Albert V. Smith

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65,520 110 255 324 h-index g-index citations papers 16 6.94 79,755 359 L-index ext. citations avg, IF ext. papers

#	Paper	IF	Citations
324	A haplotype map of the human genome. <i>Nature</i> , 2005 , 437, 1299-320	50.4	4818
323	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007 , 449, 851-61	50.4	3647
322	Biological, clinical and population relevance of 95 loci for blood lipids. <i>Nature</i> , 2010 , 466, 707-13	50.4	2742
321	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. <i>Nature Genetics</i> , 2013 , 45, 1452-8	36.3	2714
320	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
319	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010 , 42, 937-48	36.3	2267
318	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011 , 478, 103-9	50.4	1564
317	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010 , 467, 832-8	50.4	1514
316	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011 , 43, 333-8	36.3	1394
315	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007 , 449, 913-8	50.4	1367
314	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014 , 46, 1173-86	36.3	1339
313	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015 , 47, 1121-1130	36.3	1290
312	Genome-wide association study of blood pressure and hypertension. <i>Nature Genetics</i> , 2009 , 41, 677-87	36.3	1065
311	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
310	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates Alltau, immunity and lipid processing. <i>Nature Genetics</i> , 2019 , 51, 414-430	36.3	917
309	Genome-wide analysis of genetic loci associated with Alzheimer disease. <i>JAMA - Journal of the American Medical Association</i> , 2010 , 303, 1832-40	27.4	888
308	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. <i>Nature Genetics</i> , 2012 , 44, 491-501	36.3	866

(2014-2016)

307	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016 , 533, 539-42	50.4	850
306	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010 , 42, 949-60	36.3	724
305	Genome-wide association analysis identifies variants associated with nonalcoholic fatty liver disease that have distinct effects on metabolic traits. <i>PLoS Genetics</i> , 2011 , 7, e1001324	6	629
304	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012 , 44, 991-1005	36.3	621
303	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. <i>Nature Genetics</i> , 2012 , 44, 659-69	36.3	615
302	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016 , 48, 624-33	36.3	602
301	New loci associated with kidney function and chronic kidney disease. <i>Nature Genetics</i> , 2010 , 42, 376-84	36.3	599
300	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. <i>Science</i> , 2013 , 340, 1467-71	33.3	563
299	Genetic associations with valvular calcification and aortic stenosis. <i>New England Journal of Medicine</i> , 2013 , 368, 503-12	59.2	556
298	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. <i>Nature Genetics</i> , 2017 , 49, 1373-1384	36.3	508
297	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013 , 45, 145-54	36.3	505
296	Identification of common variants associated with human hippocampal and intracranial volumes. <i>Nature Genetics</i> , 2012 , 44, 552-61	36.3	498
295	Multiple loci associated with indices of renal function and chronic kidney disease. <i>Nature Genetics</i> , 2009 , 41, 712-7	36.3	469
294	The International HapMap Project Web site. <i>Genome Research</i> , 2005 , 15, 1592-3	9.7	450
293	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013 , 45, 501-12	36.3	437
292	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. <i>Nature Genetics</i> , 2012 , 44, 670-5	36.3	429
291	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
2 90	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014 , 514, 92-97	50.4	401

289	Meta-analysis of genome-wide association studies in >80 000 subjects identifies multiple loci for C-reactive protein levels. <i>Circulation</i> , 2011 , 123, 731-8	16.7	395
288	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018 , 50, 1412-1425	36.3	386
287	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2010 , 42, 1077-85	36.3	372
286	Common variants in KCNN3 are associated with lone atrial fibrillation. <i>Nature Genetics</i> , 2010 , 42, 240-4	36.3	362
285	Genome-wide association study of PR interval. <i>Nature Genetics</i> , 2010 , 42, 153-9	36.3	340
284	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011 , 43, 1005-11	36.3	338
283	Genomic inflation factors under polygenic inheritance. <i>European Journal of Human Genetics</i> , 2011 , 19, 807-12	5.3	335
282	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. <i>Nature Genetics</i> , 2011 , 43, 1082-90	36.3	313
281	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017 , 49, 1758-	1 36 .6	310
280	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. <i>Nature</i> , 2015 , 526, 112-7	50.4	308
279	Variants in ZFHX3 are associated with atrial fibrillation in individuals of European ancestry. <i>Nature Genetics</i> , 2009 , 41, 879-81	36.3	307
278	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012 , 490, 267-72	50.4	304
277	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016 , 7, 10023	17.4	295
276	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. <i>Nature Genetics</i> , 2009 , 41, 1191-8	36.3	285
275	Quality control and conduct of genome-wide association meta-analyses. <i>Nature Protocols</i> , 2014 , 9, 1192	28.8	278
274	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018 , 50, 1225-1233	36.3	277
273	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. <i>PLoS Genetics</i> , 2013 , 9, e1003500	6	277
272	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021 , 590, 290-299	50.4	268

