

Alkes Price

List of Publications by Year in descending order

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Version: 2024-02-01

123
papers

68,417
citations

11908

72
h-index

18944

123
g-index

161
all docs

161
docs citations

161
times ranked

81204
citing authors

#	ARTICLE	IF	CITATIONS
1	Leveraging gene co-regulation to identify gene sets enriched for disease heritability. American Journal of Human Genetics, 2022, 109, 393-404.	2.6	10
2	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. Nature Genetics, 2022, 54, 450-458.	9.4	109
3	Single-cell eQTL models reveal dynamic T cell state dependence of disease loci. Nature, 2022, 606, 120-128.	13.7	75
4	Combining SNP-to-gene linking strategies to identify disease genes and assess disease omnigenicity. Nature Genetics, 2022, 54, 827-836.	9.4	61
5	Incorporating family history of disease improves polygenic risk scores in diverse populations. Cell Genomics, 2022, 2, 100152.	3.0	17
6	SNP-to-gene linking strategies reveal contributions of enhancer-related and candidate master-regulator genes to autoimmune disease. Cell Genomics, 2022, 2, 100145.	3.0	19
7	miqoGraph: fitting admixture graphs using mixed-integer quadratic optimization. Bioinformatics, 2021, 37, 2488-2490.	1.8	7
8	OUP accepted manuscript. Human Molecular Genetics, 2021, 30, 1521-1534.	1.4	32
9	Population-specific causal disease effect sizes in functionally important regions impacted by selection. Nature Communications, 2021, 12, 1098.	5.8	68
10	Identifying loci with different allele frequencies among cases of eight psychiatric disorders using CC-GWAS. Nature Genetics, 2021, 53, 445-454.	9.4	61
11	Genome-wide enhancer maps link risk variants to disease genes. Nature, 2021, 593, 238-243.	13.7	332
12	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. Nature, 2021, 595, 107-113.	13.7	537
13	Combining ancient DNA and radiocarbon dating data to increase chronological accuracy. Journal of Archaeological Science, 2021, 133, 105452.	1.2	7
14	Incorporating functional priors improves polygenic prediction accuracy in UK Biobank and 23andMe data sets. Nature Communications, 2021, 12, 6052.	5.8	52
15	Annotations capturing cell type-specific TF binding explain a large fraction of disease heritability. Human Molecular Genetics, 2020, 29, 1057-1067.	1.4	16
16	Functionally informed fine-mapping and polygenic localization of complex trait heritability. Nature Genetics, 2020, 52, 1355-1363.	9.4	185
17	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.	9.4	126
18	Evaluating the informativeness of deep learning annotations for human complex diseases. Nature Communications, 2020, 11, 4703.	5.8	21

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19	GBAT: a gene-based association test for robust detection of trans-gene regulation. <i>Genome Biology</i> , 2020, 21, 211.	3.8	12
20	Improving the informativeness of Mendelian disease-derived pathogenicity scores for common disease. <i>Nature Communications</i> , 2020, 11, 6258.	5.8	8
21	Quantifying genetic effects on disease mediated by assayed gene expression levels. <i>Nature Genetics</i> , 2020, 52, 626-633.	9.4	191
22	Ancient West African foragers in the context of African population history. <i>Nature</i> , 2020, 577, 665-670.	13.7	86
23	Liability threshold modeling of case-control status and family history of disease increases association power. <i>Nature Genetics</i> , 2020, 52, 541-547.	9.4	60
24	Extreme Polygenicity of Complex Traits Is Explained by Negative Selection. <i>American Journal of Human Genetics</i> , 2019, 105, 456-476.	2.6	175
25	Reconciling S-LDSC and LDK functional enrichment estimates. <i>Nature Genetics</i> , 2019, 51, 1202-1204.	9.4	77
26	Functional disease architectures reveal unique biological role of transposable elements. <i>Nature Communications</i> , 2019, 10, 4054.	5.8	14
27	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	5.8	88
28	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. <i>ELife</i> , 2019, 8, .	2.8	276
29	Genes with High Network Connectivity Are Enriched for Disease Heritability. <i>American Journal of Human Genetics</i> , 2019, 104, 896-913.	2.6	46
30	IMPACT: Genomic Annotation of Cell-State-Specific Regulatory Elements Inferred from the Epigenome of Bound Transcription Factors. <i>American Journal of Human Genetics</i> , 2019, 104, 879-895.	2.6	49
31	Disease Heritability Enrichment of Regulatory Elements Is Concentrated in Elements with Ancient Sequence Age and Conserved Function across Species. <i>American Journal of Human Genetics</i> , 2019, 104, 611-624.	2.6	68
32	Quantification of frequency-dependent genetic architectures in 25 UK Biobank traits reveals action of negative selection. <i>Nature Communications</i> , 2019, 10, 790.	5.8	98
33	Leveraging Polygenic Functional Enrichment to Improve GWAS Power. <i>American Journal of Human Genetics</i> , 2019, 104, 65-75.	2.6	715
34	Multiethnic Genome-Wide Association Study of Diabetic Retinopathy Using Liability Threshold Modeling of Duration of Diabetes and Glycemic Control. <i>Diabetes</i> , 2019, 68, 441-456.	0.3	54
35	Estimating cross-population genetic correlations of causal effect sizes. <i>Genetic Epidemiology</i> , 2019, 43, 180-188.	0.6	70
36	Quantitative analysis of population-scale family trees with millions of relatives. <i>Science</i> , 2018, 360, 171-175.	6.0	157

