

Jennifer A Smith

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

168 papers	12,448 citations	46 h-index	110 g-index
212 ext. papers	17,848 ext. citations	11 avg, IF	4.77 L-index

#	Paper	IF	Citations
168	Epigenetics of single-site and multi-site atherosclerosis in African Americans from the Genetic Epidemiology Network of Arteriopathy (GENOA).. <i>Clinical Epigenetics</i> , 2022 , 14, 10	7.7	0
167	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed.. <i>Cell Genomics</i> , 2022 , 2, 100084-100084		1
166	Multivariate, region-based genetic analyses of facets of reproductive aging in White and Black women.. <i>Molecular Genetics & Genomic Medicine</i> , 2022 , e1896	2.3	1
165	Rare coding variants in RCN3 are associated with blood pressure.. <i>BMC Genomics</i> , 2022 , 23, 148	4.5	
164	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traits-The Hispanic/Latino Anthropometry Consortium.. <i>Human Genetics and Genomics Advances</i> , 2022 , 3, 100099	0.8	0
163	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential.. <i>Science Advances</i> , 2022 , 8, eabl6579	14.3	3
162	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. <i>Nature Genetics</i> , 2022 ,	36.3	7
161	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects.. <i>Nature Genetics</i> , 2022 , 54, 581-592	36.3	6
160	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2021 , 26, 2111-2125	15.1	3
159	Association of low-frequency and rare coding variants with information processing speed. <i>Translational Psychiatry</i> , 2021 , 11, 613	8.6	0
158	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
157	Association of mitochondrial DNA copy number with cardiometabolic diseases.. <i>Cell Genomics</i> , 2021 , 1,		1
156	Epigenome-wide association study identifies DNA methylation sites associated with target organ damage in older African Americans. <i>Epigenetics</i> , 2021 , 16, 862-875	5.7	6
155	Epigenetic age acceleration is associated with cardiometabolic risk factors and clinical cardiovascular disease risk scores in African Americans. <i>Clinical Epigenetics</i> , 2021 , 13, 55	7.7	8
154	Cumulative Genetic Risk and Are Independently Associated With Dementia Status in a Multiethnic, Population-Based Cohort. <i>Neurology: Genetics</i> , 2021 , 7, e576	3.8	2
153	Associations between polygenic risk score for age at menarche and menopause, reproductive timing, and serum hormone levels in multiple race/ethnic groups. <i>Menopause</i> , 2021 , 28, 819-828	2.5	5
152	Genetic variants predictive of reproductive aging are associated with vasomotor symptoms in a multiracial/ethnic cohort. <i>Menopause</i> , 2021 , 28, 883-892	2.5	

151	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. <i>American Journal of Human Genetics</i> , 2021 , 108, 564-582	11	7
150	A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. <i>American Journal of Epidemiology</i> , 2021 , 190, 1977-1992	3.8	3
149	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021 , 22, 194	18.3	14
148	Accelerated DNA methylation age and medication use among African Americans. <i>Aging</i> , 2021 , 13, 14604-14629	5.1	1
147	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021 , 12, 3987	17.4	3
146	The Socioeconomic Gradient in Epigenetic Ageing Clocks: Evidence from the Multi-Ethnic Study of Atherosclerosis and the Health and Retirement Study. <i>Epigenetics</i> , 2021 , 1-23	5.7	8
145	Depression and interleukin-6 signaling: A Mendelian Randomization study. <i>Brain, Behavior, and Immunity</i> , 2021 , 95, 106-114	16.6	10
144	Genetic effects and gene-by-education interactions on episodic memory performance and decline in an aging population. <i>Social Science and Medicine</i> , 2021 , 271, 112039	5.1	5
143	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. <i>EBioMedicine</i> , 2021 , 63, 103157	8.8	3
142	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021 , 590, 290-299	50.4	268
141	Bayesian hierarchical models for high-dimensional mediation analysis with coordinated selection of correlated mediators. <i>Statistics in Medicine</i> , 2021 , 40, 6038-6056	2.3	2
140	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021 , 596, 393-397	50.4	28
139	Population sequencing data reveal a compendium of mutational processes in the human germ line. <i>Science</i> , 2021 , 373, 1030-1035	33.3	7
138	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021 , 12, 7173	17.4	1
137	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021 , 12, 7174	17.4	0
136	Polygenic risk score for general cognitive function is associated with measures of cognition in South Asians from the LASI-DAD Study.. <i>Alzheimer's and Dementia</i> , 2021 , 17 Suppl 3, e053977	1.2	
135	Common and rare variants in topologically associated domains for cognitive function in South Asians from the LASI-DAD Study.. <i>Alzheimer's and Dementia</i> , 2021 , 17 Suppl 3, e054029	1.2	
134	Whole genome sequence association analyses of brain volumes in the TOPMed program. <i>Alzheimer's and Dementia</i> , 2020 , 16, e040627	1.2	

