Laura M Raffield

List of Publications by Year
in descending order

111 papers	5,414 citations	168829 31 h-index	139680 61 g-index
141 all docs	141 docs citations	141 times ranked	9955 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.	1.1	27
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	eSCAN: scan regulatory regions for aggregate association testing using whole-genome sequencing data. Briefings in Bioinformatics, 2022, 23, .	3.2	5
4	From GWAS variant to function: A study of â¼148,000 variants for blood cell traits. Human Genetics and Genomics Advances, 2022, 3, 100063.	1.0	9
5	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. Stroke, 2022, 53, 788-797.	1.0	88
6	Obesity Partially Mediates the Diabetogenic Effect of Lowering LDL Cholesterol. Diabetes Care, 2022, 45, 232-240.	4.3	10
7	Super interactive promoters provide insight into cell type-specific regulatory networks in blood lineage cell types. PLoS Genetics, 2022, 18, e1009984.	1.5	4
8	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	3.0	29
9	Transcriptome-wide association study in UK Biobank Europeans identifies associations with blood cell traits. Human Molecular Genetics, 2022, 31, 2333-2347.	1.4	6
10	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study. Diabetologia, 2022, 65, 477-489.	2.9	15
11	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	1.2	2
12	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20
13	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	4.7	36
14	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
15	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. American Journal of Human Genetics, 2022, 109, 1175-1181.	2.6	25
16	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. Kidney International, 2022, 102, 624-639.	2.6	18
17	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
18	CUE: CpG impUtation ensemble for DNA methylation levels across the human methylation450 (HM450) and EPIC (HM850) BeadChip platforms. Epigenetics, 2021, 16, 851-861.	1.3	1

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19	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	2.6	42
20	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.	2.7	14
21	Malaria is a cause of iron deficiency in African children. Nature Medicine, 2021, 27, 653-658.	15.2	35
22	Optimism and telomere length among African American adults in the Jackson Heart Study. Psychoneuroendocrinology, 2021, 125, 105124.	1.3	1
23	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. Genome Medicine, 2021, 13, 74.	3.6	20
24	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. Human Genetics and Genomics Advances, 2021, 2, 100029.	1.0	23
25	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
26	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	2.6	28
27	FGL1 as a modulator of plasma Dâ€dimer levels: Exomeâ€wide marker analysis of plasma tPA, PAIâ€1, and Dâ€dimer. Journal of Thrombosis and Haemostasis, 2021, 19, 2019-2028.	1.9	1
28	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. Aging Cell, 2021, 20, e13366.	3.0	72
29	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
30	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	3.8	90
31	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
32	DNAm-based signatures of accelerated aging and mortality in blood are associated with low renal function. Clinical Epigenetics, 2021, 13, 121.	1.8	13
33	Soluble CD14 Levels in the Jackson Heart Study: Associations With Cardiovascular Disease Risk and Genetic Variants. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, e369-e378.	1.1	5
34	Development and Validation of Machine Learningâ€“Based Race-Specific Models to Predict 10-Year Risk of Heart Failure: A Multicohort Analysis. Circulation, 2021, 143, 2370-2383.	1.6	56
35	Association of Clonal Hematopoiesis With Incident HeartÂFailure. Journal of the American College of Cardiology, 2021, 78, 42-52.	1.2	101
36	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. Genes, 2021, 12, 1049.	1.0	11

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37	Multiethnic Genome-Wide Association Study of Subclinical Atherosclerosis in Individuals With Type 2 Diabetes. Circulation Genomic and Precision Medicine, 2021, 14, e003258.	1.6	4
38	Genetic underpinnings of regional adiposity distribution in African Americans: Assessments from the Jackson Heart Study. PLoS ONE, 2021, 16, e0255609.	1.1	2
39	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
40	Presence and transmission of mitochondrial heteroplasmic mutations in human populations of European and African ancestry. Mitochondrion, 2021, 60, 33-42.	1.6	6
41	Effect of Sickle Cell Trait and APOL1 Genotype on the Association of Soluble uPAR with Kidney Function Measures in Black Americans. Clinical Journal of the American Society of Nephrology: CJASN, 2021, 16, 287-289.	2.2	3
42	Association of mitochondrial DNA copy number with cardiometabolic diseases. Cell Genomics, 2021, 1, 100006.	3.0	26
43	Soluble Urokinase Plasminogen Activator Receptor: Genetic Variation and Cardiovascular Disease Risk in Black Adults. Circulation Genomic and Precision Medicine, 2021, 14, CIRCGEN121003421.	1.6	7
44	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
45	Full title: A largeâ€scale transcriptomeâ€wide association study (TWAS) of 10 blood cell phenotypes reveals complexities of TWAS fineâ€mapping. Genetic Epidemiology, 2021, , .	0.6	2
46	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.	1.6	10
47	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
48	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376
49	Coagulation factor VIII: Relationship to cardiovascular disease risk and whole genome sequence and epigenomeâ€wide analysis in African Americans. Journal of Thrombosis and Haemostasis, 2020, 18, 1335-1347.	1.9	17
50	Common genetic risk variants identified in the SPARK cohort support DDHD2 as a candidate risk gene for autism. Translational Psychiatry, 2020, 10, 265.	2.4	56
51	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	13.5	353
52	Comparison of Proteomic Assessment Methods in Multiple Cohort Studies. Proteomics, 2020, 20, e1900278.	1.3	103
53	Importance of Genetic Studies of Cardiometabolic Disease in Diverse Populations. Circulation Research, 2020, 126, 1816-1840.	2.0	19
54	Ancestry-specific associations identified in genome-wide combined-phenotype study of red blood cell traits emphasize benefits of diversity in genomics. BMC Genomics, 2020, 21, 228.	1.2	19

