Paul I W De Bakker

List of Publications by Year in Descending Order

236 papers	80,995 citations	102 h-index	250 g-index
250 ext. papers	94,874 ext. citations	15.4 avg, IF	7.01 L-index

#	Paper	IF	Citations
236	Exome-chip association analysis of intracranial aneurysms. *Neurology*, **2020**, 94, e481-e488	6.5	3
235	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	5.3	18
234	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
233	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. *Neurology*, **2019**,	6.5	17
232	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. *Nature Communications*, **2018**, 9, 2904	17.4	39
231	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nature Genetics*, **2018**, 50, 524-537	36.3	536
230	Genetic Association of Lipids and Lipid Drug Targets With Abdominal Aortic Aneurysm: A Meta-analysis. *JAMA Cardiology*, **2018**, 3, 26-33	16.2	44
229	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. *European Heart Journal*, **2018**, 39, 3961-3969	9.5	31
228	Atrial fibrillation genetic risk differentiates cardioembolic stroke from other stroke subtypes. *Neurology: Genetics*, **2018**, 4, e293	3.8	19
227	Genetic Susceptibility Loci for Cardiovascular Disease and Their Impact on Atherosclerotic Plaques. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002115	5.2	11
226	Low-Frequency and Rare-Coding Variation Contributes to Multiple Sclerosis Risk. *Cell*, **2018**, 175, 1679-1687.e72	36.2	
225	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
224	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	5.3	43
223	Negative selection in humans and fruit flies involves synergistic epistasis. *Science*, **2017**, 356, 539-542	33.3	53
222	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. *Circulation Research*, **2017**, 120, 341-353	15.7	97
221	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. *Nature Communications*, **2017**, 8, 15805	17.4	50
220	Reply: Poor Sensitivity and Specificity of Electrocardiographic Estimation of Myocardial Mass. *Journal of the American College of Cardiology*, **2017**, 69, 1099	15.1	

219	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	5.3	11
218	Resetting the bar: Statistical significance in whole-genome sequencing-based association studies of global populations. *Genetic Epidemiology*, **2017**, 41, 145-151	2.6	36
217	Genetic variation at 16q24.2 is associated with small vessel stroke. *Annals of Neurology*, **2017**, 81, 383-394	9.4	51
216	Evaluating the Impact of Functional Genetic Variation on HIV-1 Control. *Journal of Infectious Diseases*, **2017**, 216, 1063-1069	7	18
215	A replication study of genetic risk loci for ischemic stroke in a Dutch population: a case-control study. *Scientific Reports*, **2017**, 7, 12175	4.9	7
214	A framework for the detection of de novo mutations in family-based sequencing data. *European Journal of Human Genetics*, **2017**, 25, 227-233	5.3	19
213	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
212	52 Genetic Loci Influencing Myocardial Mass. *Journal of the American College of Cardiology*, **2016**, 68, 1435-1448	15.1	76
211	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
210	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. *Nature Genetics*, **2016**, 48, 1043-8	36.3	328
209	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. *Journal of the American Heart Association*, **2016**, 5,	6	34
208	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. *Nature Communications*, **2016**, 7, 12989	17.4	70
207	Twenty-eight genetic loci associated with ST-T-wave amplitudes of the electrocardiogram. *Human Molecular Genetics*, **2016**, 25, 2093-2103	5.6	20
206	The HLA-DQ insertion is a strong achalasia risk factor and displays a geospatial north-south gradient among Europeans. *European Journal of Human Genetics*, **2016**, 24, 1228-31	5.3	16
205	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. *Lancet Neurology, The*, **2016**, 15, 174-184	24.1	159
204	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. *Human Molecular Genetics*, **2016**, 25, 1663-76	5.6	39
203	Transmission of human mtDNA heteroplasmy in the Genome of the Netherlands families: support for a variable-size bottleneck. *Genome Research*, **2016**, 26, 417-26	9.7	48
202	Seventeen years of statin pharmacogenetics: a systematic review. *Pharmacogenomics*, **2016**, 17, 163-80	2.6	37