133	Common and rare variants in Alzheimer's disease genes are associated with episodic memory in South Asians from the LASI-DAD study. <i>Alzheimer's and Dementia</i> , 2020 , 16, e045189	1.2	
132	Trans-ethnic meta-analysis of interactions between genetics and early life socioeconomic status on memory performance and decline in older Americans. <i>Alzheimer's and Dementia</i> , 2020 , 16, e045872	1.2	
131	Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020 , 11, 6285	17.4	22
130	Social regulation of inflammation related gene expression in the multi-ethnic study of atherosclerosis. <i>Psychoneuroendocrinology</i> , 2020 , 117, 104654	5	7
129	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002772	5.2	8
128	Genetic Architecture of Gene Expression in European and African Americans: An eQTL Mapping Study in GENOA. <i>American Journal of Human Genetics</i> , 2020 , 106, 496-512	11	14
127	Genome-wide association study meta-analysis identifies three novel loci for circulating anti-Müllerian hormone levels in women 2020 ,		3
126	Bayesian shrinkage estimation of high dimensional causal mediation effects in omics studies. <i>Biometrics</i> , 2020 , 76, 700-710	1.8	12
125	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020 , 586, 763-768	50.4	127
124	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	36.3	26
123	Genome-wide association study of cognitive function in diverse Hispanics/Latinos: results from the Hispanic Community Health Study/Study of Latinos. <i>Translational Psychiatry</i> , 2020 , 10, 245	8.6	1
122	Association Between Episodic Memory and Genetic Risk Factors for Alzheimer's Disease in South Asians from the Longitudinal Aging Study in India-Diagnostic Assessment of Dementia (LASI-DAD). <i>Journal of the American Geriatrics Society</i> , 2020 , 68 Suppl 3, S45-S53	5.6	0
121	Underlying features of epigenetic aging clocks in vivo and in vitro. <i>Aging Cell</i> , 2020 , 19, e13229	9.9	37
120	Genome-Wide Association Meta-Analysis of Individuals of European Ancestry Identifies Suggestive Loci for Sodium Intake, Potassium Intake, and Their Ratio Measured from 24-Hour or Half-Day Urine Samples. <i>Journal of Nutrition</i> , 2020 , 150, 2635-2645	4.1	1
119	Epigenetic loci for blood pressure are associated with hypertensive target organ damage in older African Americans from the genetic epidemiology network of Arteriopathy (GENOA) study. <i>BMC Medical Genomics</i> , 2020 , 13, 131	3.7	1
118	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. <i>Nature Genetics</i> , 2020 , 52, 969-983	36.3	33
117	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. <i>Nature Communications</i> , 2020 , 11, 6417	17.4	17
116	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020 , 25, 2392-2409	15.1	45

115	Leveraging gene co-expression patterns to infer trait-relevant tissues in genome-wide association studies. <i>PLoS Genetics</i> , 2020 , 16, e1008734	6	8
114	Intrinsic and extrinsic epigenetic age acceleration are associated with hypertensive target organ damage in older African Americans. <i>BMC Medical Genomics</i> , 2019 , 12, 141	3.7	11
113	Education and Lifestyle Factors Are Associated with DNA Methylation Clocks in Older African Americans. <i>International Journal of Environmental Research and Public Health</i> , 2019 , 16,	4.6	49
112	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. <i>Epigenomics</i> , 2019 , 11, 1487-1500	4.4	24
111	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019 , 188, 1033-1054	3.8	39
110	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019 , 10, 376	17.4	41
109	Leveraging linkage evidence to identify low-frequency and rare variants on 16p13 associated with blood pressure using TOPMed whole genome sequencing data. <i>Human Genetics</i> , 2019 , 138, 199-210	6.3	14
108	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. <i>Nature Communications</i> , 2019 , 10, 2581	17.4	31
107	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. <i>PLoS ONE</i> , 2019 , 14, e0216222	3.7	11
106	Novel DNA methylation sites associated with cigarette smoking among African Americans. <i>Epigenetics</i> , 2019 , 14, 383-391	5.7	21
105	The metabolic network coherence of human transcriptomes is associated with genetic variation at the cadherin 18 locus. <i>Human Genetics</i> , 2019 , 138, 375-388	6.3	4
104	Expression of socially sensitive genes: The multi-ethnic study of atherosclerosis. <i>PLoS ONE</i> , 2019 , 14, e0214061	3.7	5
103	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , 2019 , 28, 2615-2633	5.6	14
102	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	36.3	59
101	A Peripheral Blood DNA Methylation Signature of Hepatic Fat Reveals a Potential Causal Pathway for Nonalcoholic Fatty Liver Disease. <i>Diabetes</i> , 2019 , 68, 1073-1083	0.9	25
100	Longitudinal analysis of epigenome-wide DNA methylation reveals novel smoking-related loci in African Americans. <i>Epigenetics</i> , 2019 , 14, 171-184	5.7	4
99	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. <i>Molecular Psychiatry</i> , 2019 , 24, 1920-1932	15.1	30
98	Genome-wide meta-analysis of SNP and antihypertensive medication interactions on left ventricular traits in African Americans. <i>Molecular Genetics & Genomic Medicine</i> , 2019 , 7, e00788	2.3	3

