Myriam Fornage

List of Publications by Year
in descending order

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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	Proteomic Analysis Identifies Circulating Proteins Associated With Plasma Amyloid-Î² and Incident Dementia. Biological Psychiatry Global Open Science, 2023, 3, 490-499.	1.0	5
2	Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. Human Molecular Genetics, 2022, 31, 347-361.	1.4	9
3	Genetic Basis of Stroke Occurrence, Prevention, and Outcome. , 2022, , 237-246.e4.		0
4	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. Stroke, 2022, 53, 788-797.	1.0	88
5	Gene-mapping study of extremes of cerebral small vessel disease reveals TRIM47 as a strong candidate. Brain, 2022, 145, 1992-2007.	3.7	6
6	Identification of novel susceptibility methylation loci for pancreatic cancer in a two-phase epigenome-wide association study. Epigenetics, 2022, 17, 1357-1372.	1.3	4
7	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	3.0	29
8	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	2.6	24
9	Circulating Metabolome and White Matter Hyperintensities in Women and Men. Circulation, 2022, 145, 1040-1052.	1.6	17
10	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	1.2	2
11	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	9.4	156
12	Polygenic transcriptome risk scores for COPD and lung function improve cross-ethnic portability of prediction in the NHLBI TOPMed program. American Journal of Human Genetics, 2022, 109, 857-870.	2.6	7
13	Predicted gene expression in ancestrally diverse populations leads to discovery of susceptibility loci for lifestyle and cardiometabolic traits. American Journal of Human Genetics, 2022, 109, 669-679.	2.6	5
14	Meta-analysis of genome-wide association studies identifies ancestry-specific associations underlying circulating total tau levels. Communications Biology, 2022, 5, 336.	2.0	6
15	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	4.7	36
16	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	9.4	700
17	Integrative analysis of clinical and epigenetic biomarkers of mortality. Aging Cell, 2022, 21, e13608.	3.0	8
18	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250

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19	Pulmonary Function and Blood DNA Methylation: A Multiancestry Epigenome-Wide Association Meta-analysis. American Journal of Respiratory and Critical Care Medicine, 2022, 206, 321-336.	2.5	15
20	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations. Frontiers in Endocrinology, 2022, 13, 863893.	1.5	7
21	Gaseous air pollutants and DNA methylation in a methylome-wide association study of an ethnically and environmentally diverse population of U.S. adults. Environmental Research, 2022, 212, 113360.	3.7	7
22	Genetic Risk, Midlife Life's Simple 7, and Incident Dementia in the Atherosclerosis Risk in Communities Study. Neurology, 2022, 99, .	1.5	11
23	A multi-ethnic polygenic risk score is associated with hypertension prevalence and progression throughout adulthood. Nature Communications, 2022, 13, .	5.8	27
24	Association of Cardiovascular Health Through Young Adulthood With Genome-Wide DNA Methylation Patterns in Midlife: The CARDIA Study. Circulation, 2022, 146, 94-109.	1.6	17
25	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	1.3	12
26	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.	0.4	33
27	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.0	2
28	Association between Circulating Protein C Levels and Incident Dementia: The Atherosclerosis Risk in Communities Study. Neuroepidemiology, 2021, 55, 306-315.	1.1	2
29	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	9.4	676
30	MarkVCID cerebral small vessel consortium: I. Enrollment, clinical, fluid protocols. Alzheimer's and Dementia, 2021, 17, 704-715.	0.4	42
31	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
32	Common Medications and Intracerebral Hemorrhage: The ARIC Study. Journal of the American Heart Association, 2021, 10, e014270.	1.6	8
33	Multiomics integrative analysis identifies APOE allele-specific blood biomarkers associated to Alzheimerâ€™s disease etiopathogenesis. Aging, 2021, 13, 9277-9329.	1.4	15
34	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	4.1	13
35	Circulating trimethylamine N-oxide in association with diet and cardiometabolic biomarkers: an international pooled analysis. American Journal of Clinical Nutrition, 2021, 113, 1145-1156.	2.2	27
36	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. American Journal of Human Genetics, 2021, 108, 564-582.	2.6	18

