Myriam Fornage

List of Publications by Year
in descending order

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277 papers	44,240 citations	6254 80 h-index	2684 193 g-index
314 all docs	314 docs citations	314 times ranked	60331 citing authors

#	Article	IF	Citations
1	Heart Disease and Stroke Statisticsâ€”2017 Update: A Report From the American Heart Association. Circulation, 2017, 135, e146-e603.	1.6	7,085
2	Heart Disease and Stroke Statisticsâ€”2019 Update: A Report From the American Heart Association. Circulation, 2019, 139, e56-e528.	1.6	6,192
3	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates AÎ², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	21.4	1,962
4	Guidelines for the Primary Prevention of Stroke. Stroke, 2014, 45, 3754-3832.	2.0	1,621
5	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	21.4	1,124
6	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
7	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	21.4	783
8	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
9	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	27.8	679
10	Epigenetic Signatures of Cigarette Smoking. Circulation: Cardiovascular Genetics, 2016, 9, 436-447.	5.1	678
11	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	21.4	676
12	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	2.2	567
13	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. Lancet, The, 2015, 385, 351-361.	13.7	562
14	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
15	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	6.0	528
16	Polygenic Prediction of Weight and Obesity Trajectories from Birth to Adulthood. Cell, 2019, 177, 587-596.e9.	28.9	516
17	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
18	The genetic architecture of the human cerebral cortex. Science, 2020, 367, .	12.6	450

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19	Genomewide Association Studies of Stroke. New England Journal of Medicine, 2009, 360, 1718-1728.	27.0	420
20	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
21	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
22	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
23	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
24	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. PLoS Medicine, 2017, 14, e1002383.	8.4	341
25	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.	6.2	326
26	Epigenome-wide association study (EWAS) of BMI, BMI change and waist circumference in African American adults identifies multiple replicated loci. Human Molecular Genetics, 2015, 24, 4464-4479.	2.9	289
27	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, 223-232.	6.2	287
28	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
29	Prevention of Stroke in Patients With Silent Cerebrovascular Disease: A Scientific Statement for Healthcare Professionals From the American Heart Association/American Stroke Association. Stroke, 2017, 48, e44-e71.	2.0	284
30	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	8.8	251
31	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	12.8	250
32	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
33	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. PLoS Medicine, 2017, 14, e1002215.	8.4	246
34	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	6.2	227
35	Twenty-seven-year time trends in dementia incidence in Europe and the United States. Neurology, 2020, 95, e519-e531.	1.1	227
36	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	21.4	223

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37	Best Practices and Joint Calling of the HumanExome BeadChip: The CHARGE Consortium. PLoS ONE, 2013, 8, e68095.	2.5	219
38	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	10.2	217
39	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	14.8	213
40	Common variants at 12q14 and 12q24 are associated with hippocampal volume. Nature Genetics, 2012, 44, 545-551.	21.4	212
41	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.	3.5	203
42	Genomeâ€wide association studies of cerebral white matter lesion burden. Annals of Neurology, 2011, 69, 928-939.	5.3	201
43	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
44	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	21.4	192
45	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517.	3.5	191
46	Whole exome sequencing study identifies novel rare and common Alzheimerâ€™s-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry, 2020, 25, 1859-1875.	7.9	191
47	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	6.2	189
48	Biomarkers of Inflammation and MRI-Defined Small Vessel Disease of the Brain. Stroke, 2008, 39, 1952-1959.	2.0	179
49	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
50	Genetic variation in soluble epoxide hydrolase (EPHX2) and risk of coronary heart disease: The Atherosclerosis Risk in Communities (ARIC) study. Human Molecular Genetics, 2006, 15, 1640-1649.	2.9	171
51	Genome-Wide Association Study of Plasma N6 Polyunsaturated Fatty Acids Within the Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. Circulation: Cardiovascular Genetics, 2014, 7, 321-331.	5.1	164
52	Multiethnic Genome-Wide Association Study of Cerebral White Matter Hyperintensities on MRI. Circulation: Cardiovascular Genetics, 2015, 8, 398-409.	5.1	162
53	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	6.2	158
54	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158

