Heather J Cordell

List of Publications by Year in Descending Order

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	Increased serum miR-193a-5p during non-alcoholic fatty liver disease progression: Diagnostic and mechanistic relevance.. *JHEP Reports*, **2022**, 4, 100409	10.3	4
234	Common Genetic Variants Contribute to Risk of Transposition of the Great Arteries. *Circulation Research*, **2021**,	15.7	2
233	Macrophage Scavenger Receptor 1 mediates lipid-induced inflammation in non-alcoholic fatty liver disease.. *Journal of Hepatology*, **2021**,	13.4	4
232	Obesity, Diabetes, Coffee, Tea, and Cannabis Use Alter Risk for Alcohol-Related Cirrhosis in 2 Large Cohorts of High-Risk Drinkers. *American Journal of Gastroenterology*, **2021**, 116, 106-115	0.7	7
231	rs9459874 and rs1012656 in CCR6/FGFR1OP confer susceptibility to primary biliary cholangitis. *Journal of Autoimmunity*, **2021**, 126, 102775	15.5	1
230	A genetic risk score and diabetes predict development of alcohol-related cirrhosis in drinkers. *Journal of Hepatology*, **2021**,	13.4	4
229	Genome-wide association study identifies susceptibility loci for acute myeloid leukemia. *Nature Communications*, **2021**, 12, 6233	17.4	2
228	A Role in the Genetic Predisposition to NAFLD-HCC?. *Cancers*, **2021**, 13,	6.6	5
227	Rationale and design of the African Cardiomyopathy and Myocarditis Registry Program: The IMHOTEP study. *International Journal of Cardiology*, **2021**, 333, 119-126	3.2	0
226	X Chromosome Contribution to the Genetic Architecture of Primary Biliary Cholangitis. *Gastroenterology*, **2021**, 160, 2483-2495.e26	13.3	9
225	A Genome-wide Association Study Identifies SERPINB10, CRLF3, STX7, LAMP3, IFNG-AS1, and KRT80 As Risk Loci Contributing to Cutaneous Leishmaniasis in Brazil. *Clinical Infectious Diseases*, **2021**, 72, e515-e525	11.6	6
224	Genome-wide Association Study and Meta-analysis on Alcohol-Associated Liver Cirrhosis Identifies Genetic Risk Factors. *Hepatology*, **2021**, 73, 1920-1931	11.2	18
223	Heritability and family-based GWAS analyses of the N-acyl ethanolamine and ceramide plasma lipidome. *Human Molecular Genetics*, **2021**, 30, 500-513	5.6	4
222	Congenital heart disease risk loci identified by genome-wide association study in European patients. *Journal of Clinical Investigation*, **2021**, 131,	15.9	9
221	Common and Rare Genetic Variants That Could Contribute to Severe Otitis Media in an Australian Aboriginal Population. *Clinical Infectious Diseases*, **2021**, 73, 1860-1870	11.6	0
220	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
219	Association of Novel Locus With Rheumatic Heart Disease in Black African Individuals: Findings From the RHDGen Study. *JAMA Cardiology*, **2021**, 6, 1000-1011	16.2	7

218	A Bayesian network approach incorporating imputation of missing data enables exploratory analysis of complex causal biological relationships. *PLoS Genetics*, **2021**, 17, e1009811	6	3
217	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
216	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
215	An Intronic HCP5 Variant Is Associated With Age of Onset and Susceptibility to Graves Disease in UK and Polish Cohorts. *Journal of Clinical Endocrinology and Metabolism*, **2020**, 105,	5.6	5
214	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
213	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
212	Mutations in SPATA13/ASEF2 cause primary angle closure glaucoma. *PLoS Genetics*, **2020**, 16, e1008721	6	7
211	Cardiac Imaging of Aortic Valve Area From 34 287 UK Biobank Participants Reveals Novel Genetic Associations and Shared Genetic Comorbidity With Multiple Disease Phenotypes. *Circulation Genomic and Precision Medicine*, **2020**, 13, e003014	5.2	1
210	Early B-cell Factor 3-Related Genetic Disease Can Mimic Urofacial Syndrome. *Kidney International Reports*, **2020**, 5, 1823-1827	4.1	3
209	Transcriptomic profiling across the nonalcoholic fatty liver disease spectrum reveals gene signatures for steatohepatitis and fibrosis. *Science Translational Medicine*, **2020**, 12,	17.5	51
208	Investigation of genetically regulated gene expression and response to treatment in rheumatoid arthritis highlights an association between expression and treatment response. *Annals of the Rheumatic Diseases*, **2020**, 79, 1446-1452	2.4	2
207	Identifying genetic factors that contribute to the increased risk of congenital heart defects in infants with Down syndrome. *Scientific Reports*, **2020**, 10, 18051	4.9	4
206	Heritability of haemodynamics in the ascending aorta. *Scientific Reports*, **2020**, 10, 14356	4.9	2
205	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
204	Exploring Shared Susceptibility between Two Neural Crest Cells Originating Conditions: Neuroblastoma and Congenital Heart Disease. *Genes*, **2019**, 10,	4.2	8
203	Marked variation in heritability estimates of left ventricular mass depending on modality of measurement. *Scientific Reports*, **2019**, 9, 13556	4.9	1
202	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
201	A genome-wide association study of mitochondrial DNA copy number in two population-based cohorts. *Human Genomics*, **2019**, 13, 6	6.8	15

