Heather J Cordell

List of Publications by Citations

235 papers	18,330 citations	63 h-index	133 g-index
263 ext. papers	21,165 ext. citations	8 avg, IF	6.5 L-index

#	Paper	IF	Citations
235	Association of the T-cell regulatory gene CTLA4 with susceptibility to autoimmune disease. *Nature*, **2003**, 423, 506-11	50.4	1774
234	A genome-wide search for human type 1 diabetes susceptibility genes. *Nature*, **1994**, 371, 130-6	50.4	1175
233	Haplotype tagging for the identification of common disease genes. *Nature Genetics*, **2001**, 29, 233-7	36.3	1014
232	Detecting gene-gene interactions that underlie human diseases. *Nature Reviews Genetics*, **2009**, 10, 392-404	36.1	990
231	HLA-B*5701 genotype is a major determinant of drug-induced liver injury due to flucloxacillin. *Nature Genetics*, **2009**, 41, 816-9	36.3	818
230	Epistasis: what it means, what it doesn't mean, and statistical methods to detect it in humans. *Human Molecular Genetics*, **2002**, 11, 2463-8	5.6	725
229	Genome-wide association study identifies 12 new susceptibility loci for primary biliary cirrhosis. *Nature Genetics*, **2011**, 43, 329-32	36.3	396
228	Genetic association studies. *Lancet, The*, **2005**, 366, 1121-31	40	394
227	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
226	A unified stepwise regression procedure for evaluating the relative effects of polymorphisms within a gene using case/control or family data: application to HLA in type 1 diabetes. *American Journal of Human Genetics*, **2002**, 70, 124-41	11	360
225	Loss-of-function variants in the filaggrin gene are a significant risk factor for peanut allergy. *Journal of Allergy and Clinical Immunology*, **2011**, 127, 661-7	11.5	342
224	Meta-analysis of filaggrin polymorphisms in eczema and asthma: robust risk factors in atopic disease. *Journal of Allergy and Clinical Immunology*, **2009**, 123, 1361-70.e7	11.5	317
223	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
222	Chromosome-specific microsatellite sets for fluorescence-based, semi-automated genome mapping. *Nature Genetics*, **1994**, 7, 390-5	36.3	298
221	Polygenic control of autoimmune diabetes in nonobese diabetic mice. *Nature Genetics*, **1993**, 4, 404-9	36.3	286
220	Research capacity. Enabling the genomic revolution in Africa. *Science*, **2014**, 344, 1346-8	33.3	256
219	Dense fine-mapping study identifies new susceptibility loci for primary biliary cirrhosis. *Nature Genetics*, **2012**, 44, 1137-41	36.3	214

218	Contribution of global rare copy-number variants to the risk of sporadic congenital heart disease. *American Journal of Human Genetics*, **2012**, 91, 489-501	11	213
217	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
216	Parameters for reliable results in genetic association studies in common disease. *Nature Genetics*, **2002**, 30, 149-50	36.3	198
215	Case/pseudocontrol analysis in genetic association studies: A unified framework for detection of genotype and haplotype associations, gene-gene and gene-environment interactions, and parent-of-origin effects. *Genetic Epidemiology*, **2004**, 26, 167-85	2.6	193
214	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. *Human Molecular Genetics*, **2014**, 23, 4420-32	5.6	188
213	International genome-wide meta-analysis identifies new primary biliary cirrhosis risk loci and targetable pathogenic pathways. *Nature Communications*, **2015**, 6, 8019	17.4	185
212	The UK-PBC risk scores: Derivation and validation of a scoring system for long-term prediction of end-stage liver disease in primary biliary cholangitis. *Hepatology*, **2016**, 63, 930-50	11.2	184
211	Remapping the insulin gene/IDDM2 locus in type 1 diabetes. *Diabetes*, **2004**, 53, 1884-9	0.9	180
210	Absolute risk of childhood-onset type 1 diabetes defined by human leukocyte antigen class II genotype: a population-based study in the United Kingdom. *Journal of Clinical Endocrinology and Metabolism*, **2004**, 89, 4037-43	5.6	162
209	Intragenic copy number variation within filaggrin contributes to the risk of atopic dermatitis with a dose-dependent effect. *Journal of Investigative Dermatology*, **2012**, 132, 98-104	4.3	148
