Paul I W De Bakker

List of Publications by Citations

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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	PLINK: a tool set for whole-genome association and population-based linkage analyses. *American Journal of Human Genetics*, **2007**, 81, 559-75	11	19239
235	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature*, **2007**, 447, 799-816	50.4	4121
234	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
233	Structure validation by Calpha geometry: phi,psi and Cbeta deviation. *Proteins: Structure, Function and Bioinformatics*, **2003**, 50, 437-50	4.2	3522
232	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
231	Genome-wide association analysis identifies loci for type 2 diabetes and triglyceride levels. *Science*, **2007**, 316, 1331-6	33.3	2364
230	Integrating common and rare genetic variation in diverse human populations. *Nature*, **2010**, 467, 52-8	50.4	2135
229	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. *Nature*, **2011**, 476, 214-9	50.4	1948
228	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. *Lancet, The*, **2012**, 380, 572-80	40	1523
227	Efficiency and power in genetic association studies. *Nature Genetics*, **2005**, 37, 1217-23	36.3	1520
226	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
225	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
224	Genome-wide detection and characterization of positive selection in human populations. *Nature*, **2007**, 449, 913-8	50.4	1367
223	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
222	Risk alleles for multiple sclerosis identified by a genomewide study. *New England Journal of Medicine*, **2007**, 357, 851-62	59.2	1327
221	Common variants at 30 loci contribute to polygenic dyslipidemia. *Nature Genetics*, **2009**, 41, 56-65	36.3	1095
220	SNAP: a web-based tool for identification and annotation of proxy SNPs using HapMap. *Bioinformatics*, **2008**, 24, 2938-9	7.2	1062

219	Genome-wide association study meta-analysis identifies seven new rheumatoid arthritis risk loci. *Nature Genetics*, **2010**, 42, 508-14	36.3	969
218	The major genetic determinants of HIV-1 control affect HLA class I peptide presentation. *Science*, **2010**, 330, 1551-7	33.3	884
217	STAT4 and the risk of rheumatoid arthritis and systemic lupus erythematosus. *New England Journal of Medicine*, **2007**, 357, 977-86	59.2	786
216	Integrated detection and population-genetic analysis of SNPs and copy number variation. *Nature Genetics*, **2008**, 40, 1166-74	36.3	773
215	HLA-A*3101 and carbamazepine-induced hypersensitivity reactions in Europeans. *New England Journal of Medicine*, **2011**, 364, 1134-43	59.2	689
214	TCF7L2 polymorphisms and progression to diabetes in the Diabetes Prevention Program. *New England Journal of Medicine*, **2006**, 355, 241-50	59.2	679
213	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
212	A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. *Nature Genetics*, **2006**, 38, 1166-72	36.3	618
211	Pooled association tests for rare variants in exon-resequencing studies. *American Journal of Human Genetics*, **2010**, 86, 832-8	11	615
210	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
209	Whole-genome association study of bipolar disorder. *Molecular Psychiatry*, **2008**, 13, 558-69	15.1	571
208	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
207	Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. *Lancet, The*, **2012**, 379, 1205-13	40	522
206	Whole-genome sequence variation, population structure and demographic history of the Dutch population. *Nature Genetics*, **2014**, 46, 818-25	36.3	514
205	Two independent alleles at 6q23 associated with risk of rheumatoid arthritis. *Nature Genetics*, **2007**, 39, 1477-82	36.3	449
204	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. *Nature Genetics*, **2012**, 44, 1336-40	36.3	436
203	Imputing amino acid polymorphisms in human leukocyte antigens. *PLoS ONE*, **2013**, 8, e64683	3.7	425
202	Practical aspects of imputation-driven meta-analysis of genome-wide association studies. *Human Molecular Genetics*, **2008**, 17, R122-8	5.6	423