200	A meta-analysis of genome-wide association studies identifies multiple longevity genes. *Nature Communications*, **2019**, 10, 3669	17.4	102
199	Whole Exome Sequencing Reveals the Major Genetic Contributors to Nonsyndromic Tetralogy of Fallot. *Circulation Research*, **2019**, 124, 553-563	15.7	62
198	Analysis of BAFF gene polymorphisms in UK Graves' disease patients. *Clinical Endocrinology*, **2019**, 90, 170-174	3.4	9
197	Statistical methods for genome-wide association studies. *Seminars in Cancer Biology*, **2019**, 55, 53-60	12.7	29
196	A case-control genome wide association study of substance use disorder (SUD) identifies novel variants on chromosome 7p14.1 in patients from the United Arab Emirates (UAE). *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2019**, 180, 68-79	3.5	2
195	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
194	Evaluation of laboratory tests for cirrhosis and for alcohol use, in the context of alcoholic cirrhosis. *Alcohol*, **2018**, 66, 1-7	2.7	8
193	Arylsulphatase A Pseudodeficiency (ARSA-PD), hypertension and chronic renal disease in Aboriginal Australians. *Scientific Reports*, **2018**, 8, 10912	4.9	3
192	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
191	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
190	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
189	Application of Bayesian networks to GAW20 genetic and blood lipid data. *BMC Proceedings*, **2018**, 12, 19	2.3	3
188	Using penalized regression to predict phenotype from SNP data. *BMC Proceedings*, **2018**, 12, 38	2.3	7
187	Prediction of treatment response in rheumatoid arthritis patients using genome-wide SNP data. *Genetic Epidemiology*, **2018**, 42, 754-771	2.6	13
186	Amino acid residues in five separate HLA genes can explain most of the known associations between the MHC and primary biliary cholangitis. *PLoS Genetics*, **2018**, 14, e1007833	6	4
185	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
184	Genome-wide association study of response to tumour necrosis factor inhibitor therapy in rheumatoid arthritis. *Pharmacogenomics Journal*, **2018**, 18, 657-664	3.5	32
183	Genome-wide association study of response to methotrexate in early rheumatoid arthritis patients. *Pharmacogenomics Journal*, **2018**, 18, 528-538	3.5	25

182	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
181	A two-stage inter-rater approach for enrichment testing of variants associated with multiple traits. *European Journal of Human Genetics*, **2017**, 25, 341-349	5.3	
180	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
179	Protein-altering and regulatory genetic variants near GATA4 implicated in bicuspid aortic valve. *Nature Communications*, **2017**, 8, 15481	17.4	52
178	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
177	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
176	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
175	Further investigations of the W-test for pairwise epistasis testing. *Wellcome Open Research*, **2017**, 2, 54	4.8	1
174	Relationship of sow udder morphology with piglet suckling behavior and teat access. *Theriogenology*, **2016**, 86, 1913-20	2.8	14
173	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
172	Using gene expression data to identify causal pathways between genotype and phenotype in a complex disease: application to Genetic Analysis Workshop 19. *BMC Proceedings*, **2016**, 10, 79-84	2.3	2
171	Examination of previously identified associations within the Genetic Analysis Workshop 19 data. *BMC Proceedings*, **2016**, 10, 97-101	2.3	
170	Gene expression in large pedigrees: analytic approaches. *BMC Genetics*, **2016**, 17 Suppl 2, 3	2.6	5
169	Exome sequencing in dementia with Lewy bodies. *Translational Psychiatry*, **2016**, 6, e728	8.6	30
168	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
167	Compare and Contrast Meta Analysis (CCMA): A Method for Identification of Pleiotropic Loci in Genome-Wide Association Studies. *PLoS ONE*, **2016**, 11, e0154872	3.7	3
166	Transcriptional regulation of PNPLA3 and its impact on susceptibility to nonalcoholic fatty liver Disease (NAFLD) in humans. *Aging*, **2016**, 9, 26-40	5.6	7
165	Heritability of udder morphology and colostrum quality traits in swine. *Journal of Animal Science*, **2016**, 94, 3636-3644	0.7	11