201	Extensive Association of Common Disease Variants with Regulatory Sequence. *PLoS ONE*, **2016**, 11, e0165893	3.7	7
200	A general framework for meta-analyzing dependent studies with overlapping subjects in association mapping. *Human Molecular Genetics*, **2016**, 25, 1857-66	5.6	28
199	A genetic risk score is associated with statin-induced low-density lipoprotein cholesterol lowering. *Pharmacogenomics*, **2016**, 17, 583-91	2.6	8
198	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	6.3	9
197	Cystatin C and Cardiovascular Disease: A Mendelian Randomization Study. *Journal of the American College of Cardiology*, **2016**, 68, 934-45	15.1	65
196	Shared genetic contribution to Ischaemic Stroke and Alzheimer's Disease. *Annals of Neurology*, **2016**, 79, 739-747	9.4	42
195	Population-specific genotype imputations using minimac or IMPUTE2. *Nature Protocols*, **2015**, 10, 1285-96	8.8	59
194	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	36.3	154
193	Genetic risk scores and number of autoantibodies in patients with rheumatoid arthritis. *Annals of the Rheumatic Diseases*, **2015**, 74, 762-8	2.4	11
192	Characteristics of de novo structural changes in the human genome. *Genome Research*, **2015**, 25, 792-801	9.7	83
191	Genome-wide patterns and properties of de novo mutations in humans. *Nature Genetics*, **2015**, 47, 822-826	36.3	267
190	Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. *Lancet Diabetes and Endocrinology,the*, **2015**, 3, 243-53	18.1	81
189	Mendelian randomization of blood lipids for coronary heart disease. *European Heart Journal*, **2015**, 36, 539-50	9.5	417
188	Fine mapping in the MHC region accounts for 18% additional genetic risk for celiac disease. *Nature Genetics*, **2015**, 47, 577-8	36.3	99
187	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, 565-80	11	96
186	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, 51-9	1.9	13
185	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. *Nature Genetics*, **2015**, 47, 1085-90	36.3	112
184	Genome of The Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. *Nature Communications*, **2015**, 6, 6065	17.4	32

183	Impact of carotid atherosclerosis loci on cardiovascular events. *Atherosclerosis*, **2015**, 243, 466-8	3.1	12
182	Concept and design of a genome-wide association genotyping array tailored for transplantation-specific studies. *Genome Medicine*, **2015**, 7, 90	14.4	38
181	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	3.7	5
180	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	6	220
179	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. *Nature Communications*, **2015**, 6, 5751	17.4	44
178	Accurate and fast multiple-testing correction in eQTL studies. *American Journal of Human Genetics*, **2015**, 96, 857-68	11	18
177	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. *Nature Communications*, **2015**, 6, 6916	17.4	115
176	Major histocompatibility complex associations of ankylosing spondylitis are complex and involve further epistasis with ERAP1. *Nature Communications*, **2015**, 6, 7146	17.4	164
175	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, 14658-63	11.5	108
174	Serum lipid levels, body mass index, and their role in coronary artery calcification: a polygenic analysis. *Circulation: Cardiovascular Genetics*, **2015**, 8, 327-33		16
173	Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. *American Journal of Human Genetics*, **2015**, 97, 775-89	11	56
172	HLA-DRB1*11 and 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, 15970-5	11.5	103
171	Variants in ALOX5, ALOX5AP and LTA4H are not associated with atherosclerotic plaque phenotypes: the Athero-Express Genomics Study. *Atherosclerosis*, **2015**, 239, 528-38	3.1	13
170	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
169	Incremental value of a genetic risk score for the prediction of new vascular events in patients with clinically manifest vascular disease. *Atherosclerosis*, **2015**, 239, 451-8	3.1	27
168	Genome-wide meta-analysis in alopecia areata resolves HLA associations and reveals two new susceptibility loci. *Nature Communications*, **2015**, 6, 5966	17.4	142
167	Somatic Variation of T-Cell Receptor Genes Strongly Associate with HLA Class Restriction. *PLoS ONE*, **2015**, 10, e0140815	3.7	20
166	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170

