

# Andres Moreno-Estrada

## List of Publications by Year in descending order

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57  
papers

28,729  
citations

126858

33  
h-index

143943

57  
g-index

68  
all docs

68  
docs citations

68  
times ranked

51180  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dietary, Cultural, and Pathogens-Related Selective Pressures Shaped Differential Adaptive Evolution among Native Mexican Populations. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	6
2	Disentangling Signatures of Selection Before and After European Colonization in Latin Americans. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	16
3	The genetic legacy of the Manila galleon trade in Mexico. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20200419.	1.8	9
4	A loss-of-function <i>IFNAR1</i> allele in Polynesia underlies severe viral diseases in homozygotes. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	28
5	Clotting factor genes are associated with preeclampsia in high-altitude pregnant women in the Peruvian Andes. <i>American Journal of Human Genetics</i> , 2022, 109, 1117-1139.	2.6	10
6	Ancient DNA reveals five streams of migration into Micronesia and matrilocality in early Pacific seafarers. <i>Science</i> , 2022, 377, 72-79.	6.0	13
7	Continental-scale genomic analysis suggests shared post-admixture adaptation in the Americas. <i>Human Molecular Genetics</i> , 2021, 30, 2123-2134.	1.4	6
8	Paths and timings of the peopling of Polynesia inferred from genomic networks. <i>Nature</i> , 2021, 597, 522-526.	13.7	31
9	Evaluating the Impact of Sex-Biased Genetic Admixture in the Americas through the Analysis of Haplotype Data. <i>Genes</i> , 2021, 12, 1580.	1.0	6
10	Imputation Performance in Latin American Populations: Improving Rare Variants Representation With the Inclusion of Native American Genomes. <i>Frontiers in Genetics</i> , 2021, 12, 719791.	1.1	7
11	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
12	Paleogenomic insights into the red complex bacteria <i>Tannerella forsythia</i> in Pre-Hispanic and Colonial individuals from Mexico. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190580.	1.8	18
13	Native American gene flow into Polynesia predating Easter Island settlement. <i>Nature</i> , 2020, 583, 572-577.	13.7	64
14	Development of a small panel of SNPs to infer ancestry in Chileans that distinguishes Aymara and Mapuche components. <i>Biological Research</i> , 2020, 53, 15.	1.5	18
15	Genetic analyses of diverse populations improves discovery for complex traits. <i>Nature</i> , 2019, 570, 514-518.	13.7	679
16	A genome-wide association and admixture mapping study of bronchodilator drug response in African Americans with asthma. <i>Pharmacogenomics Journal</i> , 2019, 19, 249-259.	0.9	54
17	An admixture mapping meta-analysis implicates genetic variation at 18q21 with asthma susceptibility in Latinos. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 957-969.	1.5	33
18	A panel of 32 AIMs suitable for population stratification correction and global ancestry estimation in Mexican mestizos. <i>BMC Genetics</i> , 2019, 20, 5.	2.7	11

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19	The Genomic Impact of European Colonization of the Americas. <i>Current Biology</i> , 2019, 29, 3974-3986.e4.	1.8	89
20	Whole-Genome Sequencing of Pharmacogenetic Drug Response in Racially Diverse Children with Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 197, 1552-1564.	2.5	102
21	Genomic insights into the origin and diversification of late maritime hunter-gatherers from the Chilean Patagonia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4006-E4012.	3.3	50
22	Genetic diversity in populations across Latin America: implications for population and medical genetic studies. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 98-104.	1.5	37
23	Genome-wide Association Study in an Amerindian Ancestry Population Reveals Novel Systemic Lupus Erythematosus Risk Loci and the Role of European Admixture. <i>Arthritis and Rheumatology</i> , 2016, 68, 932-943.	2.9	138
24	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016, 538, 201-206.	13.7	1,216
25	Genomic variation in recently collected maize landraces from Mexico. <i>Genomics Data</i> , 2016, 7, 38-45.	1.3	50
26	Genomic Insights into the Ancestry and Demographic History of South America. <i>PLoS Genetics</i> , 2015, 11, e1005602.	1.5	198
27	Genome-wide association study and admixture mapping reveal new loci associated with total IgE levels in Latinos. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, 1502-1510.	1.5	52
28	Genetic ancestry influences asthma susceptibility and lung function among Latinos. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, 228-235.	1.5	113
29	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	6.0	449
30	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
31	Population Genomic Analysis of Ancient and Modern Genomes Yields New Insights into the Genetic Ancestry of the Tyrolean Iceman and the Genetic Structure of Europe. <i>PLoS Genetics</i> , 2014, 10, e1004353.	1.5	86
32	A genome-wide association study of bronchodilator response in Latinos implicates rare variants. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 133, 370-378.e15.	1.5	105
33	Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. <i>Nature Communications</i> , 2014, 5, 3934.	5.8	364
34	Genome-wide association study and admixture mapping identify different asthma-associated loci in Latinos: The Genes-environments & Admixture in Latino Americans study. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 134, 295-305.	1.5	106
35	The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. <i>Science</i> , 2014, 344, 1280-1285.	6.0	420
36	Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences. <i>Genome Biology</i> , 2014, 15, R88.	13.9	72

