Tune H Pers

List of Publications by Year
in descending order

87 papers	25,610 citations	25014 57 h-index	40954 93 g-index
109 all docs	109 docs citations	109 times ranked	37221 citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. Nature Genetics, 2018, 50, 1112-1121.	9.4	1,835
3	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
4	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
5	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
6	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
7	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
8	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	5.8	706
9	A molecular census of arcuate hypothalamus and median eminence cell types. Nature Neuroscience, 2017, 20, 484-496.	7.1	635
10	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. Nature Genetics, 2016, 48, 510-518.	9.4	617
11	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
12	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
13	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
14	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. Nature Genetics, 2019, 51, 245-257.	9.4	536
15	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	9.4	520
16	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. Nature Genetics, 2016, 48, 1043-1048.	9.4	494
17	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
18	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362

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19	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
20	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	1.5	331
21	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	2.6	326
22	Gene expression analysis identifies global gene dosage sensitivity in cancer. Nature Genetics, 2015, 47, 115-125.	9.4	313
23	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310
24	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
25	A single-cell atlas of human and mouse white adipose tissue. Nature, 2022, 603, 926-933.	13.7	277
26	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	1.4	275
27	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
28	Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13790-13794.	3.3	244
29	Mutations in FGF17, IL17RD, DUSP6, SPRY4, and FLRT3 Are Identified in Individuals with Congenital Hypogonadotropic Hypogonadism. American Journal of Human Genetics, 2013, 92, 725-743.	2.6	227
30	Population genetic differentiation of height and body mass index across Europe. Nature Genetics, 2015, 47, 1357-1362.	9.4	227
31	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. Nature Genetics, 2013, 45, 902-906.	9.4	221
32	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
33	Macrophages and Adipocytes in Human Obesity. Diabetes, 2009, 58, 1558-1567.	0.3	160
34	SNPsnap: a Web-based tool for identification and annotation of matched SNPs. Bioinformatics, 2015, 31, 418-420.	1.8	158
35	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
36	scVAE: variational auto-encoders for single-cell gene expression data. Bioinformatics, 2020, 36, 4415-4422.	1.8	144

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37	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
38	Whole-Exome Sequencing of 2,000 Danish Individuals and the Role of Rare Coding Variants in Type 2 Diabetes. American Journal of Human Genetics, 2013, 93, 1072-1086.	2.6	124
39	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194.	2.6	119
40	Modeling neural tube development by differentiation of human embryonic stem cells in a microfluidic WNT gradient. Nature Biotechnology, 2020, 38, 1265-1273.	9.4	114
41	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
42	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
43	A novel common variant in DCST2 is associated with length in early life and height in adulthood. Human Molecular Genetics, 2015, 24, 1155-1168.	1.4	109
44	Tracing the origin of adult intestinal stem cells. Nature, 2019, 570, 107-111.	13.7	107
45	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. Journal of Clinical Investigation, 2017, 127, 1798-1812.	3.9	106
46	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	0.7	103
47	Genome-wide association analyses identify variants in developmental genes associated with hypospadias. Nature Genetics, 2014, 46, 957-963.	9.4	97
48	A genome-wide association study of men with symptoms of testicular dysgenesis syndrome and its network biology interpretation. Journal of Medical Genetics, 2012, 49, 58-65.	1.5	96
49	Genome-wide association analyses identify 39 new susceptibility loci for diverticular disease. Nature Genetics, 2018, 50, 1359-1365.	9.4	93
50	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
51	Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes. Nature Communications, 2018, 9, 321.	5.8	85
52	Quantitative proteomics and single-nucleus transcriptomics of the sinus node elucidates the foundation of cardiac pacemaking. Nature Communications, 2019, 10, 2889.	5.8	84
53	Identification of epilepsy-associated neuronal subtypes and gene expression underlying epileptogenesis. Nature Communications, 2020, 11, 5038.	5.8	80
54	Genetic mapping of etiologic brain cell types for obesity. ELife, 2020, 9, .	2.8	79