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55	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
56	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	6.2	154
57	Epigenome-wide study identifies novel methylation loci associated with body mass index and waist circumference. Obesity, 2015, 23, 1493-1501.	3.0	152
58	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. Circulation, 2019, 140, 645-657.	1.6	151
59	Epigenome-wide association studies identify DNA methylation associated with kidney function. Nature Communications, 2017, 8, 1286.	12.8	145
60	Polymorphism of the Soluble Epoxide Hydrolase Is Associated With Coronary Artery Calcification in African-American Subjects. Circulation, 2004, 109, 335-339.	1.6	140
61	Common variants in Alzheimerâ€™s disease and risk stratification by polygenic risk scores. Nature Communications, 2021, 12, 3417.	12.8	140
62	Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. Nature Communications, 2019, 10, 4267.	12.8	139
63	Genome-Wide Association Study of White Blood Cell Count in 16,388 African Americans: the Continental Origins and Genetic Epidemiology Network (COGENT). PLoS Genetics, 2011, 7, e1002108.	3.5	133
64	Heritability of Leukoaraiosis in Hypertensive Sibships. Hypertension, 2004, 43, 483-487.	2.7	132
65	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
66	Common variants at 12q15 and 12q24 are associated with infant head circumference. Nature Genetics, 2012, 44, 532-538.	21.4	130
67	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.	10.2	130
68	Reversal of endothelial dysfunction reduces white matter vulnerability in cerebral small vessel disease in rats. Science Translational Medicine, 2018, 10, .	12.4	129
69	Polygenic Type 2 Diabetes Prediction at the Limit of Common Variant Detection. Diabetes, 2014, 63, 2172-2182.	0.6	127
70	Common variants at 6q22 and 17q21 are associated with intracranial volume. Nature Genetics, 2012, 44, 539-544.	21.4	126
71	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
72	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.	6.2	109

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73	Genetic variants of the NOTCH3 gene in the elderly and magnetic resonance imaging correlates of age-related cerebral small vessel disease. Brain, 2011, 134, 3384-3397.	7.6	108
74	Common variation in COL4A1/COL4A2 is associated with sporadic cerebral small vessel disease. Neurology, 2015, 84, 918-926.	1.1	106
75	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. Journal of Clinical Investigation, 2017, 127, 1798-1812.	8.2	106
76	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. Circulation, 2019, 139, 620-635.	1.6	102
77	Discovery and fine-mapping of adiposity loci using high density imputation of genome-wide association studies in individuals of African ancestry: African Ancestry Anthropometry Genetics Consortium. PLoS Genetics, 2017, 13, e1006719.	3.5	98
78	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
79	The soluble epoxide hydrolase gene harbors sequence variation associated with susceptibility to and protection from incident ischemic stroke. Human Molecular Genetics, 2005, 14, 2829-2837.	2.9	91
80	Report of the National Heart, Lung, and Blood Institute Working Group on Epigenetics and Hypertension. Hypertension, 2012, 59, 899-905.	2.7	91
81	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
82	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
83	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
84	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	12.8	89
85	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	3.5	88
86	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. Stroke, 2022, 53, 788-797.	2.0	88
87	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	12.8	85
88	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
89	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. Biological Psychiatry, 2017, 82, 322-329.	1.3	84
90	Variation at the M235T locus of the angiotensinogen gene and essential hypertension: a population-based case-control study from Rochester, Minnesota. Human Genetics, 1995, 96, 295-300.	3.8	82

