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List of Publications by Year in Descending Order

131 papers	19,903 citations	52 h-index	141 g-index
154 ext. papers	26,076 ext. citations	14.7 avg, IF	4.3 L-index

#	Paper	IF	Citations
131	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed.. *Cell Genomics*, **2022**, 2, 100084-100084		1
130	Meta-analysis of genome-wide association studies identifies ancestry-specific associations underlying circulating total tau levels.. *Communications Biology*, **2022**, 5, 336	6.7	0
129	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential.. *Science Advances*, **2022**, 8, eabl6579	14.3	3
128	New insights into the genetic etiology of Alzheimer's disease and related dementias.. *Nature Genetics*, **2022**,	36.3	27
127	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases.. *Nature Communications*, **2022**, 13, 2408	17.4	1
126	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations.. *Frontiers in Endocrinology*, **2022**, 13, 863893	5.7	
125	Association of low-frequency and rare coding variants with information processing speed. *Translational Psychiatry*, **2021**, 11, 613	8.6	0
124	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
123	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. *Stroke*, **2021**, STROKEAHA121037388	6.7	7
122	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. *Stroke*, **2021**, STROKEAHA120031792	6.7	2
121	Clonal Hematopoiesis is Associated with Reduced Risk of Alzheimer's Disease. *Blood*, **2021**, 138, 5-5	2.2	1
120	Cholesteryl ester transfer protein (CETP) as a drug target for cardiovascular disease. *Nature Communications*, **2021**, 12, 5640	17.4	7
119	Association of mitochondrial DNA copy number with cardiometabolic diseases.. *Cell Genomics*, **2021**, 1,		1
118	Multiomics integrative analysis identifies allele-specific blood biomarkers associated to Alzheimer's disease etiopathogenesis. *Aging*, **2021**, 13, 9277-9329	5.6	4
117	Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. *Molecular Psychiatry*, **2021**,	15.1	3
116	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. *Nature Communications*, **2021**, 12, 2182	17.4	5
115	Common variants in Alzheimer's disease and risk stratification by polygenic risk scores. *Nature Communications*, **2021**, 12, 3417	17.4	23

114	Meta-analysis of epigenome-wide association studies of carotid intima-media thickness. *European Journal of Epidemiology*, **2021**, 36, 1143-1155	12.1	4
113	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. *Human Molecular Genetics*, **2021**, 30, 393-409	5.6	6
112	Adverse Cardiovascular Outcomes and Antihypertensive Treatment: A Genome-Wide Interaction Meta-Analysis in the International Consortium for Antihypertensive Pharmacogenomics Studies. *Clinical Pharmacology and Therapeutics*, **2021**, 110, 723-732	6.1	2
111	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
110	Cerebral small vessel disease genomics and its implications across the lifespan. *Nature Communications*, **2020**, 11, 6285	17.4	22
109	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications*, **2020**, 11, 2542	17.4	16
108	Common Genetic Variation Indicates Separate Causes for Periventricular and Deep White Matter Hyperintensities. *Stroke*, **2020**, 51, 2111-2121	6.7	23
107	Global and Regional Development of the Human Cerebral Cortex: Molecular Architecture and Occupational Aptitudes. *Cerebral Cortex*, **2020**, 30, 4121-4139	5.1	5
106	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. *American Journal of Human Genetics*, **2020**, 106, 112-120	11	2
105	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
104	Association of CD14 with incident dementia and markers of brain aging and injury. *Neurology*, **2020**, 94, e254-e266	6.5	10
103	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. *Nature Communications*, **2020**, 11, 4796	17.4	16
102	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. *Nature*, **2020**, 586, 763-768	50.4	127
101	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
100	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
99	Genomewide Association Study of Statin-Induced Myopathy in Patients Recruited Using the UK Clinical Practice Research Datalink. *Clinical Pharmacology and Therapeutics*, **2019**, 106, 1353-1361	6.1	28
98	Analysis of Whole-Exome Sequencing Data for Alzheimer Disease Stratified by APOE Genotype. *JAMA Neurology*, **2019**, 76, 1099-1108	17.2	18
97	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