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37	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. <i>Nature Genetics</i> , 2018, 50, 621-629.	9.4	807
38	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. <i>Nature Genetics</i> , 2018, 50, 538-548.	9.4	406
39	Reconstructing the genetic history of late Neanderthals. <i>Nature</i> , 2018, 555, 652-656.	13.7	197
40	Discussion: Are the Origins of Indo-European Languages Explained by the Migration of the Yamnaya Culture to the West?. <i>European Journal of Archaeology</i> , 2018, 21, 3-17.	0.3	17
41	Functional architecture of low-frequency variants highlights strength of negative selection across coding and non-coding annotations. <i>Nature Genetics</i> , 2018, 50, 1600-1607.	9.4	132
42	Distinguishing genetic correlation from causation across 52 diseases and complex traits. <i>Nature Genetics</i> , 2018, 50, 1728-1734.	9.4	262
43	A genome-wide association study suggests new evidence for an association of the <i>NADPH Oxidase 4 (NOX4)</i> gene with severe diabetic retinopathy in type 2 diabetes. <i>Acta Ophthalmologica</i> , 2018, 96, e811-e819.	0.6	52
44	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. <i>Nature Genetics</i> , 2018, 50, 1483-1493.	9.4	55
45	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. <i>American Journal of Human Genetics</i> , 2018, 102, 1185-1194.	2.6	119
46	Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. <i>Nature Genetics</i> , 2018, 50, 1041-1047.	9.4	154
47	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, .	6.0	1,085
48	Insights into clonal haematopoiesis from 8,342 mosaic chromosomal alterations. <i>Nature</i> , 2018, 559, 350-355.	13.7	279
49	High-throughput inference of pairwise coalescence times identifies signals of selection and enriched disease heritability. <i>Nature Genetics</i> , 2018, 50, 1311-1317.	9.4	61
50	Mixed-model association for biobank-scale datasets. <i>Nature Genetics</i> , 2018, 50, 906-908.	9.4	521
51	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	9.4	426
52	Functional Architectures of Local and Distal Regulation of Gene Expression in Multiple Human Tissues. <i>American Journal of Human Genetics</i> , 2017, 100, 605-616.	2.6	76
53	Mixed Model Association with Family-Biased Case-Control Ascertainment. <i>American Journal of Human Genetics</i> , 2017, 100, 31-39.	2.6	14
54	Genetically Determined Plasma Lipid Levels and Risk of Diabetic Retinopathy: A Mendelian Randomization Study. <i>Diabetes</i> , 2017, 66, 3130-3141.	0.3	17

