Heather J Cordell

List of Publications by Year
in descending order

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235	23,495	12330 69	8866 145
papers	citations	h-index	g-index

263	263	263	28111
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Association of the T-cell regulatory gene CTLA4 with susceptibility to autoimmune disease. Nature, 2003, 423, 506-511.	27.8	1,980
2	A genome-wide search for human type 1 diabetes susceptibility genes. Nature, 1994, 371, 130-136.	27.8	1,326
3	Detecting geneâ€“gene interactions that underlie human diseases. Nature Reviews Genetics, 2009, 10, 392-404.	16.3	1,177
4	Haplotype tagging for the identification of common disease genes. Nature Genetics, 2001, 29, 233-237.	21.4	1,118
5	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
6	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
7	Epistasis: what it means, what it doesn't mean, and statistical methods to detect it in humans. Human Molecular Genetics, 2002, 11, 2463-2468.	2.9	890
8	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
9	Genetic association studies. Lancet, The, 2005, 366, 1121-1131.	13.7	462
10	Genome-wide association study identifies 12 new susceptibility loci for primary biliary cirrhosis. Nature Genetics, 2011, 43, 329-332.	21.4	441
11	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
12	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, 124-141.	6.2	393
13	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
14	Enabling the genomic revolution in Africa. Science, 2014, 344, 1346-1348.	12.6	361
15	Chromosomeâ€“specific microsatellite sets for fluorescenceâ€“based, semiâ€“automated genome mapping. Nature Genetics, 1994, 7, 390-395.	21.4	323
16	Polygenic control of autoimmune diabetes in nonobese diabetic mice. Nature Genetics, 1993, 4, 404-409.	21.4	310
17	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
18	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

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19	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
20	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
21	Dense fine-mapping study identifies new susceptibility loci for primary biliary cirrhosis. Nature Genetics, 2012, 44, 1137-1141.	21.4	251
22	International genome-wide meta-analysis identifies new primary biliary cirrhosis risk loci and targetable pathogenic pathways. Nature Communications, 2015, 6, 8019.	12.8	245
23	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
24	Parameters for reliable results in genetic association studies in common disease. Nature Genetics, 2002, 30, 149-150.	21.4	224
25	Case/pseudocontrol analysis in genetic association studies: A unified framework for detection of genotype and haplotype associations, geneâ€gene and geneâ€environment interactions, and parentâ€ofâ€origin effects. Genetic Epidemiology, 2004, 26, 167-185.	1.3	214
26	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	12.8	214
27	Transcriptomic profiling across the nonalcoholic fatty liver disease spectrum reveals gene signatures for steatohepatitis and fibrosis. Science Translational Medicine, 2020, 12, .	12.4	205
28	Remapping the Insulin Gene/IDDM2 Locus in Type 1 Diabetes. Diabetes, 2004, 53, 1884-1889.	0.6	198
29	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, 4037-4043.	3.6	189
30	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
31	Genomeâ€wide linkage analysis for human longevity: Genetics of Healthy Aging Study. Aging Cell, 2013, 12, 184-193.	6.7	170
32	SNP Selection in genomeâ€wide and candidate gene studies via penalized logistic regression. Genetic Epidemiology, 2010, 34, 879-891.	1.3	166
33	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
34	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
35	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
36	Evidence for a cluster of genes on chromosome 17q11â€“q21 controlling susceptibility to tuberculosis and leprosy in Brazilians. Genes and Immunity, 2004, 5, 46-57.	4.1	135

