Alkes Price

List of Publications by Year
in descending order

123 papers	68,417 citations	10389 72 h-index	16650 123 g-index
161 all docs	161 docs citations	161 times ranked	73592 citing authors

#	Article	IF	Citations
1	Principal components analysis corrects for stratification in genome-wide association studies. Nature Genetics, 2006, 38, 904-909.	21.4	8,889
2	PGC-1Î±-responsive genes involved in oxidative phosphorylation are coordinately downregulated in human diabetes. Nature Genetics, 2003, 34, 267-273.	21.4	8,185
3	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. Nature Genetics, 2015, 47, 291-295.	21.4	3,905
4	A Draft Sequence of the Neandertal Genome. Science, 2010, 328, 710-722.	12.6	3,588
5	An atlas of genetic correlations across human diseases and traits. Nature Genetics, 2015, 47, 1236-1241.	21.4	3,145
6	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	27.8	2,625
7	Partitioning heritability by functional annotation using genome-wide association summary statistics. Nature Genetics, 2015, 47, 1228-1235.	21.4	2,045
8	The complete genome sequence of a Neanderthal from the Altai Mountains. Nature, 2014, 505, 43-49.	27.8	1,830
9	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
10	Integrative approaches for large-scale transcriptome-wide association studies. Nature Genetics, 2016, 48, 245-252.	21.4	1,618
11	Reconstructing Indian population history. Nature, 2009, 461, 489-494.	27.8	1,442
12	Reference-based phasing using the Haplotype Reference Consortium panel. Nature Genetics, 2016, 48, 1443-1448.	21.4	1,357
13	Efficient Bayesian mixed-model analysis increases association power in large cohorts. Nature Genetics, 2015, 47, 284-290.	21.4	1,285
14	Genome-wide patterns of selection in 230 ancient Eurasians. Nature, 2015, 528, 499-503.	27.8	1,160
15	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	6.2	1,098
16	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	12.6	1,085
17	New approaches to population stratification in genome-wide association studies. Nature Reviews Genetics, 2010, 11, 459-463.	16.3	1,047
18	Genetic Signatures of Strong Recent Positive Selection at the Lactase Gene. American Journal of Human Genetics, 2004, 74, 1111-1120.	6.2	1,011

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19	The genomic landscape of Neanderthal ancestry in present-day humans. Nature, 2014, 507, 354-357.	27.8	877
20	Advantages and pitfalls in the application of mixed-model association methods. Nature Genetics, 2014, 46, 100-106.	21.4	876
21	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	21.4	838
22	LD Hub: a centralized database and web interface to perform LD score regression that maximizes the potential of summary level GWAS data for SNP heritability and genetic correlation analysis. Bioinformatics, 2017, 33, 272-279.	4.1	822
23	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. Nature Genetics, 2018, 50, 621-629.	21.4	807
24	Pooled Association Tests for Rare Variants in Exon-Resequencing Studies. American Journal of Human Genetics, 2010, 86, 832-838.	6.2	715
25	Leveraging Polygenic Functional Enrichment to Improve GWAS Power. American Journal of Human Genetics, 2019, 104, 65-75.	6.2	715
26	Pitfalls of predicting complex traits from SNPs. Nature Reviews Genetics, 2013, 14, 507-515.	16.3	617
27	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	6.2	569
28	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. Nature, 2021, 595, 107-113.	27.8	537
29	Mixed-model association for biobank-scale datasets. Nature Genetics, 2018, 50, 906-908.	21.4	521
30	Integrating Functional Data to Prioritize Causal Variants in Statistical Fine-Mapping Studies. PLoS Genetics, 2014, 10, e1004722.	3.5	475
31	Methods for High-Density Admixture Mapping of Disease Genes. American Journal of Human Genetics, 2004, 74, 979-1000.	6.2	437
32	Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. Nature Genetics, 2015, 47, 1385-1392.	21.4	431
33	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
34	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. Nature Genetics, 2018, 50, 538-548.	21.4	406
35	Linkage disequilibriumâ€“dependent architecture of human complex traits shows action of negative selection. Nature Genetics, 2017, 49, 1421-1427.	21.4	400
36	Dissecting the genetics of complex traits using summary association statistics. Nature Reviews Genetics, 2017, 18, 117-127.	16.3	379

