Paul I W De Bakker

List of Publications by Year
in descending order

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235 papers	102,807 citations	1536 106 h-index	1051 234 g-index
250 all docs	250 docs citations	250 times ranked	105559 citing authors

#	Article	IF	Citations
1	PLINK: A Tool Set for Whole-Genome Association and Population-Based Linkage Analyses. American Journal of Human Genetics, 2007, 81, 559-575.	6.2	26,761
2	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
3	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137
4	Structure validation by CÎ± geometry: Ï•,Ïˆ and CÎ² deviation. Proteins: Structure, Function and Bioinformatics, 2003, 50, 437-450.	2.6	4,134
5	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
6	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	27.8	2,625
7	Genome-Wide Association Analysis Identifies Loci for Type 2 Diabetes and Triglyceride Levels. Science, 2007, 316, 1331-1336.	12.6	2,623
8	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
9	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	27.8	2,400
10	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	13.7	1,937
11	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
12	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	27.8	1,788
13	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nature Genetics, 2008, 40, 638-645.	21.4	1,683
14	Efficiency and power in genetic association studies. Nature Genetics, 2005, 37, 1217-1223.	21.4	1,597
15	Risk Alleles for Multiple Sclerosis Identified by a Genomewide Study. New England Journal of Medicine, 2007, 357, 851-862.	27.0	1,529
16	Common variants at 30 loci contribute to polygenic dyslipidemia. Nature Genetics, 2009, 41, 56-65.	21.4	1,234
17	SNAP: a web-based tool for identification and annotation of proxy SNPs using HapMap. Bioinformatics, 2008, 24, 2938-2939.	4.1	1,201
18	Genome-wide association study meta-analysis identifies seven new rheumatoid arthritis risk loci. Nature Genetics, 2010, 42, 508-514.	21.4	1,132

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19	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	21.4	1,124
20	The Major Genetic Determinants of HIV-1 Control Affect HLA Class I Peptide Presentation. Science, 2010, 330, 1551-1557.	12.6	1,054
21	STAT4and the Risk of Rheumatoid Arthritis and Systemic Lupus Erythematosus. New England Journal of Medicine, 2007, 357, 977-986.	27.0	914
22	Integrated detection and population-genetic analysis of SNPs and copy number variation. Nature Genetics, 2008, 40, 1166-1174.	21.4	838
23	HLA-A*3101 and Carbamazepine-Induced Hypersensitivity Reactions in Europeans. New England Journal of Medicine, 2011, 364, 1134-1143.	27.0	815
24	Five amino acids in three HLA proteins explain most of the association between MHC and seropositive rheumatoid arthritis. Nature Genetics, 2012, 44, 291-296.	21.4	768
25	TCF7L2Polymorphisms and Progression to Diabetes in the Diabetes Prevention Program. New England Journal of Medicine, 2006, 355, 241-250.	27.0	762
26	Meta-analysis of genome scans and replication identify CD6, IRF8 and TNFRSF1A as new multiple sclerosis susceptibility loci. Nature Genetics, 2009, 41, 776-782.	21.4	729
27	Pooled Association Tests for Rare Variants in Exon-Resequencing Studies. American Journal of Human Genetics, 2010, 86, 832-838.	6.2	715
28	A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. Nature Genetics, 2006, 38, 1166-1172.	21.4	686
29	Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. Lancet, The, 2012, 379, 1205-1213.	13.7	668
30	Whole-genome association study of bipolar disorder. Molecular Psychiatry, 2008, 13, 558-569.	7.9	642
31	Whole-genome sequence variation, population structure and demographic history of the Dutch population. Nature Genetics, 2014, 46, 818-825.	21.4	641
32	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	2.2	567
33	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. Nature Genetics, 2012, 44, 1336-1340.	21.4	558
34	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
35	Imputing Amino Acid Polymorphisms in Human Leukocyte Antigens. PLoS ONE, 2013, 8, e64683.	2.5	538
36	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	6.0	528