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37	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
38	Regression Mapping of Association between the Human Leukocyte Antigen Region and Graves Disease. American Journal of Human Genetics, 2005, 76, 157-163.	6.2	134
39	A genome-wide scan for loci linked to forearm bone mineral density. Human Genetics, 1999, 104, 226-233.	3.8	131
40	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
41	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
42	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
43	The Interleukin 1 Gene Cluster Contains a Major Susceptibility Locus for Ankylosing Spondylitis. American Journal of Human Genetics, 2004, 75, 587-595.	6.2	122
44	Comparison of Methods to Account for Relatedness in Genome-Wide Association Studies with Family-Based Data. PLoS Genetics, 2014, 10, e1004445.	3.5	122
45	Distinct genetic loci control development of benign and malignant skin tumours in mice. Nature Genetics, 1995, 10, 424-429.	21.4	120
46	A male-female bias in type 1 diabetes and linkage to chromosome Xp in MHC HLA-DR3-positive patients. Nature Genetics, 1998, 19, 301-302.	21.4	119
47	Whole Exome Sequencing Reveals the Major Genetic Contributors to Nonsyndromic Tetralogy of Fallot. Circulation Research, 2019, 124, 553-563.	4.5	118
48	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
49	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
50	Genetic and Epigenetic Factors at COL2A1 and ABCA4 Influence Clinical Outcome in Congenital Toxoplasmosis. PLoS ONE, 2008, 3, e2285.	2.5	102
51	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
52	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
53	SLC11A1 (formerly NRAMP1) and susceptibility to visceral leishmaniasis in The Sudan. European Journal of Human Genetics, 2004, 12, 66-74.	2.8	99
54	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

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55	Multilocus Linkage Tests Based on Affected Relative Pairs. American Journal of Human Genetics, 2000, 66, 1273-1286.	6.2	96
56	Determining the Population Frequency of the CFHR3/CFHR1 Deletion at 1q32. PLoS ONE, 2013, 8, e60352.	2.5	96
57	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
58	Genome-wide scans for leprosy and tuberculosis susceptibility genes in Brazilians. Genes and Immunity, 2004, 5, 63-67.	4.1	94
59	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. Journal of Clinical Investigation, 2015, 125, 1739-1751.	8.2	94
60	Multifactorial inheritance in type 1 diabetes. Trends in Genetics, 1995, 11, 499-504.	6.7	93
61	Protein-altering and regulatory genetic variants near GATA4 implicated in bicuspid aortic valve. Nature Communications, 2017, 8, 15481.	12.8	90
62	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
63	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
64	Improved Statistics for Genome-Wide Interaction Analysis. PLoS Genetics, 2012, 8, e1002625.	3.5	82
65	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
66	Genetic susceptibility to visceral leishmaniasis in The Sudan: linkage and association with IL4 and IFNGR1. Genes and Immunity, 2003, 4, 351-355.	4.1	79
67	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
68	Common polymorphism in H19 associated with birthweight and cord blood IGF-II levels in humans. BMC Genetics, 2005, 6, 22.	2.7	72
69	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
70	Statistical Modeling of Interlocus Interactions in a Complex Disease: Rejection of the Multiplicative Model of Epistasis in Type 1 Diabetes. Genetics, 2001, 158, 357-367.	2.9	72
71	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.	4.1	71
72	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

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73	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, 184-194.	0.6	69
74	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
75	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
76	The HLA-DPB1-Associated Component of the IDDM1 and Its Relationship to the Major Loci HLA-DQB1, -DQA1, and -DRB1. Diabetes, 2001, 50, 1200-1205.	0.6	64
77	Haplotype Structure, LD Blocks, and Uneven Recombination Within the LRP5 Gene. Genome Research, 2003, 13, 845-855.	5.5	64
78	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
79	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, 1128-1133.	0.6	62
80	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
81	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
82	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
83	Statistical methods for genome-wide association studies. Seminars in Cancer Biology, 2019, 55, 53-60.	9.6	59
84	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
85	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
86	Ascertainment bias in the estimation of sibling genetic risk parameters. Genetic Epidemiology, 2000, 18, 217-235.	1.3	54
87	Properties of case/pseudocontrol analysis for genetic association studies: Effects of recombination, ascertainment, and multiple affected offspring. Genetic Epidemiology, 2004, 26, 186-205.	1.3	54
88	Genomeâ€wide Association Study and Metaâ€analysis on Alcoholâ€Associated Liver Cirrhosis Identifies Genetic Risk Factors. Hepatology, 2021, 73, 1920-1931.	7.3	54
89	Macrophage scavenger receptor 1 mediates lipid-induced inflammation in non-alcoholic fatty liver disease. Journal of Hepatology, 2022, 76, 1001-1012.	3.7	54
90	Intercellular adhesion molecule-1 K469E polymorphism: study of association with multiple sclerosis. Human Immunology, 2003, 64, 345-349.	2.4	48

