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	Exome-chip association analysis of intracranial aneurysms. Neurology, 2020, 94, e481-e488.	1.1	5
2	Genome-wide association meta-analysis of 30,000 samples identifies seven novel loci for quantitative ECG traits. European Journal of Human Genetics, 2019, 27, 952-962.	2.8	29
3	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
4	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. Neurology, 2019, 92, .	1.1	30
5	Genetic Association of Lipids and Lipid Drug Targets With Abdominal Aortic Aneurysm. JAMA Cardiology, 2018, 3, 26.	6.1	75
6	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. European Heart Journal, 2018, 39, 3961-3969.	2.2	59
7	Atrial fibrillation genetic risk differentiates cardioembolic stroke from other stroke subtypes. Neurology: Genetics, 2018, 4, e293.	1.9	35
8	Genetic Susceptibility Loci for Cardiovascular Disease and Their Impact on Atherosclerotic Plaques. Circulation Genomic and Precision Medicine, 2018, 11, e002115.	3.6	20
9	Low-Frequency and Rare-Coding Variation Contributes to Multiple Sclerosis Risk. Cell, 2018, 175, 1679-1687.e7.	28.9	115
10	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
11	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
12	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
13	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
14	Negative selection in humans and fruit flies involves synergistic epistasis. Science, 2017, 356, 539-542.	12.6	103
15	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
16	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	12.8	95
17	Reply. Journal of the American College of Cardiology, 2017, 69, 1099.	2.8	0
18	Genetic variants associated with type 2 diabetes and adiposity and risk of intracranial and abdominal aortic aneurysms. European Journal of Human Genetics, 2017, 25, 758-762.	2.8	13

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19	Resetting the bar: Statistical significance in wholeâ€genome sequencingâ€based association studies of global populations. Genetic Epidemiology, 2017, 41, 145-151.	1.3	61
20	Genetic variation at 16q24.2 is associated with small vessel stroke. Annals of Neurology, 2017, 81, 383-394.	5.3	73
21	Evaluating the Impact of Functional Genetic Variation on HIV-1 Control. Journal of Infectious Diseases, 2017, 216, 1063-1069.	4.0	20
22	A replication study of genetic risk loci for ischemic stroke in a Dutch population: a case-control study. Scientific Reports, 2017, 7, 12175.	3.3	9
23	A framework for the detection of de novo mutations in family-based sequencing data. European Journal of Human Genetics, 2017, 25, 227-233.	2.8	29
24	A general framework for meta-analyzing dependent studies with overlapping subjects in association mapping. Human Molecular Genetics, 2016, 25, 1857-1866.	2.9	42
25	A genetic risk score is associated with statin-induced low-density lipoprotein cholesterol lowering. Pharmacogenomics, 2016, 17, 583-591.	1.3	9
26	Harnessing publicly available genetic data to prioritize lipid modifying therapeutic targets for prevention of coronary heart disease based on dysglycemic risk. Human Genetics, 2016, 135, 453-467.	3.8	15
27	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	2.8	109
28	Shared genetic contribution to ischemic stroke and Alzheimer's disease. Annals of Neurology, 2016, 79, 739-747.	5.3	56
29	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
30	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
31	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
32	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
33	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. Journal of the American Heart Association, 2016, 5, .	3.7	45
34	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	12.8	99
35	Twenty-eight genetic loci associated with ST-T-wave amplitudes of the electrocardiogram. Human Molecular Genetics, 2016, 25, 2093-2103.	2.9	24
36	The HLA-DQÎ²1 insertion is a strong achalasia risk factor and displays a geospatial northâ€“south gradient among Europeans. European Journal of Human Genetics, 2016, 24, 1228-1231.	2.8	21

