

# Myriam Fornage

## List of Publications by Year in descending order

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Version: 2024-02-01

277  
papers

44,240  
citations

6250

80  
h-index

2680

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. <i>Circulation</i> , 2017, 135, e146-e603.	1.6	7,085
2	Heart Disease and Stroke Statisticsâ€™2019 Update: A Report From the American Heart Association. <i>Circulation</i> , 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. <i>Nature Genetics</i> , 2019, 51, 414-430.	9.4	1,962
4	Guidelines for the Primary Prevention of Stroke. <i>Stroke</i> , 2014, 45, 3754-3832.	1.0	1,621
5	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018, 50, 524-537.	9.4	1,124
6	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.	13.7	1,069
7	Rare coding variants in <i>PLCG2</i> , <i>ABI3</i> , and <i>TREM2</i> implicate microglial-mediated innate immunity in Alzheimer's disease. <i>Nature Genetics</i> , 2017, 49, 1373-1384.	9.4	783
8	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. <i>Nature Genetics</i> , 2022, 54, 412-436.	9.4	700
9	Genetic analyses of diverse populations improves discovery for complex traits. <i>Nature</i> , 2019, 570, 514-518.	13.7	679
10	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 436-447.	5.1	678
11	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	9.4	676
12	Mendelian randomization of blood lipids for coronary heart disease. <i>European Heart Journal</i> , 2015, 36, 539-550.	1.0	567
13	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. <i>Lancet, The</i> , 2015, 385, 351-361.	6.3	562
14	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	13.7	544
15	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. <i>BMJ, The</i> , 2014, 349, g4164-g4164.	3.0	528
16	Polygenic Prediction of Weight and Obesity Trajectories from Birth to Adulthood. <i>Cell</i> , 2019, 177, 587-596.e9.	13.5	516
17	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	9.4	470
18	The genetic architecture of the human cerebral cortex. <i>Science</i> , 2020, 367, .	6.0	450

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19	Genomewide Association Studies of Stroke. <i>New England Journal of Medicine</i> , 2009, 360, 1718-1728.	13.9	420
20	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011, 43, 1005-1011.	9.4	403
21	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.	13.7	376
22	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.	9.4	362
23	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	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. <i>PLoS Medicine</i> , 2017, 14, e1002383.	3.9	341
25	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	2.6	326
26	Epigenome-wide association study (EWAS) of BMI, BMI change and waist circumference in African American adults identifies multiple replicated loci. <i>Human Molecular Genetics</i> , 2015, 24, 4464-4479.	1.4	289
27	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, 223-232.	2.6	287
28	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.	9.4	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. <i>Stroke</i> , 2017, 48, e44-e71.	1.0	284
30	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, 255.	3.8	251
31	Novel genetic loci associated with hippocampal volume. <i>Nature Communications</i> , 2017, 8, 13624.	5.8	250
32	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	9.4	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. <i>PLoS Medicine</i> , 2017, 14, e1002215.	3.9	246
34	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. <i>American Journal of Human Genetics</i> , 2012, 91, 823-838.	2.6	227
35	Twenty-seven-year time trends in dementia incidence in Europe and the United States. <i>Neurology</i> , 2020, 95, e519-e531.	1.5	227
36	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016, 48, 1162-1170.	9.4	223

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37	Best Practices and Joint Calling of the HumanExome BeadChip: The CHARGE Consortium. PLoS ONE, 2013, 8, e68095.	1.1	219
38	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	4.9	217
39	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	7.1	213
40	Common variants at 12q14 and 12q24 are associated with hippocampal volume. Nature Genetics, 2012, 44, 545-551.	9.4	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.	1.5	203
42	Genome-wide association studies of cerebral white matter lesion burden. Annals of Neurology, 2011, 69, 928-939.	2.8	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.	2.6	193
44	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	9.4	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.	1.5	191
46	Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry, 2020, 25, 1859-1875.	4.1	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.	2.6	189
48	Biomarkers of Inflammation and MRI-Defined Small Vessel Disease of the Brain. Stroke, 2008, 39, 1952-1959.	1.0	179
49	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	5.8	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.	1.4	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.	2.6	158
54	Genome-wide physical activity interactions in adiposity • A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158