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37	Long-Range LD Can Confound Genome Scans in Admixed Populations. American Journal of Human Genetics, 2008, 83, 132-135.	6.2	366
38	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
39	Genetic evidence for two founding populations of the Americas. Nature, 2015, 525, 104-108.	27.8	348
40	Using Extended Genealogy to Estimate Components of Heritability for 23 Quantitative and Dichotomous Traits. PLoS Genetics, 2013, 9, e1003520.	3.5	345
41	Fast Principal-Component Analysis Reveals Convergent Evolution of ADH1B in Europe and East Asia. American Journal of Human Genetics, 2016, 98, 456-472.	6.2	335
42	Genome-wide enhancer maps link risk variants to disease genes. Nature, 2021, 593, 238-243.	27.8	332
43	The landscape of recombination in African Americans. Nature, 2011, 476, 170-175.	27.8	319
44	Global diversity, population stratification, and selection of human copy-number variation. Science, 2015, 349, aab3761.	12.6	293
45	Abundant contribution of short tandem repeats to gene expression variation in humans. Nature Genetics, 2016, 48, 22-29.	21.4	291
46	Fast and accurate long-range phasing in a UK Biobank cohort. Nature Genetics, 2016, 48, 811-816.	21.4	290
47	Insights into clonal haematopoiesis from 8,342 mosaic chromosomal alterations. Nature, 2018, 559, 350-355.	27.8	279
48	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. ELife, 2019, 8, .	6.0	276
49	Transethnic Genetic-Correlation Estimates from Summary Statistics. American Journal of Human Genetics, 2016, 99, 76-88.	6.2	265
50	Distinguishing genetic correlation from causation across 52 diseases and complex traits. Nature Genetics, 2018, 50, 1728-1734.	21.4	262
51	Multiethnic polygenic risk scores improve risk prediction in diverse populations. Genetic Epidemiology, 2017, 41, 811-823.	1.3	248
52	Adjusting for Heritable Covariates Can Bias Effect Estimates in Genome-Wide Association Studies. American Journal of Human Genetics, 2015, 96, 329-339.	6.2	230
53	Prospective functional classification of all possible missense variants in PPARG. Nature Genetics, 2016, 48, 1570-1575.	21.4	210
54	Reconstructing the genetic history of late Neanderthals. Nature, 2018, 555, 652-656.	27.8	197

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55	Quantifying genetic effects on disease mediated by assayed gene expression levels. Nature Genetics, 2020, 52, 626-633.	21.4	191
56	Functionally informed fine-mapping and polygenic localization of complex trait heritability. Nature Genetics, 2020, 52, 1355-1363.	21.4	185
57	Extreme Polygenicity of Complex Traits Is Explained by Negative Selection. American Journal of Human Genetics, 2019, 105, 456-476.	6.2	175
58	Single-Tissue and Cross-Tissue Heritability of Gene Expression Via Identity-by-Descent in Related or Unrelated Individuals. PLoS Genetics, 2011, 7, e1001317.	3.5	173
59	Fast and accurate imputation of summary statistics enhances evidence of functional enrichment. Bioinformatics, 2014, 30, 2906-2914.	4.1	173
60	Improved ancestry inference using weights from external reference panels. Bioinformatics, 2013, 29, 1399-1406.	4.1	163
61	Quantitative analysis of population-scale family trees with millions of relatives. Science, 2018, 360, 171-175.	12.6	157
62	New approaches to disease mapping in admixed populations. Nature Reviews Genetics, 2011, 12, 523-528.	16.3	154
63	Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. Nature Genetics, 2018, 50, 1041-1047.	21.4	154
64	Progress and promise in understanding the genetic basis of common diseases. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20151684.	2.6	147
65	A genetic method for dating ancient genomes provides a direct estimate of human generation interval in the last 45,000 years. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5652-5657.	7.1	141
66	Functional architecture of low-frequency variants highlights strength of negative selection across coding and non-coding annotations. Nature Genetics, 2018, 50, 1600-1607.	21.4	132
67	Improving the trans-ancestry portability of polygenic risk scores by prioritizing variants in predicted cell-type-specific regulatory elements. Nature Genetics, 2020, 52, 1346-1354.	21.4	126
68	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194.	6.2	119
69	Quantifying Missing Heritability at Known GWAS Loci. PLoS Genetics, 2013, 9, e1003993.	3.5	115
70	Enhanced Statistical Tests for GWAS in Admixed Populations: Assessment using African Americans from CARe and a Breast Cancer Consortium. PLoS Genetics, 2011, 7, e1001371.	3.5	110
71	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. Nature Genetics, 2022, 54, 450-458.	21.4	109
72	Quantification of frequency-dependent genetic architectures in 25 UK Biobank traits reveals action of negative selection. Nature Communications, 2019, 10, 790.	12.8	98

