Alicia R Martin

List of Publications by Year
in descending order

47 papers	26,256 citations	117625 34 h-index	206112 48 g-index
73 all docs	73 docs citations	73 times ranked	40588 citing authors

#	Article	IF	Citations
1	A roadmap to increase diversity in genomic studies. Nature Medicine, 2022, 28, 243-250.	30.7	195
2	Polygenic scores in biomedical research. Nature Reviews Genetics, 2022, 23, 524-532.	16.3	69
3	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
4	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. Nature Genetics, 2022, 54, 450-458.	21.4	109
5	Genome-wide risk prediction of common diseases across ancestries in one million people. Cell Genomics, 2022, 2, 100118.	6.5	34
6	Improving polygenic prediction in ancestrally diverse populations. Nature Genetics, 2022, 54, 573-580.	21.4	209
7	Challenges and Opportunities for Developing More Generalizable Polygenic Risk Scores. Annual Review of Biomedical Data Science, 2022, 5, 293-320.	6.5	47
8	Increasing diversity in genomics requires investment in equitable partnerships and capacity building. Nature Genetics, 2022, 54, 740-745.	21.4	20
9	Low-coverage sequencing cost-effectively detects known and novel variation in underrepresented populations. American Journal of Human Genetics, 2021, 108, 656-668.	6.2	49
10	Problems with Using Polygenic Scores to Select Embryos. New England Journal of Medicine, 2021, 385, 78-86.	27.0	105
11	Genome-wide association studies. Nature Reviews Methods Primers, 2021, 1, .	21.2	529
12	Tractor uses local ancestry to enable the inclusion of admixed individuals in GWAS and to boost power. Nature Genetics, 2021, 53, 195-204.	21.4	125
13	Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. Nature Medicine, 2021, 27, 1876-1884.	30.7	214
14	Population History and Gene Divergence in Native Mexicans Inferred from 76 Human Exomes. Molecular Biology and Evolution, 2020, 37, 994-1006.	8.9	43
15	Impact of admixture and ancestry on eQTL analysis and GWAS colocalization in GTEx. Genome Biology, 2020, 21, 233.	8.8	64
16	Population Histories of the United States Revealed through Fine-Scale Migration and Haplotype Analysis. American Journal of Human Genetics, 2020, 106, 371-388.	6.2	39
17	Analytic and Translational Genetics. Annual Review of Biomedical Data Science, 2020, 3, 217-241.	6.5	4
18	Genome-wide Association Studies in Ancestrally Diverse Populations: Opportunities, Methods, Pitfalls, and Recommendations. Cell, 2019, 179, 589-603.	28.9	428

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19	International meta-analysis of PTSD genome-wide association studies identifies sex- and ancestry-specific genetic risk loci. Nature Communications, 2019, 10, 4558.	12.8	363
20	Geographic Variation and Bias in the Polygenic Scores of Complex Diseases and Traits in Finland. American Journal of Human Genetics, 2019, 104, 1169-1181.	6.2	90
21	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. ELife, 2019, 8, .	6.0	276
22	Clinical use of current polygenic risk scores may exacerbate health disparities. Nature Genetics, 2019, 51, 584-591.	21.4	1,664
23	Neuropsychiatric Genetics of African Populations-Psychosis (NeuroGAP-Psychosis): a case-control study protocol and GWAS in Ethiopia, Kenya, South Africa and Uganda. BMJ Open, 2019, 9, e025469.	1.9	65
24	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	21.4	1,538
25	Comparative genetic architectures of schizophrenia in East Asian and European populations. Nature Genetics, 2019, 51, 1670-1678.	21.4	440
26	Predicting Polygenic Risk of Psychiatric Disorders. Biological Psychiatry, 2019, 86, 97-109.	1.3	252
27	Shades of complexity: New perspectives on the evolution and genetic architecture of human skin. American Journal of Physical Anthropology, 2019, 168, 4-26.	2.1	45
28	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	21.4	1,594
29	Haplotype Sharing Provides Insights into Fine-Scale Population History and Disease in Finland. American Journal of Human Genetics, 2018, 102, 760-775.	6.2	57
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	Rapid evolution of a skin-lightening allele in southern African KhoeSan. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 13324-13329.	7.1	17
32	The critical needs and challenges for genetic architecture studies in Africa. Current Opinion in Genetics and Development, 2018, 53, 113-120.	3.3	57
33	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. American Journal of Human Genetics, 2018, 102, 1204-1211.	6.2	102
34	Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations. American Journal of Human Genetics, 2017, 100, 635-649.	6.2	1,120
35	An Unexpectedly Complex Architecture for Skin Pigmentation in Africans. Cell, 2017, 171, 1340-1353.e14.	28.9	134
36	Fine-Scale Genetic Structure in Finland. G3: Genes, Genomes, Genetics, 2017, 7, 3459-3468.	1.8	86

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37	Fine-Scale Human Population Structure in Southern Africa Reflects Ecogeographic Boundaries. Genetics, 2016, 204, 303-314.	2.9	93
38	Distance from sub-Saharan Africa predicts mutational load in diverse human genomes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E440-9.	7.1	224
39	Strategies for Enriching Variant Coverage in Candidate Disease Loci on a Multiethnic Genotyping Array. PLoS ONE, 2016, 11, e0167758.	2.5	72
40	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
41	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. Cell, 2015, 162, 1051-1065.	28.9	304
42	Transcriptome Sequencing from Diverse Human Populations Reveals Differentiated Regulatory Architecture. PLoS Genetics, 2014, 10, e1004549.	3.5	49
43	Exome capture from saliva produces high quality genomic and metagenomic data. BMC Genomics, 2014, 15, 262.	2.8	34
44	STORMSeq: An Open-Source, User-Friendly Pipeline for Processing Personal Genomics Data in the Cloud. PLoS ONE, 2014, 9, e84860.	2.5	25
45	Imputation-based assessment of next generation rare exome variant arrays. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 241-52.	0.7	7
46	IMPUTATION-BASED ASSESSMENT OF NEXT GENERATION RARE EXOME VARIANT ARRAYS. , 2013, , .		6
47	How robust are cross-population signatures of polygenic adaptation in humans?. , 0, 1, .		3