Hilary K Finucane

List of Publications by Year
in descending order

61	28,233	81434	139680
papers	citations	41 h-index	61 g-index

85	85	85	35716
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. Nature Genetics, 2022, 54, 450-458.	9.4	109
2	Genome-wide pleiotropy analysis of coronary artery disease and pneumonia identifies shared immune pathways. Science Advances, 2022, 8, eabl4602.	4.7	4
3	OUP accepted manuscript. Human Molecular Genetics, 2021, 30, 1521-1534.	1.4	32
4	Genome-wide enhancer maps link risk variants to disease genes. Nature, 2021, 593, 238-243.	13.7	332
5	Gene Discovery in Admixed Cohorts With Tractor. Biological Psychiatry, 2021, 89, S70.	0.7	0
6	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
7	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
8	Mapping the human genetic architecture of COVID-19. Nature, 2021, 600, 472-477.	13.7	640
9	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
10	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. JAMA Psychiatry, 2021, 78, 1258.	6.0	88
11	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
12	Misuse of the term â€˜trans-ethnicâ€™ in genomics research. Nature Genetics, 2021, 53, 1520-1521.	9.4	8
13	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. Biological Psychiatry, 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. Biological Psychiatry, 2020, 88, 169-184.	0.7	137
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	Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. Nature Communications, 2020, 11, 1237.	5.8	38
18	Reconciling S-LDSC and LDAK functional enrichment estimates. Nature Genetics, 2019, 51, 1202-1204.	9.4	77

#	Article	IF	Citations
19	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
20	Genes with High Network Connectivity Are Enriched for Disease Heritability. American Journal of Human Genetics, 2019, 104, 896-913.	2.6	46
21	Interrogation of human hematopoiesis at single-cell and single-variant resolution. Nature Genetics, 2019, 51, 683-693.	9.4	147
22	Quantification of frequency-dependent genetic architectures in 25 UK Biobank traits reveals action of negative selection. Nature Communications, 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. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2019, 4, 91-100.	1.1	16
24	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
25	Estimating crossâ€population genetic correlations of causal effect sizes. Genetic Epidemiology, 2019, 43, 180-188.	0.6	70
26	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. Nature Genetics, 2018, 50, 621-629.	9.4	807
27	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. Nature Genetics, 2018, 50, 538-548.	9.4	406
28	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
29	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
30	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
31	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. Nature Genetics, 2018, 50, 1483-1493.	9.4	55
32	Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. Nature Genetics, 2018, 50, 1041-1047.	9.4	154
33	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
34	Insights into clonal haematopoiesis from 8,342 mosaic chromosomal alterations. Nature, 2018, 559, 350-355.	13.7	279
35	Dissecting the Regulation of Human Hematopoiesis at Single-Cell and Single-Variant Resolution. Blood, 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. Nature Genetics, 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. American Journal of Human Genetics, 2017, 100, 605-616.	2.6	76
38	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
39	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
40	Linkage disequilibriumâ€“dependent architecture of human complex traits shows action of negative selection. Nature Genetics, 2017, 49, 1421-1427.	9.4	400
41	Quantifying the Genetic Correlation between Multiple Cancer Types. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1427-1435.	1.1	48
42	On the scaling limit of finite vertex transitive graphs with large diameter. Combinatorica, 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. Bioinformatics, 2017, 33, 272-279.	1.8	822
44	Reference-based phasing using the Haplotype Reference Consortium panel. Nature Genetics, 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. Schizophrenia Bulletin, 2016, 42, 1176-1184.	2.3	62
46	Shared genetic aetiology of puberty timing between sexes and with health-related outcomes. Nature Communications, 2015, 6, 8842.	5.8	100
47	A recursive construction of t -wise uniform permutations. Random Structures and Algorithms, 2015, 46, 531-540.	0.6	2
48	Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. American Journal of Human Genetics, 2015, 97, 775-789.	2.6	77
49	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. Nature Genetics, 2015, 47, 291-295.	9.4	3,905
50	Efficient Bayesian mixed-model analysis increases association power in large cohorts. Nature Genetics, 2015, 47, 284-290.	9.4	1,285
51	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
52	Partitioning heritability by functional annotation using genome-wide association summary statistics. Nature Genetics, 2015, 47, 1228-1235.	9.4	2,045
53	An atlas of genetic correlations across human diseases and traits. Nature Genetics, 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. Nature Genetics, 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. Nature Genetics, 2015, 47, 1385-1392.	9.4	431
56	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. Cell, 2015, 162, 738-750.	13.5	230
57	Scenery reconstruction on finite abelian groups. Stochastic Processes and Their Applications, 2014, 124, 2754-2770.	0.4	5
58	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
59	Comparing Pedigree Graphs. Journal of Computational Biology, 2012, 19, 998-1014.	0.8	12
60	Detecting Novel Associations in Large Data Sets. Science, 2011, 334, 1518-1524.	6.0	2,252
61	Designing Floating Codes for Expected Performance. IEEE Transactions on Information Theory, 2010, 56, 968-978.	1.5	38