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37	Two independent alleles at 6q23 associated with risk of rheumatoid arthritis. Nature Genetics, 2007, 39, 1477-1482.	21.4	497
38	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. Nature Genetics, 2016, 48, 1043-1048.	21.4	494
39	Practical aspects of imputation-driven meta-analysis of genome-wide association studies. Human Molecular Genetics, 2008, 17, R122-R128.	2.9	475
40	Genetic risk factors for ischaemic stroke and its subtypes (the METASTROKE Collaboration): a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2012, 11, 951-962.	10.2	445
41	Common variants in KCNN3 are associated with lone atrial fibrillation. Nature Genetics, 2010, 42, 240-244.	21.4	438
42	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. Nature Genetics, 2012, 44, 483-489.	21.4	402
43	Common variants at ten loci influence QT interval duration in the QTGEN Study. Nature Genetics, 2009, 41, 399-406.	21.4	386
44	Genome-wide patterns and properties of de novo mutations in humans. Nature Genetics, 2015, 47, 822-826.	21.4	384
45	Exome sequencing and the genetic basis of complex traits. Nature Genetics, 2012, 44, 623-630.	21.4	340
46	Concept, Design and Implementation of a Cardiovascular Gene-Centric 50 K SNP Array for Large-Scale Genomic Association Studies. PLoS ONE, 2008, 3, e3583.	2.5	339
47	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
48	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
49	Genomeâ€wide metaâ€analysis identifies novel multiple sclerosis susceptibility loci. Annals of Neurology, 2011, 70, 897-912.	5.3	314
50	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	21.4	308
51	Meta-Analysis of Genome-Wide Association Studies in Celiac Disease and Rheumatoid Arthritis Identifies Fourteen Non-HLA Shared Loci. PLoS Genetics, 2011, 7, e1002004.	3.5	307
52	Evidence for an oligogenic basis of amyotrophic lateral sclerosis. Human Molecular Genetics, 2012, 21, 3776-3784.	2.9	307
53	Haplotype Structure and Genotype-Phenotype Correlations of the Sulfonylurea Receptor and the Islet ATP-Sensitive Potassium Channel Gene Region. Diabetes, 2004, 53, 1360-1368.	0.6	284
54	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282

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55	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
56	Evaluating and improving power in whole-genome association studies using fixed marker sets. Nature Genetics, 2006, 38, 663-667.	21.4	274
57	Common Missense Variant in the Glucokinase Regulatory Protein Gene Is Associated With Increased Plasma Triglyceride and C-Reactive Protein but Lower Fasting Glucose Concentrations. Diabetes, 2008, 57, 3112-3121.	0.6	264
58	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
59	HLA-B*13:01and the Dapsone Hypersensitivity Syndrome. New England Journal of Medicine, 2013, 369, 1620-1628.	27.0	260
60	Heterogeneity and Inaccuracy in Protein Structures Solved by X-Ray Crystallography. Structure, 2004, 12, 831-838.	3.3	252
61	Fine-Mapping the Genetic Association of the Major Histocompatibility Complex in Multiple Sclerosis: HLA and Non-HLA Effects. PLoS Genetics, 2013, 9, e1003926.	3.5	250
62	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	2.8	246
63	Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. Nature Genetics, 2012, 44, 631-635.	21.4	239
64	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 410-425.	6.2	239
65	Additive and interaction effects at three amino acid positions in HLA-DQ and HLA-DR molecules drive type 1 diabetes risk. Nature Genetics, 2015, 47, 898-905.	21.4	235
66	Common Variants in 40 Genes Assessed for Diabetes Incidence and Response to Metformin and Lifestyle Intervention in the Diabetes Prevention Program. Diabetes, 2010, 59, 2672-2681.	0.6	234
67	Mapping of multiple susceptibility variants within the MHC region for 7 immune-mediated diseases. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18680-18685.	7.1	231
68	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	6.2	227
69	Transferability of tag SNPs in genetic association studies in multiple populations. Nature Genetics, 2006, 38, 1298-1303.	21.4	224
70	Major histocompatibility complex associations of ankylosing spondylitis are complex and involve further epistasis with ERAP1. Nature Communications, 2015, 6, 7146.	12.8	220
71	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	10.2	217
72	Genome-wide meta-analysis in alopecia areata resolves HLA associations and reveals two new susceptibility loci. Nature Communications, 2015, 6, 5966.	12.8	213

