Kari E North

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6655692/publications.pdf

Version: 2024-02-01

400 papers

39,256 citations

80 h-index 4015 176 g-index

417 all docs

 $\begin{array}{c} 417 \\ \text{docs citations} \end{array}$

417 times ranked 44272 citing authors

#	Article	IF	CITATIONS
1	Analyses of biomarker traits in diverse UK biobank participants identify associations missed by European-centric analysis strategies. Journal of Human Genetics, 2022, 67, 87-93.	2.3	27
2	Do adverse childhood experiences and genetic obesity risk interact in relation to body mass index in young adulthood? Findings from the National Longitudinal Study of Adolescent to Adult Health. Pediatric Obesity, 2022, 17, e12885.	2.8	4
3	Dynamic relationships between body fat and circulating adipokine levels from adolescence to young adulthood: The Santiago Longitudinal Study. Nutrition, Metabolism and Cardiovascular Diseases, 2022, 32, 1055-1063.	2.6	3
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	Novel diabetes gene discovery through comprehensive characterization and integrative analysis of longitudinal gene expression changes. Human Molecular Genetics, 2022, 31, 3191-3205.	2.9	4
6	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study. Diabetologia, 2022, 65, 477-489.	6.3	15
7	OUP accepted manuscript. American Journal of Epidemiology, 2022, , .	3.4	1
8	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
9	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
10	The dynamic genetic architecture of early childhood BMI. Nature Metabolism, 2022, 4, 308-309.	11.9	0
11	Enrichment analyses identify shared associations for 25 quantitative traits in over 600,000 individuals from seven diverse ancestries. American Journal of Human Genetics, 2022, 109, 871-884.	6.2	6
12	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traits—The Hispanic/Latino Anthropometry Consortium. Human Genetics and Genomics Advances, 2022, 3, 100099.	1.7	3
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.	6.2	5
14	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
15	Metabolomic Associations of Asthma in the Hispanic Community Health Study/Study of Latinos. Metabolites, 2022, 12, 359.	2.9	1
16	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
17	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.	5.6	15
18	Strengthening Causal Inference in Exposomics Research: Application of Genetic Data and Methods. Environmental Health Perspectives, 2022, 130, 55001.	6.0	5

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19	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
20	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.	7.5	7
21	A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. PLoS Genetics, 2022, 18, e1010193.	3.5	12
22	Extended Human Papillomavirus Genotyping to Predict Progression to High-Grade Cervical Precancer: A Prospective Cohort Study in the Southeastern United States. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1564-1571.	2.5	3
23	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
24	Validation in a Brazilian population of gene markers of periodontitis previously investigated by GWAS and bioinformatic studies. Journal of Periodontology, 2021, 92, 689-703.	3.4	8
25	Host genetic effects in pneumonia. American Journal of Human Genetics, 2021, 108, 194-201.	6.2	17
26	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
27	Genome-wide homozygosity and risk of four non-Hodgkin lymphoma subtypes. , 2021, 5, 200-217.		0
28	Genetic variants and physical activity interact to affect bone density in Hispanic children. BMC Pediatrics, 2021, 21, 79.	1.7	1
29	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
30	Association Between Midlife Obesity and Kidney Function Trajectories: The Atherosclerosis Risk in Communities (ARIC) Study. American Journal of Kidney Diseases, 2021, 77, 376-385.	1.9	13
31	Multi-ancestry genome-wide gene–sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
32	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
33	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17
34	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. Human Genetics and Genomics Advances, 2021, 2, 100029.	1.7	23
35	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
36	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	6.2	28