208	Genome-wide linkage analysis for human longevity: Genetics of Healthy Aging Study. *Aging Cell*, **2013**, 12, 184-93	9.9	140
207	SNP selection in genome-wide and candidate gene studies via penalized logistic regression. *Genetic Epidemiology*, **2010**, 34, 879-91	2.6	133
206	Filaggrin null mutations and childhood atopic eczema: a population-based case-control study. *Journal of Allergy and Clinical Immunology*, **2008**, 121, 940-46.e3	11.5	121
205	Regression mapping of association between the human leukocyte antigen region and Graves disease. *American Journal of Human Genetics*, **2005**, 76, 157-63	11	121
204	Evidence for a cluster of genes on chromosome 17q11-q21 controlling susceptibility to tuberculosis and leprosy in Brazilians. *Genes and Immunity*, **2004**, 5, 46-57	4.4	121
203	A genome-wide scan for loci linked to forearm bone mineral density. *Human Genetics*, **1999**, 104, 226-33	6.3	121
202	Genome-wide comparative analysis of atopic dermatitis and psoriasis gives insight into opposing genetic mechanisms. *American Journal of Human Genetics*, **2015**, 96, 104-20	11	113
201	Genome-wide association study of non-alcoholic fatty liver and steatohepatitis in a histologically characterised cohort. *Journal of Hepatology*, **2020**, 73, 505-515	13.4	113

200	The interleukin 1 gene cluster contains a major susceptibility locus for ankylosing spondylitis. *American Journal of Human Genetics*, **2004**, 75, 587-95	11	109
199	Tmem79/Matt is the matted mouse gene and is a predisposing gene for atopic dermatitis in human subjects. *Journal of Allergy and Clinical Immunology*, **2013**, 132, 1121-9	11.5	108
198	A male-female bias in type 1 diabetes and linkage to chromosome Xp in MHC HLA-DR3-positive patients. *Nature Genetics*, **1998**, 19, 301-2	36.3	107
197	Distinct genetic loci control development of benign and malignant skin tumours in mice. *Nature Genetics*, **1995**, 10, 424-9	36.3	107
196	A meta-analysis of genome-wide association studies identifies multiple longevity genes. *Nature Communications*, **2019**, 10, 3669	17.4	102
195	Genomic polymorphism at the interferon-induced helicase (IFIH1) locus contributes to Graves' disease susceptibility. *Journal of Clinical Endocrinology and Metabolism*, **2007**, 92, 3338-41	5.6	101
194	Wide spectrum of filaggrin-null mutations in atopic dermatitis highlights differences between Singaporean Chinese and European populations. *British Journal of Dermatology*, **2011**, 165, 106-14	4	99
193	Genome-wide association study of multiple congenital heart disease phenotypes identifies a susceptibility locus for atrial septal defect at chromosome 4p16. *Nature Genetics*, **2013**, 45, 822-4	36.3	91
192	SLC11A1 (formerly NRAMP1) and susceptibility to visceral leishmaniasis in The Sudan. *European Journal of Human Genetics*, **2004**, 12, 66-74	5.3	89
191	Multilocus linkage tests based on affected relative pairs. *American Journal of Human Genetics*, **2000**, 66, 1273-86	11	89
190	Genetic and epigenetic factors at COL2A1 and ABCA4 influence clinical outcome in congenital toxoplasmosis. *PLoS ONE*, **2008**, 3, e2285	3.7	86
189	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. *Hypertension*, **2017**,	8.5	85
188	Phenotype-specific effect of chromosome 1q21.1 rearrangements and GJA5 duplications in 2436 congenital heart disease patients and 6760 controls. *Human Molecular Genetics*, **2012**, 21, 1513-20	5.6	83
187	Prevalent and low-frequency null mutations in the filaggrin gene are associated with early-onset and persistent atopic eczema. *Journal of Investigative Dermatology*, **2008**, 128, 1591-4	4.3	82
186	Genome-wide scans for leprosy and tuberculosis susceptibility genes in Brazilians. *Genes and Immunity*, **2004**, 5, 63-7	4.4	82
185	Multifactorial inheritance in type 1 diabetes. *Trends in Genetics*, **1995**, 11, 499-504	8.5	79
184	Filaggrin haploinsufficiency is highly penetrant and is associated with increased severity of eczema: further delineation of the skin phenotype in a prospective epidemiological study of 792 school children. *British Journal of Dermatology*, **2009**, 161, 884-9	4	77
