Heather J Cordell

List of Publications by Year
in descending order

235 papers	23,495 citations	12330 69 h-index	8866 145 g-index
263 all docs	263 docs citations	263 times ranked	28111 citing authors

#	Article	IF	Citations
1	A genetic risk score and diabetes predict development of alcohol-related cirrhosis in drinkers. Journal of Hepatology, 2022, 76, 275-282.	3.7	33
2	rs9459874 and rs1012656 in CCR6/FGFR1OP confer susceptibility to primary biliary cholangitis. Journal of Autoimmunity, 2022, 126, 102775.	6.5	6
3	Increased serum miR-193a-5p during non-alcoholic fatty liver disease progression: Diagnostic and mechanistic relevance. JHEP Reports, 2022, 4, 100409.	4.9	20
4	Common Genetic Variants Contribute to Risk of Transposition of the Great Arteries. Circulation Research, 2022, 130, 166-180.	4.5	15
5	Macrophage scavenger receptor 1 mediates lipid-induced inflammation in non-alcoholic fatty liver disease. Journal of Hepatology, 2022, 76, 1001-1012.	3.7	54
6	Rare complement factor I variants associated with reduced macular thickness and age-related macular degeneration in the UK Biobank. Human Molecular Genetics, 2022, 31, 2678-2692.	2.9	11
7	No Evidence That Genetic Variation at the Klotho Locus Is Associated With Longevity in Caucasians from the Newcastle 85+ Study and the UK Biobank. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2022, 77, 457-461.	3.6	2
8	OA13â€ƒComprehensive genetic and functional analyses of Fc gamma receptors explain response to rituximab therapy for autoimmune rheumatic diseases. Rheumatology, 2022, 61, .	1.9	0
9	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, 2022, 54, 761-771.	21.4	68
10	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.	5.8	16
11	Genomeâ€wide Association Study and Metaâ€analysis on Alcoholâ€Associated Liver Cirrhosis Identifies Genetic Risk Factors. Hepatology, 2021, 73, 1920-1931.	7.3	54
12	Heritability and family-based GWAS analyses of the N-acyl ethanolamine and ceramide plasma lipidome. Human Molecular Genetics, 2021, 30, 500-513.	2.9	13
13	Congenital heart disease risk loci identified by genome-wide association study in European patients. Journal of Clinical Investigation, 2021, 131, .	8.2	47
14	Common and Rare Genetic Variants That Could Contribute to Severe Otitis Media in an Australian Aboriginal Population. Clinical Infectious Diseases, 2021, 73, 1860-1870.	5.8	4
15	A PDCD1 Role in the Genetic Predisposition to NAFLD-HCC?. Cancers, 2021, 13, 1412.	3.7	26
16	Rationale and design of the African Cardiomyopathy and Myocarditis Registry Program: The IMHOTEP study. International Journal of Cardiology, 2021, 333, 119-126.	1.7	5
17	X Chromosome Contribution to the Genetic Architecture of Primary Biliary Cholangitis. Gastroenterology, 2021, 160, 2483-2495.e26.	1.3	27
18	An international genome-wide meta-analysis of primary biliary cholangitis: Novel risk loci and candidate drugs. Journal of Hepatology, 2021, 75, 572-581.	3.7	62

