Joanna M M Howson

List of Publications by Year in Descending Order

93 papers	13,971 citations	48 h-index	109 g-index
109 ext. papers	17,393 ext. citations	18.8 avg, IF	5.04 L-index

#	Paper	IF	Citations
93	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus.. *Nature Communications*, **2022**, 13, 1222	17.4	0
92	An atlas of mitochondrial DNA genotype-phenotype associations in the UK Biobank. *Nature Genetics*, **2021**, 53, 982-993	36.3	12
91	Mendelian randomization for studying the effects of perturbing drug targets. *Wellcome Open Research*, **2021**, 6, 16	4.8	15
90	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. *Communications Biology*, **2021**, 4, 156	6.7	11
89	A fast and efficient colocalization algorithm for identifying shared genetic risk factors across multiple traits. *Nature Communications*, **2021**, 12, 764	17.4	27
88	Mendelian randomization for studying the effects of perturbing drug targets. *Wellcome Open Research*, **2021**, 6, 16	4.8	11
87	Genetic Evidence for Repurposing of GLP1R (Glucagon-Like Peptide-1 Receptor) Agonists to Prevent Heart Failure. *Journal of the American Heart Association*, **2021**, 10, e020331	6	1
86	Mitochondrial DNA variants modulate N-formylmethionine, proteostasis and risk of late-onset human diseases. *Nature Medicine*, **2021**, 27, 1564-1575	50.5	4
85	Leveraging human genetic data to investigate the cardiometabolic effects of glucose-dependent insulinotropic polypeptide signalling. *Diabetologia*, **2021**, 64, 2773-2778	10.3	0
84	Genome-wide association study of MRI markers of cerebral small vessel disease in 42,310 participants. *Nature Communications*, **2020**, 11, 2175	17.4	21
83	A robust and efficient method for Mendelian randomization with hundreds of genetic variants. *Nature Communications*, **2020**, 11, 376	17.4	99
82	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. *Nature Genetics*, **2020**, 52, 1314-1332	36.3	26
81	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. *Cell*, **2020**, 182, 1198-1213.e14	56.2	88
80	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. *Molecular Psychiatry*, **2020**, 25, 2392-2409	15.1	45
79	Assessing the causal association of glycine with risk of cardio-metabolic diseases. *Nature Communications*, **2019**, 10, 1060	17.4	38
78	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
77	Genomic risk score offers predictive performance comparable to clinical risk factors for ischaemic stroke. *Nature Communications*, **2019**, 10, 5819	17.4	54

76	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. *Nature Genetics*, **2019**, 51, 51-62	36.3	152
75	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
74	Association of LPA Variants With Risk of Coronary Disease and the Implications for Lipoprotein(a)-Lowering Therapies: A Mendelian Randomization Analysis. *JAMA Cardiology*, **2018**, 3, 619-627	16.2	235
73	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
72	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nature Genetics*, **2018**, 50, 524-537	36.3	536
71	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
70	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. *Nature Genetics*, **2017**, 49, 403-415	36.3	313
69	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
68	Genetic invalidation of Lp-PLA as a therapeutic target: Large-scale study of five functional Lp-PLA-lowering alleles. *European Journal of Preventive Cardiology*, **2017**, 24, 492-504	3.9	16
67	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. *Journal of the American College of Cardiology*, **2017**, 69, 823-836	15.1	146
66	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	5.3	23
65	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. *Nature Genetics*, **2017**, 49, 1113-1119	36.3	184
64	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
63	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. *Circulation: Cardiovascular Genetics*, **2017**, 10,		33
62	Association analyses based on false discovery rate implicate new loci for coronary artery disease. *Nature Genetics*, **2017**, 49, 1385-1391	36.3	361
61	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
60	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. *Nature Genetics*, **2017**, 49, 1450-1457	36.3	136
59	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181