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37	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	10.2	217
38	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
39	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
40	Seventeen years of statin pharmacogenetics: a systematic review. Pharmacogenomics, 2016, 17, 163-180.	1.3	52
41	Extensive Association of Common Disease Variants with Regulatory Sequence. PLoS ONE, 2016, 11, e0165893.	2.5	7
42	Concept and design of a genome-wide association genotyping array tailored for transplantation-specific studies. Genome Medicine, 2015, 7, 90.	8.2	49
43	No Additional Prognostic Value of Genetic Information in the Prediction of Vascular Events after Cerebral Ischemia of Arterial Origin: The PROMISe Study. PLoS ONE, 2015, 10, e0119203.	2.5	5
44	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
45	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. Nature Communications, 2015, 6, 5751.	12.8	58
46	Accurate and Fast Multiple-Testing Correction in eQTL Studies. American Journal of Human Genetics, 2015, 96, 857-868.	6.2	25
47	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. Nature Communications, 2015, 6, 6916.	12.8	154
48	Major histocompatibility complex associations of ankylosing spondylitis are complex and involve further epistasis with ERAP1. Nature Communications, 2015, 6, 7146.	12.8	220
49	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
50	Serum Lipid Levels, Body Mass Index, and Their Role in Coronary Artery Calcification. Circulation: Cardiovascular Genetics, 2015, 8, 327-333.	5.1	17
51	Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. American Journal of Human Genetics, 2015, 97, 775-789.	6.2	77
52	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
53	Variants in ALOX5, ALOX5AP and LTA4H are not associated with atherosclerotic plaque phenotypes: The Athero-Express Genomics Study. Atherosclerosis, 2015, 239, 528-538.	0.8	22
54	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823

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55	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
56	Genome-wide meta-analysis in alopecia areata resolves HLA associations and reveals two new susceptibility loci. Nature Communications, 2015, 6, 5966.	12.8	213
57	Population-specific genotype imputations using minimac or IMPUTE2. Nature Protocols, 2015, 10, 1285-1296.	12.0	84
58	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
59	Genetic risk scores and number of autoantibodies in patients with rheumatoid arthritis. Annals of the Rheumatic Diseases, 2015, 74, 762-768.	0.9	14
60	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115
61	Genome-wide patterns and properties of de novo mutations in humans. Nature Genetics, 2015, 47, 822-826.	21.4	384
62	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
63	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	2.2	567
64	Fine mapping in the MHC region accounts for 18% additional genetic risk for celiac disease. Nature Genetics, 2015, 47, 577-578.	21.4	123
65	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
66	Genome-wide association study of virologic response with efavirenz-containing or abacavir-containing regimens in AIDS clinical trials group protocols. Pharmacogenetics and Genomics, 2015, 25, 51-59.	1.5	13
67	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. Nature Genetics, 2015, 47, 1085-1090.	21.4	164
68	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	12.8	45
69	Impact of carotid atherosclerosis loci on cardiovascular events. Atherosclerosis, 2015, 243, 466-468.	0.8	18
70	Somatic Variation of T-Cell Receptor Genes Strongly Associate with HLA Class Restriction. PLoS ONE, 2015, 10, e0140815.	2.5	30
71	Rs964184 (APOA5-A4-C3-A1) Is Related to Elevated Plasma Triglyceride Levels, but Not to an Increased Risk for Vascular Events in Patients with Clinically Manifest Vascular Disease. PLoS ONE, 2014, 9, e101082.	2.5	22
72	Association Claims in the Sequencing Era. Genes, 2014, 5, 196-213.	2.4	8

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73	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
74	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
75	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
76	Agreement between TOAST and CCS ischemic stroke classification. Neurology, 2014, 83, 1653-1660.	1.1	55
77	Human leukocyte antigen class II variants and adult-onset asthma: does occupational allergen exposure play a role?. European Respiratory Journal, 2014, 44, 1234-1242.	6.7	10
78	High Risk Population Isolate Reveals Low Frequency Variants Predisposing to Intracranial Aneurysms. PLoS Genetics, 2014, 10, e1004134.	3.5	55
79	Genetic risk load according to the site of intracranial aneurysms. Neurology, 2014, 83, 34-39.	1.1	28
80	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
81	No association between CYP3A4*22Âand statin effectiveness in reducing the risk for myocardial infarction. Pharmacogenomics, 2014, 15, 1471-1477.	1.3	10
82	<scp>LDL</scp>â€câ€linked <scp>SNP</scp>s are associated with <scp>LDL</scp>â€c and myocardial infarction despite lipidâ€lowering therapy in patients with established vascular disease. European Journal of Clinical Investigation, 2014, 44, 184-191.	3.4	13
83	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
84	A genome-wide association study identifies a functional ERAP2 haplotype associated with birdshot chorioretinopathy. Human Molecular Genetics, 2014, 23, 6081-6087.	2.9	115
85	Genome-Wide Association Study of Human Immunodeficiency Virus (HIV)-1 Coreceptor Usage in Treatment-Naive Patients from An AIDS Clinical Trials Group Study. Open Forum Infectious Diseases, 2014, 1, ofu018.	0.9	7
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	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
88	Predicting HLA alleles from high-resolution SNP data in three Southeast Asian populations. Human Molecular Genetics, 2014, 23, 4443-4451.	2.9	80
89	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	2.8	246
90	A gene pathway analysis highlights the role of cellular adhesion molecules in multiple sclerosis susceptibility. Genes and Immunity, 2014, 15, 126-132.	4.1	26