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91	Genome-Wide Association Studies of MRI-Defined Brain Infarcts. Stroke, 2010, 41, 210-217.	2.0	82
92	Association of Alzheimer's disease GWAS loci with MRI markers of brain aging. Neurobiology of Aging, 2015, 36, 1765.e7-1765.e16.	3.1	82
93	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
94	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949.	11.0	78
95	Circulating Monocyte Chemoattractant Protein-1 and Risk of Stroke. Circulation Research, 2019, 125, 773-782.	4.5	78
96	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.	6.2	73
97	Genetic variation at 16q24.2 is associated with small vessel stroke. Annals of Neurology, 2017, 81, 383-394.	5.3	73
98	Sequence variation in the soluble epoxide hydrolase gene and subclinical coronary atherosclerosis: Interaction with cigarette smoking. Atherosclerosis, 2007, 190, 26-34.	0.8	71
99	Common Genetic Variation Indicates Separate Causes for Periventricular and Deep White Matter Hyperintensities. Stroke, 2020, 51, 2111-2121.	2.0	71
100	Large-scale plasma proteomic analysis identifies proteins and pathways associated with dementia risk. Nature Aging, 2021, 1, 473-489.	11.6	69
101	Meta-analysis of epigenome-wide association studies of cognitive abilities. Molecular Psychiatry, 2018, 23, 2133-2144.	7.9	68
102	Genome-wide association study of selenium concentrations. Human Molecular Genetics, 2015, 24, 1469-1477.	2.9	67
103	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, 749-763.	1.3	67
104	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. Epigenomics, 2019, 11, 1487-1500.	2.1	64
105	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
106	Meta-Analysis of Genome-Wide Association Studies Identifies Genetic Risk Factors for Stroke in African Americans. Stroke, 2015, 46, 2063-2068.	2.0	63
107	Mitochondrial DNA copy number can influence mortality and cardiovascular disease via methylation of nuclear DNA CpGs. Genome Medicine, 2020, 12, 84.	8.2	63
108	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62

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109	Prevalence and correlates of mild cognitive impairment among diverse Hispanics/Latinos: Study of Latinosâ€Investigation of Neurocognitive Aging results. Alzheimer's and Dementia, 2019, 15, 1507-1515.	0.8	62
110	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. Nature Communications, 2020, 11, 4796.	12.8	61
111	Polymorphism in Soluble Epoxide Hydrolase and Blood Pressure in Spontaneously Hypertensive Rats. Hypertension, 2002, 40, 485-490.	2.7	60
112	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60
113	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. Environment International, 2019, 132, 104723.	10.0	58
114	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	1.4	55
115	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	6.2	55
116	Genome-Wide Association Analysis of Young-Onset Stroke Identifies a Locus on Chromosome 10q25 Near HABP2. Stroke, 2016, 47, 307-316.	2.0	54
117	A research framework for cognitive aging and Alzheimer's disease among diverse US Latinos: Design and implementation of the Hispanic Community Health Study/Study of Latinosâ€"Investigation of Neurocognitive Aging (SOLâ€NCA). Alzheimer's and Dementia, 2019, 15, 1624-1632.	0.8	53
118	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. PLoS ONE, 2014, 9, e100776.	2.5	52
119	Genome-Wide Association Study of Intracranial Aneurysm Identifies a New Association on Chromosome 7. Stroke, 2014, 45, 3194-3199.	2.0	52
120	Evaluation of microarray-based DNA methylation measurement using technical replicates: the Atherosclerosis Risk In Communities (ARIC) Study. BMC Bioinformatics, 2014, 15, 312.	2.6	52
121	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.	6.2	50
122	Rare and Coding Region Genetic Variants Associated With Risk of Ischemic Stroke. JAMA Neurology, 2015, 72, 781.	9.0	49
123	A prospective study of serum metabolites and risk of ischemic stroke. Neurology, 2019, 92, e1890-e1898.	1.1	48
124	Association of dietary folate and vitamin B-12 intake with genome-wide DNA methylation in blood: a large-scale epigenome-wide association analysis in 5841 individuals. American Journal of Clinical Nutrition, 2019, 110, 437-450.	4.7	46
125	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. Journal of the American Heart Association, 2016, 5, .	3.7	45
126	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.	6.2	45

