Joanna M M Howson

List of Publications by Year
in descending order

87 papers	19,903 citations	30047 54 h-index	40954 93 g-index
109 all docs	109 docs citations	109 times ranked	27684 citing authors

#	Article	IF	Citations
1	Association of the T-cell regulatory gene CTLA4 with susceptibility to autoimmune disease. Nature, 2003, 423, 506-511.	13.7	1,980
2	Robust associations of four new chromosome regions from genome-wide analyses of type 1 diabetes. Nature Genetics, 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. Nature Genetics, 2018, 50, 524-537.	9.4	1,124
4	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
5	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 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. Nature, 2010, 464, 713-720.	13.7	737
7	Shared and Distinct Genetic Variants in Type 1 Diabetes and Celiac Disease. New England Journal of Medicine, 2008, 359, 2767-2777.	13.9	654
8	Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391.	9.4	571
9	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
10	Population structure, differential bias and genomic control in a large-scale, case-control association study. Nature Genetics, 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. Nature, 2007, 450, 887-892.	13.7	493
12	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	9.4	492
13	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
14	Bayesian refinement of association signals for 14 loci in 3 common diseases. Nature Genetics, 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. Diabetes, 2004, 53, 3020-3023.	0.3	447
16	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438
17	Association ofLPAVariants With Risk of Coronary Disease and the Implications for Lipoprotein(a)-Lowering Therapies. JAMA Cardiology, 2018, 3, 619.	3.0	428
18	Coding Variation inANGPTL4,LPL,andSVEP1and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	13.9	427

#	Article	IF	Citations
19	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
20	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	13.5	353
21	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	9.4	328
22	A robust and efficient method for Mendelian randomization with hundreds of genetic variants. Nature Communications, 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. Nature Genetics, 2018, 50, 26-41.	9.4	286
24	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
25	Complete MHC Haplotype Sequencing for Common Disease Gene Mapping. Genome Research, 2004, 14, 1176-1187.	2.4	260
26	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 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. Nature Genetics, 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. PLoS Genetics, 2013, 9, e1003444.	1.5	234
29	Genome-Wide Association Analysis of Autoantibody Positivity in Type 1 Diabetes Cases. PLoS Genetics, 2011, 7, e1002216.	1.5	230
30	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. Nature Genetics, 2017, 49, 1450-1457.	9.4	218
31	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	1.2	214
32	A fast and efficient colocalization algorithm for identifying shared genetic risk factors across multiple traits. Nature Communications, 2021, 12, 764.	5.8	195
33	Interleukinâ€10, Polymorphism inSLC11A1(formerlyNRAMP1), and Susceptibility to Tuberculosis. Journal of Infectious Diseases, 2002, 186, 1808-1814.	1.9	139
34	Regression Mapping of Association between the Human Leukocyte Antigen Region and Graves Disease. American Journal of Human Genetics, 2005, 76, 157-163.	2.6	134
35	Genomic risk score offers predictive performance comparable to clinical risk factors for ischaemic stroke. Nature Communications, 2019, 10, 5819.	5.8	124
36	Genetic Analysis of Adult-Onset Autoimmune Diabetes. Diabetes, 2011, 60, 2645-2653.	0.3	115

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

#	Article	IF	Citations
55	Evidence of Gene-Gene Interaction and Age-at-Diagnosis Effects in Type 1 Diabetes. Diabetes, 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. Diabetes, 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. Journal of Autoimmunity, 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. BMC Medical Genetics, 2006, 7, 20.	2.1	51
59	An Allele ofIKZF1(Ikaros) Conferring Susceptibility to Childhood Acute Lymphoblastic Leukemia Protects Against Type 1 Diabetes. Diabetes, 2011, 60, 1041-1044.	0.3	50
60	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
61	Mendelian randomization for studying the effects of perturbing drug targets. Wellcome Open Research, 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. European Journal of Human Genetics, 2017, 25, 854-862.	1.4	45
63	Genetic association analyses of atopic illness and proinflammatory cytokine genes with type 1 diabetes. Diabetes/Metabolism Research and Reviews, 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. American Journal of Human Genetics, 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. Diabetes, 2004, 53, 870-873.	0.3	41
66	Mitochondrial DNA variants modulate N-formylmethionine, proteostasis and risk of late-onset human diseases. Nature Medicine, 2021, 27, 1564-1575.	15.2	40
67	Association of intercellular adhesion molecule-1 gene with type 1 diabetes. Lancet, The, 2003, 362, 1723-1724.	6.3	38
68	Sequencing-Based Genotyping and Association Analysis of the MICA and MICB Genes in Type 1 Diabetes. Diabetes, 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. Diabetes, 2006, 55, 559-562.	0.3	34
70	Polymorphism in NOD2, Crohn's disease, and susceptibility to pulmonary tuberculosis. FEMS Immunology and Medical Microbiology, 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. Neuroscience Letters, 2005, 374, 124-128.	1.0	32
72	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31

#	Article	IF	Citations
73	Plasma concentrations of soluble IL-2 receptor Î± (CD25) are increased in type 1 diabetes and associated with reduced C-peptide levels in young patients. Diabetologia, 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. Diabetes, 2003, 52, 1551-1556.	0.3	27
75	The Bangladesh Risk of Acute Vascular Events (BRAVE) Study: objectives and design. European Journal of Epidemiology, 2015, 30, 577-587.	2.5	25
76	Evidence of association with type 1 diabetes in the SLC11A1 gene region. BMC Medical Genetics, 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. Diabetes, 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. European Journal of Preventive Cardiology, 2017, 24, 492-504.	0.8	22
79	HLA classÂII gene associations in African American TypeÂ1 diabetes reveal a protective HLAâ€ÐRB1*03 haplotype. Diabetic Medicine, 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. Human Molecular Genetics, 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. Genetic Epidemiology, 2005, 29, 51-67.	0.6	19
82	Genetic Evidence for Repurposing of GLP1R (Glucagonâ€Like Peptideâ€1 Receptor) Agonists to Prevent Heart Failure. Journal of the American Heart Association, 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. Journal of Immunology, 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. BMC Genomics, 2014, 15, 274.	1.2	12
85	Association Analysis of the Lymphocyte-Specific Protein Tyrosine Kinase (LCK) Gene in Type 1 Diabetes. Diabetes, 2004, 53, 2479-2482.	0.3	11
86	Leveraging human genetic data to investigate the cardiometabolic effects of glucose-dependent insulinotropic polypeptide signalling. Diabetologia, 2021, 64, 2773-2778.	2.9	7
87	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. Nature Communications, 2022, 13, 1222.	5.8	5