58	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. *Science Translational Medicine*, **2016**, 8, 341ra76	17.5	77
57	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. *Science*, **2016**, 351, 1166-71	33.3	325
56	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
55	Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. *New England Journal of Medicine*, **2016**, 374, 1134-44	59.2	325
54	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	36.3	154
53	The Bangladesh Risk of Acute Vascular Events (BRAVE) Study: objectives and design. *European Journal of Epidemiology*, **2015**, 30, 577-87	12.1	16
52	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, 1774-90	5.6	11
51	A hybrid qPCR/SNP array approach allows cost efficient assessment of KIR gene copy numbers in large samples. *BMC Genomics*, **2014**, 15, 274	4.5	12
50	Plasma concentrations of soluble IL-2 receptor [(CD25) are increased in type 1 diabetes and associated with reduced C-peptide levels in young patients. *Diabetologia*, **2014**, 57, 366-72	10.3	21
49	Functional IL6R 358Ala allele impairs classical IL-6 receptor signaling and influences risk of diverse inflammatory diseases. *PLoS Genetics*, **2013**, 9, e1003444	6	170
48	HLA class II gene associations in African American type 1 diabetes reveal a protective HLA-DRB1*03 haplotype. *Diabetic Medicine*, **2013**, 30, 710-6	3.5	19
47	Evidence of gene-gene interaction and age-at-diagnosis effects in type 1 diabetes. *Diabetes*, **2012**, 61, 3012-7	0.9	49
46	Long-range DNA looping and gene expression analyses identify DEXI as an autoimmune disease candidate gene. *Human Molecular Genetics*, **2012**, 21, 322-33	5.6	91
45	Bayesian refinement of association signals for 14 loci in 3 common diseases. *Nature Genetics*, **2012**, 44, 1294-301	36.3	347
44	FUT2 nonsecretor status links type 1 diabetes susceptibility and resistance to infection. *Diabetes*, **2011**, 60, 3081-4	0.9	92
43	Evidence of association with type 1 diabetes in the SLC11A1 gene region. *BMC Medical Genetics*, **2011**, 12, 59	2.1	18
42	Genetic association analyses of atopic illness and proinflammatory cytokine genes with type 1 diabetes. *Diabetes/Metabolism Research and Reviews*, **2011**, 27, 838-43	7.5	35
41	Genetic analysis of adult-onset autoimmune diabetes. *Diabetes*, **2011**, 60, 2645-53	0.9	92

40	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, 2635-44	0.9	48
39	An allele of IKZF1 (Ikaros) conferring susceptibility to childhood acute lymphoblastic leukemia protects against type 1 diabetes. *Diabetes*, **2011**, 60, 1041-4	0.9	41
38	Genome-wide association analysis of autoantibody positivity in type 1 diabetes cases. *PLoS Genetics* , **2011**, 7, e1002216	6	195
37	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. *Nature*, **2010**, 464, 713-20	50.4	639
36	Experimental aspects of copy number variant assays at CCL3L1. *Nature Medicine*, **2009**, 15, 1115-7	50.5	63
35	Shared and distinct genetic variants in type 1 diabetes and celiac disease. *New England Journal of Medicine*, **2008**, 359, 2767-77	59.2	546
34	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, 1730-7	0.9	69
33	Sequencing-based genotyping and association analysis of the MICA and MICB genes in type 1 diabetes. *Diabetes*, **2008**, 57, 1753-6	0.9	29
32	NKG2D-RAE-1 receptor-ligand variation does not account for the NK cell defect in nonobese diabetic mice. *Journal of Immunology*, **2008**, 181, 7073-80	5.3	12
31	Robust associations of four new chromosome regions from genome-wide analyses of type 1 diabetes. *Nature Genetics*, **2007**, 39, 857-64	36.3	1159
30	Localization of type 1 diabetes susceptibility to the MHC class I genes HLA-B and HLA-A. *Nature*, **2007**, 450, 887-92	50.4	421
29	A novel and major association of HLA-C in GravesQdisease that eclipses the classical HLA-DRB1 effect. *Human Molecular Genetics*, **2007**, 16, 2149-53	5.6	72
28	Analysis of polymorphisms of the interleukin-18 gene in type 1 diabetes and Hardy-Weinberg equilibrium testing. *Diabetes*, **2006**, 55, 559-62	0.9	28
27	Association of IL13 with total IgE: evidence against an inverse association of atopy and diabetes. *Journal of Allergy and Clinical Immunology*, **2006**, 117, 1306-13	11.5	57
26	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	42
25	Regression mapping of association between the human leukocyte antigen region and Graves disease. *American Journal of Human Genetics*, **2005**, 76, 157-63	11	121
24	No evidence of association or interaction between the IL4RA, IL4, and IL13 genes in type 1 diabetes. *American Journal of Human Genetics*, **2005**, 76, 517-21	11	37
23	Candidate gene association study of solute carrier family 11a members 1 (SLC11A1) and 2 (SLC11A2) genes in AlzheimerQ disease. *Neuroscience Letters*, **2005**, 374, 124-8	3.3	26

