Donna K Arnett

List of Publications by Year
in descending order

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515 papers	61,932 citations	3334 91 h-index	1072 233 g-index
529 all docs	529 docs citations	529 times ranked	73745 citing authors

#	Article	IF	Citations
1	Dietary patterns associated with stroke among West Africans: A caseâ€“control study. International Journal of Stroke, 2023, 18, 193-200.	5.9	8
2	Tree nut consumption and prevalence of carotid artery plaques: The National Heart, Lung, and Blood Institute Family Heart Study. European Journal of Nutrition, 2022, 61, 211-218.	3.9	0
3	Risk Factor Characterization of Ischemic Stroke Subtypes Among West Africans. Stroke, 2022, 53, 134-144.	2.0	10
4	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
5	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.	6.2	24
6	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
7	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
8	Preliminary Research on a COVID-19 Test Strategy to Guide Quarantine Interval in University Students. Covid, 2022, 2, 254-260.	1.5	1
9	An Amish founder population reveals rare-population genetic determinants of the human lipidome. Communications Biology, 2022, 5, 334.	4.4	7
10	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
11	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations. Frontiers in Endocrinology, 2022, 13, 863893.	3.5	7
12	A multi-ethnic polygenic risk score is associated with hypertension prevalence and progression throughout adulthood. Nature Communications, 2022, 13, .	12.8	27
13	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	2.7	12
14	Epigenome-wide association study identifies DNA methylation sites associated with target organ damage in older African Americans. Epigenetics, 2021, 16, 862-875.	2.7	10
15	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.	1.7	2
16	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. EBioMedicine, 2021, 63, 103157.	6.1	14
17	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human Molecular Genetics, 2021, 30, 393-409.	2.9	32
18	Bending the Curve in Cardiovascular Disease Mortality. Circulation, 2021, 143, 837-851.	1.6	35

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19	Whole-Exome Sequencing and hiPSC Cardiomyocyte Models Identify MYRIP, TRAPPC11, and SLC27A6 of Potential Importance to Left Ventricular Hypertrophy in an African Ancestry Population. Frontiers in Genetics, 2021, 12, 588452.	2.3	3
20	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
21	Donor-specific phenotypic variation in hiPSC cardiomyocyte-derived exosomes impacts endothelial cell function. American Journal of Physiology - Heart and Circulatory Physiology, 2021, 320, H954-H968.	3.2	8
22	DNA Methylation and Blood Pressure Phenotypes: A Review of the Literature. American Journal of Hypertension, 2021, 34, 267-273.	2.0	9
23	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. Genome Medicine, 2021, 13, 74.	8.2	20
24	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.	6.2	18
25	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17
26	Age and sex are associated with the plasma lipidome: findings from the GOLDN study. Lipids in Health and Disease, 2021, 20, 30.	3.0	36
27	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
28	Sugar-Sweetened Beverage Consumption and Calcified Atherosclerotic Plaques in the Coronary Arteries: The NHLBI Family Heart Study. Nutrients, 2021, 13, 1775.	4.1	2
29	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
30	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	12.8	18
31	Association of high-sensitivity C-reactive protein and odds of breast cancer by molecular subtype: analysis of the MEND study. Oncotarget, 2021, 12, 1230-1242.	1.8	5
32	Widespread diabetes screening for cardiovascular disease risk estimation. Lancet, The, 2021, 397, 2228-2230.	13.7	4
33	Association of Life-Course Educational Attainment and Breast Cancer Grade in the MEND Study. Annals of Global Health, 2021, 87, 59.	2.0	2
34	Identification of novel and rare variants associated with handgrip strength using whole genome sequence data from the NHLBI Trans-Omics in Precision Medicine (TOPMed) Program. PLoS ONE, 2021, 16, e0253611.	2.5	4
35	Adverse Cardiovascular Outcomes and Antihypertensive Treatment: A Genomeâ€Wide Interaction Metaâ€Analysis in the International Consortium for Antihypertensive Pharmacogenomics Studies. Clinical Pharmacology and Therapeutics, 2021, 110, 723-732.	4.7	6
36	Population sequencing data reveal a compendium of mutational processes in the human germ line. Science, 2021, 373, 1030-1035.	12.6	43