97	A meta-analysis of genome-wide association studies identifies multiple longevity genes. <i>Nature Communications</i> , 2019 , 10, 3669	17.4	102
96	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. <i>Nature Human Behaviour</i> , 2019 , 3, 950-961	12.8	32
95	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
94	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019 , 51, 452-469	36.3	44
93	Using Genetic Burden Scores for Gene-by-Methylation Interaction Analysis on Metabolic Syndrome in African Americans. <i>Biological Research for Nursing</i> , 2019 , 21, 279-285	2.6	2
92	Genome-wide Association Study of 24-Hour Urinary Excretion of Calcium, Magnesium, and Uric Acid. <i>Mayo Clinic Proceedings Innovations, Quality & Outcomes</i> , 2019 , 3, 448-460	3.1	2
91	Associations between neighborhood built environment and cognition vary by apolipoprotein E genotype: Multi-Ethnic Study of Atherosclerosis. <i>Health and Place</i> , 2019 , 60, 102188	4.6	11
90	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. <i>PLoS Genetics</i> , 2019 , 15, e1008500	6	90
89	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. <i>American Journal of Human Genetics</i> , 2019 , 104, 260-274	11	43
88	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. <i>Nature Genetics</i> , 2019 , 51, 237-244	36.3	516
87	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. <i>Biological Psychiatry</i> , 2019 , 85, 946-955	7.9	35
86	Combined linkage and association analysis identifies rare and low frequency variants for blood pressure at 1q31. <i>European Journal of Human Genetics</i> , 2019 , 27, 269-277	5.3	3
85	Testing cross-phenotype effects of rare variants in longitudinal studies of complex traits. <i>Genetic Epidemiology</i> , 2018 , 42, 320-332	2.6	3
84	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018 , 102, 375-400	11	59
83	Joint Influence of SNPs and DNA Methylation on Lipids in African Americans From Hypertensive Sibships. <i>Biological Research for Nursing</i> , 2018 , 20, 161-167	2.6	6
82	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , 2018 , 23, 2133-2144	15.1	46
81	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. <i>Blood</i> , 2018 , 132, 1842-1850	2.2	11
80	Exome Chip Analysis Identifies Low-Frequency and Rare Variants in MRPL38 for White Matter Hyperintensities on Brain Magnetic Resonance Imaging. <i>Stroke</i> , 2018 , 49, 1812-1819	6.7	10

79	DNA methylation in the APOE genomic region is associated with cognitive function in African Americans. <i>BMC Medical Genomics</i> , 2018 , 11, 43	3.7	26
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	3.7	31
77	O3-03-03: EPIGENOME-WIDE ASSOCIATION STUDIES IMPLICATE GENES INVOLVED IN GLIAL CELL FUNCTION AND VIRAL RESPONSE IN CEREBRAL WHITE MATTER HYPERINTENSITIES 2018 , 14, P1015-P1016		
76	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018 , 9, 2098	17.4	254
75	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
74	Set-Based Tests for the Gene-Environment Interaction in Longitudinal Studies. <i>Journal of the American Statistical Association</i> , 2017 , 112, 966-978	2.8	11
73	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017 , 8, 14977	17.4	105
72	and Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2017 , 28, 981-994	12.7	30
71	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	7.9	68
70	Rare-variant association tests in longitudinal studies, with an application to the Multi-Ethnic Study of Atherosclerosis (MESA). <i>Genetic Epidemiology</i> , 2017 , 41, 801-810	2.6	0
69	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. <i>Nature Communications</i> , 2017 , 8, 910	17.4	78
68	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. <i>Circulation: Cardiovascular Genetics</i> , 2017 , 10,		33
67	Association of urinary citrate excretion, pH, and net gastrointestinal alkali absorption with diet, diuretic use, and blood glucose concentration. <i>Physiological Reports</i> , 2017 , 5, e13411	2.6	5
66	Polymorphisms in Renal Ammonia Metabolism Genes Correlate With 24-Hour Urine pH. <i>Kidney International Reports</i> , 2017 , 2, 1111-1121	4.1	6
65	The low single nucleotide polymorphism heritability of plasma and saliva cortisol levels. <i>Psychoneuroendocrinology</i> , 2017 , 85, 88-95	5	13
64	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017 , 101, 888-902	11	83
63	Neighborhood characteristics influence DNA methylation of genes involved in stress response and inflammation: The Multi-Ethnic Study of Atherosclerosis. <i>Epigenetics</i> , 2017 , 12, 662-673	5.7	73
62	Interaction between Social/Psychosocial Factors and Genetic Variants on Body Mass Index: A Gene-Environment Interaction Analysis in a Longitudinal Setting. <i>International Journal of Environmental Research and Public Health</i> , 2017 , 14,	4.6	8