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55	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. <i>Nature Genetics</i> , 2022, 54, 263-273.	9.4	156
56	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	2.6	154
57	Epigenome-wide study identifies novel methylation loci associated with body mass index and waist circumference. <i>Obesity</i> , 2015, 23, 1493-1501.	1.5	152
58	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. <i>Circulation</i> , 2019, 140, 645-657.	1.6	151
59	Epigenome-wide association studies identify DNA methylation associated with kidney function. <i>Nature Communications</i> , 2017, 8, 1286.	5.8	145
60	Polymorphism of the Soluble Epoxide Hydrolase Is Associated With Coronary Artery Calcification in African-American Subjects. <i>Circulation</i> , 2004, 109, 335-339.	1.6	140
61	Common variants in Alzheimer's disease and risk stratification by polygenic risk scores. <i>Nature Communications</i> , 2021, 12, 3417.	5.8	140
62	Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. <i>Nature Communications</i> , 2019, 10, 4267.	5.8	139
63	Genome-Wide Association Study of White Blood Cell Count in 16,388 African Americans: the Continental Origins and Genetic Epidemiology Network (COGENT). <i>PLoS Genetics</i> , 2011, 7, e1002108.	1.5	133
64	Heritability of Leukoaraiosis in Hypertensive Sibships. <i>Hypertension</i> , 2004, 43, 483-487.	1.3	132
65	Genome-wide association analysis identifies six new loci associated with forced vital capacity. <i>Nature Genetics</i> , 2014, 46, 669-677.	9.4	131
66	Common variants at 12q15 and 12q24 are associated with infant head circumference. <i>Nature Genetics</i> , 2012, 44, 532-538.	9.4	130
67	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , The, 2016, 15, 695-707.	4.9	130
68	Reversal of endothelial dysfunction reduces white matter vulnerability in cerebral small vessel disease in rats. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	129
69	Polygenic Type 2 Diabetes Prediction at the Limit of Common Variant Detection. <i>Diabetes</i> , 2014, 63, 2172-2182.	0.3	127
70	Common variants at 6q22 and 17q21 are associated with intracranial volume. <i>Nature Genetics</i> , 2012, 44, 539-544.	9.4	126
71	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.	9.4	112
72	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.	2.6	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. <i>Brain</i> , 2011, 134, 3384-3397.	3.7	108
74	Common variation in <i>COL4A1/COL4A2</i> is associated with sporadic cerebral small vessel disease. <i>Neurology</i> , 2015, 84, 918-926.	1.5	106
75	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 2017, 127, 1798-1812.	3.9	106
76	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. <i>Circulation</i> , 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. <i>PLoS Genetics</i> , 2017, 13, e1006719.	1.5	98
78	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	1.1	94
79	The soluble epoxide hydrolase gene harbors sequence variation associated with susceptibility to and protection from incident ischemic stroke. <i>Human Molecular Genetics</i> , 2005, 14, 2829-2837.	1.4	91
80	Report of the National Heart, Lung, and Blood Institute Working Group on Epigenetics and Hypertension. <i>Hypertension</i> , 2012, 59, 899-905.	1.3	91
81	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020, 52, 1314-1332.	9.4	91
82	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	3.8	90
83	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	9.4	89
84	Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020, 11, 6285.	5.8	89
85	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. <i>PLoS Genetics</i> , 2017, 13, e1006728.	1.5	88
86	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. <i>Stroke</i> , 2022, 53, 788-797.	1.0	88
87	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. <i>Nature Communications</i> , 2018, 9, 2976.	5.8	85
88	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	1.6	85
89	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. <i>Biological Psychiatry</i> , 2017, 82, 322-329.	0.7	84
90	Variation at the M235T locus of the angiotensinogen gene and essential hypertension: a population-based case-control study from Rochester, Minnesota. <i>Human Genetics</i> , 1995, 96, 295-300.	1.8	82