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73	Myosin IXB variant increases the risk of celiac disease and points toward a primary intestinal barrier defect. Nature Genetics, 2005, 37, 1341-1344.	21.4	211
74	Large-Scale Gene-Centric Analysis Identifies Novel Variants for Coronary Artery Disease. PLoS Genetics, 2011, 7, e1002260.	3.5	203
75	Causal Effects of Body Mass Index on Cardiometabolic Traits and Events: A Mendelian Randomization Analysis. American Journal of Human Genetics, 2014, 94, 198-208.	6.2	199
76	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
77	The role of the CD58 locus in multiple sclerosis. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5264-5269.	7.1	185
78	Fine Mapping Major Histocompatibility Complex Associations in Psoriasis and Its Clinical Subtypes. American Journal of Human Genetics, 2014, 95, 162-172.	6.2	182
79	GWAS Identifies Novel Susceptibility Loci on 6p21.32 and 21q21.3 for Hepatocellular Carcinoma in Chronic Hepatitis B Virus Carriers. PLoS Genetics, 2012, 8, e1002791.	3.5	177
80	Comprehensive Association Testing of Common Mitochondrial DNA Variation in Metabolic Disease. American Journal of Human Genetics, 2006, 79, 54-61.	6.2	173
81	Novel Loci for Metabolic Networks and Multi-Tissue Expression Studies Reveal Genes for Atherosclerosis. PLoS Genetics, 2012, 8, e1002907.	3.5	171
82	Angiogenin variants in Parkinson disease and amyotrophic lateral sclerosis. Annals of Neurology, 2011, 70, 964-973.	5.3	168
83	Comparative transcriptomics of extreme phenotypes of human HIV-1 infection and SIV infection in sooty mangabey and rhesus macaque. Journal of Clinical Investigation, 2011, 121, 2391-2400.	8.2	168
84	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. Circulation Research, 2017, 120, 341-353.	4.5	166
85	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. Nature Genetics, 2015, 47, 1085-1090.	21.4	164
86	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	6.2	158
87	Fine Mapping Seronegative and Seropositive Rheumatoid Arthritis to Shared and Distinct HLA Alleles by Adjusting for the Effects of Heterogeneity. American Journal of Human Genetics, 2014, 94, 522-532.	6.2	156
88	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. Nature Communications, 2015, 6, 6916.	12.8	154
89	Polymorphisms of large effect explain the majority of the host genetic contribution to variation of HIV-1 virus load. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14658-14663.	7.1	154
90	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	21.4	147