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127	Cerebral white matter hyperintensities on MRI and acceleration of epigenetic aging: the atherosclerosis risk in communities study. Clinical Epigenetics, 2017, 9, 21.	4.1	45
128	Exosome miR-371b-5p promotes proliferation of lung alveolar progenitor type II cells by using PTEN to orchestrate the PI3K/Akt signaling. Stem Cell Research and Therapy, 2017, 8, 138.	5.5	43
129	Cognitive Impairment and Dementia After Stroke: Design and Rationale for the DISCOVERY Study. Stroke, 2021, 52, e499-e516.	2.0	43
130	Genomic Susceptibility Loci for Brain Atrophy in Hypertensive Sibships From the GENOA Study. Hypertension, 2005, 45, 793-798.	2.7	42
131	17q25 Locus Is Associated With White Matter Hyperintensity Volume in Ischemic Stroke, But Not With Lacunar Stroke Status. Stroke, 2013, 44, 1609-1615.	2.0	42
132	Whole Blood DNA Methylation Signatures of Diet Are Associated With Cardiovascular Disease Risk Factors and All-Cause Mortality. Circulation Genomic and Precision Medicine, 2020, 13, e002766.	3.6	42
133	MarkVCID cerebral small vessel consortium: I. Enrollment, clinical, fluid protocols. Alzheimer's and Dementia, 2021, 17, 704-715.	0.8	42
134	Association of common genetic variants with brain microbleeds. Neurology, 2020, 95, e3331-e3343.	1.1	40
135	Genetic loci associated with circulating levels of very long-chain saturated fatty acids. Journal of Lipid Research, 2015, 56, 176-184.	4.2	38
136	Dietary fatty acids modulate associations between genetic variants and circulating fatty acids in plasma and erythrocyte membranes: Metaâ€analysis of nine studies in the CHARGE consortium. Molecular Nutrition and Food Research, 2015, 59, 1373-1383.	3.3	37
137	Association of variants inHTRA1andNOTCH3with MRI-defined extremes of cerebral small vessel disease in older subjects. Brain, 2019, 142, 1009-1023.	7.6	37
138	Parental History of Stroke Predicts Subclinical But Not Clinical Stroke. Stroke, 2000, 31, 2098-2102.	2.0	36
139	Family-based association study of matrix metalloproteinase-3 and -9 haplotypes with susceptibility to ischemic white matter injury. Human Genetics, 2007, 120, 671-680.	3.8	36
140	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. Human Molecular Genetics, 2015, 24, 559-571.	2.9	36
141	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. International Journal of Epidemiology, 2017, 46, dyw318.	1.9	36
142	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
143	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. Nature Communications, 2021, 12, 2830.	12.8	35
144	Epigenetic Age and the Risk of Incident Atrial Fibrillation. Circulation, 2021, 144, 1899-1911.	1.6	35