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55	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.	1.5	17
56	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. American Journal of Human Genetics, 2020, 106, 112-120.	2.6	9
57	Interferon gamma-induced protein 10 (IP-10) and cardiovascular disease in African Americans. PLoS ONE, 2020, 15, e0231013.	1.1	12
58	Title is missing!. , 2020, 16, e1008684.		0
59	Title is missing!. , 2020, 16, e1008684.		0
60	Title is missing!. , 2020, 16, e1008684.		0
61	Title is missing!. , 2020, 16, e1008684.		0
62	Title is missing!. , 2020, 16, e1008684.		0
63	Title is missing!. , 2020, 16, e1008684.		0
64	Genomeâ€wide metaâ€analysis of SNP and antihypertensive medication interactions on left ventricular traits in African Americans. Molecular Genetics & Genomic Medicine, 2019, 7, e00788.	0.6	4
65	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	5.8	133
66	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
67	Impact of Rare and Common Genetic Variants on Diabetes Diagnosis by Hemoglobin A1c in Multi-Ancestry Cohorts: The Trans-Omics for Precision Medicine Program. American Journal of Human Genetics, 2019, 105, 706-718.	2.6	44
68	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.	1.0	17
69	A fully adjusted twoâ€stage procedure for rankâ€normalization in genetic association studies. Genetic Epidemiology, 2019, 43, 263-275.	0.6	60
70	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
71	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
72	Whole genome sequence association with E-selectin levels reveals loss-of-function variant in African Americans. Human Molecular Genetics, 2019, 28, 515-523.	1.4	15

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73	Genome-wide association study of homocysteine in African Americans from the Jackson Heart Study, the Multi-Ethnic Study of Atherosclerosis, and the Coronary Artery Risk in Young Adults study. Journal of Human Genetics, 2018, 63, 327-337.	1.1	7
74	A robust and powerful twoâ€step testing procedure for local ancestry adjusted allelic association analysis in admixed populations. Genetic Epidemiology, 2018, 42, 288-302.	0.6	17
75	Associations of activated coagulation factor VII and factor VIIaâ€antithrombin levels with genomeâ€wide polymorphisms and cardiovascular disease risk. Journal of Thrombosis and Haemostasis, 2018, 16, 19-30.	1.9	25
76	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	5.8	119
77	KCNJ11 variants and their effect on the association between serum potassium and diabetes risk in the Atherosclerosis Risk in Communities (ARIC) Study and Jackson Heart Study (JHS) cohorts. PLoS ONE, 2018, 13, e0203213.	1.1	4
78	A common TCN1 loss-of-function variant is associated with lower vitamin B12 concentration in African Americans. Blood, 2018, 131, 2859-2863.	0.6	7
79	Associations of coronary artery calcified plaque density with mortality in type 2 diabetes: the Diabetes Heart Study. Cardiovascular Diabetology, 2018, 17, 67.	2.7	14
80	Common Î±-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. PLoS Genetics, 2018, 14, e1007293.	1.5	45
81	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. Heart Rhythm, 2017, 14, 1675-1684.	0.3	18
82	Genome-wide association study of iron traits and relation to diabetes in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL): potential genomic intersection of iron and glucose regulation?. Human Molecular Genetics, 2017, 26, 1966-1978.	1.4	31
83	Leukocyte telomere length and cardiovascular disease in African Americans: The Jackson Heart Study. Atherosclerosis, 2017, 266, 41-47.	0.4	30
84	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	5.8	118
85	D-Dimer in African Americans. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 2220-2227.	1.1	40
86	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	2.6	60
87	APOE Genotypes Associate With Cognitive Performance but Not Cerebral Structure: Diabetes Heart Study MIND. Diabetes Care, 2016, 39, 2225-2231.	4.3	12
88	Novel Genetic Variants Associated With Increased Vertebral Volumetric BMD, Reduced Vertebral Fracture Risk, and Increased Expression of SLC1A3 and EPHB2. Journal of Bone and Mineral Research, 2016, 31, 2085-2097.	3.1	42
89	The association of calcium supplementation and incident cardiovascular events in the Multi-ethnic Study of Atherosclerosis (MESA). Nutrition, Metabolism and Cardiovascular Diseases, 2016, 26, 899-907.	1.1	2
90	Dopamine pathway gene variants may modulate cognitive performance in the DHS â€“ Mind Study. Brain and Behavior, 2016, 6, e00446.	1.0	7