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37	Discrimination and Leukocyte Telomere Length by Depressive Symptomatology: The Jackson Heart Study. Healthcare (Switzerland), 2021, 9, 639.	2.0	1
38	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
39	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.	2.8	6
40	Genome-wide association study of body fat distribution traits in Hispanics/Latinos from the HCHS/SOL. Human Molecular Genetics, 2021, 30, 2190-2204.	2.9	8
41	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. Genes, 2021, 12, 1049.	2.4	11
42	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.	7.5	4
43	Sugar-Sweetened Beverage Consumption May Modify Associations Between Genetic Variants in the CHREBP (Carbohydrate Responsive Element Binding Protein) Locus and HDL-C (High-Density Lipoprotein) Tj ETQ e003288.	q1 _{3.6} 0.78	4314 rgBT /C
44	Gene-Environment Joint Linkage and Association Analysis of Arsenic Exposure and Diabetes-Related Traits in the Strong Heart Family Study. ISEE Conference Abstracts, 2021, 2021, .	0.0	0
45	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.	6.2	14
46	Tracing the Distribution of European Lactase Persistence Genotypes Along the Americas. Frontiers in Genetics, 2021, 12, 671079.	2.3	3
47	Genetic determinants of metabolic biomarkers and their associations with cardiometabolic traits in Hispanic/Latino adolescents. Pediatric Research, 2021, , .	2.3	0
48	Genomeâ€wide association study identifying novel variant for fasting insulin and allelic heterogeneity in known glycemic loci in Chilean adolescents: The Santiago Longitudinal Study. Pediatric Obesity, 2021, 16, e12765.	2.8	3
49	Demographic and sociocultural risk factors for adulthood weight gain in Hispanic/Latinos: results from the Hispanic Community Health Study / Study of Latinos (HCHS/SOL). BMC Public Health, 2021, 21, 2064.	2.9	8
50	Full title: A largeâ€scale transcriptomeâ€wide association study (TWAS) of 10 blood cell phenotypes reveals complexities of TWAS fineâ€mapping. Genetic Epidemiology, 2021, , .	1.3	2
51	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
52	Obesity Duration, Severity, and Distribution Trajectories and Cardiovascular Disease Risk in the Atherosclerosis Risk in Communities Study. Journal of the American Heart Association, 2021, 10, e019946.	3.7	10
53	Findings from the Hispanic Community Health Study/Study of Latinos on the Importance of Sociocultural Environmental Interactors: Polygenic Risk Score-by-Immigration and Dietary Interactions. Frontiers in Genetics, 2021, 12, 720750.	2.3	6
54	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	7.9	83

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55	Genetic variants affecting bone mineral density and bone mineral content at multiple skeletal sites in Hispanic children. Bone, 2020, 132, 115175.	2.9	13
56	Epigenetic reprogramming in periodontal disease: Dynamic crosstalk with potential impact in oncogenesis. Periodontology 2000, 2020, 82, 157-172.	13.4	15
57	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
58	Cohort Profile: ZOE 2.0—A Community-Based Genetic Epidemiologic Study of Early Childhood Oral Health. International Journal of Environmental Research and Public Health, 2020, 17, 8056.	2.6	20
59	A Genome-wide Association Study Discovers 46 Loci of the Human Metabolome in the Hispanic Community Health Study/Study of Latinos. American Journal of Human Genetics, 2020, 107, 849-863.	6.2	48
60	Methylome-wide association study of central adiposity implicates genes involved in immune and endocrine systems. Epigenomics, 2020, 12, 1483-1499.	2.1	6
61	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.6	26
62	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
63	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
64	Serum metabolites reflecting gut microbiome alpha diversity predict type 2 diabetes. Gut Microbes, 2020, 11, 1632-1642.	9.8	65
65	Importance of Genetic Studies of Cardiometabolic Disease in Diverse Populations. Circulation Research, 2020, 126, 1816-1840.	4.5	19
66	Maternal diet as a risk factor for primary congenital glaucoma and defects of the anterior segment of the eye in the <scp>National Birth Defects Prevention Study</scp> . Birth Defects Research, 2020, 112, 503-514.	1.5	4
67	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study. PLoS Genetics, 2020, 16, e1008684.	3.5	17
68	Sociodemographic predictors of early postnatal growth: evidence from a Chilean infancy cohort. BMJ Open, 2020, 10, e033695.	1.9	5
69	Multi-Ethnic Genome-Wide Association Study of Decomposed Cardioelectric Phenotypes Illustrates Strategies to Identify and Characterize Evidence of Shared Genetic Effects for Complex Traits. Circulation Genomic and Precision Medicine, 2020, 13, e002680.	3.6	4
70	Associations of maternal arsenic exposure with adult fasting glucose and insulin resistance in the Strong Heart Study and Strong Heart Family Study. Environment International, 2020, 137, 105531.	10.0	16
71	Nine-Year Ethanol Intake Trajectories and Their Association With 15-Year Cognitive Decline Among Black and White Adults. American Journal of Epidemiology, 2020, 189, 788-800.	3.4	1
72	Title is missing!. , 2020, 16, e1008684.		O