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37	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. <i>Science</i> , 2013, 342, 1235587.	6.0	341
38	Pulling out the 1%: Whole-Genome Capture for the Targeted Enrichment of Ancient DNA Sequencing Libraries. <i>American Journal of Human Genetics</i> , 2013, 93, 852-864.	2.6	284
39	Factors associated with degree of atopy in Latino children in a nationwide pediatric sample: The Genes-environments and Admixture in Latino Asthmatics (GALA II) study. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 132, 896-905.e1.	1.5	27
40	Reconstructing Native American Migrations from Whole-Genome and Whole-Exome Data. <i>PLoS Genetics</i> , 2013, 9, e1004023.	1.5	185
41	Reconstructing the Population Genetic History of the Caribbean. <i>PLoS Genetics</i> , 2013, 9, e1003925.	1.5	296
42	Genomic Ancestry of North Africans Supports Back-to-Africa Migrations. <i>PLoS Genetics</i> , 2012, 8, e1002397.	1.5	275
43	Type 2 Diabetes Risk Alleles Demonstrate Extreme Directional Differentiation among Human Populations, Compared to Other Diseases. <i>PLoS Genetics</i> , 2012, 8, e1002621.	1.5	106
44	New insights into the Tyrolean Iceman's origin and phenotype as inferred by whole-genome sequencing. <i>Nature Communications</i> , 2012, 3, 698.	5.8	382
45	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65.	13.7	7,199
46	Population Genetic Inference from Personal Genome Data: Impact of Ancestry and Admixture on Human Genomic Variation. <i>American Journal of Human Genetics</i> , 2012, 91, 660-671.	2.6	100
47	Melanesian Blond Hair Is Caused by an Amino Acid Change in TYRP1. <i>Science</i> , 2012, 336, 554-554.	6.0	104
48	Y-chromosome diversity in Native Mexicans reveals continental transition of genetic structure in the Americas. <i>American Journal of Physical Anthropology</i> , 2012, 148, 395-405.	2.1	26
49	EVOLUTION AND MEDICINE IN UNDERGRADUATE EDUCATION: A PRESCRIPTION FOR ALL BIOLOGY STUDENTS. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 1991-2006.	1.1	29
50	African signatures of recent positive selection in human FOXI1. <i>BMC Evolutionary Biology</i> , 2010, 10, 267.	3.2	6
51	Fine-scale population structure and the era of next-generation sequencing. <i>Human Molecular Genetics</i> , 2010, 19, R221-R226.	1.4	25
52	Genome-wide patterns of population structure and admixture among Hispanic/Latino populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8954-8961.	3.3	360
53	A functional ABCA1 gene variant is associated with low HDL-cholesterol levels and shows evidence of positive selection in Native Americans. <i>Human Molecular Genetics</i> , 2010, 19, 2877-2885.	1.4	133
54	Interrogating 11 Fast-Evolving Genes for Signatures of Recent Positive Selection in Worldwide Human Populations. <i>Molecular Biology and Evolution</i> , 2009, 26, 2285-2297.	3.5	20

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55	Decay of linkage disequilibrium within genes across HGDP-CEPH human samples: most population isolates do not show increased LD. <i>BMC Genomics</i> , 2009, 10, 338.	1.2	19
56	SNP analysis to results (SNPator): a web-based environment oriented to statistical genomics analyses upon SNP data. <i>Bioinformatics</i> , 2008, 24, 1643-1644.	1.8	61
57	Signatures of Selection in the Human Olfactory Receptor OR511 Gene. <i>Molecular Biology and Evolution</i> , 2007, 25, 144-154.	3.5	26