

# Genevieve L Wojcik

## List of Publications by Year in descending order

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Version: 2024-02-01

41  
papers

3,488  
citations

394286

19  
h-index

243529

44  
g-index

57  
all docs

57  
docs citations

57  
times ranked

7069  
citing authors

#	ARTICLE	IF	CITATIONS
1	Trans-ancestral fine-mapping of MHC reveals key amino acids associated with spontaneous clearance of hepatitis C in HLA-DQ1 <sup>2</sup> . American Journal of Human Genetics, 2022, 109, 299-310.	2.6	6
2	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study. Diabetologia, 2022, 65, 477-489.	2.9	15
3	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.	2.6	6
4	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
5	Disentangling Signatures of Selection Before and After European Colonization in Latin Americans. Molecular Biology and Evolution, 2022, 39, .	3.5	16
6	Genome-Wide Association Study of Campylobacter <i>Campylobacter</i> Positive Diarrhea Identifies Genes Involved in Toxin Processing and Inflammatory Response. MBio, 2022, 13, e0055622.	1.8	5
7	Benchmarking statistical methods for analyzing parent-child dyads in genetic association studies. Genetic Epidemiology, 2022, 46, 266-284.	0.6	2
8	Opportunities and challenges for the use of common controls in sequencing studies. Nature Reviews Genetics, 2022, 23, 665-679.	7.7	13
9	Clotting factor genes are associated with preeclampsia in high-altitude pregnant women in the Peruvian Andes. American Journal of Human Genetics, 2022, 109, 1117-1139.	2.6	10
10	A Multiancestry Sex-Stratified Genome-Wide Association Study of Spontaneous Clearance of Hepatitis C Virus. Journal of Infectious Diseases, 2021, 223, 2090-2098.	1.9	5
11	Discovering prescription patterns in pediatric acute-onset neuropsychiatric syndrome patients. Journal of Biomedical Informatics, 2021, 113, 103664.	2.5	2
12	Improving reporting standards for polygenic scores in risk prediction studies. Nature, 2021, 591, 211-219.	13.7	265
13	Host Genome-Wide Association Study of Infant Susceptibility to <i>Shigella</i> -Associated Diarrhea. Infection and Immunity, 2021, 89, .	1.0	12
14	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
15	Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. Nature Medicine, 2021, 27, 1876-1884.	15.2	214
16	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.	1.1	6
17	Multi-ancestry fine mapping of interferon lambda and the outcome of acute hepatitis C virus infection. Genes and Immunity, 2020, 21, 348-359.	2.2	5
18	Genome-Wide Association Study of Cryptosporidiosis in Infants Implicates <i>PRKCA</i> . MBio, 2020, 11, .	1.8	20

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19	Importance of Genetic Studies of Cardiometabolic Disease in Diverse Populations. <i>Circulation Research</i> , 2020, 126, 1816-1840.	2.0	19
20	Ancestry-specific associations identified in genome-wide combined-phenotype study of red blood cell traits emphasize benefits of diversity in genomics. <i>BMC Genomics</i> , 2020, 21, 228.	1.2	19
21	A common variant in PNPLA3 is associated with age at diagnosis of NAFLD in patients from a multi-ethnic biobank. <i>Journal of Hepatology</i> , 2020, 72, 1070-1081.	1.8	35
22	Native American gene flow into Polynesia predating Easter Island settlement. <i>Nature</i> , 2020, 583, 572-577.	13.7	64
23	Multi-Ethnic Genome-Wide Association Study of Decomposed Cardioelectric Phenotypes Illustrates Strategies to Identify and Characterize Evidence of Shared Genetic Effects for Complex Traits. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002680.	1.6	4
24	Genetic analyses of diverse populations improves discovery for complex traits. <i>Nature</i> , 2019, 570, 514-518.	13.7	679
25	The role of country of birth, and genetic and self-identified ancestry, in obesity susceptibility among African and Hispanic Americans. <i>American Journal of Clinical Nutrition</i> , 2019, 110, 16-23.	2.2	13
26	Multi-Ancestry Genome-Wide Association Study of Spontaneous Clearance of Hepatitis C Virus. <i>Gastroenterology</i> , 2019, 156, 1496-1507.e7.	0.6	32
27	The Future of Genomic Studies Must Be Globally Representative: Perspectives from PAGE. <i>Annual Review of Genomics and Human Genetics</i> , 2019, 20, 181-200.	2.5	33
28	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. <i>Nature Communications</i> , 2019, 10, 880.	5.8	71
29	Standardized Biogeographic Grouping System for Annotating Populations in Pharmacogenetic Research. <i>Clinical Pharmacology and Therapeutics</i> , 2019, 105, 1256-1262.	2.3	90
30	Imputation-Aware Tag SNP Selection To Improve Power for Large-Scale, Multi-ethnic Association Studies. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3255-3267.	0.8	36
31	Genome-Wide Association Study Reveals Genetic Link between Diarrhea-Associated <i>Entamoeba histolytica</i> Infection and Inflammatory Bowel Disease. <i>MBio</i> , 2018, 9, .	1.8	23
32	Ancient genomes from North Africa evidence prehistoric migrations to the Maghreb from both the Levant and Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6774-6779.	3.3	131
33	A Sex-Stratified Genome-Wide Association Study of Tuberculosis Using a Multi-Ethnic Genotyping Array. <i>Frontiers in Genetics</i> , 2018, 9, 678.	1.1	28
34	Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome. <i>Scientific Reports</i> , 2017, 7, 46398.	1.6	26
35	Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations. <i>American Journal of Human Genetics</i> , 2017, 100, 635-649.	2.6	1,120
36	Genetic identification of a common collagen disease in Puerto Ricans via identity-by-descent mapping in a health system. <i>ELife</i> , 2017, 6, .	2.8	65

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37	Role of nucleotide-binding oligomerization domain 1 (NOD1) and its variants in human cytomegalovirus control in vitro and in vivo. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7818-E7827.	3.3	30
38	Strategies for Enriching Variant Coverage in Candidate Disease Loci on a Multiethnic Genotyping Array. PLoS ONE, 2016, 11, e0167758.	1.1	72
39	Variants in HAVCR1 Gene Region Contribute to Hepatitis C Persistence in African Americans. Journal of Infectious Diseases, 2014, 209, 355-359.	1.9	13
40	Genome-Wide Association Study of Spontaneous Resolution of Hepatitis C Virus Infection: Data From Multiple Cohorts. Annals of Internal Medicine, 2013, 158, 235.	2.0	187
41	Identification of functional genetic variation in exome sequence analysis. BMC Proceedings, 2011, 5, S13.	1.8	9