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 global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
2	Clinical use of current polygenic risk scores may exacerbate health disparities. Nature Genetics, 2019, 51, 584-591.	21.4	1,664
3	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	21.4	1,594
4	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	21.4	1,538
5	Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations. American Journal of Human Genetics, 2017, 100, 635-649.	6.2	1,120
6	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
7	Genome-wide association studies. Nature Reviews Methods Primers, 2021, 1, .	21.2	529
8	Comparative genetic architectures of schizophrenia in East Asian and European populations. Nature Genetics, 2019, 51, 1670-1678.	21.4	440
9	Genome-wide Association Studies in Ancestrally Diverse Populations: Opportunities, Methods, Pitfalls, and Recommendations. Cell, 2019, 179, 589-603.	28.9	428
10	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
11	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. Cell, 2015, 162, 1051-1065.	28.9	304
12	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. ELife, 2019, 8, .	6.0	276
13	Predicting Polygenic Risk of Psychiatric Disorders. Biological Psychiatry, 2019, 86, 97-109.	1.3	252
14	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
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	Improving polygenic prediction in ancestrally diverse populations. Nature Genetics, 2022, 54, 573-580.	21.4	209
17	A roadmap to increase diversity in genomic studies. Nature Medicine, 2022, 28, 243-250.	30.7	195
18	An Unexpectedly Complex Architecture for Skin Pigmentation in Africans. Cell, 2017, 171, 1340-1353.e14.	28.9	134

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19	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
20	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. Nature Genetics, 2022, 54, 450-458.	21.4	109
21	Problems with Using Polygenic Scores to Select Embryos. New England Journal of Medicine, 2021, 385, 78-86.	27.0	105
22	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
23	Fine-Scale Human Population Structure in Southern Africa Reflects Ecogeographic Boundaries. Genetics, 2016, 204, 303-314.	2.9	93
24	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
25	Fine-Scale Genetic Structure in Finland. G3: Genes, Genomes, Genetics, 2017, 7, 3459-3468.	1.8	86
26	Strategies for Enriching Variant Coverage in Candidate Disease Loci on a Multiethnic Genotyping Array. PLoS ONE, 2016, 11, e0167758.	2.5	72
27	Polygenic scores in biomedical research. Nature Reviews Genetics, 2022, 23, 524-532.	16.3	69
28	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
29	Impact of admixture and ancestry on eQTL analysis and GWAS colocalization in GTEx. Genome Biology, 2020, 21, 233.	8.8	64
30	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
31	The critical needs and challenges for genetic architecture studies in Africa. Current Opinion in Genetics and Development, 2018, 53, 113-120.	3.3	57
32	Transcriptome Sequencing from Diverse Human Populations Reveals Differentiated Regulatory Architecture. PLoS Genetics, 2014, 10, e1004549.	3.5	49
33	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
34	Challenges and Opportunities for Developing More Generalizable Polygenic Risk Scores. Annual Review of Biomedical Data Science, 2022, 5, 293-320.	6.5	47
35	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
36	Population History and Gene Divergence in Native Mexicans Inferred from 76 Human Exomes. Molecular Biology and Evolution, 2020, 37, 994-1006.	8.9	43

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37	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
38	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
39	Exome capture from saliva produces high quality genomic and metagenomic data. BMC Genomics, 2014, 15, 262.	2.8	34
40	Genome-wide risk prediction of common diseases across ancestries in one million people. Cell Genomics, 2022, 2, 100118.	6.5	34
41	STORMSeq: An Open-Source, User-Friendly Pipeline for Processing Personal Genomics Data in the Cloud. PLoS ONE, 2014, 9, e84860.	2.5	25
42	Increasing diversity in genomics requires investment in equitable partnerships and capacity building. Nature Genetics, 2022, 54, 740-745.	21.4	20
43	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
44	Imputation-based assessment of next generation rare exome variant arrays. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 241-52.	0.7	7
45	IMPUTATION-BASED ASSESSMENT OF NEXT GENERATION RARE EXOME VARIANT ARRAYS. , 2013, , .		6
46	Analytic and Translational Genetics. Annual Review of Biomedical Data Science, 2020, 3, 217-241.	6.5	4
47	How robust are cross-population signatures of polygenic adaptation in humans?. , 0, 1, .		3