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73	Title is missing!. , 2020, 16, e1008684.		O
74	Title is missing!. , 2020, 16, e1008684.		0
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76	Title is missing!. , 2020, 16, e1008684.		0
77	Title is missing!. , 2020, 16, e1008684.		0
78	Genetic polymorphisms of diabetesâ€related genes, their interaction with diabetes status, and breast cancer incidence and mortality: The Long Island Breast Cancer Study Project. Molecular Carcinogenesis, 2019, 58, 436-446.	2.7	13
79	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. Molecular Psychiatry, 2019, 24, 1920-1932.	7.9	44
80	A trans-ancestral meta-analysis of genome-wide association studies reveals loci associated with childhood obesity. Human Molecular Genetics, 2019, 28, 3327-3338.	2.9	76
81	Gut microbiome composition in the Hispanic Community Health Study/Study of Latinos is shaped by geographic relocation, environmental factors, and obesity. Genome Biology, 2019, 20, 219.	8.8	94
82	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
83	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
84	Genetic analysis of hsCRP in American Indians: The Strong Heart Family Study. PLoS ONE, 2019, 14, e0223574.	2.5	5
85	Association of Birth Weight With Type 2 Diabetes and Glycemic Traits. JAMA Network Open, 2019, 2, e1910915.	5.9	41
86	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.8	5
87	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
88	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. Environment International, 2019, 132, 104723.	10.0	58
89	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	27.8	679
90	Genome-wide analysis of dental caries and periodontitis combining clinical and self-reported data. Nature Communications, 2019, 10, 2773.	12.8	183

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91	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
92	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	6.2	21
93	Dairy Intake and Body Composition and Cardiometabolic Traits among Adults: Mendelian Randomization Analysis of 182041 Individuals from 18 Studies. Clinical Chemistry, 2019, 65, 751-760.	3.2	20
94	Genetics of Chronic Kidney Disease Stages Across Ancestries: The PAGE Study. Frontiers in Genetics, 2019, 10, 494.	2.3	29
95	Protocols, Methods, and Tools for Genome-Wide Association Studies (GWAS) of Dental Traits. Methods in Molecular Biology, 2019, 1922, 493-509.	0.9	14
96	The Future of Genomic Studies Must Be Globally Representative: Perspectives from PAGE. Annual Review of Genomics and Human Genetics, 2019, 20, 181-200.	6.2	33
97	Multi-ancestry genome-wide gene–smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
98	Metabolomics Identifies Novel Blood Biomarkers of Pulmonary Function and COPD in the General Population. Metabolites, 2019, 9, 61.	2.9	30
99	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
100	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
101	A phenome-wide association study (PheWAS) in the Population Architecture using Genomics and Epidemiology (PAGE) study reveals potential pleiotropy in African Americans. PLoS ONE, 2019, 14, e0226771.	2.5	15
102	Fine mapping and identification of serum urate loci in American Indians: The Strong Heart Family Study. Scientific Reports, 2019, 9, 17899.	3.3	1
103	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
104	Omega-3 Fatty Acids and Genome-Wide Interaction Analyses Reveal <i>DPP10–</i> Pulmonary Function Association. American Journal of Respiratory and Critical Care Medicine, 2019, 199, 631-642.	5.6	14
105	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
106	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholâUse. Biological Psychiatry, 2019, 85, 946-955.	1.3	69
107	Genetically Determined Height and Risk of Non-hodgkin Lymphoma. Frontiers in Oncology, 2019, 9, 1539.	2.8	6
108	Abstract 002: Adherence to Ideal Life's Simple 7 Metrics is Associated With Epigenetic Biomarkers of Aging in African Americans: The Atherosclerosis Risk in Communities (ARIC) Study. Circulation, 2019, 139, .	1.6	0