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91	Methylation quantitative trait locus analysis of osteoarthritis links epigenetics with genetic risk. Human Molecular Genetics, 2015, 24, 7432-7444.	2.9	48
92	Linkage Analysis of Candidate Genes and Gene-Gene Interactions in Chinese Hypertensive Sib Pairs. Hypertension, 1999, 33, 1332-1337.	2.7	47
93	Genes at human chromosome 5q31.1 regulate delayed-type hypersensitivity responses associated with Leishmania chagasi infection. Genes and Immunity, 2007, 8, 539-551.	4.1	47
94	Fine mapping and replication of genetic risk loci in primary sclerosing cholangitis. Scandinavian Journal of Gastroenterology, 2012, 47, 820-826.	1.5	47
95	Congenital heart disease risk loci identified by genome-wide association study in European patients. Journal of Clinical Investigation, 2021, 131, .	8.2	47
96	Estimation and testing of genotype and haplotype effects in caseâ€control studies: comparison of weighted regression and multiple imputation procedures. Genetic Epidemiology, 2006, 30, 259-275.	1.3	46
97	PREMIM and EMIM: tools for estimation of maternal, imprinting and interaction effects using multinomial modelling. BMC Bioinformatics, 2012, 13, 149.	2.6	45
98	Linkage and association mapping of the LRP5 locus on chromosomeÂ11q13 in typeÂ1 diabetes. Human Genetics, 2003, 113, 99-105.	3.8	44
99	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
100	Genome-wide association study of response to methotrexate in early rheumatoid arthritis patients. Pharmacogenomics Journal, 2018, 18, 528-538.	2.0	42
101	Genome-wide association study of response to tumour necrosis factor inhibitor therapy in rheumatoid arthritis. Pharmacogenomics Journal, 2018, 18, 657-664.	2.0	41
102	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
103	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
104	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
105	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, 1294-1302.	6.2	35
106	Exome sequencing in dementia with Lewy bodies. Translational Psychiatry, 2016, 6, e728-e728.	4.8	35
107	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
108	Speed-bumps ahead for the genetics of later-life diseases. Trends in Genetics, 2011, 27, 387-388.	6.7	34

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109	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
110	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
111	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
112	A genetic risk score and diabetes predict development of alcohol-related cirrhosis in drinkers. Journal of Hepatology, 2022, 76, 275-282.	3.7	33
113	An extension of the Maximum Lod Score method to X-linked loci. Annals of Human Genetics, 1995, 59, 435-449.	0.8	31
114	Association Between C677T Polymorphism of Methylene Tetrahydrofolate Reductase and Congenital Heart Disease. Circulation: Cardiovascular Genetics, 2013, 6, 347-353.	5.1	31
115	Urinary Tract Effects of HPSE2 Mutations. Journal of the American Society of Nephrology: JASN, 2015, 26, 797-804.	6.1	31
116	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
117	Heterogeneity in the Magnitude of the Insulin Gene Effect on HLA Risk in Type 1 Diabetes. Diabetes, 2004, 53, 3286-3291.	0.6	30
118	CTLA-4 as a genetic determinant in autoimmune Addisonâ€™s disease. Genes and Immunity, 2015, 16, 430-436.	4.1	30
119	Host genetic and epigenetic factors in toxoplasmosis. Memorias Do Instituto Oswaldo Cruz, 2009, 104, 162-169.	1.6	29
120	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
121	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
122	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
123	Factors determining penetrance in familial atypical haemolytic uraemic syndrome. Journal of Medical Genetics, 2014, 51, 756-764.	3.2	28
124	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
125	Association of Autoimmune Addison's Disease with Alleles of STAT4 and GATA3 in European Cohorts. PLoS ONE, 2014, 9, e88991.	2.5	27
126	X Chromosome Contribution to the Genetic Architecture of Primary Biliary Cholangitis. Gastroenterology, 2021, 160, 2483-2495.e26.	1.3	27