165	Predicting HLA alleles from high-resolution SNP data in three Southeast Asian populations. *Human Molecular Genetics*, **2014**, 23, 4443-51	5.6	69
164	The Genome of the Netherlands: design, and project goals. *European Journal of Human Genetics*, **2014**, 22, 221-7	5.3	184
163	A gene pathway analysis highlights the role of cellular adhesion molecules in multiple sclerosis susceptibility. *Genes and Immunity*, **2014**, 15, 126-32	4.4	23
162	Cholesteryl ester transfer protein polymorphisms, statin use, and their impact on cholesterol levels and cardiovascular events. *Clinical Pharmacology and Therapeutics*, **2014**, 95, 314-20	6.1	12
161	Variation at HLA-DRB1 is associated with resistance to enteric fever. *Nature Genetics*, **2014**, 46, 1333-6	36.3	56
160	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. *Nature Genetics*, **2014**, 46, 1233-8	36.3	108
159	Genome-wide association study identifies five susceptibility loci for follicular lymphoma outside the HLA region. *American Journal of Human Genetics*, **2014**, 95, 462-71	11	74
158	Risk for ACPA-positive rheumatoid arthritis is driven by shared HLA amino acid polymorphisms in Asian and European populations. *Human Molecular Genetics*, **2014**, 23, 6916-26	5.6	114
157	No evidence for shared genetic basis of common variants in multiple sclerosis and amyotrophic lateral sclerosis. *Human Molecular Genetics*, **2014**, 23, 1916-22	5.6	14
156	Meta-analysis in more than 17,900 cases of ischemic stroke reveals a novel association at 12q24.12. *Neurology*, **2014**, 83, 678-85	6.5	78
155	Fine mapping major histocompatibility complex associations in psoriasis and its clinical subtypes. *American Journal of Human Genetics*, **2014**, 95, 162-72	11	151
154	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. *Nature Methods*, **2014**, 11, 868-74	21.6	50
153	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
152	C9orf72 and UNC13A are shared risk loci for amyotrophic lateral sclerosis and frontotemporal dementia: a genome-wide meta-analysis. *Annals of Neurology*, **2014**, 76, 120-33	9.4	61
151	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, 522-32	11	132
150	Fast pairwise IBD association testing in genome-wide association studies. *Bioinformatics*, **2014**, 30, 206-12	7.2	5
149	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. *BMJ, The*, **2014**, 349, g4164	5.9	406
148	Towards a molecular systems model of coronary artery disease. *Current Cardiology Reports*, **2014**, 16, 488	4.2	16

