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List of Publications by Year in descending order

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Version: 2024-02-01

94
papers

43,694
citations

15504

65
h-index

33894

99
g-index

109
all docs

109
docs citations

109
times ranked

43244
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic overlap analysis of endometriosis and asthma identifies shared loci implicating sex hormones and thyroid signalling pathways. <i>Human Reproduction</i> , 2022, 37, 366-383.	0.9	19
2	Multi-ancestry genome-wide association study of gestational diabetes mellitus highlights genetic links with type 2 diabetes. <i>Human Molecular Genetics</i> , 2022, 31, 3377-3391.	2.9	47
3	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	21.4	250
4	Loss-of-Function Variants in the Tumor-Suppressor Gene <i>PTPN14</i> Confer Increased Cancer Risk. <i>Cancer Research</i> , 2021, 81, 1954-1964.	0.9	15
5	Distinction between the effects of parental and fetal genomes on fetal growth. <i>Nature Genetics</i> , 2021, 53, 1135-1142.	21.4	41
6	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the <i>WNT4</i> 1p36.12 locus. <i>Human Genetics</i> , 2021, 140, 1353-1365.	3.8	18
7	Genetic propensities for verbal and spatial ability have opposite effects on body mass index and risk of schizophrenia. <i>Intelligence</i> , 2021, 88, 101565.	3.0	2
8	Large-Scale Screening for Monogenic and Clinically Defined Familial Hypercholesterolemia in Iceland. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021, 41, 2616-2628.	2.4	16
9	Large-scale integration of the plasma proteome with genetics and disease. <i>Nature Genetics</i> , 2021, 53, 1712-1721.	21.4	340
10	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. <i>European Heart Journal</i> , 2020, 41, 2618-2628.	2.2	61
11	Genetic predisposition to hypertension is associated with preeclampsia in European and Central Asian women. <i>Nature Communications</i> , 2020, 11, 5976.	12.8	102
12	Genome-wide association identifies seven loci for pelvic organ prolapse in Iceland and the UK Biobank. <i>Communications Biology</i> , 2020, 3, 129.	4.4	20
13	A PRPH splice-donor variant associates with reduced sural nerve amplitude and risk of peripheral neuropathy. <i>Nature Communications</i> , 2019, 10, 1777.	12.8	7
14	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	21.4	89
15	Lipoprotein(a) Concentration and Risks of Cardiovascular Disease and Diabetes. <i>Journal of the American College of Cardiology</i> , 2019, 74, 2982-2994.	2.8	127
16	Sequence variants associating with urinary biomarkers. <i>Human Molecular Genetics</i> , 2019, 28, 1199-1211.	2.9	28
17	Genome-wide analysis yields new loci associating with aortic valve stenosis. <i>Nature Communications</i> , 2018, 9, 987.	12.8	91
18	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.	21.4	356

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19	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018, 50, 1505-1513.	21.4	1,331
20	Variants associating with uterine leiomyoma highlight genetic background shared by various cancers and hormone-related traits. <i>Nature Communications</i> , 2018, 9, 3636.	12.8	74
21	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. <i>Nature Communications</i> , 2018, 9, 2252.	12.8	99
22	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.	21.4	286
23	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544
24	Variants in the fetal genome near FLT1 are associated with risk of preeclampsia. <i>Nature Genetics</i> , 2017, 49, 1255-1260.	21.4	205
25	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. <i>Nature Communications</i> , 2017, 8, 15539.	12.8	230
26	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017, 66, 2888-2902.	0.6	615
27	Analysis of potential protein-modifying variants in 9000 endometriosis patients and 150000 controls of European ancestry. <i>Scientific Reports</i> , 2017, 7, 11380.	3.3	16
28	Effect of sequence variants on variance in glucose levels predicts type 2 diabetes risk and accounts for heritability. <i>Nature Genetics</i> , 2017, 49, 1398-1402.	21.4	20
29	Variant <i>ASGR1</i> Associated with a Reduced Risk of Coronary Artery Disease. <i>New England Journal of Medicine</i> , 2016, 374, 2131-2141.	27.0	137
30	Variants with large effects on blood lipids and the role of cholesterol and triglycerides in coronary disease. <i>Nature Genetics</i> , 2016, 48, 634-639.	21.4	214
31	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	12.8	74
32	Common variants upstream of KDR encoding VEGFR2 and in TTC39B associate with endometriosis. <i>Nature Communications</i> , 2016, 7, 12350.	12.8	31
33	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.	3.5	331
34	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. <i>PLoS Genetics</i> , 2015, 11, e1005230.	3.5	77
35	A Splice Region Variant in LDLR Lowers Non-high Density Lipoprotein Cholesterol and Protects against Coronary Artery Disease. <i>PLoS Genetics</i> , 2015, 11, e1005379.	3.5	24
36	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	27.8	1,328

