Tune H Pers

List of Publications by Year
in descending order

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		25014	40954
87	25,610	57	93
papers	citations	h-index	g-index

109	109	109	37221
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. Biological Psychiatry, 2022, 91, 102-117.	0.7	61
2	Genetic analysis of dietary intake identifies new loci and functional links with metabolic traits. Nature Human Behaviour, 2022, 6, 155-163.	6.2	22
3	A single-cell atlas of human and mouse white adipose tissue. Nature, 2022, 603, 926-933.	13.7	277
4	A genetic map of the mouse dorsal vagal complex and its role in obesity. Nature Metabolism, 2021, 3, 530-545.	5.1	60
5	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	0.7	103
6	Hypothalamic hormone-sensitive lipase regulates appetite and energy homeostasis. Molecular Metabolism, 2021, 47, 101174.	3.0	11
7	Single-Cell Mapping of GLP-1 and GIP Receptor Expression in the Dorsal Vagal Complex. Diabetes, 2021, 70, 1945-1955.	0.3	13
8	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
9	HIV infection drives interferon signaling within intestinal SARS-CoV-2 target cells. JCI Insight, 2021, 6, .	2.3	7
10	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
11	Role of hypothalamic MAPK/ERK signaling and central action of FGF1 in diabetes remission. IScience, 2021, 24, 102944.	1.9	18
12	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
13	Identification of epilepsy-associated neuronal subtypes and gene expression underlying epileptogenesis. Nature Communications, 2020, 11, 5038.	5.8	80
14	Transcriptomic analysis links diverse hypothalamic cell types to fibroblast growth factor 1-induced sustained diabetes remission. Nature Communications, 2020, 11, 4458.	5.8	34
15	scVAE: variational auto-encoders for single-cell gene expression data. Bioinformatics, 2020, 36, 4415-4422.	1.8	144
16	Nationwide prediction of type 2 diabetes comorbidities. Scientific Reports, 2020, 10, 1776.	1.6	31
17	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
18	Genetic mapping of etiologic brain cell types for obesity. ELife, 2020, 9, .	2.8	79

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19	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
20	Quantitative proteomics and single-nucleus transcriptomics of the sinus node elucidates the foundation of cardiac pacemaking. Nature Communications, 2019, 10, 2889.	5.8	84
21	Tracing the origin of adult intestinal stem cells. Nature, 2019, 570, 107-111.	13.7	107
22	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
23	Benchmarker: An Unbiased, Association-Data-Driven Strategy to Evaluate Gene Prioritization Algorithms. American Journal of Human Genetics, 2019, 104, 1025-1039.	2.6	16
24	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
25	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
26	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
27	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
28	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
29	Genome-wide association analyses identify 39 new susceptibility loci for diverticular disease. Nature Genetics, 2018, 50, 1359-1365.	9.4	93
30	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
31	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
32	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
33	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
34	A molecular census of arcuate hypothalamus and median eminence cell types. Nature Neuroscience, 2017, 20, 484-496.	7.1	635
35	Shared genetic variants suggest common pathways in allergy and autoimmune diseases. Journal of Allergy and Clinical Immunology, 2017, 140, 771-781.	1.5	63
36	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615

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37	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
38	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
39	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
40	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
41	Gene set analysis for interpreting genetic studies. Human Molecular Genetics, 2016, 25, R133-R140.	1.4	12
42	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
43	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
44	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
45	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
46	Twenty-eight genetic loci associated with ST-T-wave amplitudes of the electrocardiogram. Human Molecular Genetics, 2016, 25, 2093-2103.	1.4	24
47	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	9.4	520
48	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
49	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
50	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
51	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
52	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
53	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	1.4	275
54	Multilocus Heterozygosity and Coronary Heart Disease: Nested Case-Control Studies in Men and Women. PLoS ONE, 2015, 10, e0124847.	1.1	3

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55	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
56	Mendelian randomization study of height and risk of colorectal cancer. International Journal of Epidemiology, 2015, 44, 662-672.	0.9	55
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	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
59	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
60	SNPsnap: a Web-based tool for identification and annotation of matched SNPs. Bioinformatics, 2015, 31, 418-420.	1.8	158
61	Gene expression analysis identifies global gene dosage sensitivity in cancer. Nature Genetics, 2015, 47, 115-125.	9.4	313
62	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	5.8	706
63	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
64	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310
65	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
66	Predicting facial characteristics from complex polygenic variations. Forensic Science International: Genetics, 2015, 19, 263-268.	1.6	11
67	Population genetic differentiation of height and body mass index across Europe. Nature Genetics, 2015, 47, 1357-1362.	9.4	227
68	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
69	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
70	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
71	Genome-wide association analyses identify variants in developmental genes associated with hypospadias. Nature Genetics, 2014, 46, 957-963.	9.4	97
72	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

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73	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. Nature Genetics, 2013, 45, 902-906.	9.4	221
74	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
75	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
76	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
77	Concordance of gene expression in human protein complexes reveals tissue specificity and pathology. Nucleic Acids Research, 2013, 41, e171-e171.	6.5	24
78	MetaRanker 2.0: a web server for prioritization of genetic variation data. Nucleic Acids Research, 2013, 41, W104-W108.	6.5	24
79	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
80	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
81	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
82	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
83	Protein Interaction-Based Genome-Wide Analysis of Incident Coronary Heart Disease. Circulation: Cardiovascular Genetics, 2011, 4, 549-556.	5.1	55
84	Metabolic Network Topology Reveals Transcriptional Regulatory Signatures of Type 2 Diabetes. PLoS Computational Biology, 2010, 6, e1000729.	1.5	75
85	Macrophages and Adipocytes in Human Obesity. Diabetes, 2009, 58, 1558-1567.	0.3	160
86	Fatness-Associated FTO Gene Variant Increases Mortality Independent of Fatness â€“ in Cohorts of Danish Men. PLoS ONE, 2009, 4, e4428.	1.1	47
87	The Validation and Assessment of Machine Learning: A Game of Prediction from High-Dimensional Data. PLoS ONE, 2009, 4, e6287.	1.1	22