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19	Association of Novel Locus With Rheumatic Heart Disease in Black African Individuals. JAMA Cardiology, 2021, 6, 1000.	6.1	18
20	A Bayesian network approach incorporating imputation of missing data enables exploratory analysis of complex causal biological relationships. PLoS Genetics, 2021, 17, e1009811.	3.5	11
21	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.	3.7	149
22	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.	0.4	25
23	Genome-wide association study identifies susceptibility loci for acute myeloid leukemia. Nature Communications, 2021, 12, 6233.	12.8	17
24	Early B-cell Factor 3â€"Related Genetic Disease Can Mimic Urofacial Syndrome. Kidney International Reports, 2020, 5, 1823-1827.	0.8	7
25	Transcriptomic profiling across the nonalcoholic fatty liver disease spectrum reveals gene signatures for steatohepatitis and fibrosis. Science Translational Medicine, 2020, 12, .	12.4	205
26	Investigation of genetically regulated gene expression and response to treatment in rheumatoid arthritis highlights an association between IL18RAP expression and treatment response. Annals of the Rheumatic Diseases, 2020, 79, 1446-1452.	0.9	13
27	Identifying genetic factors that contribute to the increased risk of congenital heart defects in infants with Down syndrome. Scientific Reports, 2020, 10, 18051.	3.3	14
28	Macrophage scavenger receptor 1 mediates lipid-induced inflammation in human obesity-related non-alcoholic fatty liver disease. Journal of Hepatology, 2020, 73, S20-S21.	3.7	0
29	Heritability of haemodynamics in the ascending aorta. Scientific Reports, 2020, 10, 14356.	3.3	5
30	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.	7.1	22
31	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, e3277-e3284.	3.6	12
32	Investigation of prediction accuracy and the impact of sample size, ancestry, and tissue in transcriptomeâ€wide association studies. Genetic Epidemiology, 2020, 44, 425-441.	1.3	19
33	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.	3.5	39
34	Mutations in SPATA13/ASEF2 cause primary angle closure glaucoma. PLoS Genetics, 2020, 16, e1008721.	3.5	12
35	Genome-wide association study of non-alcoholic fatty liver and steatohepatitis in a histologically characterised cohortâ˜†. Journal of Hepatology, 2020, 73, 505-515.	3.7	279
36	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.	3.6	16

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37	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	12.8	214
38	Exploring Shared Susceptibility between Two Neural Crest Cells Originating Conditions: Neuroblastoma and Congenital Heart Disease. Genes, 2019, 10, 663.	2.4	14
39	Marked variation in heritability estimates of left ventricular mass depending on modality of measurement. Scientific Reports, 2019, 9, 13556.	3.3	3
40	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.	2.6	11
41	The Plight of Muntaser Ibrahim. PLoS Genetics, 2019, 15, e1008100.	3.5	1
42	A genome-wide association study of mitochondrial DNA copy number in two population-based cohorts. Human Genomics, 2019, 13, 6.	2.9	25
43	Câ€…Identification of the major genetic contributors to tetralogy of fallot. , 2019, , .		0
44	Whole Exome Sequencing Reveals the Major Genetic Contributors to Nonsyndromic Tetralogy of Fallot. Circulation Research, 2019, 124, 553-563.	4.5	118
45	Analysis of BAFF gene polymorphisms in UK Gravesâ€™ disease patients. Clinical Endocrinology, 2019, 90, 170-174.	2.4	19
46	Statistical methods for genome-wide association studies. Seminars in Cancer Biology, 2019, 55, 53-60.	9.6	59
47	Phenotypic heterogeneity in m.3243A>G mitochondrial disease: The role of nuclear factors. Annals of Clinical and Translational Neurology, 2018, 5, 333-345.	3.7	102
48	Evaluation of laboratory tests for cirrhosis and for alcohol use, in the context of alcoholic cirrhosis. Alcohol, 2018, 66, 1-7.	1.7	13
49	CD4+ and B Lymphocyte Expression Quantitative Traits at Rheumatoid Arthritis Risk Loci in Patients With Untreated Early Arthritis. Arthritis and Rheumatology, 2018, 70, 361-370.	5.6	37
50	Application of Bayesian networks to GAW20 genetic and blood lipid data. BMC Proceedings, 2018, 12, 19.	1.6	5
51	Using penalized regression to predict phenotype from SNP data. BMC Proceedings, 2018, 12, 38.	1.6	10
52	Prediction of treatment response in rheumatoid arthritis patients using genomeâ€wide SNP data. Genetic Epidemiology, 2018, 42, 754-771.	1.3	15
53	A caseâ€“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, 2018, 180, 68-79.	1.7	3
54	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.	3.5	10