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91	Genome-Wide Association Studies of MRI-Defined Brain Infarcts. <i>Stroke</i> , 2010, 41, 210-217.	1.0	82
92	Association of Alzheimer's disease GWAS loci with MRI markers of brain aging. <i>Neurobiology of Aging</i> , 2015, 36, 1765.e7-1765.e16.	1.5	82
93	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. <i>American Journal of Human Genetics</i> , 2016, 99, 40-55.	2.6	82
94	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. <i>JAMA Psychiatry</i> , 2018, 75, 949.	6.0	78
95	Circulating Monocyte Chemoattractant Protein-1 and Risk of Stroke. <i>Circulation Research</i> , 2019, 125, 773-782.	2.0	78
96	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.	2.6	73
97	Genetic variation at 16q24.2 is associated with small vessel stroke. <i>Annals of Neurology</i> , 2017, 81, 383-394.	2.8	73
98	Sequence variation in the soluble epoxide hydrolase gene and subclinical coronary atherosclerosis: Interaction with cigarette smoking. <i>Atherosclerosis</i> , 2007, 190, 26-34.	0.4	71
99	Common Genetic Variation Indicates Separate Causes for Periventricular and Deep White Matter Hyperintensities. <i>Stroke</i> , 2020, 51, 2111-2121.	1.0	71
100	Large-scale plasma proteomic analysis identifies proteins and pathways associated with dementia risk. <i>Nature Aging</i> , 2021, 1, 473-489.	5.3	69
101	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , 2018, 23, 2133-2144.	4.1	68
102	Genome-wide association study of selenium concentrations. <i>Human Molecular Genetics</i> , 2015, 24, 1469-1477.	1.4	67
103	Genome-wide Studies of Verbal Declarative Memory in Nondemented Older People: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. <i>Biological Psychiatry</i> , 2015, 77, 749-763.	0.7	67
104	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. <i>Epigenomics</i> , 2019, 11, 1487-1500.	1.0	64
105	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	5.8	64
106	Meta-Analysis of Genome-Wide Association Studies Identifies Genetic Risk Factors for Stroke in African Americans. <i>Stroke</i> , 2015, 46, 2063-2068.	1.0	63
107	Mitochondrial DNA copy number can influence mortality and cardiovascular disease via methylation of nuclear DNA CpGs. <i>Genome Medicine</i> , 2020, 12, 84.	3.6	63
108	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. <i>Nature Communications</i> , 2019, 10, 5121.	5.8	62

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109	Prevalence and correlates of mild cognitive impairment among diverse Hispanics/Latinos: Study of Latinos—Investigation of Neurocognitive Aging results. <i>Alzheimer's and Dementia</i> , 2019, 15, 1507-1515.	0.4	62
110	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. <i>Nature Communications</i> , 2020, 11, 4796.	5.8	61
111	Polymorphism in Soluble Epoxide Hydrolase and Blood Pressure in Spontaneously Hypertensive Rats. <i>Hypertension</i> , 2002, 40, 485-490.	1.3	60
112	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. <i>American Journal of Human Genetics</i> , 2016, 99, 8-21.	2.6	60
113	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. <i>Environment International</i> , 2019, 132, 104723.	4.8	58
114	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. <i>Blood</i> , 2015, 126, e19-e29.	0.6	55
115	Trans-ethnic Meta-analysis and Functional Annotation Illuminates the Genetic Architecture of Fasting Glucose and Insulin. <i>American Journal of Human Genetics</i> , 2016, 99, 56-75.	2.6	55
116	Genome-Wide Association Analysis of Young-Onset Stroke Identifies a Locus on Chromosome 10q25 Near <i>HABP2</i> . <i>Stroke</i> , 2016, 47, 307-316.	1.0	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 Latinos—Investigation of Neurocognitive Aging (SOL—INCA). <i>Alzheimer's and Dementia</i> , 2019, 15, 1624-1632.	0.4	53
118	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. <i>PLoS ONE</i> , 2014, 9, e100776.	1.1	52
119	Genome-Wide Association Study of Intracranial Aneurysm Identifies a New Association on Chromosome 7. <i>Stroke</i> , 2014, 45, 3194-3199.	1.0	52
120	Evaluation of microarray-based DNA methylation measurement using technical replicates: the Atherosclerosis Risk In Communities (ARIC) Study. <i>BMC Bioinformatics</i> , 2014, 15, 312.	1.2	52
121	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.	2.6	50
122	Rare and Coding Region Genetic Variants Associated With Risk of Ischemic Stroke. <i>JAMA Neurology</i> , 2015, 72, 781.	4.5	49
123	A prospective study of serum metabolites and risk of ischemic stroke. <i>Neurology</i> , 2019, 92, e1890-e1898.	1.5	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. <i>American Journal of Clinical Nutrition</i> , 2019, 110, 437-450.	2.2	46
125	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. <i>Journal of the American Heart Association</i> , 2016, 5, .	1.6	45
126	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. <i>American Journal of Human Genetics</i> , 2017, 100, 51-63.	2.6	45