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37	Influence of age on links between major modifiable risk factors and stroke occurrence in West Africa. Journal of the Neurological Sciences, 2021, 428, 117573.	0.6	6
38	Lipid Phenotypes and DNA Methylation: a Review of the Literature. Current Atherosclerosis Reports, 2021, 23, 71.	4.8	17
39	A Novel Afrocentric Stroke Risk Assessment Score: Models from the Siren Study. Journal of Stroke and Cerebrovascular Diseases, 2021, 30, 106003.	1.6	6
40	Association of Sickle Cell Trait With Incidence of Coronary Heart Disease Among African American Individuals. JAMA Network Open, 2021, 4, e2030435.	5.9	5
41	Genetic correlations between traits associated with hyperuricemia, gout, and comorbidities. European Journal of Human Genetics, 2021, 29, 1438-1445.	2.8	11
42	Genomics of Postprandial Lipidomics in the Genetics of Lipid-Lowering Drugs and Diet Network Study. Nutrients, 2021, 13, 4000.	4.1	2
43	A 6-CpG validated methylation risk score model for metabolic syndrome: The HyperGEN and GOLDN studies. PLoS ONE, 2021, 16, e0259836.	2.5	7
44	Metabolic Syndrome and Risk of Breast Cancer by Molecular Subtype: analysis of the MEND study. Clinical Breast Cancer, 2021, , .	2.4	7
45	Proximal and distal effects of genetic susceptibility to multiple sclerosis on the T cell epigenome. Nature Communications, 2021, 12, 7078.	12.8	15
46	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
47	SNPs Filtered by Allele Frequency Improve the Prediction of Hypertension Subtypes. , 2021, , .		0
48	Genetic Contributors of Incident Stroke in 10,700 African Americans With Hypertension: A Meta-Analysis From the Genetics of Hypertension Associated Treatments and Reasons for Geographic and Racial Differences in Stroke Studies. Frontiers in Genetics, 2021, 12, 781451.	2.3	7
49	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
50	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
51	Metabolomics, Lipid Pathways, and Blood Pressure Change. Arteriosclerosis, Thrombosis, and Vascular Biology, 2020, 40, 1801-1803.	2.4	3
52	Carbohydrate and fat intake associated with risk of metabolic diseases through epigenetics of CPT1A. American Journal of Clinical Nutrition, 2020, 112, 1200-1211.	4.7	48
53	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. Journal of Nutrition, 2020, 150, 2635-2645.	2.9	4
54	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146

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55	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
56	Whole genome sequence association analyses of brain volumes in the TOPMed program. Alzheimer's and Dementia, 2020, 16, e040627.	0.8	0
57	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
58	Mendelian randomization analysis does not support causal associations of birth weight with hypertension risk and blood pressure in adulthood. European Journal of Epidemiology, 2020, 35, 685-697.	5.7	9
59	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. PLoS ONE, 2020, 15, e0230815.	2.5	10
60	A lipidome-wide association study of the lipoprotein insulin resistance index. Lipids in Health and Disease, 2020, 19, 153.	3.0	6
61	Report of the National Heart, Lung, and Blood Institute Working Group on Hypertension. Hypertension, 2020, 75, 902-917.	2.7	24
62	Salivary AMY1 Copy Number Variation Modifies Age-Related Type 2 Diabetes Risk. Clinical Chemistry, 2020, 66, 718-726.	3.2	7
63	Unraveling the risk factors for spontaneous intracerebral hemorrhage among West Africans. Neurology, 2020, 94, e998-e1012.	1.1	31
64	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
65	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
66	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
67	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
68	Genome-wide meta-analysis of SNP-by9-ACEI/ARB and SNP-by-thiazide diuretic and effect on serum potassium in cohorts of European and African ancestry. Pharmacogenomics Journal, 2019, 19, 97-108.	2.0	3
69	Clinical correlates and heritability of cardiac mechanics: The HyperGEN study. International Journal of Cardiology, 2019, 274, 208-213.	1.7	5
70	Genomeâ€wide metaâ€analysis of SNP and antihypertensive medication interactions on left ventricular traits in African Americans. Molecular Genetics & Genomic Medicine, 2019, 7, e00788.	1.2	4
71	2019 ACC/AHA Guideline on the Primary Prevention of Cardiovascular Disease: Part 1, Lifestyle and Behavioral Factors. JAMA Cardiology, 2019, 4, 1043.	6.1	100
72	A Clinician's Guide to Healthy Eating for Cardiovascular Disease Prevention. Mayo Clinic Proceedings Innovations, Quality & Outcomes, 2019, 3, 251-267.	2.4	72

