Heather M Highland

List of Publications by Year
in descending order

50 papers	4,334 citations	393982 19 h-index	214527 47 g-index
56 all docs	56 docs citations	56 times ranked	9900 citing authors

#	Article	IF	Citations
1	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
2	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	13.7	679
3	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
4	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
5	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
6	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
7	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
8	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	1.5	95
9	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
10	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	2.6	82
11	A trans-ancestral meta-analysis of genome-wide association studies reveals loci associated with childhood obesity. Human Molecular Genetics, 2019, 28, 3327-3338.	1.4	76
12	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	2.6	60
13	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
14	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
15	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
16	Trans-ethnic fine-mapping of genetic loci for body mass index in the diverse ancestral populations of the Population Architecture using Genomics and Epidemiology (PAGE) Study reveals evidence for multiple signals at established loci. Human Genetics, 2017, 136, 771-800.	1.8	31
17	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
18	Genetics of Chronic Kidney Disease Stages Across Ancestries: The PAGE Study. Frontiers in Genetics, 2019, 10, 494.	1.1	29

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19	Continued lessons from theINSgene: an intronic mutation causing diabetes through a novel mechanism. Journal of Medical Genetics, 2015, 52, 612-616.	1.5	25
20	GWAS of the electrocardiographic QT interval in Hispanics/Latinos generalizes previously identified loci and identifies population-specific signals. Scientific Reports, 2017, 7, 17075.	1.6	23
21	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. Human Genetics and Genomics Advances, 2021, 2, 100029.	1.0	23
22	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	2.6	21
23	Importance of Genetic Studies of Cardiometabolic Disease in Diverse Populations. Circulation Research, 2020, 126, 1816-1840.	2.0	19
24	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
25	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study. Diabetologia, 2022, 65, 477-489.	2.9	15
26	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
27	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. Human Molecular Genetics, 2019, 28, 1212-1224.	1.4	12
28	The interaction between physical activity and obesity gene variants in association with BMI: Does the obesogenic environment matter?. Health and Place, 2016, 42, 159-165.	1.5	10
29	GWAS of QRS duration identifies new loci specific to Hispanic/Latino populations. PLoS ONE, 2019, 14, e0217796.	1.1	8
30	Genome-wide association study of body fat distribution traits in Hispanics/Latinos from the HCHS/SOL. Human Molecular Genetics, 2021, 30, 2190-2204.	1.4	8
31	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
32	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
33	Predicted gene expression in ancestrally diverse populations leads to discovery of susceptibility loci for lifestyle and cardiometabolic traits. American Journal of Human Genetics, 2022, 109, 669-679.	2.6	5
34	Strengthening Causal Inference in Exposomics Research: Application of Genetic Data and Methods. Environmental Health Perspectives, 2022, 130, 55001.	2.8	5
35	Genome-wide association study and meta-analysis identify loci associated with ventricular and supraventricular ectopy. Scientific Reports, 2018, 8, 5675.	1.6	4
36	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.	1.6	4

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37	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.	1.4	4
38	Population-based genetic effects for developmental stuttering. Human Genetics and Genomics Advances, 2022, 3, 100073.	1.0	4
39	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.	1.4	3
40	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traitsâ€"The Hispanic/Latino Anthropometry Consortium. Human Genetics and Genomics Advances, 2022, 3, 100099.	1.0	3
41	Genome-wide association study of pancreatic fat: The Multiethnic Cohort Adiposity Phenotype Study. PLoS ONE, 2021, 16, e0249615.	1.1	2
42	Revisiting Some Useful Statistical Guidelines in Circulation Research in Response to a Changing Landscape. Circulation Research, 2021, 128, 1724-1727.	2.0	1
43	Comparison of adaptive multiple phenotype association tests using summary statistics in genome-wide association studies. Human Molecular Genetics, 2021, 30, 1371-1383.	1.4	1
44	GWAS of Variant-by-Thiazide Interaction on Lipids Identifies a Novel Low-Density Lipoprotein Cholesterol Locus. Circulation Research, 0, , .	2.0	1
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