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127	Cerebral white matter hyperintensities on MRI and acceleration of epigenetic aging: the atherosclerosis risk in communities study. <i>Clinical Epigenetics</i> , 2017, 9, 21.	1.8	45
128	Exosome miR-371b-5p promotes proliferation of lung alveolar progenitor type II cells by using PTEN to orchestrate the PI3K/Akt signaling. <i>Stem Cell Research and Therapy</i> , 2017, 8, 138.	2.4	43
129	Cognitive Impairment and Dementia After Stroke: Design and Rationale for the DISCOVERY Study. <i>Stroke</i> , 2021, 52, e499-e516.	1.0	43
130	Genomic Susceptibility Loci for Brain Atrophy in Hypertensive Sibships From the GENOA Study. <i>Hypertension</i> , 2005, 45, 793-798.	1.3	42
131	17q25 Locus Is Associated With White Matter Hyperintensity Volume in Ischemic Stroke, But Not With Lacunar Stroke Status. <i>Stroke</i> , 2013, 44, 1609-1615.	1.0	42
132	Whole Blood DNA Methylation Signatures of Diet Are Associated With Cardiovascular Disease Risk Factors and All-Cause Mortality. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002766.	1.6	42
133	MarkVCID cerebral small vessel consortium: I. Enrollment, clinical, fluid protocols. <i>Alzheimer's and Dementia</i> , 2021, 17, 704-715.	0.4	42
134	Association of common genetic variants with brain microbleeds. <i>Neurology</i> , 2020, 95, e3331-e3343.	1.5	40
135	Genetic loci associated with circulating levels of very long-chain saturated fatty acids. <i>Journal of Lipid Research</i> , 2015, 56, 176-184.	2.0	38
136	Dietary fatty acids modulate associations between genetic variants and circulating fatty acids in plasma and erythrocyte membranes: Meta-analysis of nine studies in the CHARGE consortium. <i>Molecular Nutrition and Food Research</i> , 2015, 59, 1373-1383.	1.5	37
137	Association of variants in <i>HTRA1</i> and <i>NOTCH3</i> with MRI-defined extremes of cerebral small vessel disease in older subjects. <i>Brain</i> , 2019, 142, 1009-1023.	3.7	37
138	Parental History of Stroke Predicts Subclinical But Not Clinical Stroke. <i>Stroke</i> , 2000, 31, 2098-2102.	1.0	36
139	Family-based association study of matrix metalloproteinase-3 and -9 haplotypes with susceptibility to ischemic white matter injury. <i>Human Genetics</i> , 2007, 120, 671-680.	1.8	36
140	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. <i>Human Molecular Genetics</i> , 2015, 24, 559-571.	1.4	36
141	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. <i>International Journal of Epidemiology</i> , 2017, 46, dyw318.	0.9	36
142	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. <i>Science Advances</i> , 2022, 8, eabl6579.	4.7	36
143	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. <i>Nature Communications</i> , 2021, 12, 2830.	5.8	35
144	Epigenetic Age and the Risk of Incident Atrial Fibrillation. <i>Circulation</i> , 2021, 144, 1899-1911.	1.6	35

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145	Genetic Overlap Between Diagnostic Subtypes of Ischemic Stroke. <i>Stroke</i> , 2015, 46, 615-619.	1.0	34
146	Whole genome sequence analyses of brain imaging measures in the Framingham Study. <i>Neurology</i> , 2018, 90, e188-e196.	1.5	34
147	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. <i>Blood</i> , 2019, 133, 967-977.	0.6	34
148	Genes From a Translational Analysis Support a Multifactorial Nature of White Matter Hyperintensities. <i>Stroke</i> , 2015, 46, 341-347.	1.0	33
149	Identification, Heritability, and Relation With Gene Expression of Novel DNA Methylation Loci for Blood Pressure. <i>Hypertension</i> , 2020, 76, 195-205.	1.3	33
150	<i>APOE</i> alleles' association with cognitive function differs across Hispanic/Latino groups and genetic ancestry in the study of Latinos' investigation of neurocognitive aging (HCHS/SOL). <i>Alzheimer's and Dementia</i> , 2021, 17, 466-474.	0.4	33
151	Brain Aging in African-Americans: The Atherosclerosis Risk in Communities (ARIC) Experience. <i>Current Alzheimer Research</i> , 2015, 12, 607-613.	0.7	33
152	Altered Soluble Epoxide Hydrolase Gene Expression and Function and Vascular Disease Risk in the Stroke-Prone Spontaneously Hypertensive Rat. <i>Hypertension</i> , 2008, 51, 567-573.	1.3	32
153	Analysis of Whole-Exome Sequencing Data for Alzheimer Disease Stratified by <i>APOE</i> Genotype. <i>JAMA Neurology</i> , 2019, 76, 1099.	4.5	32
154	Genome-wide association study identifies novel loci for type 2 diabetes-attributed end-stage kidney disease in African Americans. <i>Human Genomics</i> , 2019, 13, 21.	1.4	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. <i>Atherosclerosis</i> , 2007, 192, 56-66.	0.4	31
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