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List of Publications by Year in descending order

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Version: 2024-02-01

87
papers

19,903
citations

34493

54
h-index

46524

93
g-index

109
all docs

109
docs citations

109
times ranked

30421
citing authors

#	ARTICLE	IF	CITATIONS
1	Association of the T-cell regulatory gene CTLA4 with susceptibility to autoimmune disease. <i>Nature</i> , 2003, 423, 506-511.	13.7	1,980
2	Robust associations of four new chromosome regions from genome-wide analyses of type 1 diabetes. <i>Nature Genetics</i> , 2007, 39, 857-864.	9.4	1,324
3	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018, 50, 524-537.	9.4	1,124
4	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	13.7	952
5	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	9.4	924
6	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. <i>Nature</i> , 2010, 464, 713-720.	13.7	737
7	Shared and Distinct Genetic Variants in Type 1 Diabetes and Celiac Disease. <i>New England Journal of Medicine</i> , 2008, 359, 2767-2777.	13.9	654
8	Association analyses based on false discovery rate implicate new loci for coronary artery disease. <i>Nature Genetics</i> , 2017, 49, 1385-1391.	9.4	571
9	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	13.7	544
10	Population structure, differential bias and genomic control in a large-scale, case-control association study. <i>Nature Genetics</i> , 2005, 37, 1243-1246.	9.4	496
11	Localization of type 1 diabetes susceptibility to the MHC class I genes HLA-B and HLA-A. <i>Nature</i> , 2007, 450, 887-892.	13.7	493
12	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017, 49, 403-415.	9.4	492
13	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	9.4	470
14	Bayesian refinement of association signals for 14 loci in 3 common diseases. <i>Nature Genetics</i> , 2012, 44, 1294-1301.	9.4	469
15	Replication of an Association Between the Lymphoid Tyrosine Phosphatase Locus (LYP/PTPN22) With Type 1 Diabetes, and Evidence for Its Role as a General Autoimmunity Locus. <i>Diabetes</i> , 2004, 53, 3020-3023.	0.3	447
16	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. <i>Science</i> , 2016, 351, 1166-1171.	6.0	438
17	Association of <i>LPA</i> Variants With Risk of Coronary Disease and the Implications for Lipoprotein(a)-Lowering Therapies. <i>JAMA Cardiology</i> , 2018, 3, 619.	3.0	428
18	Coding Variation in <i>ANGPTL4</i> , <i>LPL</i> , and <i>SVEP1</i> and the Risk of Coronary Disease. <i>New England Journal of Medicine</i> , 2016, 374, 1134-1144.	13.9	427

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19	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.	9.4	356
20	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020, 182, 1198-1213.e14.	13.5	353
21	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. <i>Nature Genetics</i> , 2019, 51, 51-62.	9.4	328
22	A robust and efficient method for Mendelian randomization with hundreds of genetic variants. <i>Nature Communications</i> , 2020, 11, 376.	5.8	290
23	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.	9.4	286
24	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016, 48, 1151-1161.	9.4	261
25	Complete MHC Haplotype Sequencing for Common Disease Gene Mapping. <i>Genome Research</i> , 2004, 14, 1176-1187.	2.4	260
26	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. <i>Nature Genetics</i> , 2017, 49, 1113-1119.	9.4	260
27	Additive and interaction effects at three amino acid positions in HLA-DQ and HLA-DR molecules drive type 1 diabetes risk. <i>Nature Genetics</i> , 2015, 47, 898-905.	9.4	235
28	Functional IL6R 358Ala Allele Impairs Classical IL-6 Receptor Signaling and Influences Risk of Diverse Inflammatory Diseases. <i>PLoS Genetics</i> , 2013, 9, e1003444.	1.5	234
29	Genome-Wide Association Analysis of Autoantibody Positivity in Type 1 Diabetes Cases. <i>PLoS Genetics</i> , 2011, 7, e1002216.	1.5	230
30	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. <i>Nature Genetics</i> , 2017, 49, 1450-1457.	9.4	218
31	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017, 69, 823-836.	1.2	214
32	A fast and efficient colocalization algorithm for identifying shared genetic risk factors across multiple traits. <i>Nature Communications</i> , 2021, 12, 764.	5.8	195
33	Interleukin-10, Polymorphism in SLC11A1 (formerly NRAMP1), and Susceptibility to Tuberculosis. <i>Journal of Infectious Diseases</i> , 2002, 186, 1808-1814.	1.9	139
34	Regression Mapping of Association between the Human Leukocyte Antigen Region and Graves Disease. <i>American Journal of Human Genetics</i> , 2005, 76, 157-163.	2.6	134
35	Genomic risk score offers predictive performance comparable to clinical risk factors for ischaemic stroke. <i>Nature Communications</i> , 2019, 10, 5819.	5.8	124
36	Genetic Analysis of Adult-Onset Autoimmune Diabetes. <i>Diabetes</i> , 2011, 60, 2645-2653.	0.3	115