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55	Linkage disequilibriumâ€“dependent architecture of human complex traits shows action of negative selection. <i>Nature Genetics</i> , 2017, 49, 1421-1427.	9.4	400
56	Multiethnic polygenic risk scores improve risk prediction in diverse populations. <i>Genetic Epidemiology</i> , 2017, 41, 811-823.	0.6	248
57	Quantifying the Genetic Correlation between Multiple Cancer Types. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 1427-1435.	1.1	48
58	Dissecting the genetics of complex traits using summary association statistics. <i>Nature Reviews Genetics</i> , 2017, 18, 117-127.	7.7	379
59	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. <i>Bioinformatics</i> , 2017, 33, 272-279.	1.8	822
60	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.	9.4	838
61	Local Joint Testing Improves Power and Identifies Hidden Heritability in Association Studies. <i>Genetics</i> , 2016, 203, 1105-1116.	1.2	9
62	A genetic method for dating ancient genomes provides a direct estimate of human generation interval in the last 45,000 years. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5652-5657.	3.3	141
63	Reference-based phasing using the Haplotype Reference Consortium panel. <i>Nature Genetics</i> , 2016, 48, 1443-1448.	9.4	1,357
64	Meta-Analysis of Rare Variant Association Tests in Multiethnic Populations. <i>Genetic Epidemiology</i> , 2016, 40, 57-65.	0.6	9
65	Prospective functional classification of all possible missense variants in PPARC. <i>Nature Genetics</i> , 2016, 48, 1570-1575.	9.4	210
66	Response to Shen et al.. <i>American Journal of Human Genetics</i> , 2016, 99, 1220-1221.	2.6	0
67	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. <i>Nature Communications</i> , 2016, 7, 10979.	5.8	50
68	Population Structure of UK Biobank and Ancient Eurasians Reveals Adaptation at Genes Influencing Blood Pressure. <i>American Journal of Human Genetics</i> , 2016, 99, 1130-1139.	2.6	53
69	Deep targeted sequencing of 12 breast cancer susceptibility regions in 4611 women across four different ethnicities. <i>Breast Cancer Research</i> , 2016, 18, 109.	2.2	6
70	Fast and accurate long-range phasing in a UK Biobank cohort. <i>Nature Genetics</i> , 2016, 48, 811-816.	9.4	290
71	Transethnic Genetic-Correlation Estimates from Summary Statistics. <i>American Journal of Human Genetics</i> , 2016, 99, 76-88.	2.6	265
72	Abundant contribution of short tandem repeats to gene expression variation in humans. <i>Nature Genetics</i> , 2016, 48, 22-29.	9.4	291

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73	Integrative approaches for large-scale transcriptome-wide association studies. <i>Nature Genetics</i> , 2016, 48, 245-252.	9.4	1,618
74	Response to Day et al.. <i>American Journal of Human Genetics</i> , 2016, 98, 394-395.	2.6	1
75	Fast Principal-Component Analysis Reveals Convergent Evolution of ADH1B in Europe and East Asia. <i>American Journal of Human Genetics</i> , 2016, 98, 456-472.	2.6	335
76	Progress and promise in understanding the genetic basis of common diseases. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20151684.	1.2	147
77	Explicit Modeling of Ancestry Improves Polygenic Risk Scores and BLUP Prediction. <i>Genetic Epidemiology</i> , 2015, 39, 427-438.	0.6	30
78	African Ancestry Analysis and Admixture Genetic Mapping for Proliferative Diabetic Retinopathy in African Americans. , 2015, 56, 3999.		10
79	Calibrating the Human Mutation Rate via Ancestral Recombination Density in Diploid Genomes. <i>PLoS Genetics</i> , 2015, 11, e1005550.	1.5	49
80	Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. <i>American Journal of Human Genetics</i> , 2015, 97, 775-789.	2.6	77
81	Adjusting for Heritable Covariates Can Bias Effect Estimates in Genome-Wide Association Studies. <i>American Journal of Human Genetics</i> , 2015, 96, 329-339.	2.6	230
82	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. <i>Nature Genetics</i> , 2015, 47, 291-295.	9.4	3,905
83	Efficient Bayesian mixed-model analysis increases association power in large cohorts. <i>Nature Genetics</i> , 2015, 47, 284-290.	9.4	1,285
84	Global diversity, population stratification, and selection of human copy-number variation. <i>Science</i> , 2015, 349, aab3761.	6.0	293
85	Genetic evidence for two founding populations of the Americas. <i>Nature</i> , 2015, 525, 104-108.	13.7	348
86	Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. <i>American Journal of Human Genetics</i> , 2015, 96, 720-730.	2.6	60
87	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	2.6	1,098
88	Partitioning heritability by functional annotation using genome-wide association summary statistics. <i>Nature Genetics</i> , 2015, 47, 1228-1235.	9.4	2,045
89	An atlas of genetic correlations across human diseases and traits. <i>Nature Genetics</i> , 2015, 47, 1236-1241.	9.4	3,145
90	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	9.4	357