96	Quality control and integration of genotypes from two calling pipelines for whole genome sequence data in the Alzheimer's disease sequencing project. *Genomics*, **2019**, 111, 808-818	4.3	10
95	A genome-wide association study identifies genetic loci associated with specific lobar brain volumes. *Communications Biology*, **2019**, 2, 285	6.7	14
94	The impact of APOE genotype on survival: Results of 38,537 participants from six population-based cohorts (E2-CHARGE). *PLoS ONE*, **2019**, 14, e0219668	3.7	31
93	Pharmacogenomics of statin-related myopathy: Meta-analysis of rare variants from whole-exome sequencing. *PLoS ONE*, **2019**, 14, e0218115	3.7	12
92	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
91	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. *PLoS Genetics*, **2019**, 15, e1008500	6	90
90	Genetic architecture of subcortical brain structures in 38,851 individuals. *Nature Genetics*, **2019**, 51, 1624-1636	36.3	81
89	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. *American Journal of Human Genetics*, **2019**, 104, 260-274	11	43
88	Transethnic Evaluation Identifies Low-Frequency Loci Associated With 25-Hydroxyvitamin D Concentrations. *Journal of Clinical Endocrinology and Metabolism*, **2018**, 103, 1380-1392	5.6	18
87	Whole genome sequence analyses of brain imaging measures in the Framingham Study. *Neurology*, **2018**, 90, e188-e196	6.5	19
86	Analysis of shared heritability in common disorders of the brain. *Science*, **2018**, 360,	33.3	666
85	Multi-ethnic genome-wide association study for atrial fibrillation. *Nature Genetics*, **2018**, 50, 1225-1233	36.3	277
84	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
83	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. *Nature Communications*, **2018**, 9, 5141	17.4	64
82	Genome-wide association study of 23,500 individuals identifies 7 loci associated with brain ventricular volume. *Nature Communications*, **2018**, 9, 3945	17.4	16
81	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
80	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
79	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002037	5.2	11

78	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. *Nature Communications*, **2018**, 9, 2098	17.4	254
77	Novel genetic loci associated with hippocampal volume. *Nature Communications*, **2017**, 8, 13624	17.4	173
76	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
75	Discovery of novel heart rate-associated loci using the Exome Chip. *Human Molecular Genetics*, **2017**, 26, 2346-2363	5.6	17
74	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
73	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. *Nature Communications*, **2017**, 8, 15805	17.4	50
72	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
71	Genetic variation at 16q24.2 is associated with small vessel stroke. *Annals of Neurology*, **2017**, 81, 383-394	9.4	51
70	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. *Nature Genetics*, **2017**, 49, 1560-1563	36.3	68
69	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
68	Trends in the incidence of dementia: design and methods in the Alzheimer Cohorts Consortium. *European Journal of Epidemiology*, **2017**, 32, 931-938	12.1	19
67	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
66	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
65	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. *American Journal of Human Genetics*, **2017**, 101, 888-902	11	83
64	[O2□08□01]: ALZHEIMER'S DISEASE SEQUENCING PROJECT: CASE-CONTROL ANALYSES **2017**, 13, P570-P571		
63	52 Genetic Loci Influencing Myocardial□Mass. *Journal of the American College of Cardiology*, **2016**, 68, 1435-1448	15.1	76
62	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
61	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

60	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. *Science Translational Medicine*, **2016**, 8, 341ra76	17.5	77
59	Twenty-eight genetic loci associated with ST-T-wave amplitudes of the electrocardiogram. *Human Molecular Genetics*, **2016**, 25, 2093-2103	5.6	20
58	Rapid evaluation of phenotypes, SNPs and results through the dbGaP CHARGE Summary Results site. *Nature Genetics*, **2016**, 48, 702-3	36.3	10
57	Genome-Wide Association Analysis of Young-Onset Stroke Identifies a Locus on Chromosome 10q25 Near HABP2. *Stroke*, **2016**, 47, 307-16	6.7	39
56	Whole Exome Sequencing in Atrial Fibrillation. *PLoS Genetics*, **2016**, 12, e1006284	6	24
55	Rare Functional Variant in TM2D3 is Associated with Late-Onset Alzheimer's Disease. *PLoS Genetics*, **2016**, 12, e1006327	6	38
54	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
53	Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. *Journal of Medical Genetics*, **2016**, 53, 835-845	5.8	28
52	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
51	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. *Genome Biology*, **2016**, 17, 255	18.3	171
50	Evaluation of a Genetic Risk Score to Improve Risk Prediction for Alzheimer's Disease. *Journal of Alzheimer's Disease*, **2016**, 53, 921-32	4.3	54
49	Fine-mapping, novel loci identification, and SNP association transferability in a genome-wide association study of QRS duration in African Americans. *Human Molecular Genetics*, **2016**, 25, 4350-4368	5.6	20
48	Cystatin C and Cardiovascular Disease: A Mendelian Randomization Study. *Journal of the American College of Cardiology*, **2016**, 68, 934-45	15.1	65
47	Novel genetic loci underlying human intracranial volume identified through genome-wide association. *Nature Neuroscience*, **2016**, 19, 1569-1582	25.5	147
46	Common genetic variants influence human subcortical brain structures. *Nature*, **2015**, 520, 224-9	50.4	601
45	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
44	Genetic overlap between diagnostic subtypes of ischemic stroke. *Stroke*, **2015**, 46, 615-9	6.7	33
43	Meta-Analysis of Genome-Wide Association Studies Identifies Genetic Risk Factors for Stroke in African Americans. *Stroke*, **2015**, 46, 2063-8	6.7	44