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37	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	5.8	17
38	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.	1.6	29
39	Associations of circulating choline and its related metabolites with cardiometabolic biomarkers: an international pooled analysis. American Journal of Clinical Nutrition, 2021, 114, 893-906.	2.2	11
40	Plasma amyloid Î² levels are driven by genetic variants near APOE, BACE1, APP, PSEN2: A genomeâ€wide association study in over 12,000 nonâ€demented participants. Alzheimer's and Dementia, 2021, 17, 1663-1674.	0.4	20
41	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. Nature Communications, 2021, 12, 2830.	5.8	35
42	Large-scale plasma proteomic analysis identifies proteins and pathways associated with dementia risk. Nature Aging, 2021, 1, 473-489.	5.3	69
43	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	3.8	90
44	Transcriptome Profiling of Mouse Corpus Callosum After Cerebral Hypoperfusion. Frontiers in Cell and Developmental Biology, 2021, 9, 685261.	1.8	5
45	Common variants in Alzheimerâ€™s disease and risk stratification by polygenic risk scores. Nature Communications, 2021, 12, 3417.	5.8	140
46	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	5.8	18
47	Association of the V122I Transthyretin Amyloidosis Genetic Variant With Cardiac Structure and Function in Middle-aged Black Adults. JAMA Cardiology, 2021, 6, 718.	3.0	7
48	Multi-ethnic genome-wide association analyses of white blood cell and platelet traits in the Population Architecture using Genomics and Epidemiology (PAGE) study. BMC Genomics, 2021, 22, 432.	1.2	6
49	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. Genes, 2021, 12, 1049.	1.0	11
50	Epigenetically mediated electrocardiographic manifestations of sub-chronic exposures to ambient particulate matter air pollution in the Women's Health Initiative and Atherosclerosis Risk in Communities Study. Environmental Research, 2021, 198, 111211.	3.7	4
51	Cognitive Impairment and Dementia After Stroke: Design and Rationale for the DISCOVERY Study. Stroke, 2021, 52, e499-e516.	1.0	43
52	Metabolic Traits and Stroke Risk in Individuals of African Ancestry: Mendelian Randomization Analysis. Stroke, 2021, 52, 2680-2684.	1.0	22
53	Blood DNA Methylation and Incident Coronary Heart Disease. JAMA Cardiology, 2021, 6, 1237.	3.0	24
54	Epigenome-wide association study of mitochondrial genome copy number. Human Molecular Genetics, 2021, 31, 309-319.	1.4	6

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55	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	2.6	14
56	Longitudinal change in blood DNA epigenetic signature after smoking cessation. Epigenetics, 2021, , 1-12.	1.3	5
57	Epigenetic Age and the Risk of Incident Atrial Fibrillation. Circulation, 2021, 144, 1899-1911.	1.6	35
58	Cerebral Small-Vessel Disease in Individuals with a Family History of Coronary Heart Disease: The Atherosclerosis Risk in Communities Study. Neuroepidemiology, 2021, 55, 316-322.	1.1	1
59	Association of mitochondrial DNA copy number with cardiometabolic diseases. Cell Genomics, 2021, 1, 100006.	3.0	26
60	Identification of Functional Genetic Determinants of Cardiac Troponin T and I in a Multiethnic Population and Causal Associations With Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2021, 14, CIRCGEN121003460.	1.6	5
61	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. Stroke, 2021, , STROKEAHA120031792.	1.0	16
62	Association of low-frequency and rare coding variants with information processing speed. Translational Psychiatry, 2021, 11, 613.	2.4	2
63	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
64	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	5.8	30
65	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.	4.1	191
66	Epigenetic Age Acceleration and Cognitive Function in African American Adults in Midlife: The Atherosclerosis Risk in Communities Study. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2020, 75, 473-480.	1.7	15
67	Polygenic Risk, Fitness, and Obesity in the Coronary Artery Risk Development in Young Adults (CARDIA) Study. JAMA Cardiology, 2020, 5, 263.	3.0	15
68	Leukocyte Traits and Exposure to Ambient Particulate Matter Air Pollution in the Womenâ€™s Health Initiative and Atherosclerosis Risk in Communities Study. Environmental Health Perspectives, 2020, 128, 17004.	2.8	17
69	Association of CD14 with incident dementia and markers of brain aging and injury. Neurology, 2020, 94, e254-e266.	1.5	21
70	Mitochondrial DNA copy number can influence mortality and cardiovascular disease via methylation of nuclear DNA CpGs. Genome Medicine, 2020, 12, 84.	3.6	63
71	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. Nature Communications, 2020, 11, 4796.	5.8	61
72	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376