201	Mendelian randomization of blood lipids for coronary heart disease. *European Heart Journal*, **2015**, 36, 539-50	9.5	417
200	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
199	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. *BMJ, The*, **2014**, 349, g4164	5.9	406
198	Common variants in KCNN3 are associated with lone atrial fibrillation. *Nature Genetics*, **2010**, 42, 240-4	36.3	362
197	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
196	Common variants at ten loci influence QT interval duration in the QTGEN Study. *Nature Genetics*, **2009**, 41, 399-406	36.3	330
195	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
194	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. *Nature Genetics*, **2012**, 44, 483-9	36.3	326
193	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
192	Exome sequencing and the genetic basis of complex traits. *Nature Genetics*, **2012**, 44, 623-30	36.3	303
191	Genome-wide patterns and properties of de novo mutations in humans. *Nature Genetics*, **2015**, 47, 822-826	36.3	267
190	Genome-wide meta-analysis identifies novel multiple sclerosis susceptibility loci. *Annals of Neurology*, **2011**, 70, 897-912	9.4	263
189	Haplotype structure and genotype-phenotype correlations of the sulfonylurea receptor and the islet ATP-sensitive potassium channel gene region. *Diabetes*, **2004**, 53, 1360-8	0.9	261
188	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
187	Seventy-five genetic loci influencing the human red blood cell. *Nature*, **2012**, 492, 369-75	50.4	257
186	Evidence for an oligogenic basis of amyotrophic lateral sclerosis. *Human Molecular Genetics*, **2012**, 21, 3776-84	5.6	251
185	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. *Nature Genetics*, **2010**, 42, 1068-76	36.3	249
184	Evaluating and improving power in whole-genome association studies using fixed marker sets. *Nature Genetics*, **2006**, 38, 663-7	36.3	241

183	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, 3112-21	0.9	223
182	Heterogeneity and inaccuracy in protein structures solved by X-ray crystallography. *Structure*, **2004**, 12, 831-8	5.2	223
181	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
180	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
179	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
178	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
177	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
176	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. *Nature Genetics*, **2014**, 46, 826-36	36.3	199
175	Transferability of tag SNPs in genetic association studies in multiple populations. *Nature Genetics*, **2006**, 38, 1298-303	36.3	198
174	HLA-B*13:01 and the dapsone hypersensitivity syndrome. *New England Journal of Medicine*, **2013**, 369, 1620-8	59.2	193
173	Large-scale gene-centric meta-analysis across 32 studies identifies multiple lipid loci. *American Journal of Human Genetics*, **2012**, 91, 823-38	11	189
172	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
171	The Genome of the Netherlands: design, and project goals. *European Journal of Human Genetics*, **2014**, 22, 221-7	5.3	184
170	Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. *Nature Genetics*, **2012**, 44, 631-5	36.3	184
169	Myosin IXB variant increases the risk of celiac disease and points toward a primary intestinal barrier defect. *Nature Genetics*, **2005**, 37, 1341-4	36.3	184
168	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
167	Large-scale gene-centric analysis identifies novel variants for coronary artery disease. *PLoS Genetics*, **2011**, 7, e1002260	6	175
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	Major histocompatibility complex associations of ankylosing spondylitis are complex and involve further epistasis with ERAP1. *Nature Communications*, **2015**, 6, 7146	17.4	164
164	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
163	Comprehensive association testing of common mitochondrial DNA variation in metabolic disease. *American Journal of Human Genetics*, **2006**, 79, 54-61	11	160
162	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. *Lancet Neurology, The*, **2016**, 15, 174-184	24.1	159
161	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
160	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
159	Fine mapping major histocompatibility complex associations in psoriasis and its clinical subtypes. *American Journal of Human Genetics*, **2014**, 95, 162-72	11	151
158	Angiogenin variants in Parkinson disease and amyotrophic lateral sclerosis. *Annals of Neurology*, **2011**, 70, 964-73	9.4	144
157	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
156	Genome-wide meta-analysis in alopecia areata resolves HLA associations and reveals two new susceptibility loci. *Nature Communications*, **2015**, 6, 5966	17.4	142
155	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
154	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
153	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
152	Novel Loci for metabolic networks and multi-tissue expression studies reveal genes for atherosclerosis. *PLoS Genetics*, **2012**, 8, e1002907	6	125
151	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	4.2	124
150	Ab initio construction of polypeptide fragments: efficient generation of accurate, representative ensembles. *Proteins: Structure, Function and Bioinformatics*, **2003**, 51, 41-55	4.2	123
149	Loci influencing blood pressure identified using a cardiovascular gene-centric array. *Human Molecular Genetics*, **2013**, 22, 1663-78	5.6	119
148	Common NOS1AP variants are associated with a prolonged QTc interval in the Rotterdam Study. *Circulation*, **2007**, 116, 10-6	16.7	116

