Albert V. Smith

List of Publications by Year in Descending Order

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

#	Paper	IF	Citations
324	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed.. *Cell Genomics*, **2022**, 2, 100084-100084		1
323	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. *Nature Genetics*, **2022**,	36.3	7
322	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential.. *Science Advances*, **2022**, 8, eabl6579	14.3	3
321	Accounting for population structure in genetic studies of cystic fibrosis. *Human Genetics and Genomics Advances*, **2022**, 100117	0.8	
320	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. *Communications Biology*, **2022**, 5,	6.7	1
319	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. *Molecular Psychiatry*, **2021**, 26, 2111-2125	15.1	3
318	Association of low-frequency and rare coding variants with information processing speed. *Translational Psychiatry*, **2021**, 11, 613	8.6	0
317	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. *Cell Genomics*, **2021**, 1, 100029-100029		20
316	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. *Nature Genetics*, **2021**, 53, 1504-1516	36.3	7
315	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. *Nature Communications*, **2021**, 12, 2182	17.4	5
314	Allele-specific variation at APOE increases nonalcoholic fatty liver disease and obesity but decreases risk of Alzheimer's disease and myocardial infarction. *Human Molecular Genetics*, **2021**, 30, 1443-1456	5.6	5
313	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. *American Journal of Human Genetics*, **2021**, 108, 874-893	11	5
312	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
311	Gene Set Enrichment Analsyes Identiify Pathways Involved in Genetic Risk for Diabetic Retinopathy. *American Journal of Ophthalmology*, **2021**, 233, 111-123	4.9	3
310	A Noncoding Variant Near PPP1R3B Promotes Liver Glycogen Storage and MetS, but Protects Against Myocardial Infarction. *Journal of Clinical Endocrinology and Metabolism*, **2021**, 106, 372-387	5.6	3
309	rs641738C>T near MBOAT7 is associated with liver fat, ALT and fibrosis in NAFLD: A meta-analysis. *Journal of Hepatology*, **2021**, 74, 20-30	13.4	24
308	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30

307	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *Nature*, **2021**, 590, 290-299	50.4	268
306	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. *PLoS ONE*, **2021**, 16, e0253611	3.7	1
305	Multiethnic Genome-Wide Association Study of Subclinical Atherosclerosis in Individuals With Type 2 Diabetes. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003258	5.2	0
304	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28
303	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. *Scientific Reports*, **2021**, 11, 19365	4.9	0
302	Cerebral small vessel disease genomics and its implications across the lifespan. *Nature Communications*, **2020**, 11, 6285	17.4	22
301	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. *PLoS ONE*, **2020**, 15, e0230815	3.7	4
300	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications*, **2020**, 11, 2542	17.4	16
299	Common Genetic Variation Indicates Separate Causes for Periventricular and Deep White Matter Hyperintensities. *Stroke*, **2020**, 51, 2111-2121	6.7	23
298	Genetic loci associated with prevalent and incident myocardial infarction and coronary heart disease in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. *PLoS ONE*, **2020**, 15, e0230035	3.7	4
297	Genome-wide meta-analysis of variant-by-diuretic interactions as modulators of lipid traits in persons of European and African ancestry. *Pharmacogenomics Journal*, **2020**, 20, 482-493	3.5	1
296	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. *Nature*, **2020**, 586, 763-768	50.4	127
295	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. *Nature Genetics*, **2020**, 52, 1314-1332	36.3	26
294	Association of common genetic variants with brain microbleeds: A genome-wide association study. *Neurology*, **2020**, 95, e3331-e3343	6.5	10
293	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. *Nature Communications*, **2020**, 11, 6417	17.4	17
292	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
291	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
290	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		