(2011-1997)

271	The yeast Red1 protein localizes to the cores of meiotic chromosomes. <i>Journal of Cell Biology</i> , 1997 , 136, 957-67	7.3	266	
270	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017 , 49, 834-841	36.3	257	
269	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018 , 9, 2098	17.4	254	
268	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016 , 48, 1171-1184	36.3	251	
267	Genetic contributions to variation in general cognitive function: a meta-analysis of genome-wide association studies in the CHARGE consortium (N=53949). <i>Molecular Psychiatry</i> , 2015 , 20, 183-92	15.1	250	
266	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. <i>Nature Genetics</i> , 2010 , 42, 1068-76	36.3	249	
265	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. <i>Nature Genetics</i> , 2012 , 44, 260-8	36.3	243	
264	Multiple genetic loci influence serum urate levels and their relationship with gout and cardiovascular disease risk factors. <i>Circulation: Cardiovascular Genetics</i> , 2010 , 3, 523-30		243	
263	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. <i>Nature Genetics</i> , 2011 , 43, 753-60	36.3	237	
262	Association of low-frequency and rare coding-sequence variants with blood lipids and coronary heart disease in 56,000 whites and blacks. <i>American Journal of Human Genetics</i> , 2014 , 94, 223-32	11	233	
261	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. <i>Nature Neuroscience</i> , 2017 , 20, 1052-1061	25.5	228	
260	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015 , 47, 1294-1303	36.3	226	
259	Meta-analysis of genome-wide association data identifies two loci influencing age at menarche. <i>Nature Genetics</i> , 2009 , 41, 648-50	36.3	223	
258	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018 , 50, 559-571	36.3	221	
257	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015 , 11, e1005378	6	220	
256	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013 , 45, 621-31	36.3	219	
255	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019 , 51, 957-972	36.3	217	
254	Genome-wide association study for coronary artery calcification with follow-up in myocardial infarction. <i>Circulation</i> , 2011 , 124, 2855-64	16.7	213	

253	NRXN3 is a novel locus for waist circumference: a genome-wide association study from the CHARGE Consortium. <i>PLoS Genetics</i> , 2009 , 5, e1000539	6	203
252	Best practices and joint calling of the HumanExome BeadChip: the CHARGE Consortium. <i>PLoS ONE</i> , 2013 , 8, e68095	3.7	203
251	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014 , 46, 826-36	36.3	199
250	Genome-wide association for abdominal subcutaneous and visceral adipose reveals a novel locus for visceral fat in women. <i>PLoS Genetics</i> , 2012 , 8, e1002695	6	199
249	GWAS of longevity in CHARGE consortium confirms APOE and FOXO3 candidacy. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2015 , 70, 110-8	6.4	188
248	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018 , 50, 26-41	36.3	186
247	Genome-wide association meta-analysis for total serum bilirubin levels. <i>Human Molecular Genetics</i> , 2009 , 18, 2700-10	5.6	177
246	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017 , 49, 946-952	36.3	176
245	A novel Alzheimer disease locus located near the gene encoding tau protein. <i>Molecular Psychiatry</i> , 2016 , 21, 108-17	15.1	175
244	Common variants at 12q14 and 12q24 are associated with hippocampal volume. <i>Nature Genetics</i> , 2012 , 44, 545-51	36.3	175
243	Novel genetic loci associated with hippocampal volume. <i>Nature Communications</i> , 2017 , 8, 13624	17.4	173
242	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. <i>American Journal of Human Genetics</i> , 2014 , 94, 233-45	11	170
241	CUBN is a gene locus for albuminuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 55.	5 <u>172</u> 07	170
240	Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. <i>Nature Genetics</i> , 2011 , 43, 940-7	36.3	168
239	Assessing population differentiation and isolation from single-nucleotide polymorphism data. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2002 , 64, 695-715	3.9	165
238	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. <i>Nature Communications</i> , 2014 , 5, 5068	17.4	160
237	Heterogeneity in white blood cells has potential to confound DNA methylation measurements. <i>PLoS ONE</i> , 2012 , 7, e46705	3.7	156
236	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016 , 48, 1162-70	36.3	152