164	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
163	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
162	CTLA-4 as a genetic determinant in autoimmune Addison's disease. *Genes and Immunity*, **2015**, 16, 430-6	4.4	27
161	Maternal filaggrin mutations increase the risk of atopic dermatitis in children: an effect independent of mutation inheritance. *PLoS Genetics*, **2015**, 11, e1005076	6	25
160	International genome-wide meta-analysis identifies new primary biliary cirrhosis risk loci and targetable pathogenic pathways. *Nature Communications*, **2015**, 6, 8019	17.4	185
159	Methylation quantitative trait locus analysis of osteoarthritis links epigenetics with genetic risk. *Human Molecular Genetics*, **2015**, 24, 7432-44	5.6	35
158	Association analysis identifies new risk loci for congenital heart disease in Chinese populations. *Nature Communications*, **2015**, 6, 8082	17.4	19
157	A Bayesian Approach to the Overlap Analysis of Epidemiologically Linked Traits. *Genetic Epidemiology*, **2015**, 39, 624-34	2.6	3
156	Brief report: genetics of alcoholic cirrhosis-GenomALC multinational study. *Alcoholism: Clinical and Experimental Research*, **2015**, 39, 836-42	3.7	22
155	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
154	Uterine carcinosarcoma/malignant mixed M□lerian tumor incidence is increased in women with breast cancer, but independent of hormone therapy. *Journal of Gynecologic Oncology*, **2015**, 26, 249-51	4	4
153	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. *Journal of Clinical Investigation*, **2015**, 125, 1739-51	15.9	67
152	Urinary tract effects of HPSE2 mutations. *Journal of the American Society of Nephrology: JASN*, **2015** , 26, 797-804	12.7	25
151	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
150	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
149	Linkage Analysis in Autoimmune Addison's Disease: NFATC1 as a Potential Novel Susceptibility Locus. *PLoS ONE*, **2015**, 10, e0123550	3.7	8
148	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
147	Factors determining penetrance in familial atypical haemolytic uraemic syndrome. *Journal of Medical Genetics*, **2014**, 51, 756-64	5.8	20

146	Research capacity. Enabling the genomic revolution in Africa. *Science*, **2014**, 344, 1346-8	33.3	256
145	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
144	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
143	Analysis of Genetic Analysis Workshop 18 data with gene-based penalized regression. *BMC Proceedings*, **2014**, 8, S43	2.3	1
142	Accounting for relatedness in family-based association studies: application to Genetic Analysis Workshop 18 data. *BMC Proceedings*, **2014**, 8, S79	2.3	8
141	Association of autoimmune Addison's disease with alleles of STAT4 and GATA3 in European cohorts. *PLoS ONE*, **2014**, 9, e88991	3.7	25
140	Comparison of methods to account for relatedness in genome-wide association studies with family-based data. *PLoS Genetics*, **2014**, 10, e1004445	6	75
139	Imputation without doing imputation: a new method for the detection of non-genotyped causal variants. *Genetic Epidemiology*, **2014**, 38, 173-90	2.6	8
138	Summary of results and discussions from the gene-based tests group at Genetic Analysis Workshop 18. *Genetic Epidemiology*, **2014**, 38 Suppl 1, S44-8	2.6	6
137	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
136	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
135	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
134	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
133	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
132	Identification of grouped rare and common variants via penalized logistic regression. *Genetic Epidemiology*, **2013**, 37, 592-602	2.6	10
131	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
130	Genome-wide linkage analysis for human longevity: Genetics of Healthy Aging Study. *Aging Cell*, **2013**, 12, 184-93	9.9	140
129	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

128	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
127	Determining the population frequency of the CFHR3/CFHR1 deletion at 1q32. *PLoS ONE*, **2013**, 8, e60353	3.7	74
126	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
125	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
124	Dense fine-mapping study identifies new susceptibility loci for primary biliary cirrhosis. *Nature Genetics*, **2012**, 44, 1137-41	36.3	214
123	PREMIM and EMIM: tools for estimation of maternal, imprinting and interaction effects using multinomial modelling. *BMC Bioinformatics*, **2012**, 13, 149	3.6	37
122	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
121	Improved statistics for genome-wide interaction analysis. *PLoS Genetics*, **2012**, 8, e1002625	6	65
120	Fine mapping and replication of genetic risk loci in primary sclerosing cholangitis. *Scandinavian Journal of Gastroenterology*, **2012**, 47, 820-6	2.4	36
119	A common variant in the PTPN11 gene contributes to the risk of tetralogy of Fallot. *Circulation: Cardiovascular Genetics*, **2012**, 5, 287-92		25
118	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
117	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
116	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
115	Genome-wide association study identifies 12 new susceptibility loci for primary biliary cirrhosis. *Nature Genetics*, **2011**, 43, 329-32	36.3	396
114	Speed-bumps ahead for the genetics of later-life diseases. *Trends in Genetics*, **2011**, 27, 387-8	8.5	20
113	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
112	Penalized-regression-based multimarker genotype analysis of Genetic Analysis Workshop 17 data. *BMC Proceedings*, **2011**, 5 Suppl 9, S92	2.3	3
111	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