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127	Association analysis identifies new risk loci for congenital heart disease in Chinese populations. Nature Communications, 2015, 6, 8082.	12.8	26
128	A PDCD1 Role in the Genetic Predisposition to NAFLD-HCC?. Cancers, 2021, 13, 1412.	3.7	26
129	Dealing with Missing Data in Family-Based Association Studies: A Multiple Imputation Approach. Human Heredity, 2007, 63, 229-238.	0.8	25
130	A genome-wide association study of mitochondrial DNA copy number in two population-based cohorts. Human Genomics, 2019, 13, 6.	2.9	25
131	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
132	Association between Aldosterone Production and Variation in the 11Î²-Hydroxylase (CYP11B1) Gene. Journal of Clinical Endocrinology and Metabolism, 2006, 91, 5051-5056.	3.6	24
133	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
134	Heritability of udder morphology and colostrum quality traits in swine1. Journal of Animal Science, 2016, 94, 3636-3644.	0.5	23
135	Gamma regression improves Haseman-Elston and variance components linkage analysis for sib-pairs. Genetic Epidemiology, 2004, 26, 97-107.	1.3	22
136	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
137	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
138	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
139	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
140	Fieller's theorem and linkage disequilibrium mapping. , 1999, 17, 237-252.		21
141	Association mapping of complex diseases in linked regions: estimation of genetic effects and feasibility of testing rare variants. Genetic Epidemiology, 2003, 24, 36-43.	1.3	21
142	Relationship of sow udder morphology with piglet suckling behavior and teat access. Theriogenology, 2016, 86, 1913-1920.	2.1	20
143	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
144	Increased serum miR-193a-5p during non-alcoholic fatty liver disease progression: Diagnostic and mechanistic relevance. JHEP Reports, 2022, 4, 100409.	4.9	20

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145	Comparison of populationâ€•and familyâ€‘based methods for genetic association analysis in the presence of interacting loci. Genetic Epidemiology, 2005, 29, 51-67.	1.3	19
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	Analysis of BAFF gene polymorphisms in UK Gravesâ€™ disease patients. Clinical Endocrinology, 2019, 90, 170-174.	2.4	19
148	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
149	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.	0.8	19
150	Estimation and testing of geneâ€“environment interactions in family-based association studies. Genomics, 2009, 93, 5-9.	2.9	18
151	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
152	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
153	Association of Novel Locus With Rheumatic Heart Disease in Black African Individuals. JAMA Cardiology, 2021, 6, 1000.	6.1	18
154	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
155	Genome-wide association study identifies susceptibility loci for acute myeloid leukemia. Nature Communications, 2021, 12, 6233.	12.8	17
156	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
157	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
158	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
159	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
160	Prediction of treatment response in rheumatoid arthritis patients using genomeâ€‐wide SNP data. Genetic Epidemiology, 2018, 42, 754-771.	1.3	15
161	Common Genetic Variants Contribute to Risk of Transposition of the Great Arteries. Circulation Research, 2022, 130, 166-180.	4.5	15
162	Mapping multiple linked quantitative trait loci in non-obese diabetic mice using a stepwise regression strategy. Genetical Research, 1998, 71, 51-64.	0.9	14

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163	Affected-Sib-Pair Data Can Be Used to Distinguish Two-Locus Heterogeneity from Two-Locus Epistasis. American Journal of Human Genetics, 2003, 73, 1468-1470.	6.2	14
164	Exploring causality via identification of SNPs or haplotypes responsible for a linkage signal. Genetic Epidemiology, 2007, 31, 727-740.	1.3	14
165	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
166	Exploring Shared Susceptibility between Two Neural Crest Cells Originating Conditions: Neuroblastoma and Congenital Heart Disease. Genes, 2019, 10, 663.	2.4	14
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