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145	Genetic Overlap Between Diagnostic Subtypes of Ischemic Stroke. Stroke, 2015, 46, 615-619.	2.0	34
146	Whole genome sequence analyses of brain imaging measures in the Framingham Study. Neurology, 2018, 90, e188-e196.	1.1	34
147	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. Blood, 2019, 133, 967-977.	1.4	34
148	Genes From a Translational Analysis Support a Multifactorial Nature of White Matter Hyperintensities. Stroke, 2015, 46, 341-347.	2.0	33
149	Identification, Heritability, and Relation With Gene Expression of Novel DNA Methylation Loci for Blood Pressure. Hypertension, 2020, 76, 195-205.	2.7	33
150	APOE alleleså€™ association with cognitive function differs across Hispanic/Latino groups and genetic ancestry in the study of Latinosâ€investigation of neurocognitive aging (HCHS/SOL). Alzheimer's and Dementia, 2021, 17, 466-474.	0.8	33
151	Brain Aging in African-Americans: The Atherosclerosis Risk in Communities (ARIC) Experience. Current Alzheimer Research, 2015, 12, 607-613.	1.4	33
152	Altered Soluble Epoxide Hydrolase Gene Expression and Function and Vascular Disease Risk in the Stroke-Prone Spontaneously Hypertensive Rat. Hypertension, 2008, 51, 567-573.	2.7	32
153	Analysis of Whole-Exome Sequencing Data for Alzheimer Disease Stratified by APOE Genotype. JAMA Neurology, 2019, 76, 1099.	9.0	32
154	Genome-wide association study identifies novel loci for type 2 diabetes-attributed end-stage kidney disease in African Americans. Human Genomics, 2019, 13, 21.	2.9	32
155	L5, the most electronegative subfraction of plasma LDL, induces endothelial vascular cell adhesion molecule 1 and CXC chemokines, which mediate mononuclear leukocyte adhesion. Atherosclerosis, 2007, 192, 56-66.	0.8	31
156	Overlap Between Common Genetic Polymorphisms Underpinning Kidney Traits and Cardiovascular Disease Phenotypes: The CKDGen Consortium. American Journal of Kidney Diseases, 2013, 61, 889-898.	1.9	31
157	Trans-ethnic fine-mapping of genetic loci for body mass index in the diverse ancestral populations of the Population Architecture using Genomics and Epidemiology (PAGE) Study reveals evidence for multiple signals at established loci. Human Genetics, 2017, 136, 771-800.	3.8	31
158	Genome-wide association study of 23,500 individuals identifies 7 loci associated with brain ventricular volume. Nature Communications, 2018, 9, 3945.	12.8	31
159	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
160	Using previously genotyped controls in genome-wide association studies (GWAS): application to the Stroke Genetics Network (SiGN). Frontiers in Genetics, 2014, 5, 95.	2.3	30
161	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. Neurology, 2019, 92, .	1.1	30
162	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	12.8	30

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163	Inverse effects of the PPARÎ³2 Pro12Ala polymorphism on measures of adiposity over 15 years in African Americans and whites. The CARDIA study. Metabolism: Clinical and Experimental, 2005, 54, 910-917.	3.4	29
164	Fine-mapping of lipid regions in global populations discovers ethnic-specific signals and refines previously identified lipid loci. Human Molecular Genetics, 2016, 25, 5500-5512.	2.9	29
165	A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. American Journal of Epidemiology, 2021, 190, 1977-1992.	3.4	29
166	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
167	White Matter Lesion Progression. Stroke, 2015, 46, 3048-3057.	2.0	27
168	Circulating trimethylamine N-oxide in association with diet and cardiometabolic biomarkers: an international pooled analysis. American Journal of Clinical Nutrition, 2021, 113, 1145-1156.	4.7	27
169	A multi-ethnic polygenic risk score is associated with hypertension prevalence and progression throughout adulthood. Nature Communications, 2022, 13, .	12.8	27
170	Apolipoprotein E genotypes among diverse middle-aged and older Latinos: Study of Latinos-Investigation of Neurocognitive Aging results (HCHS/SOL). Scientific Reports, 2018, 8, 17578.	3.3	26
171	Genome-Wide Association Study Meta-Analysis of Stroke in 22 000 Individuals of African Descent Identifies Novel Associations With Stroke. Stroke, 2020, 51, 2454-2463.	2.0	26
172	Association of mitochondrial DNA copy number with cardiometabolic diseases. Cell Genomics, 2021, 1, 100006.	6.5	26
173	Ranking analysis of microarray data: A powerful method for identifying differentially expressed genes. Genomics, 2006, 88, 846-854.	2.9	25
174	Genetic loci associated with ideal cardiovascular health: A meta-analysis of genome-wide association studies. American Heart Journal, 2016, 175, 112-120.	2.7	25
175	A Mendelian randomization of Î³â€² and total fibrinogen levels in relation to venous thromboembolism and ischemic stroke. Blood, 2020, 136, 3062-3069.	1.4	25
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