183	Common variants in the HLA-DRB1-HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. *Nature Genetics*, **2013**, 45, 208-13	36.3	76

182	Comparison of methods to account for relatedness in genome-wide association studies with family-based data. *PLoS Genetics*, **2014**, 10, e1004445	6	75
181	Determining the population frequency of the CFHR3/CFHR1 deletion at 1q32. *PLoS ONE*, **2013**, 8, e60353	3.7	74
180	Genetic susceptibility to visceral leishmaniasis in The Sudan: linkage and association with IL4 and IFNGR1. *Genes and Immunity*, **2003**, 4, 351-5	4.4	71
179	Genome-wide association study identifies loci on 12q24 and 13q32 associated with tetralogy of Fallot. *Human Molecular Genetics*, **2013**, 22, 1473-81	5.6	68
178	Genomic DNA pooling for whole-genome association scans in complex disease: empirical demonstration of efficacy in rheumatoid arthritis. *Genes and Immunity*, **2007**, 8, 57-68	4.4	68
177	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. *Journal of Clinical Investigation*, **2015**, 125, 1739-51	15.9	67
176	Clinical and pharmacogenetic influences on response to hydroxychloroquine in discoid lupus erythematosus: a retrospective cohort study. *Journal of Investigative Dermatology*, **2011**, 131, 1981-6	4.3	66
175	Improved statistics for genome-wide interaction analysis. *PLoS Genetics*, **2012**, 8, e1002625	6	65
174	Common polymorphism in H19 associated with birthweight and cord blood IGF-II levels in humans. *BMC Genetics*, **2005**, 6, 22	2.6	65
173	Programmed death ligand 1 (PD-L1) gene variants contribute to autoimmune Addison's disease and Graves' disease susceptibility. *Journal of Clinical Endocrinology and Metabolism*, **2009**, 94, 5139-45	5.6	62
172	Whole Exome Sequencing Reveals the Major Genetic Contributors to Nonsyndromic Tetralogy of Fallot. *Circulation Research*, **2019**, 124, 553-563	15.7	62
171	Suggestive evidence for association of human chromosome 18q12-q21 and its orthologue on rat and mouse chromosome 18 with several autoimmune diseases. *Diabetes*, **2001**, 50, 184-94	0.9	61
170	Pretreatment prediction of response to ursodeoxycholic acid in primary biliary cholangitis: development and validation of the UDCA Response Score. *The Lancet Gastroenterology and Hepatology*, **2018**, 3, 626-634	18.8	60
169	Investigation of maternal effects, maternal-fetal interactions and parent-of-origin effects (imprinting), using mothers and their offspring. *Genetic Epidemiology*, **2011**, 35, 19-45	2.6	59
168	Association between anti-tumour necrosis factor treatment response and genetic variants within the TLR and NF{kappa}B signalling pathways. *Annals of the Rheumatic Diseases*, **2010**, 69, 1315-20	2.4	59
167	Maternal-fetal interactions and birth order influence insulin variable number of tandem repeats allele class associations with head size at birth and childhood weight gain. *Diabetes*, **2004**, 53, 1128-33	0.9	56
166	The HLA-DPB1--associated component of the IDDM1 and its relationship to the major loci HLA-DQB1, -DQA1, and -DRB1. *Diabetes*, **2001**, 50, 1200-5	0.9	55
165	Phenotypic heterogeneity in m.3243A>G mitochondrial disease: The role of nuclear factors. *Annals of Clinical and Translational Neurology*, **2018**, 5, 333-345	5.3	54

164	Genetic variants associated with myocardial infarction risk factors in over 8000 individuals from five ethnic groups: The INTERHEART Genetics Study. *Circulation: Cardiovascular Genetics*, **2009**, 2, 16-25		54
163	Y chromosome lineage- and village-specific genes on chromosomes 1p22 and 6q27 control visceral leishmaniasis in Sudan. *PLoS Genetics*, **2007**, 3, e71	6	54
162	Haplotype structure, LD blocks, and uneven recombination within the LRP5 gene. *Genome Research*, **2003**, 13, 845-55	9.7	54
161	Statistical modeling of interlocus interactions in a complex disease: rejection of the multiplicative model of epistasis in type 1 diabetes. *Genetics*, **2001**, 158, 357-67	4	54