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73	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
74	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.	1.0	26
75	A Mendelian randomization of Î³â€² and total fibrinogen levels in relation to venous thromboembolism and ischemic stroke. Blood, 2020, 136, 3062-3069.	0.6	25
76	Genome-wide association study of cognitive function in diverse Hispanics/Latinos: results from the Hispanic Community Health Study/Study of Latinos. Translational Psychiatry, 2020, 10, 245.	2.4	9
77	Association of blood pressure with cognitive function at midlife: a Mendelian randomization study. BMC Medical Genomics, 2020, 13, 121.	0.7	12
78	Methylome-wide association study of central adiposity implicates genes involved in immune and endocrine systems. Epigenomics, 2020, 12, 1483-1499.	1.0	6
79	Association of common genetic variants with brain microbleeds. Neurology, 2020, 95, e3331-e3343.	1.5	40
80	APOE alleles' association with neurocognitive function differ across Hispanic background groups. Alzheimer's and Dementia, 2020, 16, e044169.	0.4	3
81	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	5.8	89
82	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	4.1	17
83	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.	1.6	42
84	Identification, Heritability, and Relation With Gene Expression of Novel DNA Methylation Loci for Blood Pressure. Hypertension, 2020, 76, 195-205.	1.3	33
85	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. Circulation Genomic and Precision Medicine, 2020, 13, e002772.	1.6	11
86	Common Genetic Variation Indicates Separate Causes for Periventricular and Deep White Matter Hyperintensities. Stroke, 2020, 51, 2111-2121.	1.0	71
87	The genetic architecture of the human cerebral cortex. Science, 2020, 367, .	6.0	450
88	Global and Regional Development of the Human Cerebral Cortex: Molecular Architecture and Occupational Aptitudes. Cerebral Cortex, 2020, 30, 4121-4139.	1.6	16
89	Twenty-seven-year time trends in dementia incidence in Europe and the United States. Neurology, 2020, 95, e519-e531.	1.5	227
90	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. Circulation, 2019, 140, 645-657.	1.6	151

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91	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	5.8	62
92	Circulating Monocyte Chemoattractant Protein-1 and Risk of Stroke. Circulation Research, 2019, 125, 773-782.	2.0	78
93	Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. Nature Communications, 2019, 10, 4267.	5.8	139
94	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. Epigenomics, 2019, 11, 1487-1500.	1.0	64
95	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
96	Heart Disease and Stroke Statisticsâ€”2019 Update: A Report From the American Heart Association. Circulation, 2019, 139, e56-e528.	1.6	6,192
97	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	5.8	64
98	The emerging genetic landscape of cerebral white matter hyperintensities. Neurology, 2019, 92, 355-356.	1.5	3
99	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. Environment International, 2019, 132, 104723.	4.8	58
100	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	13.7	679
101	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.	2.2	46
102	Analysis of Whole-Exome Sequencing Data for Alzheimer Disease Stratified by APOE Genotype. JAMA Neurology, 2019, 76, 1099.	4.5	32
103	Genome-wide association study identifies novel loci for type 2 diabetes-attributed end-stage kidney disease in African Americans. Human Genomics, 2019, 13, 21.	1.4	32
104	Polygenic Prediction of Weight and Obesity Trajectories from Birth to Adulthood. Cell, 2019, 177, 587-596.e9.	13.5	516
105	Association of variants inHTRA1andNOTCH3with MRI-defined extremes of cerebral small vessel disease in older subjects. Brain, 2019, 142, 1009-1023.	3.7	37
106	A prospective study of serum metabolites and risk of ischemic stroke. Neurology, 2019, 92, e1890-e1898.	1.5	48
107	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.	1.4	31
108	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.	9.4	112

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109	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.	9.4	1,962
110	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
111	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.	0.4	62
112	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€INCA). Alzheimer's and Dementia, 2019, 15, 1624-1632.	0.4	53
113	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
114	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	9.4	192
115	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
116	Epigenetic Loci of Blood Pressure. Circulation Genomic and Precision Medicine, 2019, 12, e002341.	1.6	3
117	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. Neurology, 2019, 92, .	1.5	30
118	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. Blood, 2019, 133, 967-977.	0.6	34
119	Combined linkage and association analysis identifies rare and low frequency variants for blood pressure at 1q31. European Journal of Human Genetics, 2019, 27, 269-277.	1.4	5
120	Genomeâ€wide interaction with the insulin secretion locus MTNR1B reveals CMIP as a novel type 2 diabetes susceptibility gene in African Americans. Genetic Epidemiology, 2018, 42, 559-570.	0.6	17
121	Relationships of Clinical and Computed Tomography-Imaged Adiposity with Cognition in Middle-Aged and Older African Americans. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2018, 73, 492-498.	1.7	5
122	Whole genome sequence analyses of brain imaging measures in the Framingham Study. Neurology, 2018, 90, e188-e196.	1.5	34
123	Meta-analysis of epigenome-wide association studies of cognitive abilities. Molecular Psychiatry, 2018, 23, 2133-2144.	4.1	68
124	The genetic architecture of dementia with Lewy bodies is shaping up. Lancet Neurology, The, 2018, 17, 25-26.	4.9	2
125	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.	1.6	26
126	O3â€03â€03: EPIGENOMEâ€WIDE ASSOCIATION STUDIES IMPLICATE GENES INVOLVED IN GLIAL CELL FUNCTION AND VIRAL RESPONSE IN CEREBRAL WHITE MATTER HYPERINTENSITIES. Alzheimer's and Dementia, 2018, 14, P1015.	0.4	0