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37	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
38	Association Analysis of 29,956 Individuals Confirms That a Low-Frequency Variant at <i>CCND2</i> Halves the Risk of Type 2 Diabetes by Enhancing Insulin Secretion. <i>Diabetes</i> , 2015, 64, 2279-2285.	0.6	24
39	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015, 47, 589-597.	21.4	310
40	The epidemiology of pituitary adenomas in Iceland, 1955–2012: a nationwide population-based study. <i>European Journal of Endocrinology</i> , 2015, 173, 655-664.	3.7	255
41	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015, 47, 1415-1425.	21.4	365
42	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. <i>Nature Genetics</i> , 2014, 46, 294-298.	21.4	294
43	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. <i>Cell</i> , 2014, 156, 343-358.	28.9	113
44	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	21.4	1,818
45	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	21.4	959
46	Loss-of-function mutations in <i>SLC30A8</i> protect against type 2 diabetes. <i>Nature Genetics</i> , 2014, 46, 357-363.	21.4	428
47	InterPregGen: genetic studies of pre-eclampsia in three continents. <i>Norsk Epidemiologi</i> , 2014, 24, 141-146.	0.3	12
48	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	21.4	578
49	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	3.5	371
50	Genetic Architecture of Vitamin B12 and Folate Levels Uncovered Applying Deeply Sequenced Large Datasets. <i>PLoS Genetics</i> , 2013, 9, e1003530.	3.5	112
51	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. <i>PLoS Medicine</i> , 2013, 10, e1001474.	8.4	178
52	Stratifying Type 2 Diabetes Cases by BMI Identifies Genetic Risk Variants in <i>LAMA1</i> and Enrichment for Risk Variants in Lean Compared to Obese Cases. <i>PLoS Genetics</i> , 2012, 8, e1002741.	3.5	190
53	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. <i>PLoS Genetics</i> , 2012, 8, e1002607.	3.5	419
54	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012, 44, 981-990.	21.4	1,748

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55	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	27.8	383
56	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. <i>PLoS ONE</i> , 2012, 7, e29202.	2.5	197
57	A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. <i>Nature Genetics</i> , 2011, 43, 1098-1103.	21.4	251
58	Evaluating differences in linkage disequilibrium between populations. <i>Annals of Human Genetics</i> , 2010, 74, 233-247.	0.8	3
59	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	27.8	1,789
60	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. <i>Nature Genetics</i> , 2010, 42, 142-148.	21.4	591
61	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. <i>Nature Genetics</i> , 2010, 42, 579-589.	21.4	1,631
62	Genome-wide association study identifies a sequence variant within the DAB2IP gene conferring susceptibility to abdominal aortic aneurysm. <i>Nature Genetics</i> , 2010, 42, 692-697.	21.4	181
63	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	21.4	836
64	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	21.4	2,634
65	Genetic evidence that raised sex hormone binding globulin (SHBG) levels reduce the risk of type 2 diabetes. <i>Human Molecular Genetics</i> , 2010, 19, 535-544.	2.9	176
66	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. <i>Diabetes</i> , 2010, 59, 3229-3239.	0.6	387
67	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	21.4	1,982
68	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. <i>PLoS Genetics</i> , 2009, 5, e1000508.	3.5	453
69	The T-381C SNP in BNP gene may be modestly associated with type 2 diabetes: an updated meta-analysis in 49 279 subjects. <i>Human Molecular Genetics</i> , 2009, 18, 2495-2501.	2.9	30
70	Parental origin of sequence variants associated with complex diseases. <i>Nature</i> , 2009, 462, 868-874.	27.8	521
71	Genome-wide association yields new sequence variants at seven loci that associate with measures of obesity. <i>Nature Genetics</i> , 2009, 41, 18-24.	21.4	1,247
72	Variants in MTNR1B influence fasting glucose levels. <i>Nature Genetics</i> , 2009, 41, 77-81.	21.4	662