160	The impact of common gene variants on the response of biomarkers of cardiovascular disease (CVD) risk to increased fish oil fatty acids intakes. *Annual Review of Nutrition*, **2011**, 31, 203-34	9.9	53
159	Protein-altering and regulatory genetic variants near GATA4 implicated in bicuspid aortic valve. *Nature Communications*, **2017**, 8, 15481	17.4	52
158	Whole-genome linkage and association scan in primary, nonsyndromic vesicoureteric reflux. *Journal of the American Society of Nephrology: JASN*, **2010**, 21, 113-23	12.7	51
157	Chromosome 11q13.5 variant associated with childhood eczema: an effect supplementary to filaggrin mutations. *Journal of Allergy and Clinical Immunology*, **2010**, 125, 170-4.e1-2	11.5	51
156	Transcriptomic profiling across the nonalcoholic fatty liver disease spectrum reveals gene signatures for steatohepatitis and fibrosis. *Science Translational Medicine*, **2020**, 12,	17.5	51
155	Properties of case/pseudocontrol analysis for genetic association studies: Effects of recombination, ascertainment, and multiple affected offspring. *Genetic Epidemiology*, **2004**, 26, 186-205	2.6	50
154	Ascertainment bias in the estimation of sibling genetic risk parameters. *Genetic Epidemiology*, **2000**, 18, 217-35	2.6	48
153	Systematic survey of variants in TBX1 in non-syndromic tetralogy of Fallot identifies a novel 57 base pair deletion that reduces transcriptional activity but finds no evidence for association with common variants. *Heart*, **2010**, 96, 1651-5	5.1	47
152	Intercellular adhesion molecule-1 K469E polymorphism: study of association with multiple sclerosis. *Human Immunology*, **2003**, 64, 345-9	2.3	46
151	Estimation and testing of genotype and haplotype effects in case-control studies: comparison of weighted regression and multiple imputation procedures. *Genetic Epidemiology*, **2006**, 30, 259-75	2.6	45
150	The tryptophan 620 allele of the lymphoid tyrosine phosphatase (PTPN22) gene predisposes to autoimmune Addison's disease. *Clinical Endocrinology*, **2009**, 70, 358-62	3.4	41
149	Genes at human chromosome 5q31.1 regulate delayed-type hypersensitivity responses associated with Leishmania chagasi infection. *Genes and Immunity*, **2007**, 8, 539-51	4.4	41
148	Linkage analysis of candidate genes and gene-gene interactions in chinese hypertensive sib pairs. *Hypertension*, **1999**, 33, 1332-7	8.5	40
147	Linkage and association mapping of the LRP5 locus on chromosome 11q13 in type 1 diabetes. *Human Genetics*, **2003**, 113, 99-105	6.3	38

146	PREMIM and EMIM: tools for estimation of maternal, imprinting and interaction effects using multinomial modelling. *BMC Bioinformatics*, **2012**, 13, 149	3.6	37
145	Fine mapping and replication of genetic risk loci in primary sclerosing cholangitis. *Scandinavian Journal of Gastroenterology*, **2012**, 47, 820-6	2.4	36
144	Methylation quantitative trait locus analysis of osteoarthritis links epigenetics with genetic risk. *Human Molecular Genetics*, **2015**, 24, 7432-44	5.6	35
143	Common genetic variants in complement genes other than CFH, CD46 and the CFHRs are not associated with aHUS. *Molecular Immunology*, **2012**, 49, 640-8	4.3	33
142	Bias toward the null hypothesis in model-free linkage analysis is highly dependent on the test statistic used. *American Journal of Human Genetics*, **2004**, 74, 1294-302	11	32
141	Genome-wide association study of response to tumour necrosis factor inhibitor therapy in rheumatoid arthritis. *Pharmacogenomics Journal*, **2018**, 18, 657-664	3.5	32
140	Exome sequencing in dementia with Lewy bodies. *Translational Psychiatry*, **2016**, 6, e728	8.6	30
139	An extension of the Maximum Lod Score method to X-linked loci. *Annals of Human Genetics*, **1995**, 59, 435-49	2.2	29
138	Statistical methods for genome-wide association studies. *Seminars in Cancer Biology*, **2019**, 55, 53-60	12.7	29
137	CTLA-4 as a genetic determinant in autoimmune Addison's disease. *Genes and Immunity*, **2015**, 16, 430-6	4.4	27
136	DNA methylation abnormalities at gene promoters are extensive and variable in the elderly and phenocopy cancer cells. *FASEB Journal*, **2014**, 28, 3261-72	0.9	26
