Hilary K Finucane

List of Publications by Year
in descending order

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	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. Nature Genetics, 2015, 47, 291-295.	9.4	3,905
2	An atlas of genetic correlations across human diseases and traits. Nature Genetics, 2015, 47, 1236-1241.	9.4	3,145
3	Detecting Novel Associations in Large Data Sets. Science, 2011, 334, 1518-1524.	6.0	2,252
4	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	9.4	2,224
5	Partitioning heritability by functional annotation using genome-wide association summary statistics. Nature Genetics, 2015, 47, 1228-1235.	9.4	2,045
6	Reference-based phasing using the Haplotype Reference Consortium panel. Nature Genetics, 2016, 48, 1443-1448.	9.4	1,357
7	Efficient Bayesian mixed-model analysis increases association power in large cohorts. Nature Genetics, 2015, 47, 284-290.	9.4	1,285
8	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
9	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
10	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
11	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.	1.8	822
12	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. Nature Genetics, 2018, 50, 621-629.	9.4	807
13	Mapping the human genetic architecture of COVID-19. Nature, 2021, 600, 472-477.	13.7	640
14	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	2.6	569
15	Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. Nature Genetics, 2015, 47, 1385-1392.	9.4	431
16	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.	9.4	426
17	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. Nature Genetics, 2018, 50, 538-548.	9.4	406
18	Linkage disequilibriumâ€“dependent architecture of human complex traits shows action of negative selection. Nature Genetics, 2017, 49, 1421-1427.	9.4	400

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19	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
20	Genome-wide enhancer maps link risk variants to disease genes. Nature, 2021, 593, 238-243.	13.7	332
21	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
22	Insights into clonal haematopoiesis from 8,342 mosaic chromosomal alterations. Nature, 2018, 559, 350-355.	13.7	279
23	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. Cell, 2015, 162, 738-750.	13.5	230
24	Functionally informed fine-mapping and polygenic localization of complex trait heritability. Nature Genetics, 2020, 52, 1355-1363.	9.4	185
25	Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. Nature Genetics, 2018, 50, 1041-1047.	9.4	154
26	Interrogation of human hematopoiesis at single-cell and single-variant resolution. Nature Genetics, 2019, 51, 683-693.	9.4	147
27	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. Biological Psychiatry, 2020, 88, 169-184.	0.7	137
28	Functional architecture of low-frequency variants highlights strength of negative selection across coding and non-coding annotations. Nature Genetics, 2018, 50, 1600-1607.	9.4	132
29	Tractor uses local ancestry to enable the inclusion of admixed individuals in GWAS and to boost power. Nature Genetics, 2021, 53, 195-204.	9.4	125
30	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. Nature Genetics, 2022, 54, 450-458.	9.4	109
31	Shared genetic aetiology of puberty timing between sexes and with health-related outcomes. Nature Communications, 2015, 6, 8842.	5.8	100
32	Quantification of frequency-dependent genetic architectures in 25 UK Biobank traits reveals action of negative selection. Nature Communications, 2019, 10, 790.	5.8	98
33	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
34	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. JAMA Psychiatry, 2021, 78, 1258.	6.0	88
35	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. Biological Psychiatry, 2018, 84, 138-147.	0.7	87
36	Genomics of body fat percentage may contribute to sex bias in anorexia nervosa. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 428-438.	1.1	87

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37	Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. American Journal of Human Genetics, 2015, 97, 775-789.	2.6	77
38	Reconciling S-LDSC and LDAK functional enrichment estimates. Nature Genetics, 2019, 51, 1202-1204.	9.4	77
39	Functional Architectures of Local and Distal Regulation of Gene Expression in Multiple Human Tissues. American Journal of Human Genetics, 2017, 100, 605-616.	2.6	76
40	Estimating crossâ€population genetic correlations of causal effect sizes. Genetic Epidemiology, 2019, 43, 180-188.	0.6	70
41	Genome-Wide Association Studies Suggest Limited Immune Gene Enrichment in Schizophrenia Compared to 5 Autoimmune Diseases. Schizophrenia Bulletin, 2016, 42, 1176-1184.	2.3	62
42	Genome-wide functional screen of 3â€²UTR variants uncovers causal variants for human disease and evolution. Cell, 2021, 184, 5247-5260.e19.	13.5	62
43	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. Nature Genetics, 2018, 50, 1483-1493.	9.4	55
44	Quantifying the Genetic Correlation between Multiple Cancer Types. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1427-1435.	1.1	48
45	Genes with High Network Connectivity Are Enriched for Disease Heritability. American Journal of Human Genetics, 2019, 104, 896-913.	2.6	46
46	Leveraging supervised learning for functionallyÂinformed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs. Nature Communications, 2021, 12, 3394.	5.8	44
47	Designing Floating Codes for Expected Performance. IEEE Transactions on Information Theory, 2010, 56, 968-978.	1.5	38
48	Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. Nature Communications, 2020, 11, 1237.	5.8	38
49	Direct characterization of cis-regulatory elements and functional dissection of complex genetic associations using HCRâ€“FlowFISH. Nature Genetics, 2021, 53, 1166-1176.	9.4	36
50	OUP accepted manuscript. Human Molecular Genetics, 2021, 30, 1521-1534.	1.4	32
51	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. Biological Psychiatry, 2020, 87, 419-430.	0.7	27
52	Association of Whole-Genome and NETRIN1 Signaling Pathwayâ€“Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2019, 4, 91-100.	1.1	16
53	Annotations capturing cell type-specific TF binding explain a large fraction of disease heritability. Human Molecular Genetics, 2020, 29, 1057-1067.	1.4	16
54	Comparing Pedigree Graphs. Journal of Computational Biology, 2012, 19, 998-1014.	0.8	12

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55	Misuse of the term â€˜trans-ethnicâ€™ in genomics research. Nature Genetics, 2021, 53, 1520-1521.	9.4	8
56	Scenery reconstruction on finite abelian groups. Stochastic Processes and Their Applications, 2014, 124, 2754-2770.	0.4	5
57	On the scaling limit of finite vertex transitive graphs with large diameter. Combinatorica, 2017, 37, 333-374.	0.6	4
58	Genome-wide pleiotropy analysis of coronary artery disease and pneumonia identifies shared immune pathways. Science Advances, 2022, 8, eabl4602.	4.7	4
59	A recursive construction of t -wise uniform permutations. Random Structures and Algorithms, 2015, 46, 531-540.	0.6	2
60	Gene Discovery in Admixed Cohorts With Tractor. Biological Psychiatry, 2021, 89, S70.	0.7	0
61	Dissecting the Regulation of Human Hematopoiesis at Single-Cell and Single-Variant Resolution. Blood, 2018, 132, 531-531.	0.6	0