147	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. *Nature Communications*, **2015**, 6, 6916	17.4	115
146	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
145	Effective detection of human leukocyte antigen risk alleles in celiac disease using tag single nucleotide polymorphisms. *PLoS ONE*, **2008**, 3, e2270	3.7	113
144	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. *Nature Genetics*, **2015**, 47, 1085-90	36.3	112
143	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
142	Next-generation sequencing for HLA typing of class I loci. *BMC Genomics*, **2011**, 12, 42	4.5	112
141	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. *Nature Genetics*, **2014**, 46, 1233-8	36.3	108
140	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
139	Genome-wide association analysis identifies multiple loci related to resting heart rate. *Human Molecular Genetics*, **2010**, 19, 3885-94	5.6	106
138	Molecular dynamics simulations of the hyperthermophilic protein sac7d from Sulfolobus acidocaldarius: contribution of salt bridges to thermostability. *Journal of Molecular Biology*, **1999**, 285, 1811-30	6.5	105
137	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
136	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
135	Association of granulomatosis with polyangiitis (Wegener's) with HLA-DPB1*04 and SEMA6A gene variants: evidence from genome-wide analysis. *Arthritis and Rheumatism*, **2013**, 65, 2457-68		102
134	Fine mapping in the MHC region accounts for 18% additional genetic risk for celiac disease. *Nature Genetics*, **2015**, 47, 577-8	36.3	99
133	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
132	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
131	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
130	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

129	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
128	Characteristics of de novo structural changes in the human genome. *Genome Research*, **2015**, 25, 792-801	9.7	83
127	A genome-wide association study identifies a functional ERAP2 haplotype associated with birdshot chorioretinopathy. *Human Molecular Genetics*, **2014**, 23, 6081-7	5.6	82
126	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
125	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
124	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
123	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
122	52 Genetic Loci Influencing Myocardial Mass. *Journal of the American College of Cardiology*, **2016**, 68, 1435-1448	15.1	76
121	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. *Nature Genetics*, **2014**, 46, 901-4	36.3	75
120	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
119	Improved imputation quality of low-frequency and rare variants in European samples using the Genome of The Netherlands *European Journal of Human Genetics*, **2014**, 22, 1321-6	5.3	74
118	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
117	Low-Frequency and Rare-Coding Variation Contributes to Multiple Sclerosis Risk. *Cell*, **2018**, 175, 1679-1687.e7	36.2	72
116	Interrogating the major histocompatibility complex with high-throughput genomics. *Human Molecular Genetics*, **2012**, 21, R29-36	5.6	71
115	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
114	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. *Nature Communications*, **2016**, 7, 12989	17.4	70
113	Predicting HLA alleles from high-resolution SNP data in three Southeast Asian populations. *Human Molecular Genetics*, **2014**, 23, 4443-51	5.6	69
112	Association testing of variants in the hepatocyte nuclear factor 4alpha gene with risk of type 2 diabetes in 7,883 people. *Diabetes*, **2005**, 54, 886-92	0.9	69

111	Association of common variation in the HNF1alpha gene region with risk of type 2 diabetes. *Diabetes*, **2005**, 54, 2336-42	0.9	67
110	Classical HLA-DRB1 and DPB1 alleles account for HLA associations with primary biliary cirrhosis. *Genes and Immunity*, **2012**, 13, 461-8	4.4	66
109	Cystatin C and Cardiovascular Disease: A Mendelian Randomization Study. *Journal of the American College of Cardiology*, **2016**, 68, 934-45	15.1	65
108	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
107	IL12A, MPHOSPH9/CDK2AP1 and RGS1 are novel multiple sclerosis susceptibility loci. *Genes and Immunity*, **2010**, 11, 397-405	4.4	62
106	Searching for signals of evolutionary selection in 168 genes related to immune function. *Human Genetics*, **2006**, 119, 92-102	6.3	62
105	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
104	Population-specific genotype imputations using minimac or IMPUTE2. *Nature Protocols*, **2015**, 10, 1285-96	8.8	59
103	Variation at HLA-DRB1 is associated with resistance to enteric fever. *Nature Genetics*, **2014**, 46, 1333-6	36.3	56
102	Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. *American Journal of Human Genetics*, **2015**, 97, 775-89	11	56
101	MODBASE, a database of annotated comparative protein structure models. *Nucleic Acids Research*, **2000**, 28, 250-3	20.1	54
100	Negative selection in humans and fruit flies involves synergistic epistasis. *Science*, **2017**, 356, 539-542	33.3	53
99	Genetic variation at 16q24.2 is associated with small vessel stroke. *Annals of Neurology*, **2017**, 81, 383-394	9.4	51
98	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
97	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. *Nature Communications*, **2017**, 8, 15805	17.4	50
96	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. *Nature Methods*, **2014**, 11, 868-74	21.6	50
95	PANDIT: an evolution-centric database of protein and associated nucleotide domains with inferred trees. *Nucleic Acids Research*, **2006**, 34, D327-31	20.1	50
94	Many hypotheses but no replication for the association between PDE4D and stroke. *Nature Genetics*, **2006**, 38, 1091-2; author reply 1092-3	36.3	50