135	Association between C677T polymorphism of methylene tetrahydrofolate reductase and congenital heart disease: meta-analysis of 7697 cases and 13,125 controls. *Circulation: Cardiovascular Genetics*, **2013**, 6, 347-53		26
134	The heritability of G2 chromosomal radiosensitivity and its association with cancer in Danish cancer survivors and their offspring. *International Journal of Radiation Biology*, **2010**, 86, 986-95	2.9	26
133	CD4+ and B Lymphocyte Expression Quantitative Traits at Rheumatoid Arthritis Risk Loci in Patients With Untreated Early Arthritis: Implications for Causal Gene Identification. *Arthritis and Rheumatology*, **2018**, 70, 361-370	9.5	26
132	Maternal filaggrin mutations increase the risk of atopic dermatitis in children: an effect independent of mutation inheritance. *PLoS Genetics*, **2015**, 11, e1005076	6	25
131	Urinary tract effects of HPSE2 mutations. *Journal of the American Society of Nephrology: JASN*, **2015**, 26, 797-804	12.7	25
130	Association of autoimmune Addison's disease with alleles of STAT4 and GATA3 in European cohorts. *PLoS ONE*, **2014**, 9, e88991	3.7	25
129	A common variant in the PTPN11 gene contributes to the risk of tetralogy of Fallot. *Circulation: Cardiovascular Genetics*, **2012**, 5, 287-92		25

128	Explorative two-locus linkage analysis suggests a multiplicative interaction between the 7q32 and 16p13 myoclonic seizures-related photosensitivity loci. *Genetic Epidemiology*, **2007**, 31, 42-50	2.6	25
127	Genome-wide association study of response to methotrexate in early rheumatoid arthritis patients. *Pharmacogenomics Journal*, **2018**, 18, 528-538	3.5	25
126	A genome-wide search for type 2 diabetes susceptibility genes in an extended Arab family. *Annals of Human Genetics*, **2013**, 77, 488-503	2.2	24
125	Heterogeneity in the magnitude of the insulin gene effect on HLA risk in type 1 diabetes. *Diabetes*, **2004**, 53, 3286-91	0.9	24
124	Dealing with missing data in family-based association studies: a multiple imputation approach. *Human Heredity*, **2007**, 63, 229-38	1.1	23
123	First genome-wide association study in an Australian aboriginal population provides insights into genetic risk factors for body mass index and type 2 diabetes. *PLoS ONE*, **2015**, 10, e0119333	3.7	23
122	Brief report: genetics of alcoholic cirrhosis-GenomALC multinational study. *Alcoholism: Clinical and Experimental Research*, **2015**, 39, 836-42	3.7	22
121	Association between aldosterone production and variation in the 11beta-hydroxylase (CYP11B1) gene. *Journal of Clinical Endocrinology and Metabolism*, **2006**, 91, 5051-6	5.6	22
120	Gamma regression improves Haseman-Elston and variance components linkage analysis for sib-pairs. *Genetic Epidemiology*, **2004**, 26, 97-107	2.6	21
119	Factors determining penetrance in familial atypical haemolytic uraemic syndrome. *Journal of Medical Genetics*, **2014**, 51, 756-64	5.8	20
118	Genetic information and the prediction of incident type 2 diabetes in a high-risk multiethnic population: the EpiDREAM genetic study. *Diabetes Care*, **2013**, 36, 2836-42	14.6	20
117	Speed-bumps ahead for the genetics of later-life diseases. *Trends in Genetics*, **2011**, 27, 387-8	8.5	20
116	Association analysis identifies new risk loci for congenital heart disease in Chinese populations. *Nature Communications*, **2015**, 6, 8082	17.4	19
115	Comparison of methods for transcriptome imputation through application to two common complex diseases. *European Journal of Human Genetics*, **2018**, 26, 1658-1667	5.3	19
114	Association mapping of complex diseases in linked regions: estimation of genetic effects and feasibility of testing rare variants. *Genetic Epidemiology*, **2003**, 24, 36-43	2.6	19
113	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
112	Diagnostic accuracy of elastography and magnetic resonance imaging in patients with NAFLD: A systematic review and meta-analysis. *Journal of Hepatology*, **2021**, 75, 770-785	13.4	19