147	Whole-genome sequence variation, population structure and demographic history of the Dutch population. *Nature Genetics*, **2014**, 46, 818-25	36.3	514
146	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. *Nature Genetics*, **2014**, 46, 901-4	36.3	75
145	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. *Nature Genetics*, **2014**, 46, 826-36	36.3	199
144	Causal effects of body mass index on cardiometabolic traits and events: a Mendelian randomization analysis. *American Journal of Human Genetics*, **2014**, 94, 198-208	11	156
143	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	3.7	15
142	Association claims in the sequencing era. *Genes*, **2014**, 5, 196-213	4.2	7
141	Using previously genotyped controls in genome-wide association studies (GWAS): application to the Stroke Genetics Network (SiGN). *Frontiers in Genetics*, **2014**, 5, 95	4.5	18
140	Behçet 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, 8867-72	11.5	95
139	Improved imputation quality of low-frequency and rare variants in European samples using the QGenome of The NetherlandsQ*European Journal of Human Genetics*, **2014**, 22, 1321-6	5.3	74
138	Agreement between TOAST and CCS ischemic stroke classification: the NINDS SiGN study. *Neurology*, **2014**, 83, 1653-60	6.5	48
137	Human leukocyte antigen class II variants and adult-onset asthma: does occupational allergen exposure play a role?. *European Respiratory Journal*, **2014**, 44, 1234-42	13.6	7
136	High risk population isolate reveals low frequency variants predisposing to intracranial aneurysms. *PLoS Genetics*, **2014**, 10, e1004134	6	43
135	Genetic risk load according to the site of intracranial aneurysms. *Neurology*, **2014**, 83, 34-9	6.5	22
134	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	6	63
133	No association between CYP3A4*22 and statin effectiveness in reducing the risk for myocardial infarction. *Pharmacogenomics*, **2014**, 15, 1471-7	2.6	8
132	LDL-c-linked SNPs are associated with LDL-c and myocardial infarction despite lipid-lowering therapy in patients with established vascular disease. *European Journal of Clinical Investigation*, **2014**, 44, 184-91	4.6	9
131	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	18.3	86
130	A genome-wide association study identifies a functional ERAP2 haplotype associated with birdshot chorioretinopathy. *Human Molecular Genetics*, **2014**, 23, 6081-7	5.6	82

129	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	1	7
128	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60	11	131
127	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, 264-70		21
126	Genome-wide association study of coronary and aortic calcification implicates risk loci for coronary artery disease and myocardial infarction. *Atherosclerosis*, **2013**, 228, 400-5	3.1	78
125	The impact of susceptibility loci for coronary artery disease on other vascular domains and recurrence risk. *European Heart Journal*, **2013**, 34, 2896-904	9.5	27
124	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, 167-72	11	26
123	Loci influencing blood pressure identified using a cardiovascular gene-centric array. *Human Molecular Genetics*, **2013**, 22, 1663-78	5.6	119
122	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
121	Stroke Genetics Network (SiGN) study: design and rationale for a genome-wide association study of ischemic stroke subtypes. *Stroke*, **2013**, 44, 2694-702	6.7	43
120	Association of granulomatosis with polyangiitis (Wegener©) with HLA-DPB1*04 and SEMA6A gene variants: evidence from genome-wide analysis. *Arthritis and Rheumatism*, **2013**, 65, 2457-68		102
119	Fine-mapping the genetic association of the major histocompatibility complex in multiple sclerosis: HLA and non-HLA effects. *PLoS Genetics*, **2013**, 9, e1003926	6	186
118	Deleterious alleles in the human genome are on average younger than neutral alleles of the same frequency. *PLoS Genetics*, **2013**, 9, e1003301	6	49
117	Association study of common genetic variants and HIV-1 acquisition in 6,300 infected cases and 7,200 controls. *PLoS Pathogens*, **2013**, 9, e1003515	7.6	86
116	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	5.6	73
115	HLA-B*13:01 and the dapsone hypersensitivity syndrome. *New England Journal of Medicine*, **2013**, 369, 1620-8	59.2	193
114	Imputing amino acid polymorphisms in human leukocyte antigens. *PLoS ONE*, **2013**, 8, e64683	3.7	425
113	Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. *Lancet, The*, **2012**, 379, 1205-13	40	522
112	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. *Lancet, The*, **2012**, 380, 572-80	40	1523