61	Gene-by-Psychosocial Factor Interactions Influence Diastolic Blood Pressure in European and African Ancestry Populations: Meta-Analysis of Four Cohort Studies. <i>International Journal of Environmental Research and Public Health</i> , 2017 , 14,	4.6	3
60	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017 , 13, e1006528	6	103
59	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. <i>PLoS Genetics</i> , 2017 , 13, e1006678	6	11
58	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	6	60
57	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	6	58
56	The complex genetics of gait speed: genome-wide meta-analysis approach. <i>Aging</i> , 2017 , 9, 209-246	5.6	16
55	Applying Novel Methods for Assessing Individual- and Neighborhood-Level Social and Psychosocial Environment Interactions with Genetic Factors in the Prediction of Depressive Symptoms in the Multi-Ethnic Study of Atherosclerosis. <i>Behavior Genetics</i> , 2016 , 46, 89-99	3.2	6
54	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016 , 9, 436-447		442
53	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016 , 48, 1162-70	36.3	152
52	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. <i>Science Translational Medicine</i> , 2016 , 8, 341ra76	17.5	77
51	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016 , 48, 1462-1472	36.3	198
50	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 13366-13371	11.5	90
49	Key influence of sex on urine volume and osmolality. <i>Biology of Sex Differences</i> , 2016 , 7, 12	9.3	13
48	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	11	41
47	Heritability of dietary traits that contribute to nephrolithiasis in a cohort of adult sibships. <i>Journal of Nephrology</i> , 2016 , 29, 45-51	4.8	7
46	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016 , 7, 10023	17.4	295
45	A Statistical Approach for Testing Cross-Phenotype Effects of Rare Variants. <i>American Journal of Human Genetics</i> , 2016 , 98, 525-540	11	40
44	An Empirical Comparison of Joint and Stratified Frameworks for Studying G x E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Gene-Lifestyle Interactions Working Group. <i>Genetic Epidemiology</i> , 2016 , 40, 404-15	2.6	15

43	GENOME-WIDE ASSOCIATION STUDY (GWAS) AND GENOME-WIDE BY ENVIRONMENT INTERACTION STUDY (GWEIS) OF DEPRESSIVE SYMPTOMS IN AFRICAN AMERICAN AND HISPANIC/LATINA WOMEN. <i>Depression and Anxiety</i> , 2016 , 33, 265-80	8.4	76
42	Personality Polygenes, Positive Affect, and Life Satisfaction. <i>Twin Research and Human Genetics</i> , 2016 , 19, 407-17	2.2	10
41	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016 , 17, 255	18.3	171
40	P1-118: Association of Low-Frequency and Rare Coding Variants with Information Processing Speed 2016 , 12, P448-P448		
39	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016 , 48, 624-33	36.3	602
38	Estimating Telomere Length Heritability in an Unrelated Sample of Adults: Is Heritability of Telomere Length Modified by Life Course Socioeconomic Status?. <i>Biodemography and Social Biology</i> , 2016 , 62, 73-86	1.1	13
37	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016 , 533, 539-42	50.4	850
36	GWAS analysis of handgrip and lower body strength in older adults in the CHARGE consortium. <i>Aging Cell</i> , 2016 , 15, 792-800	9.9	33
35	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015 , 523, 459-462	60.4	119
34	A statistical approach for rare-variant association testing in affected sibships. <i>American Journal of Human Genetics</i> , 2015 , 96, 543-54	11	14
33	Multiethnic genome-wide association study of cerebral white matter hyperintensities on MRI. <i>Circulation: Cardiovascular Genetics</i> , 2015 , 8, 398-409		119
32	The cis and trans effects of the risk variants of coronary artery disease in the Chr9p21 region. <i>BMC Medical Genomics</i> , 2015 , 8, 21	3.7	15
31	GWAS of longevity in CHARGE consortium confirms APOE and FOXO3 candidacy. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2015 , 70, 110-8	6.4	188
30	Contribution of common non-synonymous variants in PCSK1 to body mass index variation and risk of obesity: a systematic review and meta-analysis with evidence from up to 331 175 individuals. <i>Human Molecular Genetics</i> , 2015 , 24, 3582-94	5.6	34
29	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015 , 47, 1294-1303	36.3	226
28	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015 , 6, 8570	17.4	335
27	Current Applications of Genetic Risk Scores to Cardiovascular Outcomes and Subclinical Phenotypes. <i>Current Epidemiology Reports</i> , 2015 , 2, 180-190	2.9	58
26	Life course socioeconomic status and DNA methylation in genes related to stress reactivity and inflammation: The multi-ethnic study of atherosclerosis. <i>Epigenetics</i> , 2015 , 10, 958-69	5.7	110