93	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
92	Deleterious alleles in the human genome are on average younger than neutral alleles of the same frequency. *PLoS Genetics*, **2013**, 9, e1003301	6	49
91	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
90	Agreement between TOAST and CCS ischemic stroke classification: the NINDS SiGN study. *Neurology*, **2014**, 83, 1653-60	6.5	48
89	Modeling the cumulative genetic risk for multiple sclerosis from genome-wide association data. *Genome Medicine*, **2011**, 3, 3	14.4	48
88	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. *Nature Communications*, **2015**, 6, 5751	17.4	44
87	Multiethnic genetic association studies improve power for locus discovery. *PLoS ONE*, **2010**, 5, e12600	3.7	44
86	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
85	Genetic Association of Lipids and Lipid Drug Targets With Abdominal Aortic Aneurysm: A Meta-analysis. *JAMA Cardiology*, **2018**, 3, 26-33	16.2	44
84	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
83	High risk population isolate reveals low frequency variants predisposing to intracranial aneurysms. *PLoS Genetics*, **2014**, 10, e1004134	6	43
82	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
81	Crystallographic refinement by knowledge-based exploration of complex energy landscapes. *Structure*, **2005**, 13, 1311-9	5.2	42
80	Shared genetic contribution to Ischaemic Stroke and Alzheimer Disease. *Annals of Neurology*, **2016**, 79, 739-747	9.4	42
79	Pandit: a database of protein and associated nucleotide domains with inferred trees. *Bioinformatics* , **2003**, 19, 1556-63	7.2	40
78	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
77	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
76	Concept and design of a genome-wide association genotyping array tailored for transplantation-specific studies. *Genome Medicine*, **2015**, 7, 90	14.4	38

75	Principal-component analysis for assessment of population stratification in mitochondrial medical genetics. *American Journal of Human Genetics*, **2010**, 86, 904-17	11	38
74	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, 825-34	5.6	38
73	Biases and reconciliation in estimates of linkage disequilibrium in the human genome. *American Journal of Human Genetics*, **2006**, 78, 588-603	11	38
72	Seventeen years of statin pharmacogenetics: a systematic review. *Pharmacogenomics*, **2016**, 17, 163-80	2.6	37
71	Resetting the bar: Statistical significance in whole-genome sequencing-based association studies of global populations. *Genetic Epidemiology*, **2017**, 41, 145-151	2.6	36
70	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. *Journal of the American Heart Association*, **2016**, 5,	6	34
69	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
68	Genome of The Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. *Nature Communications*, **2015**, 6, 6065	17.4	32
67	Common mitochondrial sequence variants in ischemic stroke. *Annals of Neurology*, **2011**, 69, 471-80	9.4	31
66	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. *European Heart Journal*, **2018**, 39, 3961-3969	9.5	31
65	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
64	A general framework for meta-analyzing dependent studies with overlapping subjects in association mapping. *Human Molecular Genetics*, **2016**, 25, 1857-66	5.6	28
63	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
62	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
61	Genetic modulation of lipid profiles following lifestyle modification or metformin treatment: the Diabetes Prevention Program. *PLoS Genetics*, **2012**, 8, e1002895	6	27
60	Knowledge-based real-space explorations for low-resolution structure determination. *Structure*, **2006**, 14, 1313-20	5.2	27
59	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
58	Advantages of fine-grained side chain conformer libraries. *Protein Engineering, Design and Selection*, **2003**, 16, 963-9	1.9	25

57	Discrete restraint-based protein modeling and the Calpha-trace problem. *Protein Science*, **2003**, 12, 2032-46	6.5	25
56	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
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