(2015-2018)

235	Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018 , 103, 691-706	11	151	
234	Omega-6 fatty acid biomarkers and incident type 2 diabetes: pooled analysis of individual-level data for 39 740 adults from 20 prospective cohort studies. <i>Lancet Diabetes and Endocrinology,the</i> , 2017 , 5, 965-974	18.1	150	
233	KLB is associated with alcohol drinking, and its gene product EKlotho is necessary for FGF21 regulation of alcohol preference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 14372-14377	11.5	150	
232	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015 , 6, 5897	17.4	147	
231	Novel genetic loci underlying human intracranial volume identified through genome-wide association. <i>Nature Neuroscience</i> , 2016 , 19, 1569-1582	25.5	147	•
230	Convergent genetic and expression data implicate immunity in Alzheimer's disease. <i>Alzheimerls and Dementia</i> , 2015 , 11, 658-71	1.2	146	
229	Genome-wide association studies of cerebral white matter lesion burden: the CHARGE consortium. <i>Annals of Neurology</i> , 2011 , 69, 928-39	9.4	146	
228	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. <i>Human Molecular Genetics</i> , 2011 , 20, 2273-8	34 ⁶	146	
227	Genome-wide association studies of serum magnesium, potassium, and sodium concentrations identify six Loci influencing serum magnesium levels. <i>PLoS Genetics</i> , 2010 , 6, e1001045	6	144	
226	Genome-wide association and functional follow-up reveals new loci for kidney function. <i>PLoS Genetics</i> , 2012 , 8, e1002584	6	143	
225	A genome-wide association study of depressive symptoms. <i>Biological Psychiatry</i> , 2013 , 73, 667-78	7.9	135	
224	Association of low-density lipoprotein cholesterol-related genetic variants with aortic valve calcium and incident aortic stenosis. <i>JAMA - Journal of the American Medical Association</i> , 2014 , 312, 1764-71	27.4	134	
223	Genome-wide association studies identify CHRNA5/3 and HTR4 in the development of airflow obstruction. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2012 , 186, 622-32	10.2	131	
222	The Promises and Pitfalls of Genoeconomics*. <i>Annual Review of Economics</i> , 2012 , 4, 627-662	5	130	
221	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020 , 586, 763-768	50.4	127	
220	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019 , 51, 1459-1474	36.3	122	
219	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015 , 523, 459-4	63 0.4	119	
218	Multiethnic genome-wide association study of cerebral white matter hyperintensities on MRI. <i>Circulation: Cardiovascular Genetics</i> , 2015 , 8, 398-409		119	

217	Biomarkers of Dietary Omega-6 Fatty Acids and Incident Cardiovascular Disease and Mortality. <i>Circulation</i> , 2019 , 139, 2422-2436	16.7	118
216	Interactions of dietary whole-grain intake with fasting glucose- and insulin-related genetic loci in individuals of European descent: a meta-analysis of 14 cohort studies. <i>Diabetes Care</i> , 2010 , 33, 2684-91	14.6	112
215	Four novel Loci (19q13, 6q24, 12q24, and 5q14) influence the microcirculation in vivo. <i>PLoS Genetics</i> , 2010 , 6, e1001184	6	111
214	A genome-wide association study of aging. <i>Neurobiology of Aging</i> , 2011 , 32, 2109.e15-28	5.6	110
213	Genome-wide joint meta-analysis of SNP and SNP-by-smoking interaction identifies novel loci for pulmonary function. <i>PLoS Genetics</i> , 2012 , 8, e1003098	6	108
212	A meta-analysis of four genome-wide association studies of survival to age 90 years or older: the Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2010 , 65, 478-87	6.4	107
211	Genome-wide association analysis identifies multiple loci related to resting heart rate. <i>Human Molecular Genetics</i> , 2010 , 19, 3885-94	5.6	106
210	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017 , 8, 14977	17.4	105
209	Genome-wide association analysis identifies six new loci associated with forced vital capacity. <i>Nature Genetics</i> , 2014 , 46, 669-77	36.3	104
208	Common variants at 6q22 and 17q21 are associated with intracranial volume. <i>Nature Genetics</i> , 2012 , 44, 539-44	36.3	104
207	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017 , 13, e1006528	6	103
206	A meta-analysis of genome-wide association studies identifies multiple longevity genes. <i>Nature Communications</i> , 2019 , 10, 3669	17.4	102
205	Novel genetic markers associate with atrial fibrillation risk in Europeans and Japanese. <i>Journal of the American College of Cardiology</i> , 2014 , 63, 1200-1210	15.1	102
204	Meta-analysis of genome-wide association studies identifies six new Loci for serum calcium concentrations. <i>PLoS Genetics</i> , 2013 , 9, e1003796	6	100
203	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology, The</i> , 2016 , 15, 695-707	24.1	100
202	A genome-wide association study identifies LIPA as a susceptibility gene for coronary artery disease. <i>Circulation: Cardiovascular Genetics</i> , 2011 , 4, 403-12		98
201	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , 2016 , 65, 803-17	0.9	96
200	Genome-wide association study meta-analysis of chronic widespread pain: evidence for involvement of the 5p15.2 region. <i>Annals of the Rheumatic Diseases</i> , 2013 , 72, 427-36	2.4	96