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73	Gene Variants at Loci Related to Blood Pressure Account for Variation in Response to Antihypertensive Drugs Between Black and White Individuals. Hypertension, 2019, 74, 614-622.	2.7	14
74	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
75	Association of Birth Weight With Type 2 Diabetes and Glycemic Traits. JAMA Network Open, 2019, 2, e1910915.	5.9	41
76	Tracing and Assessing the Evolution of Clinical Guidelines. Journal of the American Heart Association, 2019, 8, e014060.	3.7	3
77	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.8	5
78	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. Epigenomics, 2019, 11, 1487-1500.	2.1	64
79	Genome-Wide Association Study of Apparent Treatment-Resistant Hypertension in the CHARGE Consortium: The CHARGE Pharmacogenetics Working Group. American Journal of Hypertension, 2019, 32, 1146-1153.	2.0	17
80	Genetic influences on susceptibility to rheumatoid arthritis in African-Americans. Human Molecular Genetics, 2019, 28, 858-874.	2.9	55
81	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
82	Leveraging linkage evidence to identify low-frequency and rare variants on 16p13 associated with blood pressure using TOPMed whole genome sequencing data. Human Genetics, 2019, 138, 199-210.	3.8	29
83	A PheWAS study of a large observational epidemiological cohort of African Americans from the REGARDS study. BMC Medical Genomics, 2019, 12, 26.	1.5	9
84	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
85	Echocardiographic Abnormalities and Determinants of 1â€Month Outcome of Stroke Among West Africans in the SIREN Study. Journal of the American Heart Association, 2019, 8, e010814.	3.7	3
86	Collaborative Molecular Epidemiology Study of Metabolic Dysregulation, DNA Methylation, and Breast Cancer Risk Among Nigerian Women: MEND Study Objectives and Design. Journal of Global Oncology, 2019, 5, 1-9.	0.5	6
87	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. Nature Communications, 2019, 10, 2581.	12.8	62
88	2019 ACC/AHA Guideline on the Primary Prevention of Cardiovascular Disease: A Report of the American College of Cardiology/American Heart Association Task Force on Clinical Practice Guidelines. Circulation, 2019, 140, e596-e646.	1.6	1,789
89	Differential Impact of Risk Factors on Stroke Occurrence Among Men Versus Women in West Africa. Stroke, 2019, 50, 820-827.	2.0	26
90	An Exome-Wide Sequencing Study of the GOLDN Cohort Reveals Novel Associations of Coding Variants and Fasting Plasma Lipids. Frontiers in Genetics, 2019, 10, 158.	2.3	2