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91	Cholesteryl Ester Transfer Protein Polymorphisms, Statin Use, and Their Impact on Cholesterol Levels and Cardiovascular Events. Clinical Pharmacology and Therapeutics, 2014, 95, 314-320.	4.7	12
92	Variation at HLA-DRB1 is associated with resistance to enteric fever. Nature Genetics, 2014, 46, 1333-1336.	21.4	85
93	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	21.4	147
94	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
95	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
96	No evidence for shared genetic basis of common variants in multiple sclerosis and amyotrophic lateral sclerosis. Human Molecular Genetics, 2014, 23, 1916-1922.	2.9	23
97	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
98	Fine Mapping Major Histocompatibility Complex Associations in Psoriasis and Its Clinical Subtypes. American Journal of Human Genetics, 2014, 95, 162-172.	6.2	182
99	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. Nature Methods, 2014, 11, 868-874.	19.0	70
100	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
101	<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
102	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
103	Fast pairwise IBD association testing in genome-wide association studies. Bioinformatics, 2014, 30, 206-213.	4.1	5
104	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	6.0	528
105	Towards a Molecular Systems Model of Coronary Artery Disease. Current Cardiology Reports, 2014, 16, 488.	2.9	19
106	Whole-genome sequence variation, population structure and demographic history of the Dutch population. Nature Genetics, 2014, 46, 818-825.	21.4	641
107	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. Nature Genetics, 2014, 46, 901-904.	21.4	104
108	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281

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109	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
110	Impact of Inherited Genetic Variants Associated With Lipid Profile, Hypertension, and Coronary Artery Disease on the Risk of Intracranial and Abdominal Aortic Aneurysms. Circulation: Cardiovascular Genetics, 2013, 6, 264-270.	5.1	27
111	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
112	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
113	Coding Variants at Hexa-allelic Amino Acid 13 of HLA-DRB1 Explain Independent SNP Associations with Follicular Lymphoma Risk. American Journal of Human Genetics, 2013, 93, 167-172.	6.2	26
114	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	2.9	141
115	Granulomatosis with polyangiitis (Wegener's) is associated with HLA-DPB1*04 and EMA6A gene variants. Evidence from a genome-wide analysis. Presse Medicale, 2013, 42, 668.	1.9	1
116	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
117	Stroke Genetics Network (SiGN) Study. Stroke, 2013, 44, 2694-2702.	2.0	62
118	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 3394-3395.	2.9	1
119	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
120	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
121	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
122	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
123	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
124	HLA-B*13:01and the Dapsone Hypersensitivity Syndrome. New England Journal of Medicine, 2013, 369, 1620-1628.	27.0	260
125	Imputing Amino Acid Polymorphisms in Human Leukocyte Antigens. PLoS ONE, 2013, 8, e64683.	2.5	538
126	Novel Loci for Metabolic Networks and Multi-Tissue Expression Studies Reveal Genes for Atherosclerosis. PLoS Genetics, 2012, 8, e1002907.	3.5	171