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55	Metabolic Network Topology Reveals Transcriptional Regulatory Signatures of Type 2 Diabetes. PLoS Computational Biology, 2010, 6, e1000729.	1.5	75
56	Comprehensive analysis of schizophrenia-associated loci highlights ion channel pathways and biologically plausible candidate causal genes. Human Molecular Genetics, 2016, 25, 1247-1254.	1.4	69
57	Mendelian Randomization Study of Body Mass Index and Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1024-1031.	1.1	67
58	Genome-wide Analysis of Body Proportion Classifies Height-Associated Variants by Mechanism of Action and Implicates Genes Important for Skeletal Development. American Journal of Human Genetics, 2015, 96, 695-708.	2.6	67
59	Novel Microcephalic Primordial Dwarfism Disorder Associated with Variants in the Centrosomal Protein Ninein. Journal of Clinical Endocrinology and Metabolism, 2012, 97, E2140-E2151.	1.8	64
60	Shared genetic variants suggest common pathways in allergy and autoimmune diseases. Journal of Allergy and Clinical Immunology, 2017, 140, 771-781.	1.5	63
61	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. Nature Human Behaviour, 2021, 5, 1717-1730.	6.2	62
62	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. Biological Psychiatry, 2022, 91, 102-117.	0.7	61
63	A genetic map of the mouse dorsal vagal complex and its role in obesity. Nature Metabolism, 2021, 3, 530-545.	5.1	60
64	Protein Interaction-Based Genome-Wide Analysis of Incident Coronary Heart Disease. Circulation: Cardiovascular Genetics, 2011, 4, 549-556.	5.1	55
65	Mendelian randomization study of height and risk of colorectal cancer. International Journal of Epidemiology, 2015, 44, 662-672.	0.9	55
66	Gene-based meta-analysis of genome-wide association studies implicates new loci involved in obesity. Human Molecular Genetics, 2015, 24, 6849-6860.	1.4	55
67	A distinct adipose tissue gene expression response to caloric restriction predicts 6-mo weight maintenance in obese subjects. American Journal of Clinical Nutrition, 2011, 94, 1399-1409.	2.2	54
68	A Low-Frequency Inactivating *AKT2* Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
69	Fatness-Associated FTO Gene Variant Increases Mortality Independent of Fatness – in Cohorts of Danish Men. PLoS ONE, 2009, 4, e4428.	1.1	47
70	Transcriptomic analysis links diverse hypothalamic cell types to fibroblast growth factor 1-induced sustained diabetes remission. Nature Communications, 2020, 11, 4458.	5.8	34
71	Meta-analysis of heterogeneous data sources for genome-scale identification of risk genes in complex phenotypes. Genetic Epidemiology, 2011, 35, 318-332.	0.6	31
72	Nationwide prediction of type 2 diabetes comorbidities. Scientific Reports, 2020, 10, 1776.	1.6	31

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73	Concordance of gene expression in human protein complexes reveals tissue specificity and pathology. Nucleic Acids Research, 2013, 41, e171-e171.	6.5	24
74	MetaRanker 2.0: a web server for prioritization of genetic variation data. Nucleic Acids Research, 2013, 41, W104-W108.	6.5	24
75	Twenty-eight genetic loci associated with ST-T-wave amplitudes of the electrocardiogram. Human Molecular Genetics, 2016, 25, 2093-2103.	1.4	24
76	Genetic analysis of dietary intake identifies new loci and functional links with metabolic traits. Nature Human Behaviour, 2022, 6, 155-163.	6.2	22
77	The Validation and Assessment of Machine Learning: A Game of Prediction from High-Dimensional Data. PLoS ONE, 2009, 4, e6287.	1.1	22
78	Role of hypothalamic MAPK/ERK signaling and central action of FGF1 in diabetes remission. IScience, 2021, 24, 102944.	1.9	18
79	Benchmarker: An Unbiased, Association-Data-Driven Strategy to Evaluate Gene Prioritization Algorithms. American Journal of Human Genetics, 2019, 104, 1025-1039.	2.6	16
80	PAIRUP-MS: Pathway analysis and imputation to relate unknowns in profiles from mass spectrometry-based metabolite data. PLoS Computational Biology, 2019, 15, e1006734.	1.5	13
81	Single-Cell Mapping of GLP-1 and GIP Receptor Expression in the Dorsal Vagal Complex. Diabetes, 2021, 70, 1945-1955.	0.3	13
82	Gene set analysis for interpreting genetic studies. Human Molecular Genetics, 2016, 25, R133-R140.	1.4	12
83	Predicting facial characteristics from complex polygenic variations. Forensic Science International: Genetics, 2015, 19, 263-268.	1.6	11
84	Hypothalamic hormone-sensitive lipase regulates appetite and energy homeostasis. Molecular Metabolism, 2021, 47, 101174.	3.0	11
85	RhoA in tyrosine hydroxylase neurones regulates food intake and body weight via altered sensitivity to peripheral hormones. Journal of Neuroendocrinology, 2019, 31, e12761.	1.2	10
86	HIV infection drives interferon signaling within intestinal SARS-CoV-2 target cells. JCI Insight, 2021, 6, .	2.3	7
87	Multilocus Heterozygosity and Coronary Heart Disease: Nested Case-Control Studies in Men and Women. PLoS ONE, 2015, 10, e0124847.	1.1	3