

Alicia R Martin

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

26,256
citations

134610

34
h-index

232693

48
g-index

73
all docs

73
docs citations

73
times ranked

44502
citing authors

#	ARTICLE	IF	CITATIONS
1	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
2	Clinical use of current polygenic risk scores may exacerbate health disparities. <i>Nature Genetics</i> , 2019, 51, 584-591.	9.4	1,664
3	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. <i>Nature Genetics</i> , 2019, 51, 63-75.	9.4	1,594
4	Identification of common genetic risk variants for autism spectrum disorder. <i>Nature Genetics</i> , 2019, 51, 431-444.	9.4	1,538
5	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
6	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	13.7	929
7	Genome-wide association studies. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	529
8	Comparative genetic architectures of schizophrenia in East Asian and European populations. <i>Nature Genetics</i> , 2019, 51, 1670-1678.	9.4	440
9	Genome-wide Association Studies in Ancestrally Diverse Populations: Opportunities, Methods, Pitfalls, and Recommendations. <i>Cell</i> , 2019, 179, 589-603.	13.5	428
10	International meta-analysis of PTSD genome-wide association studies identifies sex- and ancestry-specific genetic risk loci. <i>Nature Communications</i> , 2019, 10, 4558.	5.8	363
11	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. <i>Cell</i> , 2015, 162, 1051-1065.	13.5	304
12	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. <i>ELife</i> , 2019, 8, .	2.8	276
13	Predicting Polygenic Risk of Psychiatric Disorders. <i>Biological Psychiatry</i> , 2019, 86, 97-109.	0.7	252
14	Distance from sub-Saharan Africa predicts mutational load in diverse human genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E440-9.	3.3	224
15	Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. <i>Nature Medicine</i> , 2021, 27, 1876-1884.	15.2	214
16	Improving polygenic prediction in ancestrally diverse populations. <i>Nature Genetics</i> , 2022, 54, 573-580.	9.4	209
17	A roadmap to increase diversity in genomic studies. <i>Nature Medicine</i> , 2022, 28, 243-250.	15.2	195
18	An Unexpectedly Complex Architecture for Skin Pigmentation in Africans. <i>Cell</i> , 2017, 171, 1340-1353.e14.	13.5	134

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19	Tractor uses local ancestry to enable the inclusion of admixed individuals in GWAS and to boost power. <i>Nature Genetics</i> , 2021, 53, 195-204.	9.4	125
20	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. <i>Nature Genetics</i> , 2022, 54, 450-458.	9.4	109
21	Problems with Using Polygenic Scores to Select Embryos. <i>New England Journal of Medicine</i> , 2021, 385, 78-86.	13.9	105
22	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. <i>American Journal of Human Genetics</i> , 2018, 102, 1204-1211.	2.6	102
23	Fine-Scale Human Population Structure in Southern Africa Reflects Ecogeographic Boundaries. <i>Genetics</i> , 2016, 204, 303-314.	1.2	93
24	Geographic Variation and Bias in the Polygenic Scores of Complex Diseases and Traits in Finland. <i>American Journal of Human Genetics</i> , 2019, 104, 1169-1181.	2.6	90
25	Fine-Scale Genetic Structure in Finland. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3459-3468.	0.8	86
26	Strategies for Enriching Variant Coverage in Candidate Disease Loci on a Multiethnic Genotyping Array. <i>PLoS ONE</i> , 2016, 11, e0167758.	1.1	72
27	Polygenic scores in biomedical research. <i>Nature Reviews Genetics</i> , 2022, 23, 524-532.	7.7	69
28	Neuropsychiatric Genetics of African Populations-Psychosis (NeuroGAP-Psychosis): a case-control study protocol and GWAS in Ethiopia, Kenya, South Africa and Uganda. <i>BMJ Open</i> , 2019, 9, e025469.	0.8	65
29	Impact of admixture and ancestry on eQTL analysis and GWAS colocalization in GTEx. <i>Genome Biology</i> , 2020, 21, 233.	3.8	64
30	Haplotype Sharing Provides Insights into Fine-Scale Population History and Disease in Finland. <i>American Journal of Human Genetics</i> , 2018, 102, 760-775.	2.6	57
31	The critical needs and challenges for genetic architecture studies in Africa. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 113-120.	1.5	57
32	Transcriptome Sequencing from Diverse Human Populations Reveals Differentiated Regulatory Architecture. <i>PLoS Genetics</i> , 2014, 10, e1004549.	1.5	49
33	Low-coverage sequencing cost-effectively detects known and novel variation in underrepresented populations. <i>American Journal of Human Genetics</i> , 2021, 108, 656-668.	2.6	49
34	Challenges and Opportunities for Developing More Generalizable Polygenic Risk Scores. <i>Annual Review of Biomedical Data Science</i> , 2022, 5, 293-320.	2.8	47
35	Shades of complexity: New perspectives on the evolution and genetic architecture of human skin. <i>American Journal of Physical Anthropology</i> , 2019, 168, 4-26.	2.1	45
36	Population History and Gene Divergence in Native Mexicans Inferred from 76 Human Exomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 994-1006.	3.5	43

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37	Population Histories of the United States Revealed through Fine-Scale Migration and Haplotype Analysis. <i>American Journal of Human Genetics</i> , 2020, 106, 371-388.	2.6	39
38	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
39	Exome capture from saliva produces high quality genomic and metagenomic data. <i>BMC Genomics</i> , 2014, 15, 262.	1.2	34
40	Genome-wide risk prediction of common diseases across ancestries in one million people. <i>Cell Genomics</i> , 2022, 2, 100118.	3.0	34
41	STORMSeq: An Open-Source, User-Friendly Pipeline for Processing Personal Genomics Data in the Cloud. <i>PLoS ONE</i> , 2014, 9, e84860.	1.1	25
42	Increasing diversity in genomics requires investment in equitable partnerships and capacity building. <i>Nature Genetics</i> , 2022, 54, 740-745.	9.4	20
43	Rapid evolution of a skin-lightening allele in southern African KhoeSan. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 13324-13329.	3.3	17
44	Imputation-based assessment of next generation rare exome variant arrays. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2014, , 241-52.	0.7	7
45	IMPUTATION-BASED ASSESSMENT OF NEXT GENERATION RARE EXOME VARIANT ARRAYS. , 2013, , .		6
46	Analytic and Translational Genetics. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 217-241.	2.8	4
47	How robust are cross-population signatures of polygenic adaptation in humans?. , 0, 1, .		3