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91	Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. <i>Nature Genetics</i> , 2015, 47, 1385-1392.	9.4	431
92	Two-Variance-Component Model Improves Genetic Prediction in Family Datasets. <i>American Journal of Human Genetics</i> , 2015, 97, 677-690.	2.6	26
93	Genome-wide patterns of selection in 230 ancient Eurasians. <i>Nature</i> , 2015, 528, 499-503.	13.7	1,160
94	Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. <i>ELife</i> , 2015, 4, .	2.8	95
95	Fast and accurate imputation of summary statistics enhances evidence of functional enrichment. <i>Bioinformatics</i> , 2014, 30, 2906-2914.	1.8	173
96	Integrating Functional Data to Prioritize Causal Variants in Statistical Fine-Mapping Studies. <i>PLoS Genetics</i> , 2014, 10, e1004722.	1.5	475
97	The complete genome sequence of a Neanderthal from the Altai Mountains. <i>Nature</i> , 2014, 505, 43-49.	13.7	1,830
98	The genomic landscape of Neanderthal ancestry in present-day humans. <i>Nature</i> , 2014, 507, 354-357.	13.7	877
99	Improving the Power of GWAS and Avoiding Confounding from Population Stratification with PC-Select. <i>Genetics</i> , 2014, 197, 1045-1049.	1.2	59
100	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. <i>American Journal of Human Genetics</i> , 2014, 95, 535-552.	2.6	569
101	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
102	Advantages and pitfalls in the application of mixed-model association methods. <i>Nature Genetics</i> , 2014, 46, 100-106.	9.4	876
103	Pitfalls of predicting complex traits from SNPs. <i>Nature Reviews Genetics</i> , 2013, 14, 507-515.	7.7	617
104	Using Extended Genealogy to Estimate Components of Heritability for 23 Quantitative and Dichotomous Traits. <i>PLoS Genetics</i> , 2013, 9, e1003520.	1.5	345
105	Quantifying Missing Heritability at Known GWAS Loci. <i>PLoS Genetics</i> , 2013, 9, e1003993.	1.5	115
106	Improved ancestry inference using weights from external reference panels. <i>Bioinformatics</i> , 2013, 29, 1399-1406.	1.8	163
107	Informed Conditioning on Clinical Covariates Increases Power in Case-Control Association Studies. <i>PLoS Genetics</i> , 2012, 8, e1003032.	1.5	78
108	New approaches to disease mapping in admixed populations. <i>Nature Reviews Genetics</i> , 2011, 12, 523-528.	7.7	154

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109	The landscape of recombination in African Americans. <i>Nature</i> , 2011, 476, 170-175.	13.7	319
110	Single-Tissue and Cross-Tissue Heritability of Gene Expression Via Identity-by-Descent in Related or Unrelated Individuals. <i>PLoS Genetics</i> , 2011, 7, e1001317.	1.5	173
111	Enhanced Statistical Tests for GWAS in Admixed Populations: Assessment using African Americans from CARE and a Breast Cancer Consortium. <i>PLoS Genetics</i> , 2011, 7, e1001371.	1.5	110
112	A Draft Sequence of the Neandertal Genome. <i>Science</i> , 2010, 328, 710-722.	6.0	3,588
113	Pooled Association Tests for Rare Variants in Exon-Resequencing Studies. <i>American Journal of Human Genetics</i> , 2010, 86, 832-838.	2.6	715
114	Integrating common and rare genetic variation in diverse human populations. <i>Nature</i> , 2010, 467, 52-58.	13.7	2,625
115	New approaches to population stratification in genome-wide association studies. <i>Nature Reviews Genetics</i> , 2010, 11, 459-463.	7.7	1,047
116	The Impact of Divergence Time on the Nature of Population Structure: An Example from Iceland. <i>PLoS Genetics</i> , 2009, 5, e1000505.	1.5	90
117	Reconstructing Indian population history. <i>Nature</i> , 2009, 461, 489-494.	13.7	1,442
118	Long-Range LD Can Confound Genome Scans in Admixed Populations. <i>American Journal of Human Genetics</i> , 2008, 83, 132-135.	2.6	366
119	Effects of cis and trans Genetic Ancestry on Gene Expression in African Americans. <i>PLoS Genetics</i> , 2008, 4, e1000294.	1.5	91
120	Principal components analysis corrects for stratification in genome-wide association studies. <i>Nature Genetics</i> , 2006, 38, 904-909.	9.4	8,889
121	Methods for High-Density Admixture Mapping of Disease Genes. <i>American Journal of Human Genetics</i> , 2004, 74, 979-1000.	2.6	437
122	Genetic Signatures of Strong Recent Positive Selection at the Lactase Gene. <i>American Journal of Human Genetics</i> , 2004, 74, 1111-1120.	2.6	1,011
123	PGC-1 α -responsive genes involved in oxidative phosphorylation are coordinately downregulated in human diabetes. <i>Nature Genetics</i> , 2003, 34, 267-273.	9.4	8,185