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127	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
128	Genetic Modulation of Lipid Profiles following Lifestyle Modification or Metformin Treatment: The Diabetes Prevention Program. PLoS Genetics, 2012, 8, e1002895.	3.5	29
129	Interrogating the major histocompatibility complex with high-throughput genomics. Human Molecular Genetics, 2012, 21, R29-R36.	2.9	85
130	Evidence for an oligogenic basis of amyotrophic lateral sclerosis. Human Molecular Genetics, 2012, 21, 3776-3784.	2.9	307
131	Classical HLA-DRB1 and DPB1 alleles account for HLA associations with primary biliary cirrhosis. Genes and Immunity, 2012, 13, 461-468.	4.1	75
132	Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. Lancet, The, 2012, 379, 1205-1213.	13.7	668
133	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	13.7	1,937
134	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. Nature Genetics, 2012, 44, 1336-1340.	21.4	558
135	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
136	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
137	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. Nature Genetics, 2012, 44, 483-489.	21.4	402
138	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
139	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
140	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
141	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
142	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
143	Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. Nature Genetics, 2012, 44, 631-635.	21.4	239
144	Exome sequencing and the genetic basis of complex traits. Nature Genetics, 2012, 44, 623-630.	21.4	340

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145	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
146	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2012, 90, 1116-1117.	6.2	0
147	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	27.8	2,400
148	HLA-A*3101 and Carbamazepine-Induced Hypersensitivity Reactions in Europeans. New England Journal of Medicine, 2011, 364, 1134-1143.	27.0	815
149	Modeling the cumulative genetic risk for multiple sclerosis from genome-wide association data. Genome Medicine, 2011, 3, 3.	8.2	63
150	IL28B Alleles Exert an Additive Dose Effect When Applied to HCV-HIV Coinfected Persons Undergoing Peginterferon and Ribavirin Therapy. PLoS ONE, 2011, 6, e25753.	2.5	19
151	Large-Scale Gene-Centric Analysis Identifies Novel Variants for Coronary Artery Disease. PLoS Genetics, 2011, 7, e1002260.	3.5	203
152	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
153	Next-generation sequencing for HLA typing of class I loci. BMC Genomics, 2011, 12, 42.	2.8	135
154	Common mitochondrial sequence variants in ischemic stroke. Annals of Neurology, 2011, 69, 471-480.	5.3	35
155	Genomeâ€wide metaâ€analysis identifies novel multiple sclerosis susceptibility loci. Annals of Neurology, 2011, 70, 897-912.	5.3	314
156	Angiogenin variants in Parkinson disease and amyotrophic lateral sclerosis. Annals of Neurology, 2011, 70, 964-973.	5.3	168
157	Meta-analysis of genome-wide association studies in celiac disease and rheumatoid arthritis identifies fourteen non-HLA shared loci. Annals of the Rheumatic Diseases, 2011, 70, A21-A21.	0.9	0
158	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
159	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
160	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
161	Pooled Association Tests for Rare Variants in Exon-Resequencing Studies. American Journal of Human Genetics, 2010, 86, 832-838.	6.2	715
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	IL12A, MPHOSPH9/CDK2AP1 and RGS1 are novel multiple sclerosis susceptibility loci. Genes and Immunity, 2010, 11, 397-405.	4.1	70
164	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	27.8	2,625
165	Common variants in KCNN3 are associated with lone atrial fibrillation. Nature Genetics, 2010, 42, 240-244.	21.4	438
166	Genome-wide association study meta-analysis identifies seven new rheumatoid arthritis risk loci. Nature Genetics, 2010, 42, 508-514.	21.4	1,132
167	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	21.4	308
168	Infectious diseases not immune to genome-wide association. Nature Genetics, 2010, 42, 731-732.	21.4	23
169	Multiethnic Genetic Association Studies Improve Power for Locus Discovery. PLoS ONE, 2010, 5, e12600.	2.5	50
170	Meta-Analysis of Genome-Wide Association Studies. Cold Spring Harbor Protocols, 2010, 2010, pdb.top81.	0.3	16
171	Genome-wide association analysis identifies multiple loci related to resting heart rate. Human Molecular Genetics, 2010, 19, 3885-3894.	2.9	133
172	The Major Genetic Determinants of HIV-1 Control Affect HLA Class I Peptide Presentation. Science, 2010, 330, 1551-1557.	12.6	1,054
173	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
174	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
175	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
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