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109	DNA methylation of imprinted gene control regions in the regression of lowâ€grade cervical lesions. International Journal of Cancer, 2018, 143, 552-560.	5.1	9
110	Arsenic-gene interactions and beta-cell function in the Strong Heart Family Study. Toxicology and Applied Pharmacology, 2018, 348, 123-129.	2.8	7
111	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
112	The perils of standardizing infant weight to assess weight change differences across exposure groups. Annals of Epidemiology, 2018, 28, 515-520.	1.9	4
113	Profiles of internalizing and externalizing symptoms associated with bullying victimization. Journal of Adolescence, 2018, 65, 101-110.	2.4	54
114	Sugar-sweetened beverage intake associations with fasting glucose and insulin concentrations are not modified by selected genetic variants in a ChREBP-FGF21 pathway: a meta-analysis. Diabetologia, 2018, 61, 317-330.	6.3	32
115	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
116	Exploring the genomic basis of early childhood caries: a pilot study. International Journal of Paediatric Dentistry, 2018, 28, 217-225.	1.8	24
117	Genetics of Obesity in Diverse Populations. Current Diabetes Reports, 2018, 18, 145.	4.2	27
118	Complex patterns of direct and indirect association between the transcription Factor-7 like 2 gene, body mass index and type 2 diabetes diagnosis in adulthood in the Hispanic Community Health Study/Study of Latinos. BMC Obesity, 2018, 5, 26.	3.1	6
119	Two high-risk susceptibility loci at 6p25.3 and 14q32.13 for Waldenström macroglobulinemia. Nature Communications, 2018, 9, 4182.	12.8	15
120	Characterization of the contribution of shared environmental and genetic factors to metabolic syndrome methylation heritability and familial correlations. BMC Genetics, 2018, 19, 69.	2.7	3
121	Direct and indirect genetic effects on triglycerides through omics and correlated phenotypes. BMC Proceedings, 2018, 12, 22.	1.6	5
122	Genetic Variants Related to Cardiometabolic Traits Are Associated to B Cell Function, Insulin Resistance, and Diabetes Among AmeriCan Indians: The Strong Heart Family Study. Frontiers in Genetics, 2018, 9, 466.	2.3	4
123	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.	2.3	9
124	GWAS for Interleukin- $1\hat{l}^2$ levels in gingival crevicular fluid identifies IL37 variants in periodontal inflammation. Nature Communications, 2018, 9, 3686.	12.8	63
125	Targeting epigenetic mechanisms in periodontal diseases. Periodontology 2000, 2018, 78, 174-184.	13.4	22
126	Melanocortin 4 Receptor Pathway Dysfunction in Obesity: Patient Stratification Aimed at MC4R Agonist Treatment. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 2601-2612.	3.6	50

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127	A high throughput, functional screen of human Body Mass Index GWAS loci using tissue-specific RNAi Drosophila melanogaster crosses. PLoS Genetics, 2018, 14, e1007222.	3.5	22
128	Reply to â€~Misestimation of heritability and prediction accuracy of male-pattern baldness'. Nature Communications, 2018, 9, 2538.	12.8	0
129	The genetic underpinnings of variation in ages at menarche and natural menopause among women from the multi-ethnic Population Architecture using Genomics and Epidemiology (PAGE) Study: A trans-ethnic meta-analysis. PLoS ONE, 2018, 13, e0200486.	2.5	25
130	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.	4.1	5
131	An epigenome-wide study of obesity in African American youth and young adults: novel findings, replication in neutrophils, and relationship with gene expression. Clinical Epigenetics, 2018, 10, 3.	4.1	33
132	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	12.8	85
133	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.	2.9	16
134	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
135	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	1.8	19
136	Abstract 053: Genome-wide Tcea3 -SNP Interaction Study Identifies Novel QT Interval Loci. Circulation, 2018, 137, .	1.6	0
137	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.	0.7	19
138	Genetic evidence of assortative mating in humans. Nature Human Behaviour, 2017, 1, .	12.0	242
139	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
140	A powerful statistical framework for generalization testing in GWAS, with application to the HCHS/SOL. Genetic Epidemiology, 2017, 41, 251-258.	1.3	41
141	Genetic loci associated with chronic obstructive pulmonary disease overlap with loci for lung function and pulmonary fibrosis. Nature Genetics, 2017, 49, 426-432.	21.4	306
142	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175.	12.8	75
143	Trans-ethnic fine-mapping of genetic loci for body mass index in the diverse ancestral populations of the Population Architecture using Genomics and Epidemiology (PAGE) Study reveals evidence for multiple signals at established loci. Human Genetics, 2017, 136, 771-800.	3.8	31
144	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169