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91	A Large-Scale Genetic Analysis Reveals a Strong Contribution of the HLA Class II Region to Giant Cell Arteritis Susceptibility. American Journal of Human Genetics, 2015, 96, 565-580.	6.2	144
92	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	2.9	141
93	HLA-DRB1*11and variants of the MHC class II locus are strong risk factors for systemic juvenile idiopathic arthritis. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15970-15975.	7.1	139
94	Association of Granulomatosis With Polyangiitis (Wegener's) With HLAâ€“DPB1*04 and SEMA6A Gene Variants: Evidence From Genomeâ€Wide Analysis. Arthritis and Rheumatism, 2013, 65, 2457-2468.	6.7	138
95	Risk for myasthenia gravis maps to a ¹⁵¹Proâ†'Ala change in TNIP1 and to human leukocyte antigenâ€B*08. Annals of Neurology, 2012, 72, 927-935.	5.3	137
96	Effective Detection of Human Leukocyte Antigen Risk Alleles in Celiac Disease Using Tag Single Nucleotide Polymorphisms. PLoS ONE, 2008, 3, e2270.	2.5	136
97	Ab initio construction of polypeptide fragments: Accuracy of loop decoy discrimination by an all-atom statistical potential and the AMBER force field with the Generalized Born solvation model. Proteins: Structure, Function and Bioinformatics, 2003, 51, 21-40.	2.6	135
98	Next-generation sequencing for HLA typing of class I loci. BMC Genomics, 2011, 12, 42.	2.8	135
99	Risk for ACPA-positive rheumatoid arthritis is driven by shared HLA amino acid polymorphisms in Asian and European populations. Human Molecular Genetics, 2014, 23, 6916-6926.	2.9	135
100	Ab initio construction of polypeptide fragments: Efficient generation of accurate, representative ensembles. Proteins: Structure, Function and Bioinformatics, 2003, 51, 41-55.	2.6	134
101	Common NOS1AP Variants Are Associated With a Prolonged QTc Interval in the Rotterdam Study. Circulation, 2007, 116, 10-16.	1.6	134
102	Genome-wide association analysis identifies multiple loci related to resting heart rate. Human Molecular Genetics, 2010, 19, 3885-3894.	2.9	133
103	BehÃ§et disease-associated MHC class I residues implicate antigen binding and regulation of cell-mediated cytotoxicity. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8867-8872.	7.1	123
104	Fine mapping in the MHC region accounts for 18% additional genetic risk for celiac disease. Nature Genetics, 2015, 47, 577-578.	21.4	123
105	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	6.2	122
106	A genome-wide association study identifies a functional ERAP2 haplotype associated with birdshot chorioretinopathy. Human Molecular Genetics, 2014, 23, 6081-6087.	2.9	115
107	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115
108	Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. Lancet Diabetes and Endocrinology,the, 2015, 3, 243-253.	11.4	115

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109	Low-Frequency and Rare-Coding Variation Contributes to Multiple Sclerosis Risk. Cell, 2018, 175, 1679-1687.e7.	28.9	115
110	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
111	Association Study of Common Genetic Variants and HIV-1 Acquisition in 6,300 Infected Cases and 7,200 Controls. PLoS Pathogens, 2013, 9, e1003515.	4.7	109
112	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	2.8	109
113	Molecular dynamics simulations of the hyperthermophilic protein sac7d from Sulfolobus acidocaldarius : contribution of salt bridges to thermostability 1 1Edited by B. Honig. Journal of Molecular Biology, 1999, 285, 1811-1830.	4.2	108
114	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. Nature Genetics, 2014, 46, 901-904.	21.4	104
115	Negative selection in humans and fruit flies involves synergistic epistasis. Science, 2017, 356, 539-542.	12.6	103
116	An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge. Genome Biology, 2014, 15, R53.	9.6	101
117	Genome-wide association study of coronary and aortic calcification implicates risk loci for coronary artery disease and myocardial infarction. Atherosclerosis, 2013, 228, 400-405.	0.8	100
118	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	12.8	99
119	Genome-wide Association Study Identifies Five Susceptibility Loci for Follicular Lymphoma outside the HLA Region. American Journal of Human Genetics, 2014, 95, 462-471.	6.2	96
120	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	12.8	95
121	Improved imputation quality of low-frequency and rare variants in European samples using the â€˜Genome of The Netherlandsâ€™. European Journal of Human Genetics, 2014, 22, 1321-1326.	2.8	92
122	<scp>C9orf72</scp> and <scp>UNC13A</scp> are shared risk loci for amyotrophic lateral sclerosis and frontotemporal dementia: A genomeâ€wide metaâ€analysis. Annals of Neurology, 2014, 76, 120-133.	5.3	91
123	Meta-analysis in more than 17,900 cases of ischemic stroke reveals a novel association at 12q24.12. Neurology, 2014, 83, 678-685.	1.1	89
124	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
125	Interrogating the major histocompatibility complex with high-throughput genomics. Human Molecular Genetics, 2012, 21, R29-R36.	2.9	85
126	Variation at HLA-DRB1 is associated with resistance to enteric fever. Nature Genetics, 2014, 46, 1333-1336.	21.4	85

