Alicia R Martin

List of Publications by Year in Descending Order

61 papers	13,729 citations	26 h-index	73 g-index
73 ext. papers	20,964 ext. citations	21.5 avg, IF	5.65 L-index

#	Paper	IF	Citations
61	A roadmap to increase diversity in genomic studies.. *Nature Medicine*, **2022**,	50.5	18
60	Mapping genomic loci implicates genes and synaptic biology in schizophrenia.. *Nature*, **2022**,	50.4	35
59	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores.. *Nature Genetics*, **2022**, 54, 450-458	36.3	3
58	Improving polygenic prediction in ancestrally diverse populations.. *Nature Genetics*, **2022**, 54, 573-580	36.3	5
57	Challenges and Opportunities for Developing More Generalizable Polygenic Risk Scores.. *Annual Review of Biomedical Data Science*, **2022**,	5.6	1
56	Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. *Nature Medicine*, **2021**, 27, 1876-1884	50.5	25
55	Low-coverage sequencing cost-effectively detects known and novel variation in underrepresented populations. *American Journal of Human Genetics*, **2021**, 108, 656-668	11	10
54	Problems with Using Polygenic Scores to Select Embryos. *New England Journal of Medicine*, **2021**, 385, 78-86	59.2	23
53	Genome-wide association studies. *Nature Reviews Methods Primers*, **2021**, 1,		50
52	Tractor uses local ancestry to enable the inclusion of admixed individuals in GWAS and to boost power. *Nature Genetics*, **2021**, 53, 195-204	36.3	26
51	Population Histories of the United States Revealed through Fine-Scale Migration and Haplotype Analysis. *American Journal of Human Genetics*, **2020**, 106, 371-388	11	15
50	Analytic and Translational Genetics. *Annual Review of Biomedical Data Science*, **2020**, 3, 217-241	5.6	0
49	Population History and Gene Divergence in Native Mexicans Inferred from 76 Human Exomes. *Molecular Biology and Evolution*, **2020**, 37, 994-1006	8.3	19
48	Impact of admixture and ancestry on eQTL analysis and GWAS colocalization in GTEx. *Genome Biology*, **2020**, 21, 233	18.3	19
47	Geographic Variation and Bias in the Polygenic Scores of Complex Diseases and Traits in Finland. *American Journal of Human Genetics*, **2019**, 104, 1169-1181	11	50
46	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. *ELife*, **2019**, 8,	8.9	166
45	Clinical use of current polygenic risk scores may exacerbate health disparities. *Nature Genetics*, **2019**, 51, 584-591	36.3	711

44	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	3	28
43	Identification of common genetic risk variants for autism spectrum disorder. *Nature Genetics*, **2019**, 51, 431-444	36.3	746
42	Genome-wide Association Studies in Ancestrally Diverse Populations: Opportunities, Methods, Pitfalls, and Recommendations. *Cell*, **2019**, 179, 589-603	56.2	145
41	International meta-analysis of PTSD genome-wide association studies identifies sex- and ancestry-specific genetic risk loci. *Nature Communications*, **2019**, 10, 4558	17.4	151
40	Comparative genetic architectures of schizophrenia in East Asian and European populations. *Nature Genetics*, **2019**, 51, 1670-1678	36.3	185
39	Predicting Polygenic Risk of Psychiatric Disorders. *Biological Psychiatry*, **2019**, 86, 97-109	7.9	170
38	Shades of complexity: New perspectives on the evolution and genetic architecture of human skin. *American Journal of Physical Anthropology*, **2019**, 168 Suppl 67, 4-26	2.5	28
37	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. *Nature Genetics*, **2019**, 51, 63-75	36.3	826
36	Haplotype Sharing Provides Insights into Fine-Scale Population History and Disease in Finland. *American Journal of Human Genetics*, **2018**, 102, 760-775	11	34
35	Imputation-Aware Tag SNP Selection To Improve Power for Large-Scale, Multi-ethnic Association Studies. *G3: Genes, Genomes, Genetics*, **2018**, 8, 3255-3267	3.2	17
34	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	11.5	12
33	The critical needs and challenges for genetic architecture studies in Africa. *Current Opinion in Genetics and Development*, **2018**, 53, 113-120	4.9	32
32	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. *American Journal of Human Genetics*, **2018**, 102, 1204-1211	11	59
31	Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations. *American Journal of Human Genetics*, **2017**, 100, 635-649	11	665
30	An Unexpectedly Complex Architecture for Skin Pigmentation in Africans. *Cell*, **2017**, 171, 1340-1353.e14	56.2	85
29	Fine-Scale Genetic Structure in Finland. *G3: Genes, Genomes, Genetics*, **2017**, 7, 3459-3468	3.2	50
28	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	11.5	149
27	Strategies for Enriching Variant Coverage in Candidate Disease Loci on a Multiethnic Genotyping Array. *PLoS ONE*, **2016**, 11, e0167758	3.7	39

26	Fine-Scale Human Population Structure in Southern Africa Reflects Ecogeographic Boundaries. *Genetics*, **2016**, 204, 303-14	4	59
25	A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74	50.4	8599
24	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. *Cell*, **2015**, 162, 1051-65	56.2	240
23	Exome capture from saliva produces high quality genomic and metagenomic data. *BMC Genomics*, **2014**, 15, 262	4.5	26
22	Transcriptome sequencing from diverse human populations reveals differentiated regulatory architecture. *PLoS Genetics*, **2014**, 10, e1004549	6	35
21	STORMSeq: an open-source, user-friendly pipeline for processing personal genomics data in the cloud. *PLoS ONE*, **2014**, 9, e84860	3.7	21
20	Imputation-based assessment of next generation rare exome variant arrays. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2014**, 241-52	1.3	7
19	Global biobank analyses provide lessons for computing polygenic risk scores across diverse cohorts		3
18	How robust are cross-population signatures of polygenic adaptation in humans?1,		2
17	Haplotype sharing provides insights into fine-scale population history and disease in Finland		2
16	Population histories of the United States revealed through fine-scale migration and haplotype analysis		1
15	Human demographic history impacts genetic risk prediction across diverse populations		7
14	Imputation aware tag SNP selection to improve power for multi-ethnic association studies		1
13	Low-coverage sequencing cost-effectively detects known and novel variation in underrepresented populations		2
12	Tractor: A framework allowing for improved inclusion of admixed individuals in large-scale association studies		2
11	How robust are cross-population signatures of polygenic adaptation in humans?		4
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