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145	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	12.8	95
146	Genome-wide association of white blood cell counts in Hispanic/Latino Americans: the Hispanic Community Health Study/Study of Latinos. Human Molecular Genetics, 2017, 26, 1193-1204.	2.9	38
147	Genome-wide association study of 1,5-anhydroglucitol identifies novel genetic loci linked to glucose metabolism. Scientific Reports, 2017, 7, 2812.	3.3	26
148	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	21.4	260
149	Objectively Measured Physical Activity, Sedentary Behavior, and Genetic Predisposition to Obesity in U.S. Hispanics/Latinos: Results From the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Diabetes, 2017, 66, 3001-3012.	0.6	28
150	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	12.8	118
151	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.	6.3	20
152	Lupus-related single nucleotide polymorphisms and risk of diffuse large B-cell lymphoma. Lupus Science and Medicine, 2017, 4, e000187.	2.7	15
153	GWAS for male-pattern baldness identifies 71 susceptibility loci explaining 38% of the risk. Nature Communications, 2017, 8, 1584.	12.8	61
154	Identifying gene–gene interactions that are highly associated with four quantitative lipid traits across multiple cohorts. Human Genetics, 2017, 136, 165-178.	3.8	11
155	Genetic architecture of lipid traits in the Hispanic community health study/study of Latinos. Lipids in Health and Disease, 2017, 16, 200.	3.0	18
156	Gene-by-Psychosocial Factor Interactions Influence Diastolic Blood Pressure in European and African Ancestry Populations: Meta-Analysis of Four Cohort Studies. International Journal of Environmental Research and Public Health, 2017, 14, 1596.	2.6	5
157	Admixture mapping of pelvic organ prolapse in African Americans from the Women's Health Initiative Hormone Therapy trial. PLoS ONE, 2017, 12, e0178839.	2.5	4
158	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
159	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. BioData Mining, 2017, 10, 25.	4.0	7
160	Association of Cardiometabolic Genes with Arsenic Metabolism Biomarkers in American Indian Communities: The Strong Heart Family Study (SHFS). Environmental Health Perspectives, 2017, 125, 15-22.	6.0	32
161	Genome-wide Association Study of Susceptibility to Particulate Matter–Associated QT Prolongation. Environmental Health Perspectives, 2017, 125, 067002.	6.0	7
162	Genetic identification of a common collagen disease in Puerto Ricans via identity-by-descent mapping in a health system. ELife, 2017, 6, .	6.0	65

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163	Genome-wide physical activity interactions in adiposity ― A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
164	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
165	Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. PLoS Genetics, 2017, 13, e1006760.	3.5	53
166	Variant Discovery and Fine Mapping of Genetic Loci Associated with Blood Pressure Traits in Hispanics and African Americans. PLoS ONE, 2016, 11, e0164132.	2.5	24
167	Metaâ€Analysis of Genomeâ€Wide Association Studies with Correlated Individuals: Application to the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Genetic Epidemiology, 2016, 40, 492-501.	1.3	16
168	Mapping adipose and muscle tissue expression quantitative trait loci in African Americans to identify genes for type 2 diabetes and obesity. Human Genetics, 2016, 135, 869-880.	3.8	44
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170	A genome-wide association study meta-analysis of clinical fracture in 10,012 African American women. Bone Reports, 2016, 5, 233-242.	0.4	20
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