42	PLD3 variants in population studies. *Nature*, **2015**, 520, E2-3	50.4	47
41	White Matter Lesion Progression: Genome-Wide Search for Genetic Influences. *Stroke*, **2015**, 46, 3048-57	6.7	18
40	Genome of The Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. *Nature Communications*, **2015**, 6, 6065	17.4	32
39	Convergent genetic and expression data implicate immunity in Alzheimer's disease. *Alzheimerts and Dementia*, **2015**, 11, 658-71	1.2	146
38	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
37	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
36	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
35	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
34	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. *Human Molecular Genetics*, **2015**, 24, 559-71	5.6	31
33	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
32	Population genomic analysis of 962 whole genome sequences of humans reveals natural selection in non-coding regions. *PLoS ONE*, **2015**, 10, e0121644	3.7	12
31	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
30	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
29	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
28	Lower risk of cardiovascular events in postmenopausal women taking oral estradiol compared with oral conjugated equine estrogens. *JAMA Internal Medicine*, **2014**, 174, 25-31	11.5	70
27	Targeted sequencing in candidate genes for atrial fibrillation: the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Targeted Sequencing Study. *Heart Rhythm*, **2014**, 11, 452-7	6.7	18
26	Gene-age interactions in blood pressure regulation: a large-scale investigation with the CHARGE, Global BPgen, and ICBP Consortia. *American Journal of Human Genetics*, **2014**, 95, 24-38	11	80
25	Effects of long-term averaging of quantitative blood pressure traits on the detection of genetic associations. *American Journal of Human Genetics*, **2014**, 95, 49-65	11	52

24	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. *Nature Genetics*, **2014**, 46, 989-93	36.3	1261
23	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. *Nature Genetics*, **2014**, 46, 826-36	36.3	199
22	No evidence for genome-wide interactions on plasma fibrinogen by smoking, alcohol consumption and body mass index: results from meta-analyses of 80,607 subjects. *PLoS ONE*, **2014**, 9, e111156	3.7	5
21	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. *Nature Communications*, **2014**, 5, 5068	17.4	160
20	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
19	GATM locus does not replicate in rhabdomyolysis study. *Nature*, **2014**, 513, E1-3	50.4	25
18	Genetic evidence for a normal-weight "metabolically obese" phenotype linking insulin resistance, hypertension, coronary artery disease, and type 2 diabetes. *Diabetes*, **2014**, 63, 4369-77	0.9	131
17	Gene-wide analysis detects two new susceptibility genes for Alzheimer's disease. *PLoS ONE*, **2014**, 9, e94661	3.7	90
16	Associations of NINJ2 sequence variants with incident ischemic stroke in the Cohorts for Heart and Aging in Genomic Epidemiology (CHARGE) consortium. *PLoS ONE*, **2014**, 9, e99798	3.7	8
15	Sequence analysis of six blood pressure candidate regions in 4,178 individuals: the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) targeted sequencing study. *PLoS ONE*, **2014**, 9, e109155	3.7	15
14	The challenges of genome-wide interaction studies: lessons to learn from the analysis of HDL blood levels. *PLoS ONE*, **2014**, 9, e109290	3.7	12
13	Prospective associations of coronary heart disease loci in African Americans using the MetaboChip: the PAGE study. *PLoS ONE*, **2014**, 9, e113203	3.7	17
12	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. *Nature Genetics*, **2013**, 45, 1452-8	36.3	2714
11	A genome-wide association study for venous thromboembolism: the extended cohorts for heart and aging research in genomic epidemiology (CHARGE) consortium. *Genetic Epidemiology*, **2013**, 37, 512-521	2.6	80
10	Best practices and joint calling of the HumanExome BeadChip: the CHARGE Consortium. *PLoS ONE*, **2013**, 8, e68095	3.7	203
9	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. *Nature Genetics*, **2012**, 44, 670-5	36.3	429
8	Common variants at 12q14 and 12q24 are associated with hippocampal volume. *Nature Genetics*, **2012**, 44, 545-51	36.3	175
7	Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. *Nature Genetics*, **2011**, 43, 940-7	36.3	168

6	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
5	Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. *Nature Genetics*, **2010**, 42, 1118-25	36.3	1946
4	Variants in ZFHX3 are associated with atrial fibrillation in individuals of European ancestry. *Nature Genetics*, **2009**, 41, 879-81	36.3	307
3	Variation in inflammation-related genes and risk of incident nonfatal myocardial infarction or ischemic stroke. *Atherosclerosis*, **2008**, 198, 166-73	3.1	65
2	Exome sequencing identifies rare damaging variants in the ATP8B4 and ABCA1 genes as novel risk factors for Alzheimer□ Disease		1
1	Inherited Causes of Clonal Hematopoiesis of Indeterminate Potential in TOPMed Whole Genomes		11