111	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. *Nature Genetics*, **2012**, 44, 1336-40	36.3	436
110	Risk for myasthenia gravis maps to a (151) Pro-Ala change in TNIP1 and to human leukocyte antigen-B*08. *Annals of Neurology*, **2012**, 72, 927-35	9.4	112
109	Seventy-five genetic loci influencing the human red blood cell. *Nature*, **2012**, 492, 369-75	50.4	257
108	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. *Nature Genetics*, **2012**, 44, 483-9	36.3	326
107	Fine-mapping classical HLA variation associated with durable host control of HIV-1 infection in African Americans. *Human Molecular Genetics*, **2012**, 21, 4334-47	5.6	51
106	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, 951-62	24.1	359
105	Large-scale gene-centric meta-analysis across 32 studies identifies multiple lipid loci. *American Journal of Human Genetics*, **2012**, 91, 823-38	11	189
104	Five amino acids in three HLA proteins explain most of the association between MHC and seropositive rheumatoid arthritis. *Nature Genetics*, **2012**, 44, 291-6	36.3	607
103	Amino acid position 11 of HLA-DR□ is a major determinant of chromosome 6p association with ulcerative colitis. *Genes and Immunity*, **2012**, 13, 245-52	4.4	30
102	Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. *Nature Genetics*, **2012**, 44, 631-5	36.3	184
101	Exome sequencing and the genetic basis of complex traits. *Nature Genetics*, **2012**, 44, 623-30	36.3	303
100	Large-scale gene-centric meta-analysis across 39 studies identifies type 2 diabetes loci. *American Journal of Human Genetics*, **2012**, 90, 410-25	11	214
99	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2012**, 90, 1116-1117	11	78
98	Novel Loci for metabolic networks and multi-tissue expression studies reveal genes for atherosclerosis. *PLoS Genetics*, **2012**, 8, e1002907	6	125
97	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	6	142
96	Genetic modulation of lipid profiles following lifestyle modification or metformin treatment: the Diabetes Prevention Program. *PLoS Genetics*, **2012**, 8, e1002895	6	27
95	Interrogating the major histocompatibility complex with high-throughput genomics. *Human Molecular Genetics*, **2012**, 21, R29-36	5.6	71
94	Evidence for an oligogenic basis of amyotrophic lateral sclerosis. *Human Molecular Genetics*, **2012**, 21, 3776-84	5.6	251

93	Classical HLA-DRB1 and DPB1 alleles account for HLA associations with primary biliary cirrhosis. *Genes and Immunity*, **2012**, 13, 461-8	4.4	66
92	HLA-A*3101 and carbamazepine-induced hypersensitivity reactions in Europeans. *New England Journal of Medicine*, **2011**, 364, 1134-43	59.2	689
91	Modeling the cumulative genetic risk for multiple sclerosis from genome-wide association data. *Genome Medicine*, **2011**, 3, 3	14.4	48
90	IL28B alleles exert an additive dose effect when applied to HCV-HIV coinfected persons undergoing peginterferon and ribavirin therapy. *PLoS ONE*, **2011**, 6, e25753	3.7	19
89	Large-scale gene-centric analysis identifies novel variants for coronary artery disease. *PLoS Genetics* , **2011**, 7, e1002260	6	175
88	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2011**, 88, 6-18	11	103
87	Next-generation sequencing for HLA typing of class I loci. *BMC Genomics*, **2011**, 12, 42	4.5	112
86	Common mitochondrial sequence variants in ischemic stroke. *Annals of Neurology*, **2011**, 69, 471-80	9.4	31
85	Genome-wide meta-analysis identifies novel multiple sclerosis susceptibility loci. *Annals of Neurology*, **2011**, 70, 897-912	9.4	263
84	Angiogenin variants in Parkinson disease and amyotrophic lateral sclerosis. *Annals of Neurology*, **2011**, 70, 964-73	9.4	144
83	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. *Nature*, **2011**, 476, 214-9	50.4	1948
82	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	2.4	
81	Meta-analysis of genome-wide association studies in celiac disease and rheumatoid arthritis identifies fourteen non-HLA shared loci. *PLoS Genetics*, **2011**, 7, e1002004	6	260
80	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, 2391-400	15.9	144
79	IL12A, MPHOSPH9/CDK2AP1 and RGS1 are novel multiple sclerosis susceptibility loci. *Genes and Immunity*, **2010**, 11, 397-405	4.4	62
78	Integrating common and rare genetic variation in diverse human populations. *Nature*, **2010**, 467, 52-8	50.4	2135
77	Common variants in KCNN3 are associated with lone atrial fibrillation. *Nature Genetics*, **2010**, 42, 240-4	36.3	362
76	Genome-wide association study meta-analysis identifies seven new rheumatoid arthritis risk loci. *Nature Genetics*, **2010**, 42, 508-14	36.3	969

