

Tune H Pers

List of Publications by Year in Descending Order

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Version: 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

94
papers

16,676
citations

49
h-index

109
g-index

109
ext. papers

22,215
ext. citations

18.1
avg, IF

5.08
L-index

#	Paper	IF	Citations
94	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. <i>Biological Psychiatry</i> , 2022 , 91, 102-117	7.9	11
93	A single-cell atlas of human and mouse white adipose tissue.. <i>Nature</i> , 2022 ,	50.4	15
92	A genetic map of the mouse dorsal vagal complex and its role in obesity. <i>Nature Metabolism</i> , 2021 , 3, 530-545	14.6	17
91	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. <i>Biological Psychiatry</i> , 2021 , 90, 611-620	7.9	17
90	Hypothalamic hormone-sensitive lipase regulates appetite and energy homeostasis. <i>Molecular Metabolism</i> , 2021 , 47, 101174	8.8	3
89	Single-Cell Mapping of GLP-1 and GIP Receptor Expression in the Dorsal Vagal Complex. <i>Diabetes</i> , 2021 , 70, 1945-1955	0.9	1
88	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. <i>Nature Human Behaviour</i> , 2021 ,	12.8	5
87	HIV infection drives interferon signaling within intestinal SARS-CoV-2 target cells. <i>JCI Insight</i> , 2021 , 6,	9.9	3
86	Genetic analysis of dietary intake identifies new loci and functional links with metabolic traits. <i>Nature Human Behaviour</i> , 2021 ,	12.8	5
85	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021 , 596, 393-397	50.4	28
84	Role of hypothalamic MAPK/ERK signaling and central action of FGF1 in diabetes remission. <i>IScience</i> , 2021 , 24, 102944	6.1	2
83	scVAE: variational auto-encoders for single-cell gene expression data. <i>Bioinformatics</i> , 2020 , 36, 4415-4422	22	53
82	Nationwide prediction of type 2 diabetes comorbidities. <i>Scientific Reports</i> , 2020 , 10, 1776	4.9	13
81	Genetic mapping of etiologic brain cell types for obesity. <i>ELife</i> , 2020 , 9,	8.9	21
80	Modeling neural tube development by differentiation of human embryonic stem cells in a microfluidic WNT gradient. <i>Nature Biotechnology</i> , 2020 , 38, 1265-1273	44.5	44
79	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. <i>Biological Psychiatry</i> , 2020 , 88, 169-184	7.9	57
78	Identification of epilepsy-associated neuronal subtypes and gene expression underlying epileptogenesis. <i>Nature Communications</i> , 2020 , 11, 5038	17.4	17

77	Transcriptomic analysis links diverse hypothalamic cell types to fibroblast growth factor 1-induced sustained diabetes remission. <i>Nature Communications</i> , 2020 , 11, 4458	17.4	16
76	Tracing the origin of adult intestinal stem cells. <i>Nature</i> , 2019 , 570, 107-111	50.4	67
75	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , 2019 , 51, 793-803	36.3	662
74	Benchmarker: An Unbiased, Association-Data-Driven Strategy to Evaluate Gene Prioritization Algorithms. <i>American Journal of Human Genetics</i> , 2019 , 104, 1025-1039	11	4
73	RhoA in tyrosine hydroxylase neurones regulates food intake and body weight via altered sensitivity to peripheral hormones. <i>Journal of Neuroendocrinology</i> , 2019 , 31, e12761	3.8	7
72	Quantitative proteomics and single-nucleus transcriptomics of the sinus node elucidates the foundation of cardiac pacemaking. <i>Nature Communications</i> , 2019 , 10, 2889	17.4	51
71	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019 , 51, 452-469	36.3	44
70	PAIRUP-MS: Pathway analysis and imputation to relate unknowns in profiles from mass spectrometry-based metabolite data. <i>PLoS Computational Biology</i> , 2019 , 15, e1006734	5	9
69	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. <i>Nature Genetics</i> , 2019 , 51, 245-257	36.3	259
68	Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes. <i>Nature Communications</i> , 2018 , 9, 321	17.4	50
67	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. <i>Nature Genetics</i> , 2018 , 50, 1112-1121	36.3	950
66	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018 , 50, 26-41	36.3	186
65	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018 , 103, 691-706	11	151
64	Genome-wide association analyses identify 39 new susceptibility loci for diverticular disease. <i>Nature Genetics</i> , 2018 , 50, 1359-1365	36.3	49
63	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. <i>American Journal of Human Genetics</i> , 2018 , 102, 1185-1194	11	55
62	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
61	A molecular census of arcuate hypothalamus and median eminence cell types. <i>Nature Neuroscience</i> , 2017 , 20, 484-496	25.5	401
60	Shared genetic variants suggest common pathways in allergy and autoimmune diseases. <i>Journal of Allergy and Clinical Immunology</i> , 2017 , 140, 771-781	11.5	36