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91	2019 ACC/AHA Guideline on the Primary Prevention of Cardiovascular Disease: Executive Summary. Journal of the American College of Cardiology, 2019, 74, 1376-1414.	2.8	820
92	2019 ACC/AHA Guideline on the Primary Prevention of Cardiovascular Disease: Executive Summary: A Report of the American College of Cardiology/American Heart Association Task Force on Clinical Practice Guidelines. Circulation, 2019, 140, e563-e595.	1.6	1,676
93	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
94	Associations between SLC16A11 variants and diabetes in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Scientific Reports, 2019, 9, 843.	3.3	9
95	Systematic Error Removal Using Random Forest for Normalizing Large-Scale Untargeted Lipidomics Data. Analytical Chemistry, 2019, 91, 3590-3596.	6.5	163
96	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
97	Integrating hypertension phenotype and genotype with hybrid non-negative matrix factorization. Bioinformatics, 2019, 35, 1395-1403.	4.1	12
98	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	6.2	106
99	The Interaction of a Diabetes Gene Risk Score With 3 Different Antihypertensive Medications for Incident Glucose-level Elevation. American Journal of Hypertension, 2019, 32, 343-349.	2.0	0
100	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.	2.8	5
101	An exome-wide sequencing study of lipid response to high-fat meal and fenofibrate in Caucasians from the GOLDN cohort. Journal of Lipid Research, 2018, 59, 722-729.	4.2	10
102	Dominant modifiable risk factors for stroke in Ghana and Nigeria (SIREN): a case-control study. The Lancet Global Health, 2018, 6, e436-e446.	6.3	183
103	Association of Sickle Cell Trait With Ischemic Stroke Among African Americans. JAMA Neurology, 2018, 75, 802.	9.0	25
104	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor Î±. JAMA Cardiology, 2018, 3, 463.	6.1	33
105	Epigenome-wide association study of metabolic syndrome in African-American adults. Clinical Epigenetics, 2018, 10, 49.	4.1	49
106	Genomeâ€Wide Interactions with Dairy Intake for Body Mass Index in Adults of European Descent. Molecular Nutrition and Food Research, 2018, 62, 1700347.	3.3	9
107	Dairy Consumption and Body Mass Index Among Adults: Mendelian Randomization Analysis of 184802 Individuals from 25 Studies. Clinical Chemistry, 2018, 64, 183-191.	3.2	34
108	Hypermethylation of MIR21 in CD4+ T cells from patients with relapsing-remitting multiple sclerosis associates with lower miRNA-21 levels and concomitant up-regulation of its target genes. Multiple Sclerosis Journal, 2018, 24, 1288-1300.	3.0	33

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109	Data for GAW20: genome-wide DNA sequence variation and epigenome-wide DNA methylation before and after fenofibrate treatment in a family study of metabolic phenotypes. BMC Proceedings, 2018, 12, 35.	1.6	11
110	Genome-wide association meta-analysis of circulating odd-numbered chain saturated fatty acids: Results from the CHARGE Consortium. PLoS ONE, 2018, 13, e0196951.	2.5	14
111	Genome-wide association study of response to methotrexate in early rheumatoid arthritis patients. Pharmacogenomics Journal, 2018, 18, 528-538.	2.0	42
112	Metabolic and inflammatory biomarkers are associated with epigenetic aging acceleration estimates in the GOLDN study. Clinical Epigenetics, 2018, 10, 56.	4.1	68
113	Omics of Blood Pressure and Hypertension. Circulation Research, 2018, 122, 1409-1419.	4.5	74
114	Epigenomics and metabolomics reveal the mechanism of the APOA2-saturated fat intake interaction affecting obesity. American Journal of Clinical Nutrition, 2018, 108, 188-200.	4.7	54
115	Epigenetic Patterns in Blood Associated With Lipid Traits Predict Incident Coronary Heart Disease Events and Are Enriched for Results From Genome-Wide Association Studies. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	104
116	Sickle Cell Trait and the Risk of ESRD in Blacks. Journal of the American Society of Nephrology: JASN, 2017, 28, 2180-2187.	6.1	79
117	Phenomapping for the Identification of Hypertensive Patients with the Myocardial Substrate for Heart Failure with Preserved Ejection Fraction. Journal of Cardiovascular Translational Research, 2017, 10, 275-284.	2.4	61
118	Interleukinâ€“6 (IL-6) rs1800796 and cyclin dependent kinase inhibitor (CDKN2A/CDKN2B) rs2383207 are associated with ischemic stroke in indigenous West African Men. Journal of the Neurological Sciences, 2017, 379, 229-235.	0.6	31
119	Genome- and CD4 + T-cell methylome-wide association study of circulating trimethylamine-N-oxide in the Genetics of Lipid Lowering Drugs and Diet Network (GOLDN). Journal of Nutrition & Intermediary Metabolism, 2017, 8, 1-7.	1.7	11
120	Non-linear patterns in age-related DNA methylation may reflect CD4⁺ T cell differentiation. Epigenetics, 2017, 12, 492-503.	2.7	24
121	Stroke in Indigenous Africans, African Americans, and European Americans. Stroke, 2017, 48, 1169-1175.	2.0	44
122	Genetic associations with lipoprotein subfraction measures differ by ethnicity in the multi-ethnic study of atherosclerosis (MESA). Human Genetics, 2017, 136, 715-726.	3.8	12
123	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.	4.2	18
124	Coffee consumption and calcified atherosclerotic plaques in the coronary arteries: The NHLBI Family Heart Study. Clinical Nutrition ESPEN, 2017, 17, 18-21.	1.2	10
125	Genetic variation at 16q24.2 is associated with small vessel stroke. Annals of Neurology, 2017, 81, 383-394.	5.3	73
126	Detection of gene-environment interactions in a family-based population using SCAD. Statistics in Medicine, 2017, 36, 3547-3559.	1.6	4