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37	<i>FUT2</i> Nonsecretor Status Links Type 1 Diabetes Susceptibility and Resistance to Infection. <i>Diabetes</i> , 2011, 60, 3081-3084.	0.3	111
38	Long-range DNA looping and gene expression analyses identify DEXI as an autoimmune disease candidate gene. <i>Human Molecular Genetics</i> , 2012, 21, 322-333.	1.4	100
39	A genomic approach to therapeutic target validation identifies a glucose-lowering <i>GLP1R</i> variant protective for coronary heart disease. <i>Science Translational Medicine</i> , 2016, 8, 341ra76.	5.8	100
40	Genome-wide association study of MRI markers of cerebral small vessel disease in 42,310 participants. <i>Nature Communications</i> , 2020, 11, 2175.	5.8	93
41	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020, 52, 1314-1332.	9.4	91
42	Mendelian randomization for studying the effects of perturbing drug targets. <i>Wellcome Open Research</i> , 2021, 6, 16.	0.9	90
43	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	9.4	89
44	Assessing the causal association of glycine with risk of cardio-metabolic diseases. <i>Nature Communications</i> , 2019, 10, 1060.	5.8	85
45	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020, 25, 2392-2409.	4.1	83
46	A novel and major association of HLA-C in Graves' disease that eclipses the classical HLA-DRB1 effect. <i>Human Molecular Genetics</i> , 2007, 16, 2149-2153.	1.4	82
47	<i>PTPN22</i> Trp620 Explains the Association of Chromosome 1p13 With Type 1 Diabetes and Shows a Statistical Interaction With HLA Class II Genotypes. <i>Diabetes</i> , 2008, 57, 1730-1737.	0.3	78
48	Analysis of the Vitamin D Receptor Gene Sequence Variants in Type 1 Diabetes. <i>Diabetes</i> , 2004, 53, 2709-2712.	0.3	76
49	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. <i>Communications Biology</i> , 2021, 4, 156.	2.0	72
50	An atlas of mitochondrial DNA genotype-phenotype associations in the UK Biobank. <i>Nature Genetics</i> , 2021, 53, 982-993.	9.4	72
51	Experimental aspects of copy number variant assays at CCL3L1. <i>Nature Medicine</i> , 2009, 15, 1115-1117.	15.2	69
52	Assessing the validity of the association between the SUMO4 M55V variant and risk of type 1 diabetes. <i>Nature Genetics</i> , 2005, 37, 110-111.	9.4	65
53	Haplotype Structure, LD Blocks, and Uneven Recombination Within the LRP5 Gene. <i>Genome Research</i> , 2003, 13, 845-855.	2.4	64
54	Association of IL13 with total IgE: Evidence against an inverse association of atopy and diabetes. <i>Journal of Allergy and Clinical Immunology</i> , 2006, 117, 1306-1313.	1.5	61