110	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
109	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
108	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
107	Reply to 'Associations of CFHR1–CFHR3 deletion and a CFH SNP to age-related macular degeneration are not independent'. *Nature Genetics*, **2010**, 42, 555-556	36.3	16
106	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
105	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
104	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
103	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
102	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
101	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
100	SNP selection in genome-wide and candidate gene studies via penalized logistic regression. *Genetic Epidemiology*, **2010**, 34, 879-91	2.6	133
99	Host genetic and epigenetic factors in toxoplasmosis. *Memorias Do Instituto Oswaldo Cruz*, **2009**, 104, 162-9	2.6	18
98	Genetic variation in VEGF does not contribute significantly to the risk of congenital cardiovascular malformation. *PLoS ONE*, **2009**, 4, e4978	3.7	13
97	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
96	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
95	Analysis of North American Rheumatoid Arthritis Consortium data using a penalized logistic regression approach. *BMC Proceedings*, **2009**, 3 Suppl 7, S61	2.3	10
94	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
93	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

92	A composite-likelihood approach for identifying polymorphisms that are potentially directly associated with disease. *European Journal of Human Genetics*, **2009**, 17, 644-50	5.3	3
91	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
90	Detecting gene-gene interactions that underlie human diseases. *Nature Reviews Genetics*, **2009**, 10, 392-404	30.1	990
89	Estimation and testing of gene-environment interactions in family-based association studies. *Genomics*, **2009**, 93, 5-9	4.3	17
88	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
87	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
86	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
85	Genetic and epigenetic factors at COL2A1 and ABCA4 influence clinical outcome in congenital toxoplasmosis. *PLoS ONE*, **2008**, 3, e2285	3.7	86
84	Dealing with missing data in family-based association studies: a multiple imputation approach. *Human Heredity*, **2007**, 63, 229-38	1.1	23
83	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
82	Exploring causality via identification of SNPs or haplotypes responsible for a linkage signal. *Genetic Epidemiology*, **2007**, 31, 727-40	2.6	14
81	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
80	A genome-wide scan for type 1 diabetes susceptibility genes in nuclear families with multiple affected siblings in Finland. *BMC Genetics*, **2007**, 8, 84	2.6	6
79	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
78	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
77	Y chromosome lineage- and village-specific genes on chromosomes 1p22 and 6q27 control visceral leishmaniasis in Sudan. *PLoS Genetics*, **2007**, 3, e71	6	54
76	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
75	Genetic Analysis Workshop 15: gene expression analysis and approaches to detecting multiple functional loci. *BMC Proceedings*, **2007**, 1 Suppl 1, S1	2.3	6

74	Linkage and association analysis of GAW15 simulated data: fine-mapping of chromosome 6 region. *BMC Proceedings*, **2007**, 1 Suppl 1, S23	2.3	5
73	Joint linkage and association analysis for identification of potentially causal polymorphisms in GAW15 data. *BMC Proceedings*, **2007**, 1 Suppl 1, S36	2.3	4
72	A multimarker regression-based test of linkage for affected sib-pairs at two linked loci. *Genetic Epidemiology*, **2006**, 30, 191-208	2.6	4
71	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
70	Perils and pitfalls of permutation tests for distinguishing the effects of neighbouring polymorphisms. *Genetic Epidemiology*, **2006**, 30, 582-9	2.6	2
69	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
68	Genome-wide scan for loci influencing quantitative immune response traits in the Beln family study: comparison of methods and summary of results. *Annals of Human Genetics*, **2006**, 70, 78-97	2.2	10
67	Genetic association studies. *Lancet, The*, **2005**, 366, 1121-31	40	394
66	Regression mapping of association between the human leukocyte antigen region and Graves disease. *American Journal of Human Genetics*, **2005**, 76, 157-63	11	121
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
64	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
63	Summary of contributions to GAW Group 5: linkage mapping methods, Problem 2. *Genetic Epidemiology*, **2005**, 29 Suppl 1, S35-40	2.6	
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9	Heritability and family-based GWAS analyses of the N-acyl ethanolamine and ceramide plasma lipidome		1
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7	Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney		1
6	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
5	A genome-wide association study highlights a regulatory role for IFNG-AS1 contributing to cutaneous leishmaniasis in Brazil		2
4	Macrophage Scavenger Receptor 1 mediates lipid-induced inflammation in non-alcoholic fatty liver disease		1
3	Bayesian network analysis incorporating genetic anchors complements conventional Mendelian randomization approaches for exploratory analysis of causal relationships in complex data		2

2	A trans-ancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation		5
1	A multiancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation. *Nature Genetics*,	36.3	2