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55	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
56	Genome-wide association study of response to tumour necrosis factor inhibitor therapy in rheumatoid arthritis. Pharmacogenomics Journal, 2018, 18, 657-664.	2.0	41
57	Genome-wide association study of response to methotrexate in early rheumatoid arthritis patients. Pharmacogenomics Journal, 2018, 18, 528-538.	2.0	42
58	Arylsulphatase A Pseudodeficiency (ARSA-PD), hypertension and chronic renal disease in Aboriginal Australians. Scientific Reports, 2018, 8, 10912.	3.3	5
59	Comparison of methods for transcriptome imputation through application to two common complex diseases. European Journal of Human Genetics, 2018, 26, 1658-1667.	2.8	22
60	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.	8.1	103
61	Genetic Variants of Microtubule Actin Cross-linking Factor 1 (MACF1) Confer Risk for Parkinsonâ€™s Disease. Molecular Neurobiology, 2017, 54, 2878-2888.	4.0	22
62	A two-stage inter-rater approach for enrichment testing of variants associated with multiple traits. European Journal of Human Genetics, 2017, 25, 341-349.	2.8	0
63	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	21.4	492
64	Protein-altering and regulatory genetic variants near GATA4 implicated in bicuspid aortic valve. Nature Communications, 2017, 8, 15481.	12.8	90
65	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
66	A comparison of methods for inferring causal relationships between genotype and phenotype using additional biological measurements. Genetic Epidemiology, 2017, 41, 577-586.	1.3	20
67	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.	3.3	17
68	05.10â€...Comparison of cd4+ and b lymphocyte expression quantitative trait associations at ra risk loci in untreated early arthritis patients. , 2017, , .		0
69	Further investigations of the W-test for pairwise epistasis testing. Wellcome Open Research, 2017, 2, 54.	1.8	1
70	Heritability of udder morphology and colostrum quality traits in swine1. Journal of Animal Science, 2016, 94, 3636-3644.	0.5	23
71	The UKâ€PBC risk scores: Derivation and validation of a scoring system for longâ€term prediction of endâ€stage liver disease in primary biliary cholangitis. Hepatology, 2016, 63, 930-950.	7.3	269
72	A Variant in theBACH2Gene Is Associated With Susceptibility to Autoimmune Addisonâ€™s Disease in Humans. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 3865-3869.	3.6	18

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73	Relationship of sow udder morphology with piglet suckling behavior and teat access. Theriogenology, 2016, 86, 1913-1920.	2.1	20
74	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
75	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.	1.6	3
76	Examination of previously identified associations within the Genetic Analysis Workshop 19 data. BMC Proceedings, 2016, 10, 97-101.	1.6	0
77	Gene expression in large pedigrees: analytic approaches. BMC Genetics, 2016, 17, 3.	2.7	8
78	Exome sequencing in dementia with Lewy bodies. Translational Psychiatry, 2016, 6, e728-e728.	4.8	35
79	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.	2.9	31
80	Compare and Contrast Meta Analysis (CCMA): A Method for Identification of Pleiotropic Loci in Genome-Wide Association Studies. PLoS ONE, 2016, 11, e0154872.	2.5	3
81	Transcriptional regulation of PNPLA3 and its impact on susceptibility to nonalcoholic fatty liver Disease (NAFLD) in humans. Aging, 2016, 9, 26-40.	3.1	11
82	A Bayesian Approach to the Overlap Analysis of Epidemiologically Linked Traits. Genetic Epidemiology, 2015, 39, 624-634.	1.3	4
83	Brief Report: Genetics of Alcoholic Cirrhosisâ€"<scp>G</scp>enom<scp>ALC</scp> Multinational Study. Alcoholism: Clinical and Experimental Research, 2015, 39, 836-842.	2.4	29
84	Increased Power for Detection of Parent-of-Origin Effects via the Use of Haplotype Estimation. American Journal of Human Genetics, 2015, 97, 419-434.	6.2	15
85	Uterine carcinosarcoma/malignant mixed MÃ¼llerian tumor incidence is increased in women with breast cancer, but independent of hormone therapy. Journal of Gynecologic Oncology, 2015, 26, 249.	2.2	6
86	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. Journal of Clinical Investigation, 2015, 125, 1739-1751.	8.2	94
87	Urinary Tract Effects of HPSE2 Mutations. Journal of the American Society of Nephrology: JASN, 2015, 26, 797-804.	6.1	31
88	Genome-wide Comparative Analysis of Atopic Dermatitis and Psoriasis Gives Insight into Opposing Genetic Mechanisms. American Journal of Human Genetics, 2015, 96, 104-120.	6.2	163
89	CTLA-4 as a genetic determinant in autoimmune Addisonâ€™s disease. Genes and Immunity, 2015, 16, 430-436.	4.1	30
90	Maternal Filaggrin Mutations Increase the Risk of Atopic Dermatitis in Children: An Effect Independent of Mutation Inheritance. PLoS Genetics, 2015, 11, e1005076.	3.5	33