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127	Population-specific genotype imputations using minimac or IMPUTE2. Nature Protocols, 2015, 10, 1285-1296.	12.0	84
128	Transmission of human mtDNA heteroplasmy in the Genome of the Netherlands families: support for a variable-size bottleneck. Genome Research, 2016, 26, 417-426.	5.5	84
129	Gene-centric meta-analyses of 108 912 individuals confirm known body mass index loci and reveal three novel signals. Human Molecular Genetics, 2013, 22, 184-201.	2.9	82
130	Quantitative Trait Loci for CD4:CD8 Lymphocyte Ratio Are Associated with Risk of Type 1 Diabetes and HIV-1 Immune Control. American Journal of Human Genetics, 2010, 86, 88-92.	6.2	80
131	Predicting HLA alleles from high-resolution SNP data in three Southeast Asian populations. Human Molecular Genetics, 2014, 23, 4443-4451.	2.9	80
132	Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. American Journal of Human Genetics, 2015, 97, 775-789.	6.2	77
133	Association Testing of Variants in the Hepatocyte Nuclear Factor 4Â Gene With Risk of Type 2 Diabetes in 7,883 People. Diabetes, 2005, 54, 886-892.	0.6	75
134	Classical HLA-DRB1 and DPB1 alleles account for HLA associations with primary biliary cirrhosis. Genes and Immunity, 2012, 13, 461-468.	4.1	75
135	A Novel MMP12 Locus Is Associated with Large Artery Atherosclerotic Stroke Using a Genome-Wide Age-at-Onset Informed Approach. PLoS Genetics, 2014, 10, e1004469.	3.5	75
136	Genetic Association of Lipids and Lipid Drug Targets With Abdominal Aortic Aneurysm. JAMA Cardiology, 2018, 3, 26.	6.1	75
137	Association of Common Variation in the HNF1Â Gene Region With Risk of Type 2 Diabetes. Diabetes, 2005, 54, 2336-2342.	0.6	73
138	Genetic variation at 16q24.2 is associated with small vessel stroke. Annals of Neurology, 2017, 81, 383-394.	5.3	73
139	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	12.8	71
140	IL12A, MPHOSPH9/CDK2AP1 and RGS1 are novel multiple sclerosis susceptibility loci. Genes and Immunity, 2010, 11, 397-405.	4.1	70
141	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. Nature Methods, 2014, 11, 868-874.	19.0	70
142	Searching for signals of evolutionary selection in 168 genes related to immune function. Human Genetics, 2006, 119, 92-102.	3.8	67
143	Missing heritability: is the gap closing? An analysis of 32 complex traits in the Lifelines Cohort Study. European Journal of Human Genetics, 2017, 25, 877-885.	2.8	67
144	Modeling the cumulative genetic risk for multiple sclerosis from genome-wide association data. Genome Medicine, 2011, 3, 3.	8.2	63