22	Genetic and functional association of the immune signaling molecule 4-1BB (CD137/TNFRSF9) with type 1 diabetes. *Journal of Autoimmunity*, **2005**, 25, 13-20	15.5	50
21	Assessing the validity of the association between the SUMO4 M55V variant and risk of type 1 diabetes. *Nature Genetics*, **2005**, 37, 110-1; author reply 112-3	36.3	56
20	Population structure, differential bias and genomic control in a large-scale, case-control association study. *Nature Genetics*, **2005**, 37, 1243-6	36.3	458
19	Comparison of population- and family-based methods for genetic association analysis in the presence of interacting loci. *Genetic Epidemiology*, **2005**, 29, 51-67	2.6	19
18	Complete MHC haplotype sequencing for common disease gene mapping. *Genome Research*, **2004**, 14, 1176-87	9.7	235
17	Analysis of the vitamin D receptor gene sequence variants in type 1 diabetes. *Diabetes*, **2004**, 53, 2709-12	2.9	65
16	Lack of association of the Ala(45)Thr polymorphism and other common variants of the NeuroD gene with type 1 diabetes. *Diabetes*, **2004**, 53, 1158-61	0.9	19
15	Association analysis of the lymphocyte-specific protein tyrosine kinase (LCK) gene in type 1 diabetes. *Diabetes*, **2004**, 53, 2479-82	0.9	8
14	Analysis of the type 2 diabetes-associated single nucleotide polymorphisms in the genes IRS1, KCNJ11, and PPARG2 in type 1 diabetes. *Diabetes*, **2004**, 53, 870-3	0.9	34
13	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, 3020-3	0.9	401
12	Polymorphism in NOD2, Crohn's disease, and susceptibility to pulmonary tuberculosis. *FEMS Immunology and Medical Microbiology*, **2004**, 41, 157-60		32
11	Association of the T-cell regulatory gene CTLA4 with susceptibility to autoimmune disease. *Nature*, **2003**, 423, 506-11	50.4	1774
10	Association of intercellular adhesion molecule-1 gene with type 1 diabetes. *Lancet, The*, **2003**, 362, 1723-4	4.0	37
9	Identification of a structurally distinct CD101 molecule encoded in the 950-kb Idd10 region of NOD mice. *Diabetes*, **2003**, 52, 1551-6	0.9	25
8	Haplotype structure, LD blocks, and uneven recombination within the LRP5 gene. *Genome Research*, **2003**, 13, 845-55	9.7	54
7	Interleukin-10, polymorphism in SLC11A1 (formerly NRAMP1), and susceptibility to tuberculosis. *Journal of Infectious Diseases*, **2002**, 186, 1808-14	7	126
6	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
5	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4

List of Publications

4	The Polygenic and Monogenic Basis of Blood Traits and Diseases	3
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2	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution	1
1	A fast and efficient colocalization algorithm for identifying shared genetic risk factors across multiple traits	13