289	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
288	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. *Nature Communications*, **2019**, 10, 4130	17.4	43
287	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. *Nature Genetics*, **2019**, 51, 1459-1474	36.3	122
286	Genome-Wide Association Study of Apparent Treatment-Resistant Hypertension in the CHARGE Consortium: The CHARGE Pharmacogenetics Working Group. *American Journal of Hypertension*, **2019**, 32, 1146-1153	2.3	2
285	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
284	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*, **2019**, 188, 1033-1054	3.8	39
283	Assessment of the Relationship Between Genetic Determinants of Thyroid Function and Atrial Fibrillation: A Mendelian Randomization Study. *JAMA Cardiology*, **2019**, 4, 144-152	16.2	36
282	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. *Nature Communications*, **2019**, 10, 376	17.4	41
281	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
280	Biomarkers of Dietary Omega-6 Fatty Acids and Incident Cardiovascular Disease and Mortality. *Circulation*, **2019**, 139, 2422-2436	16.7	118
279	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. *Human Molecular Genetics*, **2019**, 28, 2615-2633	5.6	14
278	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. *Nature Genetics*, **2019**, 51, 636-648	36.3	59
277	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. *Pharmacogenomics Journal*, **2019**, 19, 97-108	3.5	3
276	A genome-wide association study identifies genetic loci associated with specific lobar brain volumes. *Communications Biology*, **2019**, 2, 285	6.7	14
275	A meta-analysis of genome-wide association studies identifies multiple longevity genes. *Nature Communications*, **2019**, 10, 3669	17.4	102
274	Insulin Resistance Exacerbates Genetic Predisposition to Nonalcoholic Fatty Liver Disease in Individuals Without Diabetes. *Hepatology Communications*, **2019**, 3, 894-907	6	21
273	Disentangling the genetics of lean mass. *American Journal of Clinical Nutrition*, **2019**, 109, 276-287	7	24
272	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40

271	HDAC9 is implicated in atherosclerotic aortic calcification and affects vascular smooth muscle cell phenotype. *Nature Genetics*, **2019**, 51, 1580-1587	36.3	45
270	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A tau, immunity and lipid processing. *Nature Genetics*, **2019**, 51, 414-430	36.3	917
269	Genetic architecture of subcortical brain structures in 38,851 individuals. *Nature Genetics*, **2019**, 51, 1624-1636	36.3	81
268	Genetic overlap between vascular pathologies and Alzheimer's dementia and potential causal mechanisms. *Alzheimerls and Dementia*, **2019**, 15, 65-75	1.2	24
267	Omega-3 Fatty Acids and Genome-Wide Interaction Analyses Reveal DPP10-Pulmonary Function Association. *American Journal of Respiratory and Critical Care Medicine*, **2019**, 199, 631-642	10.2	5
266	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. *Circulation*, **2019**, 139, 620-635	16.7	51
265	Effect of Genetically Low 25-Hydroxyvitamin D on Mortality Risk: Mendelian Randomization Analysis in 3 Large European Cohorts. *Nutrients*, **2019**, 11,	6.7	20
264	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
263	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. *Neurology*, **2019**,	6.5	17
262	Multiethnic Genome-Wide Association Study of Diabetic Retinopathy Using Liability Threshold Modeling of Duration of Diabetes and Glycemic Control. *Diabetes*, **2019**, 68, 441-456	0.9	31
261	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
260	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. *American Journal of Human Genetics*, **2018**, 102, 375-400	11	59
259	Large-scale pharmacogenomic study of sulfonylureas and the QT, JT and QRS intervals: CHARGE Pharmacogenomics Working Group. *Pharmacogenomics Journal*, **2018**, 18, 127-135	3.5	9
258	Heritability and genome-wide associations studies of cerebral blood flow in the general population. *Journal of Cerebral Blood Flow and Metabolism*, **2018**, 38, 1598-1608	7.3	8
257	Pharmacogenomics study of thiazide diuretics and QT interval in multi-ethnic populations: the cohorts for heart and aging research in genomic epidemiology. *Pharmacogenomics Journal*, **2018**, 18, 215-226	3.5	2
256	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
255	Exome Chip Analysis Identifies Low-Frequency and Rare Variants in MRPL38 for White Matter Hyperintensities on Brain Magnetic Resonance Imaging. *Stroke*, **2018**, 49, 1812-1819	6.7	10
254	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. *Genome Biology*, **2018**, 19, 87	18.3	25

