Alkes Price

List of Publications by Year in Descending Order

146 papers	45,027 citations	67 h-index	161 g-index
161 ext. papers	59,514 ext. citations	21.9 avg, IF	7.16 L-index

#	Paper	IF	Citations
146	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores.. *Nature Genetics*, **2022**, 54, 450-458	36.3	3
145	Single-cell eQTL models reveal dynamic T cell state dependence of disease loci.. *Nature*, **2022**,	50.4	4
144	miqoGraph: fitting admixture graphs using mixed-integer quadratic optimization. *Bioinformatics*, **2021**, 37, 2488-2490	7.2	2
143	Incorporating functional priors improves polygenic prediction accuracy in UK Biobank and 23andMe data sets. *Nature Communications*, **2021**, 12, 6052	17.4	7
142	Identifying disease-critical cell types and cellular processes across the human body by integration of single-cell profiles and human genetics **2021**,		6
141	Identifying loci with different allele frequencies among cases of eight psychiatric disorders using CC-GWAS. *Nature Genetics*, **2021**, 53, 445-454	36.3	16
140	Genome-wide enhancer maps link risk variants to disease genes. *Nature*, **2021**, 593, 238-243	50.4	45
139	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. *Nature*, **2021**, 595, 107-113	50.4	124
138	Estimating heritability and its enrichment in tissue-specific gene sets in admixed populations. *Human Molecular Genetics*, **2021**, 30, 1521-1534	5.6	6
137	Population-specific causal disease effect sizes in functionally important regions impacted by selection. *Nature Communications*, **2021**, 12, 1098	17.4	16
136	A single-cell and spatial atlas of autopsy tissues reveals pathology and cellular targets of SARS-CoV-2 **2021**,		15
135	COMBINING ANCIENT DNA AND RADIOCARBON DATING DATA TO INCREASE CHRONOLOGICAL ACCURACY. *Journal of Archaeological Science*, **2021**, 133, 105452-105452	2.9	1
134	Quantifying genetic effects on disease mediated by assayed gene expression levels. *Nature Genetics*, **2020**, 52, 626-633	36.3	69
133	Ancient West African foragers in the context of African population history. *Nature*, **2020**, 577, 665-670	50.4	47
132	Annotations capturing cell type-specific TF binding explain a large fraction of disease heritability. *Human Molecular Genetics*, **2020**, 29, 1057-1067	5.6	7
131	Functionally informed fine-mapping and polygenic localization of complex trait heritability. *Nature Genetics*, **2020**, 52, 1355-1363	36.3	45
130	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	36.3	37

129	Evaluating the informativeness of deep learning annotations for human complex diseases. *Nature Communications*, **2020**, 11, 4703	17.4	7
128	GBAT: a gene-based association test for robust detection of trans-gene regulation. *Genome Biology*, **2020**, 21, 211	18.3	3
127	Improving the informativeness of Mendelian disease-derived pathogenicity scores for common disease. *Nature Communications*, **2020**, 11, 6258	17.4	2
126	Liability threshold modeling of case-control status and family history of disease increases association power. *Nature Genetics*, **2020**, 52, 541-547	36.3	21
125	Functional disease architectures reveal unique biological role of transposable elements. *Nature Communications*, **2019**, 10, 4054	17.4	8
124	Shared heritability and functional enrichment across six solid cancers. *Nature Communications*, **2019** , 10, 431	17.4	45
123	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. *ELife*, **2019**, 8,	8.9	166
122	Genes with High Network Connectivity Are Enriched for Disease Heritability. *American Journal of Human Genetics*, **2019**, 104, 896-913	11	19
121	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	11	21
120	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	11	29
119	Extreme Polygenicity of Complex Traits Is Explained by Negative Selection. *American Journal of Human Genetics*, **2019**, 105, 456-476	11	76
118	Reconciling S-LDSC and LDAK functional enrichment estimates. *Nature Genetics*, **2019**, 51, 1202-1204	36.3	40
117	Quantification of frequency-dependent genetic architectures in 25 UK Biobank traits reveals action of negative selection. *Nature Communications*, **2019**, 10, 790	17.4	55
116	Leveraging Polygenic Functional Enrichment to Improve GWAS Power. *American Journal of Human Genetics*, **2019**, 104, 65-75	11	348
115	Multiethnic Genome-Wide Association Study of Diabetic Retinopathy Using Liability Threshold Modeling of Duration of Diabetes and Glycemic Control. *Diabetes*, **2019**, 68, 441-456	0.9	31
114	Estimating cross-population genetic correlations of causal effect sizes. *Genetic Epidemiology*, **2019**, 43, 180-188	2.6	25
113	Quantitative analysis of population-scale family trees with millions of relatives. *Science*, **2018**, 360, 171-175	353	94
112	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. *Nature Genetics*, **2018**, 50, 621-629	36.3	400