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91	International genome-wide meta-analysis identifies new primary biliary cirrhosis risk loci and targetable pathogenic pathways. Nature Communications, 2015, 6, 8019.	12.8	245
92	Methylation quantitative trait locus analysis of osteoarthritis links epigenetics with genetic risk. Human Molecular Genetics, 2015, 24, 7432-7444.	2.9	48
93	Association analysis identifies new risk loci for congenital heart disease in Chinese populations. Nature Communications, 2015, 6, 8082.	12.8	26
94	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.	2.5	35
95	Linkage Analysis in Autoimmune Addisonâ€™s Disease: NFATC1 as a Potential Novel Susceptibility Locus. PLoS ONE, 2015, 10, e0123550.	2.5	10
96	Association of Autoimmune Addison's Disease with Alleles of STAT4 and GATA3 in European Cohorts. PLoS ONE, 2014, 9, e88991.	2.5	27
97	Comparison of Methods to Account for Relatedness in Genome-Wide Association Studies with Family-Based Data. PLoS Genetics, 2014, 10, e1004445.	3.5	122
98	Imputation Without Doing Imputation: A New Method for the Detection of Nonâ€Genotyped Causal Variants. Genetic Epidemiology, 2014, 38, 173-190.	1.3	10
99	Summary of Results and Discussions From the Geneâ€Based Tests Group at Genetic Analysis Workshop 18. Genetic Epidemiology, 2014, 38, S44-8.	1.3	6
100	DNA methylation abnormalities at gene promoters are extensive and variable in the elderly and phenocopy cancer cells. FASEB Journal, 2014, 28, 3261-3272.	0.5	33
101	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.	1.2	23
102	Factors determining penetrance in familial atypical haemolytic uraemic syndrome. Journal of Medical Genetics, 2014, 51, 756-764.	3.2	28
103	Enabling the genomic revolution in Africa. Science, 2014, 344, 1346-1348.	12.6	361
104	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. Human Molecular Genetics, 2014, 23, 4420-4432.	2.9	227
105	Genetic Analysis Workshop 18: Methods and strategies for analyzing human sequence and phenotype data in members of extended pedigrees. BMC Proceedings, 2014, 8, S1.	1.6	12
106	Analysis of Genetic Analysis Workshop 18 data with gene-based penalized regression. BMC Proceedings, 2014, 8, S43.	1.6	1
107	Accounting for relatedness in family-based association studies: application to Genetic Analysis Workshop 18 data. BMC Proceedings, 2014, 8, S79.	1.6	9
108	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, 822-824.	21.4	123

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109	Genetic Information and the Prediction of Incident Type 2 Diabetes in a High-Risk Multiethnic Population. Diabetes Care, 2013, 36, 2836-2842.	8.6	22
110	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, 1121-1129.	2.9	135
111	A Genomeâ€Wide Search for Type 2 Diabetes Susceptibility Genes in an Extended Arab Family. Annals of Human Genetics, 2013, 77, 488-503.	0.8	28
112	Identification of Grouped Rare and Common Variants via Penalized Logistic Regression. Genetic Epidemiology, 2013, 37, 592-602.	1.3	11
113	Common variants in the HLA-DRB1â€"HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. Nature Genetics, 2013, 45, 208-213.	21.4	86
114	Genomeâ€wide linkage analysis for human longevity: Genetics of Healthy Aging Study. Aging Cell, 2013, 12, 184-193.	6.7	170
115	Association Between C677T Polymorphism of Methylene Tetrahydrofolate Reductase and Congenital Heart Disease. Circulation: Cardiovascular Genetics, 2013, 6, 347-353.	5.1	31
116	Genome-wide association study identifies loci on 12q24 and 13q32 associated with Tetralogy of Fallot. Human Molecular Genetics, 2013, 22, 1473-1481.	2.9	82
117	Determining the Population Frequency of the CFHR3/CFHR1 Deletion at 1q32. PLoS ONE, 2013, 8, e60352.	2.5	96
118	Improved Statistics for Genome-Wide Interaction Analysis. PLoS Genetics, 2012, 8, e1002625.	3.5	82
119	Fine mapping and replication of genetic risk loci in primary sclerosing cholangitis. Scandinavian Journal of Gastroenterology, 2012, 47, 820-826.	1.5	47
120	A Common Variant in the PTPN11 Gene Contributes to the Risk of Tetralogy of Fallot. Circulation: Cardiovascular Genetics, 2012, 5, 287-292.	5.1	34
121	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, 1513-1520.	2.9	101
122	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.	0.7	185
123	Dense fine-mapping study identifies new susceptibility loci for primary biliary cirrhosis. Nature Genetics, 2012, 44, 1137-1141.	21.4	251
124	PREMIM and EMIM: tools for estimation of maternal, imprinting and interaction effects using multinomial modelling. BMC Bioinformatics, 2012, 13, 149.	2.6	45
125	Contribution of Global Rare Copy-Number Variants to the Risk of Sporadic Congenital Heart Disease. American Journal of Human Genetics, 2012, 91, 489-501.	6.2	272
126	Common genetic variants in complement genes other than CFH, CD46 and the CFHRs are not associated with aHUS. Molecular Immunology, 2012, 49, 640-648.	2.2	37

