Genevieve L Wojcik

List of Publications by Year
in descending order

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41 papers	3,488 citations	394421 19 h-index	243625 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-DQβ1. American Journal of Human Genetics, 2022, 109, 299-310.	6.2	6
2	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study. Diabetologia, 2022, 65, 477-489.	6.3	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.	6.2	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.	6.2	5
5	Disentangling Signatures of Selection Before and After European Colonization in Latin Americans. Molecular Biology and Evolution, 2022, 39, .	8.9	16
6	Genome-Wide Association Study of Campylobacter - Positive Diarrhea Identifies Genes Involved in Toxin Processing and Inflammatory Response. MBio, 2022, 13, e0055622.	4.1	5
7	Benchmarking statistical methods for analyzing parentâ€“child dyads in genetic association studies. Genetic Epidemiology, 2022, 46, 266-284.	1.3	2
8	Opportunities and challenges for the use of common controls in sequencing studies. Nature Reviews Genetics, 2022, 23, 665-679.	16.3	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.	6.2	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.	4.0	5
11	Discovering prescription patterns in pediatric acute-onset neuropsychiatric syndrome patients. Journal of Biomedical Informatics, 2021, 113, 103664.	4.3	2
12	Improving reporting standards for polygenic scores in risk prediction studies. Nature, 2021, 591, 211-219.	27.8	265
13	Host Genome-Wide Association Study of Infant Susceptibility toShigella-Associated Diarrhea. Infection and Immunity, 2021, 89, .	2.2	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.	2.8	6
15	Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. Nature Medicine, 2021, 27, 1876-1884.	30.7	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.	2.3	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.	4.1	5
18	Genome-Wide Association Study of Cryptosporidiosis in Infants Implicates PRKCA. MBio, 2020, 11, .	4.1	20

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19	Importance of Genetic Studies of Cardiometabolic Disease in Diverse Populations. Circulation Research, 2020, 126, 1816-1840.	4.5	19
20	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.	2.8	19
21	A common variant in PNPLA3 is associated with age at diagnosis of NAFLD in patients from a multi-ethnic biobank. Journal of Hepatology, 2020, 72, 1070-1081.	3.7	35
22	Native American gene flow into Polynesia predating Easter Island settlement. Nature, 2020, 583, 572-577.	27.8	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. Circulation Genomic and Precision Medicine, 2020, 13, e002680.	3.6	4
24	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	27.8	679
25	The role of country of birth, and genetic and self-identified ancestry, in obesity susceptibility among African and Hispanic Americans. American Journal of Clinical Nutrition, 2019, 110, 16-23.	4.7	13
26	Multi-Ancestry Genome-Wide Association Study of Spontaneous Clearance of Hepatitis C Virus. Gastroenterology, 2019, 156, 1496-1507.e7.	1.3	32
27	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
28	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. Nature Communications, 2019, 10, 880.	12.8	71
29	Standardized Biogeographic Grouping System for Annotating Populations in Pharmacogenetic Research. Clinical Pharmacology and Therapeutics, 2019, 105, 1256-1262.	4.7	90
30	Imputation-Aware Tag SNP Selection To Improve Power for Large-Scale, Multi-ethnic Association Studies. G3: Genes, Genomes, Genetics, 2018, 8, 3255-3267.	1.8	36
31	Genome-Wide Association Study Reveals Genetic Link between Diarrhea-Associated Entamoeba histolytica Infection and Inflammatory Bowel Disease. MBio, 2018, 9, .	4.1	23
32	Ancient genomes from North Africa evidence prehistoric migrations to the Maghreb from both the Levant and Europe. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6774-6779.	7.1	131
33	A Sex-Stratified Genome-Wide Association Study of Tuberculosis Using a Multi-Ethnic Genotyping Array. Frontiers in Genetics, 2018, 9, 678.	2.3	28
34	Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome. Scientific Reports, 2017, 7, 46398.	3.3	26
35	Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations. American Journal of Human Genetics, 2017, 100, 635-649.	6.2	1,120
36	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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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.	7.1	30
38	Strategies for Enriching Variant Coverage in Candidate Disease Loci on a Multiethnic Genotyping Array. PLoS ONE, 2016, 11, e0167758.	2.5	72
39	Variants in HAVCR1 Gene Region Contribute to Hepatitis C Persistence in African Americans. Journal of Infectious Diseases, 2014, 209, 355-359.	4.0	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.	3.9	187
41	Identification of functional genetic variation in exome sequence analysis. BMC Proceedings, 2011, 5, S13.	1.6	9