(2010-2012)

199	Common variants at 12q15 and 12q24 are associated with infant head circumference. <i>Nature Genetics</i> , 2012 , 44, 532-538	36.3	94
198	Multiple loci are associated with white blood cell phenotypes. <i>PLoS Genetics</i> , 2011 , 7, e1002113	6	92
197	Characterization of European ancestry nonalcoholic fatty liver disease-associated variants in individuals of African and Hispanic descent. <i>Hepatology</i> , 2013 , 58, 966-75	11.2	91
196	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 13366-13371	11.5	90
195	Gene-wide analysis detects two new susceptibility genes for Alzheimer's disease. <i>PLoS ONE</i> , 2014 , 9, e94661	3.7	90
194	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017 , 8, 80	17.4	88
193	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019 , 73, 58-66	15.1	86
192	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. <i>Molecular Psychiatry</i> , 2016 , 21, 189-197	15.1	85
191	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017 ,	8.5	85
190	Genome-wide association study of kidney function decline in individuals of European descent. <i>Kidney International</i> , 2015 , 87, 1017-29	9.9	83
189	A genome-wide association study of early menopause and the combined impact of identified variants. <i>Human Molecular Genetics</i> , 2013 , 22, 1465-72	5.6	82
188	Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. <i>Lancet Diabetes and Endocrinology,the</i> , 2015 , 3, 243-53	18.1	81
187	Genetic architecture of subcortical brain structures in 38,851 individuals. <i>Nature Genetics</i> , 2019 , 51, 16	243663	6 81
186	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. <i>Nature Genetics</i> , 2017 , 49, 125-130	36.3	80
185	Gene-age interactions in blood pressure regulation: a large-scale investigation with the CHARGE, Global BPgen, and ICBP Consortia. <i>American Journal of Human Genetics</i> , 2014 , 95, 24-38	11	80
184	Insights into the genetic architecture of early stage age-related macular degeneration: a genome-wide association study meta-analysis. <i>PLoS ONE</i> , 2013 , 8, e53830	3.7	79
183	Genetic determinants of heel bone properties: genome-wide association meta-analysis and replication in the GEFOS/GENOMOS consortium. <i>Human Molecular Genetics</i> , 2014 , 23, 3054-68	5.6	78
182	Common variants in the calcium-sensing receptor gene are associated with total serum calcium levels. <i>Human Molecular Genetics</i> , 2010 , 19, 4296-303	5.6	77