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91	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics, 2016, 9, 511-520.	5.1	54
92	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	2.6	82
93	Genetic analysis of advanced glycation end products in the DHS MIND study. Gene, 2016, 584, 173-179.	1.0	11
94	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. American Journal of Human Genetics, 2016, 99, 22-39.	2.6	50
95	Analysis of advanced glycation end products in the DHS Mind Study. Journal of Diabetes and Its Complications, 2016, 30, 262-268.	1.2	8
96	Associations between anxiety and depression symptoms and cognitive testing and neuroimaging in type 2 diabetes. Journal of Diabetes and Its Complications, 2016, 30, 143-149.	1.2	23
97	Analysis of the relationships between type 2 diabetes status, glycemic control, and neuroimaging measures in the Diabetes Heart Study Mind. Acta Diabetologica, 2016, 53, 439-447.	1.2	25
98	Criteria for level 1 and level 2 trauma codes: Are pelvic ring injuries undertriaged?. World Journal of Orthopedics, 2016, 7, 481.	0.8	0
99	Structural and functional assessment of the brain in European Americans with mild-to-moderate kidney disease: Diabetes Heart Study-MIND. Nephrology Dialysis Transplantation, 2015, 30, 1322-1329.	0.4	23
100	Relationships between Cognitive Performance, Neuroimaging and Vascular Disease: The DHS-MIND Study. Neuroepidemiology, 2015, 45, 1-11.	1.1	8
101	Analysis of a cardiovascular disease genetic risk score in the Diabetes Heart Study. Acta Diabetologica, 2015, 52, 743-751.	1.2	11
102	Predictors of all-cause and cardiovascular disease mortality in type 2 diabetes: Diabetes Heart Study. Diabetology and Metabolic Syndrome, 2015, 7, 58.	1.2	25
103	Heritability and genetic association analysis of neuroimaging measures in the Diabetes Heart Study. Neurobiology of Aging, 2015, 36, 1602.e7-1602.e15.	1.5	16
104	APOL1 associations with nephropathy, atherosclerosis, and all-cause mortality in African Americans with type 2 diabetes. Kidney International, 2015, 87, 176-181.	2.6	71
105	Heritability and genetic association analysis of cognition in theÂDiabetes Heart Study. Neurobiology of Aging, 2014, 35, 1958.e3-1958.e12.	1.5	26
106	Genomeâ€Wide Familyâ€Based Linkage Analysis of Exome Chip Variants and Cardiometabolic Risk. Genetic Epidemiology, 2014, 38, 345-352.	0.6	15
107	Cross-sectional analysis of calcium intake for associations with vascular calcification and mortality in individuals with type 2 diabetes from the Diabetes Heart Study. American Journal of Clinical Nutrition, 2014, 100, 1029-1035.	2.2	13
108	Analysis of common and coding variants with cardiovascular disease in the diabetes heart study. Cardiovascular Diabetology, 2014, 13, 77.	2.7	35

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109	Impact of HDL genetic risk scores on coronary artery calcified plaque and mortality in individuals with type 2 diabetes from the Diabetes Heart Study. Cardiovascular Diabetology, 2013, 12, 95.	2.7	9
110	Systemic Lupus Erythematosus and Vitamin D Deficiency Are Associated with Shorter Telomere Length among African Americans: A Case-Control Study. PLoS ONE, 2013, 8, e63725.	1.1	39
111	GWAS of Variant-by-Thiazide Interaction on Lipids Identifies a Novel Low-Density Lipoprotein Cholesterol Locus. Circulation Research, 0, , .	2.0	1