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73	Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. ELife, 2015, 4, .	6.0	95
74	Effects of cis and trans Genetic Ancestry on Gene Expression in African Americans. PLoS Genetics, 2008, 4, e1000294.	3.5	91
75	The Impact of Divergence Time on the Nature of Population Structure: An Example from Iceland. PLoS Genetics, 2009, 5, e1000505.	3.5	90
76	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
77	Ancient West African foragers in the context of African population history. Nature, 2020, 577, 665-670.	27.8	86
78	Informed Conditioning on Clinical Covariates Increases Power in Case-Control Association Studies. PLoS Genetics, 2012, 8, e1003032.	3.5	78
79	Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. American Journal of Human Genetics, 2015, 97, 775-789.	6.2	77
80	Reconciling S-LDSC and LDAK functional enrichment estimates. Nature Genetics, 2019, 51, 1202-1204.	21.4	77
81	Functional Architectures of Local and Distal Regulation of Gene Expression in Multiple Human Tissues. American Journal of Human Genetics, 2017, 100, 605-616.	6.2	76
82	Single-cell eQTL models reveal dynamic T cell state dependence of disease loci. Nature, 2022, 606, 120-128.	27.8	75
83	Estimating crossâ€population genetic correlations of causal effect sizes. Genetic Epidemiology, 2019, 43, 180-188.	1.3	70
84	Disease Heritability Enrichment of Regulatory Elements Is Concentrated in Elements with Ancient Sequence Age and Conserved Function across Species. American Journal of Human Genetics, 2019, 104, 611-624.	6.2	68
85	Population-specific causal disease effect sizes in functionally important regions impacted by selection. Nature Communications, 2021, 12, 1098.	12.8	68
86	High-throughput inference of pairwise coalescence times identifies signals of selection and enriched disease heritability. Nature Genetics, 2018, 50, 1311-1317.	21.4	61
87	Identifying loci with different allele frequencies among cases of eight psychiatric disorders using CC-GWAS. Nature Genetics, 2021, 53, 445-454.	21.4	61
88	Combining SNP-to-gene linking strategies to identify disease genes and assess disease omnigenicity. Nature Genetics, 2022, 54, 827-836.	21.4	61
89	Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. American Journal of Human Genetics, 2015, 96, 720-730.	6.2	60
90	Liability threshold modeling of caseâ€“control status and family history of disease increases association power. Nature Genetics, 2020, 52, 541-547.	21.4	60