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73	Sequence variants affecting eosinophil numbers associate with asthma and myocardial infarction. Nature Genetics, 2009, 41, 342-347.	21.4	709
74	Genome-wide association study identifies sequence variants on 6q21 associated with age at menarche. Nature Genetics, 2009, 41, 734-738.	21.4	199
75	New common variants affecting susceptibility to basal cell carcinoma. Nature Genetics, 2009, 41, 909-914.	21.4	303
76	Genetics of gene expression and its effect on disease. Nature, 2008, 452, 423-428.	27.8	1,209
77	Many sequence variants affecting diversity of adult human height. Nature Genetics, 2008, 40, 609-615.	21.4	615
78	The same sequence variant on 9p21 associates with myocardial infarction, abdominal aortic aneurysm and intracranial aneurysm. Nature Genetics, 2008, 40, 217-224.	21.4	668
79	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nature Genetics, 2008, 40, 638-645.	21.4	1,683
80	A variant in CDKAL1 influences insulin response and risk of type 2 diabetes. Nature Genetics, 2007, 39, 770-775.	21.4	966
81	Two variants on chromosome 17 confer prostate cancer risk, and the one in TCF2 protects against type 2 diabetes. Nature Genetics, 2007, 39, 977-983.	21.4	670
82	Abstract 2318: The Type 2 Diabetes Gene <i>CDKAL1</i> Discovered by Genome-wide Association is Expressed in Beta Cells and Modulated by Glucose Concentration. Circulation, 2007, 116, .	1.6	1
83	Recurrence of hypertensive disorder in second pregnancy. American Journal of Obstetrics and Gynecology, 2006, 194, 916-920.	1.3	66
84	A common inversion under selection in Europeans. Nature Genetics, 2005, 37, 129-137.	21.4	747
85	Neuregulin 1 and schizophrenia. Annals of Medicine, 2004, 36, 62-71.	3.8	119
86	Paternity Change and the Recurrence Risk in Familial Hypertensive Disorder in Pregnancy. Hypertension in Pregnancy, 2004, 23, 219-225.	1.1	19
87	Multiple novel transcription initiation sites for NRG1. Gene, 2004, 342, 97-105.	2.2	139
88	Association of Neuregulin 1 with Schizophrenia Confirmed in a Scottish Population. American Journal of Human Genetics, 2003, 72, 83-87.	6.2	518
89	Neuregulin 1 and Susceptibility to Schizophrenia. American Journal of Human Genetics, 2002, 71, 877-892.	6.2	1,550
90	Clostridium perfringens beta-toxin forms multimeric transmembrane pores in human endothelial cells. Microbial Pathogenesis, 2000, 28, 45-50.	2.9	72

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91	Properties of the Adenovirus Type 40 E1B Promoter That Contribute to Its Low Transcriptional Activity. <i>Virology</i> , 1999, 265, 10-19.	2.4	11
92	Site-directed mutagenesis of <i>Clostridium perfringens</i> beta-toxin: expression of wild-type and mutant toxins in <i>Bacillus subtilis</i> . <i>FEMS Microbiology Letters</i> , 1998, 158, 17-23.	1.8	41
93	Enteric adenovirus type 40: E1B transcription map and identification of novel E1A-E1B cotranscripts in lytically infected cells. <i>Virology</i> , 1991, 181, 139-149.	2.4	13
94	Complementation of enteric adenovirus type 40 for lytic growth in tissue culture by E1B 55K function of adenovirus types 5 and 12. <i>Virology</i> , 1989, 171, 619-622.	2.4	34