Hailiang Huang

List of Publications by Year
in descending order

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74 papers	24,482 citations	70961 41 h-index	71532 76 g-index
99 all docs	99 docs citations	99 times ranked	33834 citing authors

#	Article	IF	Citations
1	Biological insights from 108 schizophrenia-associated genetic loci. Nature, 2014, 511, 421-427.	13.7	6,934
2	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. Nature Genetics, 2015, 47, 979-986.	9.4	1,965
3	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	9.4	1,594
4	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	13.5	1,422
5	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
6	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
7	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
8	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	6.0	851
9	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	9.4	838
10	Intra- and Inter-cellular Rewiring of the Human Colon during Ulcerative Colitis. Cell, 2019, 178, 714-730.e22.	13.5	806
11	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
12	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	9.4	520
13	Fine-mapping inflammatory bowel disease loci to single-variant resolution. Nature, 2017, 547, 173-178.	13.7	473
14	Comparative genetic architectures of schizophrenia in East Asian and European populations. Nature Genetics, 2019, 51, 1670-1678.	9.4	440
15	Genome-wide Association Studies in Ancestrally Diverse Populations: Opportunities, Methods, Pitfalls, and Recommendations. Cell, 2019, 179, 589-603.	13.5	428
16	Genome-wide enhancer maps link risk variants to disease genes. Nature, 2021, 593, 238-243.	13.7	332
17	Rare coding variants in ten genes confer substantial risk for schizophrenia. Nature, 2022, 604, 509-516.	13.7	326
18	Complex host genetics influence the microbiome in inflammatory bowel disease. Genome Medicine, 2014, 6, 107.	3.6	322

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19	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
20	High-density mapping of the MHC identifies a shared role for HLA-DRB1*01:03 in inflammatory bowel diseases and heterozygous advantage in ulcerative colitis. Nature Genetics, 2015, 47, 172-179.	9.4	280
21	A systems biology analysis of the Drosophila phagosome. Nature, 2007, 445, 95-101.	13.7	216
22	Improving polygenic prediction in ancestrally diverse populations. Nature Genetics, 2022, 54, 573-580.	9.4	209
23	RICOPILI: Rapid Imputation for COnsortias PIpeLIne. Bioinformatics, 2020, 36, 930-933.	1.8	201
24	Probing Nucleosome Function: A Highly Versatile Library of Synthetic Histone H3 and H4 Mutants. Cell, 2008, 134, 1066-1078.	13.5	198
25	Clozapine-induced agranulocytosis is associated with rare HLA-DQB1 and HLA-B alleles. Nature Communications, 2014, 5, 4757.	5.8	153
26	Where Have All the Interactions Gone? Estimating the Coverage of Two-Hybrid Protein Interaction Maps. PLoS Computational Biology, 2007, 3, e214.	1.5	151
27	Multi-trait analysis for genome-wide association study of five psychiatric disorders. Translational Psychiatry, 2020, 10, 209.	2.4	132
28	Whole genome sequencing in psychiatric disorders: the WGSPD consortium. Nature Neuroscience, 2017, 20, 1661-1668.	7.1	122
29	Genetic Coding Variant in GPR65 Alters Lysosomal pH and Links Lysosomal Dysfunction with Colitis Risk. Immunity, 2016, 44, 1392-1405.	6.6	106
30	Ubiquitin Ligase TRIM62 Regulates CARD9-Mediated Anti-fungal Immunity and Intestinal Inflammation. Immunity, 2015, 43, 715-726.	6.6	102
31	Temporal Profiling of the Secretome during Adipogenesis in Humans. Journal of Proteome Research, 2010, 9, 5228-5238.	1.8	100
32	Gene-Based Tests of Association. PLoS Genetics, 2011, 7, e1002177.	1.5	90
33	Differential Effect of Genetic Burden on Disease Phenotypes in Crohn's Disease and Ulcerative Colitis: Analysis of a North American Cohort. American Journal of Gastroenterology, 2014, 109, 395-400.	0.2	77
34	Population-specific causal disease effect sizes in functionally important regions impacted by selection. Nature Communications, 2021, 12, 1098.	5.8	68
35	Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population. PLoS Genetics, 2018, 14, e1007329.	1.5	66
36	Precision and recall estimates for two-hybrid screens. Bioinformatics, 2009, 25, 372-378.	1.8	65