111	A genome-wide association study of congenital cardiovascular left-sided lesions shows association with a locus on chromosome 20. *Human Molecular Genetics*, **2016**, 25, 2331-2341	5.6	18

110	Host genetic and epigenetic factors in toxoplasmosis. *Memorias Do Instituto Oswaldo Cruz*, **2009**, 104, 162-9	2.6	18
109	Genome-wide Association Study and Meta-analysis on Alcohol-Associated Liver Cirrhosis Identifies Genetic Risk Factors. *Hepatology*, **2021**, 73, 1920-1931	11.2	18
108	A new genome scan for primary nonsyndromic vesicoureteric reflux emphasizes high genetic heterogeneity and shows linkage and association with various genes already implicated in urinary tract development. *Molecular Genetics & Genomic Medicine*, **2014**, 2, 7-29	2.3	17
107	Estimation and testing of gene-environment interactions in family-based association studies. *Genomics*, **2009**, 93, 5-9	4.3	17
106	Adaptation of the extended transmission/disequilibrium test to distinguish disease associations of multiple loci: the Conditional Extended Transmission/Disequilibrium Test. *Annals of Human Genetics* , **2000**, 64, 207-13	2.2	17
105	Genetic Variants of Microtubule Actin Cross-linking Factor 1 (MACF1) Confer Risk for Parkinson's Disease. *Molecular Neurobiology*, **2017**, 54, 2878-2888	6.2	16
104	Reply to Associations of CFHR1CFHR3 deletion and a CFH SNP to age-related macular degeneration are not independent*Nature Genetics*, **2010**, 42, 555-556	36.3	16
103	Fieller's theorem and linkage disequilibrium mapping. *Genetic Epidemiology*, **1999**, 17, 237-52	2.6	16
102	A genome-wide association study of mitochondrial DNA copy number in two population-based cohorts. *Human Genomics*, **2019**, 13, 6	6.8	15
101	Genetic and functional evidence implicating DLL1 as the gene that influences susceptibility to visceral leishmaniasis at chromosome 6q27. *Journal of Infectious Diseases*, **2011**, 204, 467-77	7	15
100	A Variant in the BACH2 Gene Is Associated With Susceptibility to Autoimmune Addison's Disease in Humans. *Journal of Clinical Endocrinology and Metabolism*, **2016**, 101, 3865-3869	5.6	15
99	Bayesian network analysis incorporating genetic anchors complements conventional Mendelian randomization approaches for exploratory analysis of causal relationships in complex data. *PLoS Genetics*, **2020**, 16, e1008198	6	14
98	Relationship of sow udder morphology with piglet suckling behavior and teat access. *Theriogenology*, **2016**, 86, 1913-20	2.8	14
97	Exploring causality via identification of SNPs or haplotypes responsible for a linkage signal. *Genetic Epidemiology*, **2007**, 31, 727-40	2.6	14
96	Mapping multiple linked quantitative trait loci in non-obese diabetic mice using a stepwise regression strategy. *Genetical Research*, **1998**, 71, 51-64	1.1	14
95	Mouse genetics reveals Barttin as a genetic modifier of Joubert syndrome. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 1113-1118	11.5	13
94	A comparison of methods for inferring causal relationships between genotype and phenotype using additional biological measurements. *Genetic Epidemiology*, **2017**, 41, 577-586	2.6	13
93	Genetic variation in VEGF does not contribute significantly to the risk of congenital cardiovascular malformation. *PLoS ONE*, **2009**, 4, e4978	3.7	13

92	Quantitative trait association in parent offspring trios: Extension of case/pseudocontrol method and comparison of prospective and retrospective approaches. *Genetic Epidemiology*, **2007**, 31, 813-33	2.6	13
91	Affected-sib-pair data can be used to distinguish two-locus heterogeneity from two-locus epistasis. *American Journal of Human Genetics*, **2003**, 73, 1468-71; author reply 1471-3	11	13
90	Prediction of treatment response in rheumatoid arthritis patients using genome-wide SNP data. *Genetic Epidemiology*, **2018**, 42, 754-771	2.6	13
89	Genetic Analysis Workshop 18: Methods and strategies for analyzing human sequence and phenotype data in members of extended pedigrees. *BMC Proceedings*, **2014**, 8, S1	2.3	12