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127	Advancing stroke genomic research in the age of Trans-Omics big data science: Emerging priorities and opportunities. Journal of the Neurological Sciences, 2017, 382, 18-28.	0.6	15
128	Testing Two Evolutionary Theories of Human Aging with DNA Methylation Data. Genetics, 2017, 207, 1547-1560.	2.9	12
129	An epigenome-wide association study of inflammatory response to fenofibrate in the Genetics of Lipid Lowering Drugs and Diet Network. Pharmacogenomics, 2017, 18, 1333-1341.	1.3	16
130	Association of Estimated SodiumÂIntakeÂWith Adverse Cardiac Structure andÂFunction. Journal of the American College of Cardiology, 2017, 70, 715-724.	2.8	21
131	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	6.2	154
132	Sex Differences in Blood HDLâ€¢, the Total Cholesterol/HDLâ€¢ Ratio, and Palmitoleic Acid are Not Associated with Variants in Common Candidate Genes. Lipids, 2017, 52, 969-980.	1.7	19
133	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
134	Dense Genotyping of Immune-Related Regions Identifies Loci for Rheumatoid Arthritis Risk and Damage in African Americans. Molecular Medicine, 2017, 23, 177-187.	4.4	18
135	Exploring Overlaps Between the Genomic and Environmental Determinants of LVH and Stroke: A Multicenter Study in West Africa. Global Heart, 2017, 12, 107.	2.3	10
136	Prevalence and Prognostic Features of ECG Abnormalities in Acute Stroke: Findings From the SIREN Study Among Africans. Global Heart, 2017, 12, 99.	2.3	26
137	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
138	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
139	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
140	Behavior related genes, dietary preferences and anthropometric traits. FASEB Journal, 2017, 31, .	0.5	1
141	Whole Exome Analyses to Examine the Impact of Rare Variants on Left Ventricular Traits in African American Participants from the HyperGEN and GENOA Studies. Journal of Hypertension and Management, 2017, 3, .	0.2	0
142	An Empirical Comparison of Joint and Stratified Frameworks for Studying G Ã— E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Geneâ€Lifestyle Interactions Working Group. Genetic Epidemiology, 2016, 40, 404-415.	1.3	18
143	A genome-wide study of lipid response to fenofibrate in Caucasians. Pharmacogenetics and Genomics, 2016, 26, 324-333.	1.5	12
144	Higher chylomicron remnants and LDL particle numbers associate with CD36 SNPs and DNA methylation sites that reduce CD36. Journal of Lipid Research, 2016, 57, 2176-2184.	4.2	26