111	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. *Nature Genetics*, **2018**, 50, 538-548	36.3	222
110	Reconstructing the genetic history of late Neanderthals. *Nature*, **2018**, 555, 652-656	50.4	138
109	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	0.7	10
108	Analysis of shared heritability in common disorders of the brain. *Science*, **2018**, 360,	33.3	666
107	Insights into clonal haematopoiesis from 8,342 mosaic chromosomal alterations. *Nature*, **2018**, 559, 350-355	36.4	144
106	High-throughput inference of pairwise coalescence times identifies signals of selection and enriched disease heritability. *Nature Genetics*, **2018**, 50, 1311-1317	36.3	32
105	Mixed-model association for biobank-scale datasets. *Nature Genetics*, **2018**, 50, 906-908	36.3	297
104	Functional architecture of low-frequency variants highlights strength of negative selection across coding and non-coding annotations. *Nature Genetics*, **2018**, 50, 1600-1607	36.3	72
103	Distinguishing genetic correlation from causation across 52 diseases and complex traits. *Nature Genetics*, **2018**, 50, 1728-1734	36.3	137
102	A genome-wide association study suggests new evidence for an association of the NADPH Oxidase 4 (NOX4) gene with severe diabetic retinopathy in type 2 diabetes. *Acta Ophthalmologica*, **2018**, 96, e811-e819	3.7	36
101	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. *Nature Genetics*, **2018**, 50, 1483-1493	36.3	34
100	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. *American Journal of Human Genetics*, **2018**, 102, 1185-1194	11	55
99	Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. *Nature Genetics*, **2018**, 50, 1041-1047	36.3	67
98	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	36.3	257
97	Functional Architectures of Local and Distal Regulation of Gene Expression in Multiple Human Tissues. *American Journal of Human Genetics*, **2017**, 100, 605-616	11	50
96	Mixed Model Association with Family-Biased Case-Control Ascertainment. *American Journal of Human Genetics*, **2017**, 100, 31-39	11	13
95	Genetically Determined Plasma Lipid Levels and Risk of Diabetic Retinopathy: A Mendelian Randomization Study. *Diabetes*, **2017**, 66, 3130-3141	0.9	13
94	Linkage disequilibrium-dependent architecture of human complex traits shows action of negative selection. *Nature Genetics*, **2017**, 49, 1421-1427	36.3	204

93	Multiethnic polygenic risk scores improve risk prediction in diverse populations. *Genetic Epidemiology*, **2017**, 41, 811-823	2.6	132
92	Quantifying the Genetic Correlation between Multiple Cancer Types. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 1427-1435	4	25
91	Dissecting the genetics of complex traits using summary association statistics. *Nature Reviews Genetics*, **2017**, 18, 117-127	30.1	252
90	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	7.2	541
89	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. *Nature Genetics*, **2017**, 49, 27-35	36.3	530
88	Prospective functional classification of all possible missense variants in PPARG. *Nature Genetics*, **2016**, 48, 1570-1575	36.3	149
87	Response to Shen et al. *American Journal of Human Genetics*, **2016**, 99, 1220-1221	11	
86	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. *Nature Communications*, **2016**, 7, 10979	17.4	37
85	Population Structure of UK Biobank and Ancient Eurasians Reveals Adaptation at Genes Influencing Blood Pressure. *American Journal of Human Genetics*, **2016**, 99, 1130-1139	11	36
84	Deep targeted sequencing of 12 breast cancer susceptibility regions in 4611 women across four different ethnicities. *Breast Cancer Research*, **2016**, 18, 109	8.3	4
83	Fast and accurate long-range phasing in a UK Biobank cohort. *Nature Genetics*, **2016**, 48, 811-6	36.3	148
82	Transethnic Genetic-Correlation Estimates from Summary Statistics. *American Journal of Human Genetics*, **2016**, 99, 76-88	11	124
81	Abundant contribution of short tandem repeats to gene expression variation in humans. *Nature Genetics*, **2016**, 48, 22-9	36.3	184
80	Integrative approaches for large-scale transcriptome-wide association studies. *Nature Genetics*, **2016**, 48, 245-52	36.3	843
79	Response to Day et al. *American Journal of Human Genetics*, **2016**, 98, 394-5	11	1
78	Fast Principal-Component Analysis Reveals Convergent Evolution of ADH1B in Europe and East Asia. *American Journal of Human Genetics*, **2016**, 98, 456-472	11	201
77	Local Joint Testing Improves Power and Identifies Hidden Heritability in Association Studies. *Genetics*, **2016**, 203, 1105-16	4	3
76	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, 5652-7	11.5	75