253	Reversal of Aging-Induced Increases in Aortic Stiffness by Targeting Cytoskeletal Protein-Protein Interfaces. *Journal of the American Heart Association*, **2018**, 7,	6	14
252	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. *Nature Communications*, **2018**, 9, 2976	17.4	45
251	Multi-ethnic genome-wide association study for atrial fibrillation. *Nature Genetics*, **2018**, 50, 1225-1233	36.3	277
250	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. *PLoS ONE*, **2018**, 13, e0198166	3.7	31
249	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*, **2018**, 3, 4	4.8	16
248	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
247	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. *Nature Communications*, **2018**, 9, 5141	17.4	64
246	Genome-wide association study of 23,500 individuals identifies 7 loci associated with brain ventricular volume. *Nature Communications*, **2018**, 9, 3945	17.4	16
245	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. *Circulation Genomic and Precision Medicine*, **2018**, 11, e001758	5.2	14
244	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. *American Journal of Human Genetics*, **2018**, 103, 691-706	11	151
243	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
242	Meta-analysis across Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium provides evidence for an association of serum vitamin D with pulmonary function. *British Journal of Nutrition*, **2018**, 120, 1159-1170	3.6	7
241	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002037	5.2	11
240	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. *Nature Communications*, **2018**, 9, 2098	17.4	254
239	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. *International Journal of Epidemiology*, **2017**, 46, 894-904	7.8	25
238	Novel genetic loci associated with hippocampal volume. *Nature Communications*, **2017**, 8, 13624	17.4	173
237	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
236	A genome-wide interaction analysis of tricyclic/tetracyclic antidepressants and RR and QT intervals: a pharmacogenomics study from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium. *Journal of Medical Genetics*, **2017**, 54, 313-323	5.8	5

235	Discovery of novel heart rate-associated loci using the Exome Chip. *Human Molecular Genetics*, **2017**, 26, 2346-2363	5.6	17
234	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. *Nature Genetics*, **2017**, 49, 834-841	36.3	257
233	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. *Nature Genetics*, **2017**, 49, 946-952	36.3	176
232	Loss of Cardioprotective Effects at the Locus as a Result of Gene-Smoking Interactions. *Circulation*, **2017**, 135, 2336-2353	16.7	36
231	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. *Nature Communications*, **2017**, 8, 14977	17.4	105
230	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. *Scientific Reports*, **2017**, 7, 45040	4.9	70
229	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. *Nature Genetics*, **2017**, 49, 125-130	36.3	80
228	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. *Nature Neuroscience*, **2017**, 20, 1052-1061	25.5	228
227	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. *Journal of the American Heart Association*, **2017**, 6,	6	65
226	Association of Triglyceride-Related Genetic Variants With Mitral Annular Calcification. *Journal of the American College of Cardiology*, **2017**, 69, 2941-2948	15.1	16
225	and Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. *Journal of the American Society of Nephrology: JASN*, **2017**, 28, 981-994	12.7	30
224	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. *American Journal of Human Genetics*, **2017**, 100, 51-63	11	30
223	Genetic Obesity and the Risk of Atrial Fibrillation: Causal Estimates from Mendelian Randomization. *Circulation*, **2017**, 135, 741-754	16.7	62
222	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
221	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. *Lancet Diabetes and Endocrinology,the*, **2017**, 5, 965-974	18.1	150
220	Genetically Determined Plasma Lipid Levels and Risk of Diabetic Retinopathy: A Mendelian Randomization Study. *Diabetes*, **2017**, 66, 3130-3141	0.9	13
219	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. *Circulation: Cardiovascular Genetics*, **2017**, 10,		33
218	Genetic Interactions with Age, Sex, Body Mass Index, and Hypertension in Relation to Atrial Fibrillation: The AFGen Consortium. *Scientific Reports*, **2017**, 7, 11303	4.9	14