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91	Improving the Power of GWAS and Avoiding Confounding from Population Stratification with PC-Select. Genetics, 2014, 197, 1045-1049.	2.9	59
92	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. Nature Genetics, 2018, 50, 1483-1493.	21.4	55
93	Multiethnic Genome-Wide Association Study of Diabetic Retinopathy Using Liability Threshold Modeling of Duration of Diabetes and Glycemic Control. Diabetes, 2019, 68, 441-456.	0.6	54
94	Population Structure of UK Biobank and Ancient Eurasians Reveals Adaptation at Genes Influencing Blood Pressure. American Journal of Human Genetics, 2016, 99, 1130-1139.	6.2	53
95	A genomeâ€wide association study suggests new evidence for an association of the <scp>NADPH</scp> Oxidase 4 (<scp>NOX</scp>4) gene with severe diabetic retinopathy in type 2 diabetes. Acta Ophthalmologica, 2018, 96, e811-e819.	1.1	52
96	Incorporating functional priors improves polygenic prediction accuracy in UK Biobank and 23andMe data sets. Nature Communications, 2021, 12, 6052.	12.8	52
97	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	12.8	50
98	Calibrating the Human Mutation Rate via Ancestral Recombination Density in Diploid Genomes. PLoS Genetics, 2015, 11, e1005550.	3.5	49
99	IMPACT: Genomic Annotation of Cell-State-Specific Regulatory Elements Inferred from the Epigenome of Bound Transcription Factors. American Journal of Human Genetics, 2019, 104, 879-895.	6.2	49
100	Quantifying the Genetic Correlation between Multiple Cancer Types. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1427-1435.	2.5	48
101	Genes with High Network Connectivity Are Enriched for Disease Heritability. American Journal of Human Genetics, 2019, 104, 896-913.	6.2	46
102	OUP accepted manuscript. Human Molecular Genetics, 2021, 30, 1521-1534.	2.9	32
103	Explicit Modeling of Ancestry Improves Polygenic Risk Scores and BLUP Prediction. Genetic Epidemiology, 2015, 39, 427-438.	1.3	30
104	Two-Variance-Component Model Improves Genetic Prediction in Family Datasets. American Journal of Human Genetics, 2015, 97, 677-690.	6.2	26
105	Evaluating the informativeness of deep learning annotations for human complex diseases. Nature Communications, 2020, 11, 4703.	12.8	21
106	SNP-to-gene linking strategies reveal contributions of enhancer-related and candidate master-regulator genes to autoimmune disease. Cell Genomics, 2022, 2, 100145.	6.5	19
107	Genetically Determined Plasma Lipid Levels and Risk of Diabetic Retinopathy: A Mendelian Randomization Study. Diabetes, 2017, 66, 3130-3141.	0.6	17
108	Discussion: Are the Origins of Indo-European Languages Explained by the Migration of the Yamnaya Culture to the West?. European Journal of Archaeology, 2018, 21, 3-17.	0.5	17

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109	Incorporating family history of disease improves polygenic risk scores in diverse populations. Cell Genomics, 2022, 2, 100152.	6.5	17
110	Annotations capturing cell type-specific TF binding explain a large fraction of disease heritability. Human Molecular Genetics, 2020, 29, 1057-1067.	2.9	16
111	Mixed Model Association with Family-Biased Case-Control Ascertainment. American Journal of Human Genetics, 2017, 100, 31-39.	6.2	14
112	Functional disease architectures reveal unique biological role of transposable elements. Nature Communications, 2019, 10, 4054.	12.8	14
113	GBAT: a gene-based association test for robust detection of trans-gene regulation. Genome Biology, 2020, 21, 211.	8.8	12
114	African Ancestry Analysis and Admixture Genetic Mapping for Proliferative Diabetic Retinopathy in African Americans. , 2015, 56, 3999.		10
115	Leveraging gene co-regulation to identify gene sets enriched for disease heritability. American Journal of Human Genetics, 2022, 109, 393-404.	6.2	10
116	Local Joint Testing Improves Power and Identifies Hidden Heritability in Association Studies. Genetics, 2016, 203, 1105-1116.	2.9	9
117	Metaâ€Analysis of Rare Variant Association Tests in Multiethnic Populations. Genetic Epidemiology, 2016, 40, 57-65.	1.3	9
118	Improving the informativeness of Mendelian disease-derived pathogenicity scores for common disease. Nature Communications, 2020, 11, 6258.	12.8	8
119	miqoGraph: fitting admixture graphs using mixed-integer quadratic optimization. Bioinformatics, 2021, 37, 2488-2490.	4.1	7
120	Combining ancient DNA and radiocarbon dating data to increase chronological accuracy. Journal of Archaeological Science, 2021, 133, 105452.	2.4	7
121	Deep targeted sequencing of 12 breast cancer susceptibility regions in 4611 women across four different ethnicities. Breast Cancer Research, 2016, 18, 109.	5.0	6
122	Response to Day etÂal.. American Journal of Human Genetics, 2016, 98, 394-395.	6.2	1
123	Response to Shen etÂal.. American Journal of Human Genetics, 2016, 99, 1220-1221.	6.2	0