75	Reference-based phasing using the Haplotype Reference Consortium panel. *Nature Genetics*, **2016**, 48, 1443-1448	36.3	699
74	Meta-Analysis of Rare Variant Association Tests in Multiethnic Populations. *Genetic Epidemiology*, **2016**, 40, 57-65	2.6	6
73	Global diversity, population stratification, and selection of human copy-number variation. *Science*, **2015**, 349, aab3761	33.3	224
72	Genetic evidence for two founding populations of the Americas. *Nature*, **2015**, 525, 104-8	50.4	220
71	Mixed model with correction for case-control ascertainment increases association power. *American Journal of Human Genetics*, **2015**, 96, 720-30	11	47
70	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. *American Journal of Human Genetics*, **2015**, 97, 576-92	11	649
69	Partitioning heritability by functional annotation using genome-wide association summary statistics. *Nature Genetics*, **2015**, 47, 1228-35	36.3	1143
68	An atlas of genetic correlations across human diseases and traits. *Nature Genetics*, **2015**, 47, 1236-41	36.3	1841
67	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303	36.3	226
66	Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. *Nature Genetics*, **2015**, 47, 1385-92	36.3	299
65	Two-Variance-Component Model Improves Genetic Prediction in Family Datasets. *American Journal of Human Genetics*, **2015**, 97, 677-90	11	20
64	Genome-wide patterns of selection in 230 ancient Eurasians. *Nature*, **2015**, 528, 499-503	50.4	774
63	Progress and promise in understanding the genetic basis of common diseases. *Proceedings of the Royal Society B: Biological Sciences*, **2015**, 282, 20151684	4.4	98
62	Explicit Modeling of Ancestry Improves Polygenic Risk Scores and BLUP Prediction. *Genetic Epidemiology*, **2015**, 39, 427-38	2.6	18
61	African Ancestry Analysis and Admixture Genetic Mapping for Proliferative Diabetic Retinopathy in African Americans **2015**, 56, 3999-4005		8
60	Calibrating the Human Mutation Rate via Ancestral Recombination Density in Diploid Genomes. *PLoS Genetics*, **2015**, 11, e1005550	6	37
59	Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. *American Journal of Human Genetics*, **2015**, 97, 775-89	11	56
58	Adjusting for heritable covariates can bias effect estimates in genome-wide association studies. *American Journal of Human Genetics*, **2015**, 96, 329-39	11	155

57	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. *Nature Genetics*, **2015**, 47, 291-5	36.3	2096
56	Efficient Bayesian mixed-model analysis increases association power in large cohorts. *Nature Genetics*, **2015**, 47, 284-90	36.3	758
55	Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. *ELife*, **2015**, 4,	8.9	57
54	The complete genome sequence of a Neanderthal from the Altai Mountains. *Nature*, **2014**, 505, 43-9	50.4	1339
53	The genomic landscape of Neanderthal ancestry in present-day humans. *Nature*, **2014**, 507, 354-7	50.4	615
52	Improving the power of GWAS and avoiding confounding from population stratification with PC-Select. *Genetics*, **2014**, 197, 1045-9	4	37
51	Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases. *American Journal of Human Genetics*, **2014**, 95, 535-52	11	411
50	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
49	Advantages and pitfalls in the application of mixed-model association methods. *Nature Genetics*, **2014**, 46, 100-6	36.3	520
48	Fast and accurate imputation of summary statistics enhances evidence of functional enrichment. *Bioinformatics*, **2014**, 30, 2906-14	7.2	123
47	Integrating functional data to prioritize causal variants in statistical fine-mapping studies. *PLoS Genetics*, **2014**, 10, e1004722	6	305
46	Pitfalls of predicting complex traits from SNPs. *Nature Reviews Genetics*, **2013**, 14, 507-15	30.1	457
45	Using extended genealogy to estimate components of heritability for 23 quantitative and dichotomous traits. *PLoS Genetics*, **2013**, 9, e1003520	6	258
44	Quantifying missing heritability at known GWAS loci. *PLoS Genetics*, **2013**, 9, e1003993	6	87
43	Improved ancestry inference using weights from external reference panels. *Bioinformatics*, **2013**, 29, 1399-406	7.2	85
42	Informed conditioning on clinical covariates increases power in case-control association studies. *PLoS Genetics*, **2012**, 8, e1003032	6	58
41	New approaches to disease mapping in admixed populations. *Nature Reviews Genetics*, **2011**, 12, 523-8	30.1	124
40	The landscape of recombination in African Americans. *Nature*, **2011**, 476, 170-5	50.4	243