181	Novel loci associated with usual sleep duration: the CHARGE Consortium Genome-Wide Association Study. <i>Molecular Psychiatry</i> , 2015 , 20, 1232-9	15.1	76
180	52 Genetic Loci Influencing MyocardiallMass. <i>Journal of the American College of Cardiology</i> , 2016 , 68, 1435-1448	15.1	76
179	Common genetic variation in the 3'-BCL11B gene desert is associated with carotid-femoral pulse wave velocity and excess cardiovascular disease risk: the AortaGen Consortium. <i>Circulation: Cardiovascular Genetics</i> , 2012 , 5, 81-90		76
178	Genome-wide association studies of MRI-defined brain infarcts: meta-analysis from the CHARGE Consortium. <i>Stroke</i> , 2010 , 41, 210-7	6.7	74
177	Candidate gene association study for diabetic retinopathy in persons with type 2 diabetes: the Candidate gene Association Resource (CARe) 2011 , 52, 7593-602		73
176	Sequence features in regions of weak and strong linkage disequilibrium. <i>Genome Research</i> , 2005 , 15, 1519-34	9.7	71
175	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017 , 7, 45040	4.9	70
174	Meta-analysis of genome-wide association for migraine in six population-based European cohorts. <i>European Journal of Human Genetics</i> , 2011 , 19, 901-7	5.3	70
173	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 2017 , 127, 1798-1812	15.9	68
172	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program		68
171	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. <i>Journal of the American Heart Association</i> , 2017 , 6,	6	65
170	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. <i>Nature Communications</i> , 2018 , 9, 5141	17.4	64
169	Association of Alzheimer's disease GWAS loci with MRI markers of brain aging. <i>Neurobiology of Aging</i> , 2015 , 36, 1765.e7-1765.e16	5.6	63
168	Genetic Obesity and the Risk of Atrial Fibrillation: Causal Estimates from Mendelian Randomization. <i>Circulation</i> , 2017 , 135, 741-754	16.7	62
167	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. <i>American Journal of Human Genetics</i> , 2016 , 99, 40-55	11	61
166	Identification of nine novel loci associated with white blood cell subtypes in a Japanese population. <i>PLoS Genetics</i> , 2011 , 7, e1002067	6	61
165	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019 , 51, 636-648	36.3	59
164	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018 , 102, 375-400	11	59

(2014-2005)

163	Isolation and characterization of a thermostable RNA ligase 1 from a Thermus scotoductus bacteriophage TS2126 with good single-stranded DNA ligation properties. <i>Nucleic Acids Research</i> , 2005 , 33, 135-42	20.1	59	
162	Discovery and fine mapping of serum protein loci through transethnic meta-analysis. <i>American Journal of Human Genetics</i> , 2012 , 91, 744-53	11	58	
161	Large scale international replication and meta-analysis study confirms association of the 15q14 locus with myopia. The CREAM consortium. <i>Human Genetics</i> , 2012 , 131, 1467-80	6.3	57	
160	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. <i>Human Molecular Genetics</i> , 2012 , 21, 5329-43	5.6	54	
159	Genome-Wide Association Study for Incident Myocardial Infarction and Coronary Heart Disease in Prospective Cohort Studies: The CHARGE Consortium. <i>PLoS ONE</i> , 2016 , 11, e0144997	3.7	53	
158	Molecular mechanisms underlying variations in lung function: a systems genetics analysis. <i>Lancet Respiratory Medicine,the</i> , 2015 , 3, 782-95	35.1	52	
157	Effects of long-term averaging of quantitative blood pressure traits on the detection of genetic associations. <i>American Journal of Human Genetics</i> , 2014 , 95, 49-65	11	52	
156	HapMap methylation-associated SNPs, markers of germline DNA methylation, positively correlate with regional levels of human meiotic recombination. <i>Genome Research</i> , 2009 , 19, 581-9	9.7	51	
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152	A novel cyclin gene from Drosophila complements CLN function in yeast. <i>Genes and Development</i> , 1991 , 5, 2166-75	12.6	48	
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150	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. <i>American Journal of Human Genetics</i> , 2016 , 99, 8-21	11	47	
149	Genetic variation associated with circulating monocyte count in the eMERGE Network. <i>Human Molecular Genetics</i> , 2013 , 22, 2119-27	5.6	46	
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147	HDAC9 is implicated in atherosclerotic aortic calcification and affects vascular smooth muscle cell phenotype. <i>Nature Genetics</i> , 2019 , 51, 1580-1587	36.3	45	
146	Trans-ethnic meta-analysis of white blood cell phenotypes. <i>Human Molecular Genetics</i> , 2014 , 23, 6944-60	05.6	45	