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127	Genome-wide association study of 23,500 individuals identifies 7 loci associated with brain ventricular volume. Nature Communications, 2018, 9, 3945.	5.8	31
128	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.	2.6	326
129	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.	1.2	9
130	Genome-wide association meta-analysis of circulating odd-numbered chain saturated fatty acids: Results from the CHARGE Consortium. PLoS ONE, 2018, 13, e0196951.	1.1	14
131	Imaging Endophenotypes of Stroke as a Target for Genetic Studies. Stroke, 2018, 49, 1557-1562.	1.0	10
132	Reversal of endothelial dysfunction reduces white matter vulnerability in cerebral small vessel disease in rats. Science Translational Medicine, 2018, 10, .	5.8	129
133	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.	1.0	17
134	Generalization and fine mapping of red blood cell trait genetic associations to multiâ€ethnic populations: The PAGE study. American Journal of Hematology, 2018, 93, 1061-1073.	2.0	5
135	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949.	6.0	78
136	Top research priorities for stroke genetics. Lancet Neurology, The, 2018, 17, 663-665.	4.9	7
137	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	5.8	85
138	Discovery, fine-mapping, and conditional analyses of genetic variants associated with C-reactive protein in multiethnic populations using the Metabochip in the Population Architecture using Genomics and Epidemiology (PAGE) study. Human Molecular Genetics, 2018, 27, 2940-2953.	1.4	16
139	Associations of plasma clusterin and Alzheimerâ€™s disease-related MRI markers in adults at mid-life: The CARDIA Brain MRI sub-study. PLoS ONE, 2018, 13, e0190478.	1.1	15
140	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
141	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
142	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	9.4	1,124
143	Associations of Brain Structure With Adiposity and Changes in Adiposity in a Middle-Aged and Older Biracial Population. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2017, 72, glw239.	1.7	12
144	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. International Journal of Epidemiology, 2017, 46, dyw318.	0.9	36

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145	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	5.8	250
146	Fine mapping of QT interval regions in global populations refines previously identified QT interval loci and identifies signals unique to African and Hispanic descent populations. Heart Rhythm, 2017, 14, 572-580.	0.3	19
147	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
148	Heart Disease and Stroke Statisticsâ€”2017 Update: A Report From the American Heart Association. Circulation, 2017, 135, e146-e603.	1.6	7,085
149	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.	1.8	31
150	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.	2.4	43
151	Discovery and fine-mapping of loci associated with MUFAs through trans-ethnic meta-analysis in Chinese and European populations. Journal of Lipid Research, 2017, 58, 974-981.	2.0	18
152	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.	2.6	45
153	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. Biological Psychiatry, 2017, 82, 322-329.	0.7	84
154	Genetic variation at 16q24.2 is associated with small vessel stroke. Annals of Neurology, 2017, 81, 383-394.	2.8	73
155	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.	1.0	284
156	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
157	Transethnic insight into the genetics of glycaemic traits: fine-mapping results from the Population Architecture using Genomics and Epidemiology (PAGE) consortium. Diabetologia, 2017, 60, 2384-2398.	2.9	20
158	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	9.4	783
159	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	2.6	154
160	Epigenome-wide association studies identify DNA methylation associated with kidney function. Nature Communications, 2017, 8, 1286.	5.8	145
161	Cerebral white matter hyperintensities on MRI and acceleration of epigenetic aging: the atherosclerosis risk in communities study. Clinical Epigenetics, 2017, 9, 21.	1.8	45
162	Genome-Wide Association Analysis of the Sense of Smell in U.S. Older Adults: Identification of Novel Risk Loci in African-Americans and European-Americans. Molecular Neurobiology, 2017, 54, 8021-8032.	1.9	17

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163	[O1â€“03â€“03]: GENOMEâ€WIDE ASSOCIATION STUDY IDENTIFIES NOVEL GENETIC VARIANTS FOR NEUROCOGNITIVE FUNCTION AMONG HISPANICS/LATINOS: THE HCHS/SOL STUDY. Alzheimer's and Dementia, 2017, 13, P191.	0.4	0
164	Blood Pressure and Hispanic/Latino Cognitive Function: Hispanic Community Health Study/Study of Latinos Results. Journal of Alzheimer's Disease, 2017, 59, 31-42.	1.2	18
165	Whole exome sequence-based association analyses of plasma amyloid-Î² in African and European Americans; the Atherosclerosis Risk in Communities-Neurocognitive Study. PLoS ONE, 2017, 12, e0180046.	1.1	18
166	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.	3.9	341
167	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.	3.9	246
168	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. Journal of Clinical Investigation, 2017, 127, 1798-1812.	3.9	106
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