75	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. *Nature Genetics*, **2010**, 42, 1068-76	36.3	249
74	Multiethnic genetic association studies improve power for locus discovery. *PLoS ONE*, **2010**, 5, e12600	3.7	44
73	Meta-analysis of genome-wide association studies. *Cold Spring Harbor Protocols*, **2010**, 2010, pdb.top81	1.2	12
72	Genome-wide association analysis identifies multiple loci related to resting heart rate. *Human Molecular Genetics*, **2010**, 19, 3885-94	5.6	106
71	The major genetic determinants of HIV-1 control affect HLA class I peptide presentation. *Science*, **2010**, 330, 1551-7	33.3	884
70	Common variants in 40 genes assessed for diabetes incidence and response to metformin and lifestyle intervention in the diabetes prevention program. *Diabetes*, **2010**, 59, 2672-81	0.9	200
69	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	11	71
68	Pooled association tests for rare variants in exon-resequencing studies. *American Journal of Human Genetics*, **2010**, 86, 832-8	11	615
67	Principal-component analysis for assessment of population stratification in mitochondrial medical genetics. *American Journal of Human Genetics*, **2010**, 86, 904-17	11	38
66	The role of the CD58 locus in multiple sclerosis. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 5264-9	11.5	160
65	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, 18680-5	11.5	204
64	F.27. Meta-analysis of Genome Scans and Replication Identify CD6, ICSBP1, and TNFRSF1A as Novel Multiple Sclerosis Susceptibility Loci. *Clinical Immunology*, **2009**, 131, S101	9	2
63	Common variants at 30 loci contribute to polygenic dyslipidemia. *Nature Genetics*, **2009**, 41, 56-65	36.3	1095
62	Common variants at ten loci influence QT interval duration in the QTGEN Study. *Nature Genetics*, **2009**, 41, 399-406	36.3	330
61	Meta-analysis of genome scans and replication identify CD6, IRF8 and TNFRSF1A as new multiple sclerosis susceptibility loci. *Nature Genetics*, **2009**, 41, 776-82	36.3	621
60	Selection and evaluation of Tag-SNPs using Tagger and HapMap. *Cold Spring Harbor Protocols*, **2009**, 2009, pdb.ip67	1.2	12
59	The Duffy antigen receptor for chemokines null promoter variant does not influence HIV-1 acquisition or disease progression. *Cell Host and Microbe*, **2009**, 5, 408-10; author reply 418-9	23.4	33
58	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	3.7	50

57	Integrated detection and population-genetic analysis of SNPs and copy number variation. *Nature Genetics*, **2008**, 40, 1166-74	36.3	773
56	Whole-genome association study of bipolar disorder. *Molecular Psychiatry*, **2008**, 13, 558-69	15.1	571
55	Concept, design and implementation of a cardiovascular gene-centric 50 k SNP array for large-scale genomic association studies. *PLoS ONE*, **2008**, 3, e3583	3.7	321
54	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. *Nature Genetics*, **2008**, 40, 638-45	36.3	1496
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6	Thermodynamic Correlation with Kinetic Association Rates for Several Mutants of Mouse Acetylcholinesterase **1998**, 345-350		
5	Discovering patterns of pleiotropy in genome-wide association studies		1
4	A reference panel of 64,976 haplotypes for genotype imputation		15

List of Publications

3	A high-quality reference panel reveals the complexity and distribution of structural genome changes in a human population	3
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