

Hilary K Finucane

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

28,233
citations

70961

41
h-index

123241

61
g-index

85
all docs

85
docs citations

85
times ranked

32409
citing authors

#	ARTICLE	IF	CITATIONS
1	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. <i>Nature Genetics</i> , 2022, 54, 450-458.	9.4	109
2	Genome-wide pleiotropy analysis of coronary artery disease and pneumonia identifies shared immune pathways. <i>Science Advances</i> , 2022, 8, eabl4602.	4.7	4
3	OUP accepted manuscript. <i>Human Molecular Genetics</i> , 2021, 30, 1521-1534.	1.4	32
4	Genome-wide enhancer maps link risk variants to disease genes. <i>Nature</i> , 2021, 593, 238-243.	13.7	332
5	Gene Discovery in Admixed Cohorts With Tractor. <i>Biological Psychiatry</i> , 2021, 89, S70.	0.7	0
6	Leveraging supervised learning for functionally informed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs. <i>Nature Communications</i> , 2021, 12, 3394.	5.8	44
7	Direct characterization of cis-regulatory elements and functional dissection of complex genetic associations using HCR "FlowFISH. <i>Nature Genetics</i> , 2021, 53, 1166-1176.	9.4	36
8	Mapping the human genetic architecture of COVID-19. <i>Nature</i> , 2021, 600, 472-477.	13.7	640
9	Genome-wide functional screen of 3' UTR variants uncovers causal variants for human disease and evolution. <i>Cell</i> , 2021, 184, 5247-5260.e19.	13.5	62
10	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. <i>JAMA Psychiatry</i> , 2021, 78, 1258.	6.0	88
11	Tractor uses local ancestry to enable the inclusion of admixed individuals in GWAS and to boost power. <i>Nature Genetics</i> , 2021, 53, 195-204.	9.4	125
12	Misuse of the term "trans-ethnic" in genomics research. <i>Nature Genetics</i> , 2021, 53, 1520-1521.	9.4	8
13	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. <i>Biological Psychiatry</i> , 2020, 87, 419-430.	0.7	27
14	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. <i>Biological Psychiatry</i> , 2020, 88, 169-184.	0.7	137
15	Annotations capturing cell type-specific TF binding explain a large fraction of disease heritability. <i>Human Molecular Genetics</i> , 2020, 29, 1057-1067.	1.4	16
16	Functionally informed fine-mapping and polygenic localization of complex trait heritability. <i>Nature Genetics</i> , 2020, 52, 1355-1363.	9.4	185
17	Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. <i>Nature Communications</i> , 2020, 11, 1237.	5.8	38
18	Reconciling S-LDSC and LDK functional enrichment estimates. <i>Nature Genetics</i> , 2019, 51, 1202-1204.	9.4	77

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19	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	5.8	88
20	Genes with High Network Connectivity Are Enriched for Disease Heritability. <i>American Journal of Human Genetics</i> , 2019, 104, 896-913.	2.6	46
21	Interrogation of human hematopoiesis at single-cell and single-variant resolution. <i>Nature Genetics</i> , 2019, 51, 683-693.	9.4	147
22	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
23	Association of Whole-Genome and NETRIN1 Signaling Pathwayâ€Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , 2019, 4, 91-100.	1.1	16
24	Genomics of body fat percentage may contribute to sex bias in anorexia nervosa. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 428-438.	1.1	87
25	Estimating crossâ€population genetic correlations of causal effect sizes. <i>Genetic Epidemiology</i> , 2019, 43, 180-188.	0.6	70
26	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. <i>Nature Genetics</i> , 2018, 50, 621-629.	9.4	807
27	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. <i>Nature Genetics</i> , 2018, 50, 538-548.	9.4	406
28	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	9.4	2,224
29	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , 2018, 84, 138-147.	0.7	87
30	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
31	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. <i>Nature Genetics</i> , 2018, 50, 1483-1493.	9.4	55
32	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
33	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, .	6.0	1,085
34	Insights into clonal haematopoiesis from 8,342 mosaic chromosomal alterations. <i>Nature</i> , 2018, 559, 350-355.	18.7	279
35	Dissecting the Regulation of Human Hematopoiesis at Single-Cell and Single-Variant Resolution. <i>Blood</i> , 2018, 132, 531-531.	0.6	0
36	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

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37	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
38	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
39	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
40	Linkage disequilibrium-dependent architecture of human complex traits shows action of negative selection. <i>Nature Genetics</i> , 2017, 49, 1421-1427.	9.4	400
41	Quantifying the Genetic Correlation between Multiple Cancer Types. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 1427-1435.	1.1	48
42	On the scaling limit of finite vertex transitive graphs with large diameter. <i>Combinatorica</i> , 2017, 37, 333-374.	0.6	4
43	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
44	Reference-based phasing using the Haplotype Reference Consortium panel. <i>Nature Genetics</i> , 2016, 48, 1443-1448.	9.4	1,357
45	Genome-Wide Association Studies Suggest Limited Immune Gene Enrichment in Schizophrenia Compared to 5 Autoimmune Diseases. <i>Schizophrenia Bulletin</i> , 2016, 42, 1176-1184.	2.3	62
46	Shared genetic aetiology of puberty timing between sexes and with health-related outcomes. <i>Nature Communications</i> , 2015, 6, 8842.	5.8	100
47	A recursive construction of i -wise uniform permutations. <i>Random Structures and Algorithms</i> , 2015, 46, 531-540.	0.6	2
48	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
49	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. <i>Nature Genetics</i> , 2015, 47, 291-295.	9.4	3,905
50	Efficient Bayesian mixed-model analysis increases association power in large cohorts. <i>Nature Genetics</i> , 2015, 47, 284-290.	9.4	1,285
51	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	2.6	1,098
52	Partitioning heritability by functional annotation using genome-wide association summary statistics. <i>Nature Genetics</i> , 2015, 47, 1228-1235.	9.4	2,045
53	An atlas of genetic correlations across human diseases and traits. <i>Nature Genetics</i> , 2015, 47, 1236-1241.	9.4	3,145
54	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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55	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
56	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. <i>Cell</i> , 2015, 162, 738-750.	13.5	230
57	Scenery reconstruction on finite abelian groups. <i>Stochastic Processes and Their Applications</i> , 2014, 124, 2754-2770.	0.4	5
58	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
59	Comparing Pedigree Graphs. <i>Journal of Computational Biology</i> , 2012, 19, 998-1014.	0.8	12
60	Detecting Novel Associations in Large Data Sets. <i>Science</i> , 2011, 334, 1518-1524.	6.0	2,252
61	Designing Floating Codes for Expected Performance. <i>IEEE Transactions on Information Theory</i> , 2010, 56, 968-978.	1.5	38