59	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017 , 66, 2888-2902	414
58	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017 , 66, 2019-2032	0.9 29
57	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017 , 49, 27-35	36.3 530
56	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 2017 , 127, 1798-1812	15.9 68
55	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016 , 68, 1435-1448	15.1 76
54	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016 , 48, 1171-1184	36.3 251
53	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. <i>Nature Genetics</i> , 2016 , 48, 1043-8	36.3 328
52	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 13366-13371	11.5 90
51	Twenty-eight genetic loci associated with ST-T-wave amplitudes of the electrocardiogram. <i>Human Molecular Genetics</i> , 2016 , 25, 2093-2103	5.6 20
50	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. <i>Nature Genetics</i> , 2016 , 48, 856-66	36.3 355
49	Comprehensive analysis of schizophrenia-associated loci highlights ion channel pathways and biologically plausible candidate causal genes. <i>Human Molecular Genetics</i> , 2016 , 25, 1247-54	5.6 42
48	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016 , 7, 10495	17.4 180
47	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016 , 7, 10494	17.4 107
46	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016 , 7, 10023	17.4 295
45	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. <i>Nature Genetics</i> , 2016 , 48, 510-8	36.3 404
44	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. <i>Human Molecular Genetics</i> , 2016 , 25, 389-403	5.6 202
43	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016 , 533, 539-42	50.4 850
42	Gene set analysis for interpreting genetic studies. <i>Human Molecular Genetics</i> , 2016 , 25, R133-R140	5.6 10

41	Gene expression analysis identifies global gene dosage sensitivity in cancer. <i>Nature Genetics</i> , 2015 , 47, 115-25	36.3	219
40	Biological interpretation of genome-wide association studies using predicted gene functions. <i>Nature Communications</i> , 2015 , 6, 5890	17.4	489
39	Genome-wide Analysis of Body Proportion Classifies Height-Associated Variants by Mechanism of Action and Implicates Genes Important for Skeletal Development. <i>American Journal of Human Genetics</i> , 2015 , 96, 695-708	11	44
38	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015 , 47, 589-97	36.3	229
37	Gene-based meta-analysis of genome-wide association studies implicates new loci involved in obesity. <i>Human Molecular Genetics</i> , 2015 , 24, 6849-60	5.6	44
36	Predicting facial characteristics from complex polygenic variations. <i>Forensic Science International: Genetics</i> , 2015 , 19, 263-268	4.3	7
35	Population genetic differentiation of height and body mass index across Europe. <i>Nature Genetics</i> , 2015 , 47, 1357-62	36.3	186
34	A novel common variant in DCST2 is associated with length in early life and height in adulthood. <i>Human Molecular Genetics</i> , 2015 , 24, 1155-68	5.6	77
33	Multilocus heterozygosity and coronary heart disease: nested case-control studies in men and women. <i>PLoS ONE</i> , 2015 , 10, e0124847	3.7	2
32	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015 , 11, e1005378	6	220
31	Mendelian randomization study of height and risk of colorectal cancer. <i>International Journal of Epidemiology</i> , 2015 , 44, 662-72	7.8	44
30	Mendelian Randomization Study of Body Mass Index and Colorectal Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 1024-31	4	54
29	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
28	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
27	SNPsnap: a Web-based tool for identification and annotation of matched SNPs. <i>Bioinformatics</i> , 2015 , 31, 418-20	7.2	104
26	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014 , 514, 92-97	50.4	401
25	Genome-wide association analyses identify variants in developmental genes associated with hypospadias. <i>Nature Genetics</i> , 2014 , 46, 957-63	36.3	81
24	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014 , 46, 1173-86	36.3	1339