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145	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	8.8	251
146	A Genome-wide study of blood pressure in African Americans accounting for gene-smoking interaction. Scientific Reports, 2016, 6, 18812.	3.3	34
147	The US Cancer Moonshot initiative. Lancet Oncology, The, 2016, 17, e178-e180.	10.7	15
148	The Heart of 25 by 25: Achieving the Goal of Reducing Global and Regional Premature Deaths From Cardiovascular Diseases and Stroke. Circulation, 2016, 133, e674-90.	1.6	155
149	Walking and Calcified Atherosclerotic Plaque in the Coronary Arteries. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, 1272-1277.	2.4	12
150	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
151	The Role of Healthy Lifestyle in the Primordial Prevention of Cardiovascular Disease. Current Cardiology Reports, 2016, 18, 56.	2.9	61
152	Evidence-Based Policy Making: Assessment of the American Heart Associationâ€™s Strategic Policy Portfolio. Circulation, 2016, 133, e615-53.	1.6	36
153	Neurogenomics in Africa: Perspectives, progress, possibilities and priorities. Journal of the Neurological Sciences, 2016, 366, 213-223.	0.6	30
154	Assessment of postprandial triglycerides in clinical practice: Validation in a general population and coronary heart disease patients. Journal of Clinical Lipidology, 2016, 10, 1163-1171.	1.5	22
155	Editorial: A Novel Genetic Association With Systemic Sclerosis: The Utility of Wholeâ€Exome Sequencing in Autoimmune Disease. Arthritis and Rheumatology, 2016, 68, 27-30.	5.6	0
156	Mediterranean diet score and left ventricular structure and function: the Multi-Ethnic Study of Atherosclerosis,. American Journal of Clinical Nutrition, 2016, 104, 595-602.	4.7	22
157	Epigenetics of Lipid Phenotypes. Current Cardiovascular Risk Reports, 2016, 10, 1.	2.0	20
158	Research Needs to Improve Hypertension Treatment and Control in African Americans. Hypertension, 2016, 68, 1066-1072.	2.7	78
159	Epigenetic Signatures of Cigarette Smoking. Circulation: Cardiovascular Genetics, 2016, 9, 436-447.	5.1	678
160	Interaction of an S100A9 gene variant with saturated fat and carbohydrates to modulate insulin resistance in 3 populations of different ancestries1â€“3. American Journal of Clinical Nutrition, 2016, 104, 508-517.	4.7	11
161	Epigenome-wide association study of triglyceride postprandial responses to a high-fat dietary challenge. Journal of Lipid Research, 2016, 57, 2200-2207.	4.2	40
162	Associations of the MCM6-rs3754686 proxy for milk intake in Mediterranean and American populations with cardiovascular biomarkers, disease and mortality: Mendelian randomization. Scientific Reports, 2016, 6, 33188.	3.3	18

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163	Association of Central Adiposity With Adverse Cardiac Mechanics. Circulation: Cardiovascular Imaging, 2016, 9, .	2.6	65
164	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	12.8	94
165	Precision Medicine, Genomics, and Public Health. Diabetes Care, 2016, 39, 1870-1873.	8.6	16
166	The effects of omegaâ€3 polyunsaturated fatty acids and genetic variants on methylation levels of the interleukinâ€6 gene promoter. Molecular Nutrition and Food Research, 2016, 60, 410-419.	3.3	41
167	Archeological Echocardiography: Digitization and Speckle Tracking Analysis of Archival Echocardiograms in the Hyper<scp>GEN</scp> Study. Echocardiography, 2016, 33, 386-397.	0.9	24
168	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
169	Clock Genes Explain a Large Proportion of Phenotypic Variance in Systolic Blood Pressure and This Control Is Not Modified by Environmental Temperature. American Journal of Hypertension, 2016, 29, 132-140.	2.0	20
170	Heart Disease and Stroke Statisticsâ€”2016 Update. Circulation, 2016, 133, e38-360.	1.6	5,447
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172	Using genomic approaches to identify CVD-causing variants. Nature Reviews Cardiology, 2016, 13, 72-74.	13.7	4
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