217	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. *Hypertension*, **2017**,	8.5	85
216	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. *Nature Genetics*, **2017**, 49, 1373-1384	36.3	508
215	Genetic improvement of runtime and its fitness landscape in a bioinformatics application **2017**,		9
214	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. *Nature Communications*, **2017**, 8, 80	17.4	88
213	Loss-of-Function Variants, Low-Density Lipoprotein Cholesterol, and Risk of Coronary Heart Disease and Stroke: Data From 9 Studies of Blacks and Whites. *Circulation: Cardiovascular Genetics*, **2017**, 10, e001632		39
212	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. *Journal of Clinical Investigation*, **2017**, 127, 1798-1812	15.9	68
211	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103
210	The complex genetics of gait speed: genome-wide meta-analysis approach. *Aging*, **2017**, 9, 209-246	5.6	16
209	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. *Molecular Psychiatry*, **2016**, 21, 189-197	15.1	85
208	A novel Alzheimer disease locus located near the gene encoding tau protein. *Molecular Psychiatry*, **2016**, 21, 108-17	15.1	175
207	KLB is associated with alcohol drinking, and its gene product Klotho is necessary for FGF21 regulation of alcohol preference. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 14372-14377	11.5	150
206	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. *Circulation: Cardiovascular Genetics*, **2016**, 9, 511-520		34
205	52 Genetic Loci Influencing Myocardial Mass. *Journal of the American College of Cardiology*, **2016**, 68, 1435-1448	15.1	76
204	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. *Nature Genetics*, **2016**, 48, 1162-70	36.3	152
203	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
202	Gene-gene Interaction Analyses for Atrial Fibrillation. *Scientific Reports*, **2016**, 6, 35371	4.9	11
201	Genetic variants linked to education predict longevity. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 13366-13371	11.5	90
200	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. *American Journal of Human Genetics*, **2016**, 99, 40-55	11	61

199	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. *American Journal of Human Genetics*, **2016**, 99, 22-39	11	42
198	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. *Diabetes*, **2016**, 65, 803-17	0.9	96
197	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
196	Novel Genetic Loci Associated With Retinal Microvascular Diameter. *Circulation: Cardiovascular Genetics*, **2016**, 9, 45-54		18
195	Six Novel Loci Associated with Circulating VEGF Levels Identified by a Meta-analysis of Genome-Wide Association Studies. *PLoS Genetics*, **2016**, 12, e1005874	6	43
194	Rare Functional Variant in TM2D3 is Associated with Late-Onset Alzheimer's Disease. *PLoS Genetics*, **2016**, 12, e1006327	6	38
193	Genome-Wide Association Study for Incident Myocardial Infarction and Coronary Heart Disease in Prospective Cohort Studies: The CHARGE Consortium. *PLoS ONE*, **2016**, 11, e0144997	3.7	53
192	Association of Lipid-Related Genetic Variants with the Incidence of Atrial Fibrillation: The AFGen Consortium. *PLoS ONE*, **2016**, 11, e0151932	3.7	12
191	An Empirical Comparison of Joint and Stratified Frameworks for Studying G E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Gene-Lifestyle Interactions Working Group. *Genetic Epidemiology*, **2016**, 40, 404-15	2.6	15
190	G-STRATEGY: Optimal Selection of Individuals for Sequencing in Genetic Association Studies. *Genetic Epidemiology*, **2016**, 40, 446-60	2.6	2
189	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. *American Journal of Human Genetics*, **2016**, 99, 8-21	11	47
188	Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. *Journal of Medical Genetics*, **2016**, 53, 835-845	5.8	28
187	Meta-analysis of 49 549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in ANGPTL4 determining fasting TG levels. *Journal of Medical Genetics*, **2016**, 53, 441-9	5.8	27
186	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. *Lancet Neurology, The*, **2016**, 15, 695-707	24.1	100
185	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. *Nature Genetics*, **2016**, 48, 624-33	36.3	602
184	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
183	Novel genetic loci underlying human intracranial volume identified through genome-wide association. *Nature Neuroscience*, **2016**, 19, 1569-1582	25.5	147
182	GWAS analysis of handgrip and lower body strength in older adults in the CHARGE consortium. *Aging Cell*, **2016**, 15, 792-800	9.9	33