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55	Evidence of Gene-Gene Interaction and Age-at-Diagnosis Effects in Type 1 Diabetes. <i>Diabetes</i> , 2012, 61, 3012-3017.	0.3	60
56	Evidence That HLA Class I and II Associations With Type 1 Diabetes, Autoantibodies to GAD and Autoantibodies to IA-2, Are Distinct. <i>Diabetes</i> , 2011, 60, 2635-2644.	0.3	57
57	Genetic and functional association of the immune signaling molecule 4-1BB (CD137/TNFRSF9) with type 1 diabetes. <i>Journal of Autoimmunity</i> , 2005, 25, 13-20.	3.0	54
58	Analysis of polymorphisms in 16 genes in type 1 diabetes that have been associated with other immune-mediated diseases. <i>BMC Medical Genetics</i> , 2006, 7, 20.	2.1	51
59	An Allele of IKZF1 (Ikaros) Conferring Susceptibility to Childhood Acute Lymphoblastic Leukemia Protects Against Type 1 Diabetes. <i>Diabetes</i> , 2011, 60, 1041-1044.	0.3	50
60	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475,000 Individuals. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	48
61	Mendelian randomization for studying the effects of perturbing drug targets. <i>Wellcome Open Research</i> , 2021, 6, 16.	0.9	48
62	A comparison of Cox and logistic regression for use in genome-wide association studies of cohort and case-cohort design. <i>European Journal of Human Genetics</i> , 2017, 25, 854-862.	1.4	45
63	Genetic association analyses of atopic illness and proinflammatory cytokine genes with type 1 diabetes. <i>Diabetes/Metabolism Research and Reviews</i> , 2011, 27, 838-843.	1.7	43
64	No Evidence of Association or Interaction between the IL4RA, IL4, and IL13 Genes in Type 1 Diabetes. <i>American Journal of Human Genetics</i> , 2005, 76, 517-521.	2.6	42
65	Analysis of the Type 2 Diabetes-Associated Single Nucleotide Polymorphisms in the Genes IRS1, KCNJ11, and PPARG2 in Type 1 Diabetes. <i>Diabetes</i> , 2004, 53, 870-873.	0.3	41
66	Mitochondrial DNA variants modulate N-formylmethionine, proteostasis and risk of late-onset human diseases. <i>Nature Medicine</i> , 2021, 27, 1564-1575.	15.2	40
67	Association of intercellular adhesion molecule-1 gene with type 1 diabetes. <i>Lancet, The</i> , 2003, 362, 1723-1724.	6.3	38
68	Sequencing-Based Genotyping and Association Analysis of the MICA and MICB Genes in Type 1 Diabetes. <i>Diabetes</i> , 2008, 57, 1753-1756.	0.3	35
69	Analysis of Polymorphisms of the Interleukin-18 Gene in Type 1 Diabetes and Hardy-Weinberg Equilibrium Testing. <i>Diabetes</i> , 2006, 55, 559-562.	0.3	34
70	Polymorphism in NOD2, Crohn's disease, and susceptibility to pulmonary tuberculosis. <i>FEMS Immunology and Medical Microbiology</i> , 2004, 41, 157-160.	2.7	33
71	Candidate gene association study of solute carrier family 11a members 1 (SLC11A1) and 2 (SLC11A2) genes in Alzheimer's disease. <i>Neuroscience Letters</i> , 2005, 374, 124-128.	1.0	32
72	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	2.4	31

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73	Plasma concentrations of soluble IL-2 receptor $\hat{\pm}$ (CD25) are increased in type 1 diabetes and associated with reduced C-peptide levels in young patients. <i>Diabetologia</i> , 2014, 57, 366-372.	2.9	30
74	Identification of a Structurally Distinct CD101 Molecule Encoded in the 950-kb Idd10 Region of NOD Mice. <i>Diabetes</i> , 2003, 52, 1551-1556.	0.3	27
75	The Bangladesh Risk of Acute Vascular Events (BRAVE) Study: objectives and design. <i>European Journal of Epidemiology</i> , 2015, 30, 577-587.	2.5	25
76	Evidence of association with type 1 diabetes in the SLC11A1 gene region. <i>BMC Medical Genetics</i> , 2011, 12, 59.	2.1	24
77	Lack of Association of the Ala45Thr Polymorphism and Other Common Variants of the NeuroD Gene With Type 1 Diabetes. <i>Diabetes</i> , 2004, 53, 1158-1161.	0.3	22
78	Genetic invalidation of Lp-PLA2 as a therapeutic target: Large-scale study of five functional Lp-PLA2-lowering alleles. <i>European Journal of Preventive Cardiology</i> , 2017, 24, 492-504.	0.8	22
79	HLA class II gene associations in African American Type 1 diabetes reveal a protective HLA-DRB1*03 haplotype. <i>Diabetic Medicine</i> , 2013, 30, 710-716.	1.2	21
80	Detection and correction of artefacts in estimation of rare copy number variants and analysis of rare deletions in type 1 diabetes. <i>Human Molecular Genetics</i> , 2015, 24, 1774-1790.	1.4	20
81	Comparison of population- and family-based methods for genetic association analysis in the presence of interacting loci. <i>Genetic Epidemiology</i> , 2005, 29, 51-67.	0.6	19
82	Genetic Evidence for Repurposing of GLP1R (Glucagon-Like Peptide-1 Receptor) Agonists to Prevent Heart Failure. <i>Journal of the American Heart Association</i> , 2021, 10, e020331.	1.6	13
83	NKG2D-RAE-1 Receptor-Ligand Variation Does Not Account for the NK Cell Defect in Nonobese Diabetic Mice. <i>Journal of Immunology</i> , 2008, 181, 7073-7080.	0.4	12
84	A hybrid qPCR/SNP array approach allows cost efficient assessment of KIR gene copy numbers in large samples. <i>BMC Genomics</i> , 2014, 15, 274.	1.2	12
85	Association Analysis of the Lymphocyte-Specific Protein Tyrosine Kinase (LCK) Gene in Type 1 Diabetes. <i>Diabetes</i> , 2004, 53, 2479-2482.	0.3	11
86	Leveraging human genetic data to investigate the cardiometabolic effects of glucose-dependent insulinotropic polypeptide signalling. <i>Diabetologia</i> , 2021, 64, 2773-2778.	2.9	7
87	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. <i>Nature Communications</i> , 2022, 13, 1222.	5.8	5