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144	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021 , 53, 840-860	36.3	44
143	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019 , 10, 4130	17.4	43
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141	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. <i>American Journal of Human Genetics</i> , 2016 , 99, 22-39	11	42
140	Large-scale genome-wide association studies and meta-analyses of longitudinal change in adult lung function. <i>PLoS ONE</i> , 2014 , 9, e100776	3.7	42
139	Shared genetic contribution to Ischaemic Stroke and Alzheimer's Disease. <i>Annals of Neurology</i> , 2016 , 79, 739-747	9.4	42
138	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019 , 10, 376	17.4	41
137	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
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135	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018 , 9, 2904	17.4	39
134	Loss-of-Function Variants, Low-Density Lipoprotein Cholesterol, and Risk of Coronary Heart Disease and Stroke: Data From 9 Studies of Blacks and Whites. <i>Circulation: Cardiovascular Genetics</i> , 2017 , 10, e001632		39
133	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25,000 subjects. <i>Molecular Psychiatry</i> , 2015 , 20, 735-43	15.1	39
132	Rare Functional Variant in TM2D3 is Associated with Late-Onset Alzheimer's Disease. <i>PLoS Genetics</i> , 2016 , 12, e1006327	6	38
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130	Assessment of the Relationship Between Genetic Determinants of Thyroid Function and Atrial Fibrillation: A Mendelian Randomization Study. <i>JAMA Cardiology</i> , 2019 , 4, 144-152	16.2	36
129	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. <i>Circulation: Cardiovascular Genetics</i> , 2016 , 9, 511-520		34
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123	Modulation of genetic associations with serum urate levels by body-mass-index in humans. <i>PLoS ONE</i> , 2015 , 10, e0119752	3.7	31	
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95	Effect of Genetically Low 25-Hydroxyvitamin D on Mortality Risk: Mendelian Randomization Analysis in 3 Large European Cohorts. <i>Nutrients</i> , 2019 , 11,	6.7	20
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64	Genome-wide association study of retinopathy in individuals without diabetes. <i>PLoS ONE</i> , 2013 , 8, e542	23327	11
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53	Browsing HapMap Data Using the Genome Browser. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot	5 02 3	7
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50	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals <i>Nature Genetics</i> , 2022 ,	36.3	7
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34	Generating HapMap Data Text Reports Using the Genome Browser. <i>Cold Spring Harbor Protocols</i> , 2008 , 2008, pdb.prot5024	1.2	4
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31	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
30	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation		4
29	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2021 , 26, 2111-2125	15.1	3
28	Genome-wide meta-analysis of SNP-by9-ACEI/ARB and SNP-by-thiazide diuretic and effect on serum potassium in cohorts of European and African ancestry. <i>Pharmacogenomics Journal</i> , 2019 , 19, 97-	108	3
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25	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential <i>Science Advances</i> , 2022 , 8, eabl6579	14.3	3
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22	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer disease		2
21	G-STRATEGY: Optimal Selection of Individuals for Sequencing in Genetic Association Studies. <i>Genetic Epidemiology</i> , 2016 , 40, 446-60	2.6	2
20	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed <i>Cell Genomics</i> , 2022 , 2, 100084-100084		1

19	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> ,3, 4	4.8	1
18	The Trans-Ancestral Genomic Architecture of Glycaemic Traits		1
17	Discovering patterns of pleiotropy in genome-wide association studies		1
16	Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney		1
15	Whole genome sequencing association analysis of quantitative red blood cell phenotypes: the NHLBI TOPMed program		1
14	Genomic analyses for age at menarche identify 389 independent signals and indicate BMI-independent effects of puberty timing on cancer susceptibility		1
13	Genome-wide meta-analysis of variant-by-diuretic interactions as modulators of lipid traits in persons of European and African ancestry. <i>Pharmacogenomics Journal</i> , 2020 , 20, 482-493	3.5	1
12	Identification of novel and rare variants associated with handgrip strength using whole genome sequence data from the NHLBI Trans-Omics in Precision Medicine (TOPMed) Program. <i>PLoS ONE</i> , 2021 , 16, e0253611	3.7	1
11	Whole genome sequencing identifies common and rare structural variants contributing to hematologic traits in the NHLBI TOPMed program		1
10	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022 , 5,	6.7	1
9	Association of low-frequency and rare coding variants with information processing speed. <i>Translational Psychiatry</i> , 2021 , 11, 613	8.6	0
8	Multiethnic Genome-Wide Association Study of Subclinical Atherosclerosis in Individuals With Type 2 Diabetes. <i>Circulation Genomic and Precision Medicine</i> , 2021 , 14, e003258	5.2	O
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6	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. <i>Obstetrical and Gynecological Survey</i> , 2015 , 70, 758-70	62 ^{2.4}	
5	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose 2020 , 15, e0230815		
4	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose 2020 , 15, e0230815		
3	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose 2020 , 15, e0230815		
2	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose 2020 , 15, e0230815		

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