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37	BlueSNP: R package for highly scalable genome-wide association studies using Hadoop clusters. Bioinformatics, 2013, 29, 135-136.	1.8	56
38	Blood transcriptomic comparison of individuals with and without autism spectrum disorder: A combinedâ€samples megaâ€analysis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 181-201.	1.1	54
39	Transcriptome-scale RNase-footprinting of RNA-protein complexes. Nature Biotechnology, 2016, 34, 410-413.	9.4	49
40	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. Nature Communications, 2020, 11, 3368.	5.8	49
41	Sprouty-2 regulates HIV-specific T cell polyfunctionality. Journal of Clinical Investigation, 2014, 124, 198-208.	3.9	49
42	HistoneHits: A database for histone mutations and their phenotypes. Genome Research, 2009, 19, 674-681.	2.4	47
43	Fast Association Tests for Genes with FAST. PLoS ONE, 2013, 8, e68585.	1.1	39
44	Cyclosporine modulates neutrophil functions via the SIRT6â€“HIFâ€1Îâ€“glycolysis axis to alleviate severe ulcerative colitis. Clinical and Translational Medicine, 2021, 11, e334.	1.7	36
45	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. International Journal of Epidemiology, 2020, 49, 1022-1031.	0.9	34
46	Integrative Genetic and Epigenetic Analysis Uncovers Regulatory Mechanisms of Autoimmune Disease. American Journal of Human Genetics, 2017, 101, 75-86.	2.6	29
47	Polygenic prediction and GWAS of depression, PTSD, and suicidal ideation/self-harm in a Peruvian cohort. Neuropsychopharmacology, 2020, 45, 1595-1602.	2.8	27
48	Repeat oral dose toxicity studies of melamine in rats and monkeys. Archives of Toxicology, 2013, 87, 517-527.	1.9	22
49	Habitual sleep disturbances and migraine: a Mendelian randomization study. Annals of Clinical and Translational Neurology, 2020, 7, 2370-2380.	1.7	18
50	Genome-wide association analysis of opioid use disorder: A novel approach using clinical data. Drug and Alcohol Dependence, 2020, 217, 108276.	1.6	17
51	Novel genetic susceptibility loci identified by family based whole exome sequencing in Han Chinese schizophrenia patients. Translational Psychiatry, 2020, 10, 5.	2.4	16
52	Late-Onset Crohnâ€™s Disease Is A Subgroup Distinct in Genetic and Behavioral Risk Factors With UC-Like Characteristics. Inflammatory Bowel Diseases, 2018, 24, 2413-2422.	0.9	14
53	CELLCOUNTER: Novel Open-Source Software for Counting Cell Migration and InvasionIn Vitro. BioMed Research International, 2014, 2014, 1-6.	0.9	12
54	Wholeâ€exome sequencing predicted cancer epitope trees of 23 early cervical cancers in Chinese women. Cancer Medicine, 2017, 6, 207-219.	1.3	12

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55	Genome-wide association analysis of insomnia using data from Partners Biobank. Scientific Reports, 2020, 10, 6928.	1.6	11
56	Wnt activation promotes memory T cell polyfunctionality via epigenetic regulator PRMT1. Journal of Clinical Investigation, 2022, 132, .	3.9	11
57	Genome-wide association study of actinic keratosis identifies new susceptibility loci implicated in pigmentation and immune regulation pathways. Communications Biology, 2022, 5, 386.	2.0	9
58	Genetic variants in cellular transport do not affect mesalamine response in ulcerative colitis. PLoS ONE, 2018, 13, e0192806.	1.1	8
59	A next generation sequencing combined genome-wide association study identifies novel tuberculosis susceptibility loci in Chinese population. Genomics, 2021, 113, 2377-2384.	1.3	8
60	Genome-wide analysis of DNA methylation in 106 schizophrenia family trios in Han Chinese. EBioMedicine, 2021, 72, 103609.	2.7	8
61	Powerful and robust inference of complex phenotypes' causal genes with dependent expression quantitative loci by a median-based Mendelian randomization. American Journal of Human Genetics, 2022, 109, 838-856.	2.6	8
62	Methods for statistical fine-mapping and their applications to auto-immune diseases. Seminars in Immunopathology, 2022, 44, 101-113.	2.8	7
63	Elucidating the relationship between migraine risk and brain structure using genetic data. Brain, 2022, 145, 3214-3224.	3.7	7
64	Fine-mapping of genetic loci driving spontaneous clearance of hepatitis C virus infection. Scientific Reports, 2017, 7, 15843.	1.6	6
65	GABAergic Abnormalities Associated with Sensorimotor Cortico-striatal Community Structural Deficits in ErbB4 Knockout Mice and First-Episode Treatment-NaÃ¯ve Patients with Schizophrenia. Neuroscience Bulletin, 2020, 36, 97-109.	1.5	6
66	Synthetic immunity to break down the bottleneck of cancer immunotherapy. Science Bulletin, 2015, 60, 977-985.	4.3	4
67	O-002â€ƒGenes in IBD-Associated Risk Loci Demonstrate Genotype-, Tissue-, and Inflammation-Specific Patterns of Expression in Terminal Ileum and Colon Mucosal Tissue. Inflammatory Bowel Diseases, 2016, 22, S1.	0.9	4
68	Host Genetic Variant in CXCL16 May Be Associated With Hepatitis B Virusâ€“Related Acute LiverÂFailure. Cellular and Molecular Gastroenterology and Hepatology, 2019, 7, 477-479.e4.	2.3	4
69	Genetic liability in individuals at ultra-high risk of psychosis: A comparison study of 9 psychiatric traits. PLoS ONE, 2020, 15, e0243104.	1.1	3
70	Populationâ€based identityâ€byâ€descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 223-231.	1.1	2
71	Omics in schizophrenia: current progress and future directions of antipsychotic treatments. Journal of Bio-X Research, 2019, 2, 145-152.	0.3	2
72	Genetic Architecture of Bipolar Disorder in Individuals of Han Chinese and European Ancestries. JAMA Psychiatry, 2021, 78, 248.	6.0	1

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73	Where have all the interactions gone? Estimating the coverage of two-hybrid protein interaction maps. PLoS Computational Biology, 2005, preprint, e214.	1.5	0
74	Sequencing and Mapping IBD Genes to Individual Causative Variants and Their Clinical Relevance. , 2019, , 117-139.		0