39	Single-tissue and cross-tissue heritability of gene expression via identity-by-descent in related or unrelated individuals. *PLoS Genetics*, **2011**, 7, e1001317	6	138
38	Enhanced statistical tests for GWAS in admixed populations: assessment using African Americans from CARe and a Breast Cancer Consortium. *PLoS Genetics*, **2011**, 7, e1001371	6	86
37	Integrating common and rare genetic variation in diverse human populations. *Nature*, **2010**, 467, 52-8	50.4	2135
36	New approaches to population stratification in genome-wide association studies. *Nature Reviews Genetics*, **2010**, 11, 459-63	30.1	774
35	A draft sequence of the Neandertal genome. *Science*, **2010**, 328, 710-722	33.3	2599
34	Pooled association tests for rare variants in exon-resequencing studies. *American Journal of Human Genetics*, **2010**, 86, 832-8	11	615
33	The impact of divergence time on the nature of population structure: an example from Iceland. *PLoS Genetics*, **2009**, 5, e1000505	6	71
32	Reconstructing Indian population history. *Nature*, **2009**, 461, 489-94	50.4	1075
31	Effects of cis and trans genetic ancestry on gene expression in African Americans. *PLoS Genetics*, **2008**, 4, e1000294	6	75
30	Long-range LD can confound genome scans in admixed populations. *American Journal of Human Genetics*, **2008**, 83, 132-5; author reply 135-9	11	253
29	Principal components analysis corrects for stratification in genome-wide association studies. *Nature Genetics*, **2006**, 38, 904-9	36.3	7055
28	Methods for high-density admixture mapping of disease genes. *American Journal of Human Genetics* , **2004**, 74, 979-1000	11	386
27	Genetic signatures of strong recent positive selection at the lactase gene. *American Journal of Human Genetics*, **2004**, 74, 1111-20	11	769
26	PGC-1alpha-responsive genes involved in oxidative phosphorylation are coordinately downregulated in human diabetes. *Nature Genetics*, **2003**, 34, 267-73	36.3	5810
25	Improving the informativeness of Mendelian disease-derived pathogenicity scores for common disease		2
24	Low-frequency variant functional architectures reveal strength of negative selection across coding and non-coding annotations		1
23	IMPACT: Genomic annotation of cell-state-specific regulatory elements inferred from the epigenome of bound transcription factors		1
22	Annotations capturing cell-type-specific TF binding explain a large fraction of disease heritability		1

21	Evaluating the informativeness of deep learning annotations for human complex diseases	3
20	Quantification of frequency-dependent genetic architectures and action of negative selection in 25 UK Biobank traits	18
19	Mixed model association for biobank-scale data sets	27
18	In silico integration of thousands of epigenetic datasets into 707 cell type regulatory annotations improves the trans-ethnic portability of polygenic risk scores	1
17	Identifying loci with different allele frequencies among cases of eight psychiatric disorders using CC-GWAS	1
16	Genome-wide maps of enhancer regulation connect risk variants to disease genes	7
15	Contribution of enhancer-driven and master-regulator genes to autoimmune disease revealed using functionally informed SNP-to-gene linking strategies	3
14	Integrative approaches to improve the informativeness of deep learning models for human complex diseases	2
13	Negative short-range genomic autocorrelation of causal effects on human complex traits	2
12	Leveraging polygenic functional enrichment to improve GWAS power	6
11	Reconciling S-LDSC and LDAK models and functional enrichment estimates	9
10	LDpred-funct: incorporating functional priors improves polygenic prediction accuracy in UK Biobank and 23andMe data sets	29
9	Functional disease architectures reveal unique biological role of transposable elements	3
8	Estimating heritability and its enrichment in tissue-specific gene sets in admixed populations	4
7	Quantifying genetic effects on disease mediated by assayed gene expression levels	6
6	Population-specific causal disease effect sizes in functionally important regions impacted by selection	4
5	Functionally-informed fine-mapping and polygenic localization of complex trait heritability	13
4	Leveraging molecular QTL to understand the genetic architecture of diseases and complex traits	5

3	Incorporating family history of disease improves polygenic risk scores in diverse populations	4
2	Modeling memory T cell states at single-cell resolution identifies in vivo state-dependence of eQTLs influencing disease	1
1	Leveraging fine-mapping and non-European training data to improve cross-population polygenic risk scores	14