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127	Loss-of-function variants in the filaggrin gene are a significant risk factor for peanut allergy. Journal of Allergy and Clinical Immunology, 2011, 127, 661-667.	2.9	424
128	Wide spectrum of filaggrin-null mutations in atopic dermatitis highlights differences between Singaporean Chinese and European populations. British Journal of Dermatology, 2011, 165, 106-114.	1.5	123
129	Genome-wide association study identifies 12 new susceptibility loci for primary biliary cirrhosis. Nature Genetics, 2011, 43, 329-332.	21.4	441
130	Speed-bumps ahead for the genetics of later-life diseases. Trends in Genetics, 2011, 27, 387-388.	6.7	34
131	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, 203-234.	10.1	61
132	Penalized-regression-based multimarker genotype analysis of Genetic Analysis Workshop 17 data. BMC Proceedings, 2011, 5, S92.	1.6	3
133	Investigation of maternal effects, maternal-fetal interactions and parent-of-origin effects (imprinting), using mothers and their offspring. Genetic Epidemiology, 2011, 35, 19-45.	1.3	71
134	Genetic and Functional Evidence Implicating DLL1 as the Gene That Influences Susceptibility to Visceral Leishmaniasis at Chromosome 6q27. Journal of Infectious Diseases, 2011, 204, 467-477.	4.0	15
135	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, 760-766.	4.5	13
136	Clinical and Pharmacogenetic Influences on Response to Hydroxychloroquine in Discoid Lupus Erythematosus: A Retrospective Cohort Study. Journal of Investigative Dermatology, 2011, 131, 1981-1986.	0.7	84
137	Polymorphisms spanning the TNFR2 and TACE genes do not contribute towards variable anti-TNF treatment response. Pharmacogenetics and Genomics, 2010, 20, 338-341.	1.5	12
138	SNP Selection in genomeâ€wide and candidate gene studies via penalized logistic regression. Genetic Epidemiology, 2010, 34, 879-891.	1.3	166
139	Reply to â€œAssociations of CFHR1â€“CFHR3 deletion and a CFH SNP to age-related macular degeneration are not independentâ€• Nature Genetics, 2010, 42, 555-556.	21.4	18
140	The heritability of G₂chromosomal radiosensitivity and its association with cancer in Danish cancer survivors and their offspring. International Journal of Radiation Biology, 2010, 86, 986-995.	1.8	27
141	Whole-Genome Linkage and Association Scan in Primary, Nonsyndromic Vesicoureteric Reflux. Journal of the American Society of Nephrology: JASN, 2010, 21, 113-123.	6.1	58
142	Association between anti-tumour necrosis factor treatment response and genetic variants within the TLR and NFÂB signalling pathways. Annals of the Rheumatic Diseases, 2010, 69, 1315-1320.	0.9	74
143	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, 1651-1655.	2.9	61
144	Chromosome 11q13.5 variant associated with childhood eczema: An effect supplementary to filaggrin mutations. Journal of Allergy and Clinical Immunology, 2010, 125, 170-174.e2.	2.9	58