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145	Deleterious Alleles in the Human Genome Are on Average Younger Than Neutral Alleles of the Same Frequency. PLoS Genetics, 2013, 9, e1003301.	3.5	63
146	Stroke Genetics Network (SiGN) Study. Stroke, 2013, 44, 2694-2702.	2.0	62
147	Fine-mapping classical HLA variation associated with durable host control of HIV-1 infection in African Americans. Human Molecular Genetics, 2012, 21, 4334-4347.	2.9	61
148	Resetting the bar: Statistical significance in wholeâ€genome sequencingâ€based association studies of global populations. Genetic Epidemiology, 2017, 41, 145-151.	1.3	61
149	MODBASE, a database of annotated comparative protein structure models. Nucleic Acids Research, 2000, 28, 250-253.	14.5	59
150	PANDIT: an evolution-centric database of protein and associated nucleotide domains with inferred trees. Nucleic Acids Research, 2006, 34, D327-D331.	14.5	59
151	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. European Heart Journal, 2018, 39, 3961-3969.	2.2	59
152	Many hypotheses but no replication for the association between PDE4D and stroke. Nature Genetics, 2006, 38, 1091-1092.	21.4	58
153	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. Nature Communications, 2015, 6, 5751.	12.8	58
154	Shared genetic contribution to ischemic stroke and Alzheimer's disease. Annals of Neurology, 2016, 79, 739-747.	5.3	56
155	Agreement between TOAST and CCS ischemic stroke classification. Neurology, 2014, 83, 1653-1660.	1.1	55
156	High Risk Population Isolate Reveals Low Frequency Variants Predisposing to Intracranial Aneurysms. PLoS Genetics, 2014, 10, e1004134.	3.5	55
157	Common Genetic Variation Near the Phospholamban Gene Is Associated with Cardiac Repolarisation: Meta-Analysis of Three Genome-Wide Association Studies. PLoS ONE, 2009, 4, e6138.	2.5	53
158	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. Human Molecular Genetics, 2016, 25, 1663-1676.	2.9	52
159	Seventeen years of statin pharmacogenetics: a systematic review. Pharmacogenomics, 2016, 17, 163-180.	1.3	52
160	Multiethnic Genetic Association Studies Improve Power for Locus Discovery. PLoS ONE, 2010, 5, e12600.	2.5	50
161	Concept and design of a genome-wide association genotyping array tailored for transplantation-specific studies. Genome Medicine, 2015, 7, 90.	8.2	49
162	Principal-Component Analysis for Assessment of Population Stratification in Mitochondrial Medical Genetics. American Journal of Human Genetics, 2010, 86, 904-917.	6.2	45

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163	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	12.8	45
164	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. Journal of the American Heart Association, 2016, 5, .	3.7	45
165	Pandit: a database of protein and associated nucleotide domains with inferred trees. Bioinformatics, 2003, 19, 1556-1563.	4.1	44
166	Crystallographic Refinement by Knowledge-Based Exploration of Complex Energy Landscapes. Structure, 2005, 13, 1311-1319.	3.3	44
167	Biases and Reconciliation in Estimates of Linkage Disequilibrium in the Human Genome. American Journal of Human Genetics, 2006, 78, 588-603.	6.2	43
168	The Duffy Antigen Receptor for Chemokines Null Promoter Variant Does Not Influence HIV-1 Acquisition or Disease Progression. Cell Host and Microbe, 2009, 5, 408-410.	11.0	43
169	Comprehensive association testing of common genetic variation in DNA repair pathway genes in relationship with breast cancer risk in multiple populations. Human Molecular Genetics, 2008, 17, 825-834.	2.9	42
170	A general framework for meta-analyzing dependent studies with overlapping subjects in association mapping. Human Molecular Genetics, 2016, 25, 1857-1866.	2.9	42
171	Common mitochondrial sequence variants in ischemic stroke. Annals of Neurology, 2011, 69, 471-480.	5.3	35
172	Amino acid position 11 of HLA-DRÎ²1 is a major determinant of chromosome 6p association with ulcerative colitis. Genes and Immunity, 2012, 13, 245-252.	4.1	35
173	Atrial fibrillation genetic risk differentiates cardioembolic stroke from other stroke subtypes. Neurology: Genetics, 2018, 4, e293.	1.9	35
174	The impact of susceptibility loci for coronary artery disease on other vascular domains and recurrence risk. European Heart Journal, 2013, 34, 2896-2904.	2.2	32
175	Incremental value of a genetic risk score for the prediction of new vascular events in patients with clinically manifest vascular disease. Atherosclerosis, 2015, 239, 451-458.	0.8	31
176	Using previously genotyped controls in genome-wide association studies (GWAS): application to the Stroke Genetics Network (SiGN). Frontiers in Genetics, 2014, 5, 95.	2.3	30
177	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. Neurology, 2019, 92, .	1.1	30
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