88	Genome-wide linkage and association study implicates the 10q26 region as a major genetic contributor to primary nonsyndromic vesicoureteric reflux. *Scientific Reports*, **2017**, 7, 14595	4.9	12
87	Primary, nonsyndromic vesicoureteric reflux and nephropathy in sibling pairs: a United Kingdom cohort for a DNA bank. *Clinical Journal of the American Society of Nephrology: CJASN*, **2011**, 6, 760-6	6.9	12
86	Increased Power for Detection of Parent-of-Origin Effects via the Use of Haplotype Estimation. *American Journal of Human Genetics*, **2015**, 97, 419-34	11	11
85	Overview of model-free methods for linkage analysis. *Advances in Genetics*, **2001**, 42, 135-50	3.3	11
84	Correcting for ascertainment bias of relative-risk estimates obtained using affected-sib-pair linkage data. *Genetic Epidemiology*, **2000**, 18, 307-21	2.6	11
83	Heritability of udder morphology and colostrum quality traits in swine. *Journal of Animal Science*, **2016**, 94, 3636-3644	0.7	11
82	Investigation of prediction accuracy and the impact of sample size, ancestry, and tissue in transcriptome-wide association studies. *Genetic Epidemiology*, **2020**, 44, 425-441	2.6	10
81	Identification of grouped rare and common variants via penalized logistic regression. *Genetic Epidemiology*, **2013**, 37, 592-602	2.6	10
80	Analysis of North American Rheumatoid Arthritis Consortium data using a penalized logistic regression approach. *BMC Proceedings*, **2009**, 3 Suppl 7, S61	2.3	10
79	Polymorphisms spanning the TNFR2 and TACE genes do not contribute towards variable anti-TNF treatment response. *Pharmacogenetics and Genomics*, **2010**, 20, 338-41	1.9	10
78	Genome-wide scan for loci influencing quantitative immune response traits in the Belfh family study: comparison of methods and summary of results. *Annals of Human Genetics*, **2006**, 70, 78-97	2.2	10
77	X Chromosome Contribution to the Genetic Architecture of Primary Biliary Cholangitis. *Gastroenterology*, **2021**, 160, 2483-2495.e26	13.3	9
76	Analysis of BAFF gene polymorphisms in UK Graves' disease patients. *Clinical Endocrinology*, **2019**, 90, 170-174	3.4	9
75	Congenital heart disease risk loci identified by genome-wide association study in European patients. *Journal of Clinical Investigation*, **2021**, 131,	15.9	9

74	Exploring Shared Susceptibility between Two Neural Crest Cells Originating Conditions: Neuroblastoma and Congenital Heart Disease. *Genes*, **2019**, 10,	4.2	8
73	Haplin power analysis: a software module for power and sample size calculations in genetic association analyses of family triads and unrelated controls. *BMC Bioinformatics*, **2019**, 20, 165	3.6	8
72	Evaluation of laboratory tests for cirrhosis and for alcohol use, in the context of alcoholic cirrhosis. *Alcohol*, **2018**, 66, 1-7	2.7	8
71	Accounting for relatedness in family-based association studies: application to Genetic Analysis Workshop 18 data. *BMC Proceedings*, **2014**, 8, S79	2.3	8
70	Imputation without doing imputation: a new method for the detection of non-genotyped causal variants. *Genetic Epidemiology*, **2014**, 38, 173-90	2.6	8
69	Genome instability in ataxia telangiectasia (A-T) families: camptothecin-induced damage to replicating DNA discriminates between obligate A-T heterozygotes, A-T homozygotes and controls. *Bioscience Reports*, **2004**, 24, 617-29	4.1	8
68	Linkage Analysis in Autoimmune Addison's Disease: NFATC1 as a Potential Novel Susceptibility Locus. *PLoS ONE*, **2015**, 10, e0123550	3.7	8
67	An international genome-wide meta-analysis of primary biliary cholangitis: Novel risk loci and candidate drugs. *Journal of Hepatology*, **2021**, 75, 572-581	13.4	8
66	Mutations in SPATA13/ASEF2 cause primary angle closure glaucoma. *PLoS Genetics*, **2020**, 16, e1008721	6	7
65	A conditional-on-exchangeable-parental-genotypes likelihood that remains unbiased at the causal locus under multiple-affected-sibling ascertainment. *Genetic Epidemiology*, **2005**, 29, 87-90	2.6	7
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9	Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney		1
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