25	Effect of Demographics on Excretion of Key Urinary Factors Related to Kidney Stone Risk. <i>Urology</i> , 2015 , 86, 690-6	1.6	11
24	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, 749-63	7.9	48
23	Comparative genome-wide association studies of a depressive symptom phenotype in a repeated measures setting by race/ethnicity in the Multi-Ethnic Study of Atherosclerosis. <i>BMC Genetics</i> , 2015 , 16, 118	2.6	11
22	Set-based tests for genetic association in longitudinal studies. <i>Biometrics</i> , 2015 , 71, 606-15	1.8	11
21	Association between Stress Response Genes and Features of Diurnal Cortisol Curves in the Multi-Ethnic Study of Atherosclerosis: A New Multi-Phenotype Approach for Gene-Based Association Tests. <i>PLoS ONE</i> , 2015 , 10, e0126637	3.7	5
20	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
19	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015 , 6, 5897	17.4	147
18	Meta-analysis of correlated traits via summary statistics from GWASs with an application in hypertension. <i>American Journal of Human Genetics</i> , 2015 , 96, 21-36	11	186
17	SLC2A9 Genotype Is Associated with SLC2A9 Gene Expression and Urinary Uric Acid Concentration. <i>PLoS ONE</i> , 2015 , 10, e0128593	3.7	9
16	Meta-analysis of loci associated with age at natural menopause in African-American women. <i>Human Molecular Genetics</i> , 2014 , 23, 3327-42	5.6	44
15	Epigenomic Indicators of Age in African Americans. <i>Hereditary Genetics: Current Research</i> , 2014 , 3,		8
14	Genetic diversity is a predictor of mortality in humans. <i>BMC Genetics</i> , 2014 , 15, 159	2.6	6
13	Pleiotropic genes for metabolic syndrome and inflammation. <i>Molecular Genetics and Metabolism</i> , 2014 , 112, 317-38	3.7	81
12	Epigenomic association analysis identifies smoking-related DNA methylation sites in African Americans. <i>Human Genetics</i> , 2013 , 132, 1027-37	6.3	119
11	Genome-wide association analysis of blood-pressure traits in African-ancestry individuals reveals common associated genes in African and non-African populations. <i>American Journal of Human Genetics</i> , 2013 , 93, 545-54	11	145
10	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. <i>Science</i> , 2013 , 340, 1467-71	33.3	563
9	Epigenetic markers of renal function in african americans. <i>Nursing Research and Practice</i> , 2013 , 2013, 687519	1.9	9
8	Comparison of the DNA methylation profiles of human peripheral blood cells and transformed B-lymphocytes. <i>Human Genetics</i> , 2010 , 127, 651-8	6.3	49

7	Complexity in the genetic architecture of leukoaraiosis in hypertensive sibships from the GENOA Study. <i>BMC Medical Genomics</i> , 2009 , 2, 16	3.7	20
6	The genetic architecture of fasting plasma triglyceride response to fenofibrate treatment. <i>European Journal of Human Genetics</i> , 2008 , 16, 603-13	5.3	28
5	Anti-CD8 monoclonal antibody therapy is effective in the prevention and treatment of experimental autoimmune glomerulonephritis. <i>Journal of the American Society of Nephrology: JASN</i> , 2002 , 13, 359-369	12.7	63
4	Rare Non-coding Variation Identified by Large Scale Whole Genome Sequencing Reveals Unexplained Heritability of Type 2 Diabetes		2
3	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution		1
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