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145	Host genetic and epigenetic factors in toxoplasmosis. Memorias Do Instituto Oswaldo Cruz, 2009, 104, 162-169.	1.6	29
146	Genetic Variation in VEGF Does Not Contribute Significantly to the Risk of Congenital Cardiovascular Malformation. PLoS ONE, 2009, 4, e4978.	2.5	19
147	Programmed Death Ligand 1 (PD-L1) Gene Variants Contribute to Autoimmune Addisonâ€™s Disease and Gravesâ€™ Disease Susceptibility. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 5139-5145.	3.6	72
148	Genetic Variants Associated With Myocardial Infarction Risk Factors in Over 8000 Individuals From Five Ethnic Groups. Circulation: Cardiovascular Genetics, 2009, 2, 16-25.	5.1	67
149	Analysis of North American Rheumatoid Arthritis Consortium data using a penalized logistic regression approach. BMC Proceedings, 2009, 3, S61.	1.6	12
150	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, 884-889.	1.5	98
151	The tryptophan 620 allele of the lymphoid tyrosine phosphatase (PTPN22) gene predisposes to autoimmune Addison's disease. Clinical Endocrinology, 2009, 70, 358-362.	2.4	42
152	A composite-likelihood approach for identifying polymorphisms that are potentially directly associated with disease. European Journal of Human Genetics, 2009, 17, 644-650.	2.8	3
153	HLA-B*5701 genotype is a major determinant of drug-induced liver injury due to flucloxacillin. Nature Genetics, 2009, 41, 816-819.	21.4	950
154	Detecting geneâ€"gene interactions that underlie human diseases. Nature Reviews Genetics, 2009, 10, 392-404.	16.3	1,177
155	Estimation and testing of geneâ€"environment interactions in family-based association studies. Genomics, 2009, 93, 5-9.	2.9	18
156	Meta-analysis of filaggrin polymorphisms in eczema and asthma: Robust risk factors in atopic disease. Journal of Allergy and Clinical Immunology, 2009, 123, 1361-1370.e7.	2.9	374
157	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, 1591-1594.	0.7	95
158	Filaggrin null mutations and childhood atopic eczema: A population-based case-control study. Journal of Allergy and Clinical Immunology, 2008, 121, 940-946.e3.	2.9	143
159	Genetic and Epigenetic Factors at COL2A1 and ABCA4 Influence Clinical Outcome in Congenital Toxoplasmosis. PLoS ONE, 2008, 3, e2285.	2.5	102
160	Y Chromosome Lineage- and Village-Specific Genes on Chromosomes 1p22 and 6q27 Control Visceral Leishmaniasis in Sudan. PLoS Genetics, 2007, 3, e71.	3.5	64
161	Genomic Polymorphism at the Interferon-Induced Helicase (IFIH1) Locus Contributes to Gravesâ€™ Disease Susceptibility. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 3338-3341.	3.6	104
162	Genetic Analysis Workshop 15: gene expression analysis and approaches to detecting multiple functional loci. BMC Proceedings, 2007, 1, S1.	1.6	8

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163	Linkage and association analysis of GAW15 simulated data: fine-mapping of chromosome 6 region. BMC Proceedings, 2007, 1, S23.	1.6	5
164	Joint linkage and association analysis for identification of potentially causal polymorphisms in GAW15 data. BMC Proceedings, 2007, 1, S36.	1.6	4
165	Dealing with Missing Data in Family-Based Association Studies: A Multiple Imputation Approach. Human Heredity, 2007, 63, 229-238.	0.8	25
166	Explorative twoâ€locus linkage analysis suggests a multiplicative interaction between the 7q32 and 16p13 myoclonic seizuresâ€related photosensitivity loci. Genetic Epidemiology, 2007, 31, 42-50.	1.3	28
167	Exploring causality via identification of SNPs or haplotypes responsible for a linkage signal. Genetic Epidemiology, 2007, 31, 727-740.	1.3	14
168	Quantitative trait association in parent offspring trios: Extension of case/pseudocontrol method and comparison of prospective and retrospective approaches. Genetic Epidemiology, 2007, 31, 813-833.	1.3	14
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