23	Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 13790-4	11.5	181
22	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. <i>Nature Genetics</i> , 2013 , 45, 902-906	36.3	191
21	Integrative annotation of variants from 1092 humans: application to cancer genomics. <i>Science</i> , 2013 , 342, 1235587	33.3	281
20	Whole-exome sequencing of 2,000 Danish individuals and the role of rare coding variants in type 2 diabetes. <i>American Journal of Human Genetics</i> , 2013 , 93, 1072-86	11	109
19	Mutations in FGF17, IL17RD, DUSP6, SPRY4, and FLRT3 are identified in individuals with congenital hypogonadotropic hypogonadism. <i>American Journal of Human Genetics</i> , 2013 , 92, 725-43	11	178
18	Concordance of gene expression in human protein complexes reveals tissue specificity and pathology. <i>Nucleic Acids Research</i> , 2013 , 41, e171	20.1	19
17	MetaRanker 2.0: a web server for prioritization of genetic variation data. <i>Nucleic Acids Research</i> , 2013 , 41, W104-8	20.1	24
16	A genome-wide association study of men with symptoms of testicular dysgenesis syndrome and its network biology interpretation. <i>Journal of Medical Genetics</i> , 2012 , 49, 58-65	5.8	86
15	Novel microcephalic primordial dwarfism disorder associated with variants in the centrosomal protein ninein. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2012 , 97, E2140-51	5.6	49
14	Meta-analysis of heterogeneous data sources for genome-scale identification of risk genes in complex phenotypes. <i>Genetic Epidemiology</i> , 2011 , 35, 318-32	2.6	28
13	A distinct adipose tissue gene expression response to caloric restriction predicts 6-mo weight maintenance in obese subjects. <i>American Journal of Clinical Nutrition</i> , 2011 , 94, 1399-409	7	48
12	Protein interaction-based genome-wide analysis of incident coronary heart disease. <i>Circulation: Cardiovascular Genetics</i> , 2011 , 4, 549-56		53
11	Metabolic network topology reveals transcriptional regulatory signatures of type 2 diabetes. <i>PLoS Computational Biology</i> , 2010 , 6, e1000729	5	66
10	Macrophages and adipocytes in human obesity: adipose tissue gene expression and insulin sensitivity during calorie restriction and weight stabilization. <i>Diabetes</i> , 2009 , 58, 1558-67	0.9	142
9	Fatness-associated FTO gene variant increases mortality independent of fatness--in cohorts of Danish men. <i>PLoS ONE</i> , 2009 , 4, e4428	3.7	40
8	The validation and assessment of machine learning: a game of prediction from high-dimensional data. <i>PLoS ONE</i> , 2009 , 4, e6287	3.7	18
7	Single-cell analysis reveals cellular heterogeneity and molecular determinants of hypothalamic leptin-receptor cells		1
6	Genome-wide association study of febrile seizures identifies seven new loci implicating fever response and neuronal excitability genes		2

5	A single cell atlas of human and mouse white adipose tissue	1
4	Mapping heritability of obesity by brain cell types	2
3	Identification of 370 genetic loci for age at first sex and birth linked to externalising behaviour	3
2	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences ¹	4
1	Multi-trait genome-wide association meta-analysis of dietary intake identifies new loci and genetic and functional links with metabolic traits	3