181	Novel Genetic Variants Associated With Increased Vertebral Volumetric BMD, Reduced Vertebral Fracture Risk, and Increased Expression of SLC1A3 and EPHB2. *Journal of Bone and Mineral Research*, **2016**, 31, 2085-2097	6.3	33
180	Shared genetic contribution to Ischaemic Stroke and Alzheimer's Disease. *Annals of Neurology*, **2016**, 79, 739-747	9.4	42
179	Association of Alzheimer's disease GWAS loci with MRI markers of brain aging. *Neurobiology of Aging*, **2015**, 36, 1765.e7-1765.e16	5.6	63
178	Genetic contributions to variation in general cognitive function: a meta-analysis of genome-wide association studies in the CHARGE consortium (N=53949). *Molecular Psychiatry*, **2015**, 20, 183-92	15.1	250
177	Circadian clock genes and risk of fatal prostate cancer. *Cancer Causes and Control*, **2015**, 26, 25-33	2.8	26
176	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119
175	Is the adiposity-associated FTO gene variant related to all-cause mortality independent of adiposity? Meta-analysis of data from 169,551 Caucasian adults. *Obesity Reviews*, **2015**, 16, 327-340	10.6	7
174	Multiethnic genome-wide association study of cerebral white matter hyperintensities on MRI. *Circulation: Cardiovascular Genetics*, **2015**, 8, 398-409		119
173	GWAS of longevity in CHARGE consortium confirms APOE and FOXO3 candidacy. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2015**, 70, 110-8	6.4	188
172	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
171	PLD3 variants in population studies. *Nature*, **2015**, 520, E2-3	50.4	47
170	Molecular mechanisms underlying variations in lung function: a systems genetics analysis. *Lancet Respiratory Medicine,the*, **2015**, 3, 782-95	35.1	52
169	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303	36.3	226
168	Integrative pathway genomics of lung function and airflow obstruction. *Human Molecular Genetics*, **2015**, 24, 6836-48	5.6	20
167	White Matter Lesion Progression: Genome-Wide Search for Genetic Influences. *Stroke*, **2015**, 46, 3048-57	6.7	18
166	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. *Nature*, **2015**, 526, 112-7	50.4	308
165	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130	36.3	1290
164	Convergent genetic and expression data implicate immunity in Alzheimer's disease. *Alzheimerls and Dementia*, **2015**, 11, 658-71	1.2	146

163	Genome-wide association study of kidney function decline in individuals of European descent. *Kidney International*, **2015**, 87, 1017-29	9.9	83
162	Novel loci associated with usual sleep duration: the CHARGE Consortium Genome-Wide Association Study. *Molecular Psychiatry*, **2015**, 20, 1232-9	15.1	76
161	Genome-wide studies of verbal declarative memory in nondemented older people: the Cohorts for Heart and Aging Research in Genomic Epidemiology consortium. *Biological Psychiatry*, **2015**, 77, 749-63	7.9	48
160	Fine mapping the region reveals a common intronic insertion associated to HDL-C. *Npj Aging and Mechanisms of Disease*, **2015**, 1, 15011	5.5	5
159	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. *Obstetrical and Gynecological Survey*, **2015**, 70, 758-762	2.4	
158	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
157	Drug-Gene Interactions of Antihypertensive Medications and Risk of Incident Cardiovascular Disease: A Pharmacogenomics Study from the CHARGE Consortium. *PLoS ONE*, **2015**, 10, e0140496	3.7	12
156	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25,000 subjects. *Molecular Psychiatry*, **2015**, 20, 735-43	15.1	39
155	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
154	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
153	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
152	Modulation of genetic associations with serum urate levels by body-mass-index in humans. *PLoS ONE*, **2015**, 10, e0119752	3.7	31
151	Novel genetic markers associate with atrial fibrillation risk in Europeans and Japanese. *Journal of the American College of Cardiology*, **2014**, 63, 1200-1210	15.1	102
150	Association of low-frequency and rare coding-sequence variants with blood lipids and coronary heart disease in 56,000 whites and blacks. *American Journal of Human Genetics*, **2014**, 94, 223-32	11	233
149	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
148	Genome-wide association analysis identifies six new loci associated with forced vital capacity. *Nature Genetics*, **2014**, 46, 669-77	36.3	104
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13	The Trans-Ancestral Genomic Architecture of Glycaemic Traits		1
12	Discovering patterns of pleiotropy in genome-wide association studies		1
11	Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney		1
10	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
9	Genetic Architecture of Subcortical Brain Structures in Over 40,000 Individuals Worldwide		5
8	Ninety-nine independent genetic loci influencing general cognitive function include genes associated with brain health and structure (N = 280,360)		6
7	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
6	Whole genome sequencing association analysis of quantitative red blood cell phenotypes: the NHLBI TOPMed program		1
5	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program		68
4	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation		4
3	Genomic analyses for age at menarche identify 389 independent signals and indicate BMI-independent effects of puberty timing on cancer susceptibility		1
2	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer disease		2

1 Whole genome sequencing identifies common and rare structural variants contributing to hematologic traits in the NHLBI TOPMed program 1