

# J VÃ-ctor Moreno-Mayar

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

4,938  
citations

186265

28  
h-index

377865

34  
g-index

39  
all docs

39  
docs citations

39  
times ranked

6498  
citing authors

#	ARTICLE	IF	CITATIONS
1	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. <i>Science</i> , 2011, 334, 94-98.	12.6	675
2	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	12.6	449
3	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214.	27.8	439
4	137 ancient human genomes from across the Eurasian steppes. <i>Nature</i> , 2018, 557, 369-374.	27.8	325
5	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , 2018, 553, 203-207.	27.8	304
6	The prehistoric peopling of Southeast Asia. <i>Science</i> , 2018, 361, 88-92.	12.6	291
7	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , 2018, 360, .	12.6	262
8	The ancestry and affiliations of Kennewick Man. <i>Nature</i> , 2015, 523, 455-458.	27.8	241
9	Early human dispersals within the Americas. <i>Science</i> , 2018, 362, .	12.6	230
10	Bacterial natural transformation by highly fragmented and damaged DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19860-19865.	7.1	170
11	Population genomics of the Viking world. <i>Nature</i> , 2020, 585, 390-396.	27.8	143
12	Ancient genomics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130387.	4.0	142
13	Early Pleistocene enamel proteome from Dmanisi resolves <i>Stephanorhinus</i> phylogeny. <i>Nature</i> , 2019, 574, 103-107.	27.8	135
14	Genome Sequence of a 5,310-Year-Old Maize Cob Provides Insights into the Early Stages of Maize Domestication. <i>Current Biology</i> , 2016, 26, 3195-3201.	3.9	130
15	Genome-wide ancestry of 17th-century enslaved Africans from the Caribbean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3669-3673.	7.1	110
16	Application and comparison of large-scale solution-based DNA capture-enrichment methods on ancient DNA. <i>Scientific Reports</i> , 2011, 1, 74.	3.3	106
17	Recent Diversification of a Marine Genus ( <i>Tursiops</i> spp.) Tracks Habitat Preference and Environmental Change. <i>Systematic Biology</i> , 2013, 62, 865-877.	5.6	84
18	Ancient Biomolecules and Evolutionary Inference. <i>Annual Review of Biochemistry</i> , 2018, 87, 1029-1060.	11.1	76

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19	Human Disease Variation in the Light of Population Genomics. <i>Cell</i> , 2019, 177, 115-131.	28.9	75
20	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014, 24, R1035-R1037.	3.9	73
21	Origins and genetic legacies of the Caribbean Taino. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2341-2346.	7.1	64
22	Native American gene flow into Polynesia predating Easter Island settlement. <i>Nature</i> , 2020, 583, 572-577.	27.8	64
23	Genome-wide Ancestry Patterns in Rapanui Suggest Pre-European Admixture with Native Americans. <i>Current Biology</i> , 2014, 24, 2518-2525.	3.9	50
24	Genome-wide Ancestry and Demographic History of African-Descendant Maroon Communities from French Guiana and Suriname. <i>American Journal of Human Genetics</i> , 2017, 101, 725-736.	6.2	50
25	The limits and potential of paleogenomic techniques for reconstructing grapevine domestication. <i>Journal of Archaeological Science</i> , 2016, 72, 57-70.	2.4	43
26	The genomic history of the Aegean palatial civilizations. <i>Cell</i> , 2021, 184, 2565-2586.e21.	28.9	43
27	<i>bammds</i> : a tool for assessing the ancestry of low-depth whole-genome data using multidimensional scaling (MDS). <i>Bioinformatics</i> , 2014, 30, 2962-2964.	4.1	40
28	Speciation and demographic history of Atlantic eels ( <i>Anguilla anguilla</i> and <i>A. rostrata</i> ) revealed by mitogenome sequencing. <i>Heredity</i> , 2014, 113, 432-442.	2.6	38
29	Genetic diversity among pandemic 2009 influenza viruses isolated from a transmission chain. <i>Virology Journal</i> , 2013, 10, 116.	3.4	22
30	Revisiting the Kalahari debate in the highlands: ancient DNA provides new faunal identifications at Sehonghong, Lesotho. <i>Azania</i> , 2016, 51, 295-306.	0.9	18
31	A likelihood method for estimating present-day human contamination in ancient male samples using low-depth X-chromosome data. <i>Bioinformatics</i> , 2020, 36, 828-841.	4.1	14
32	Ancient Human Genomes and Environmental DNA from the Cement Attaching 2,000-Year-Old Head Lice Nits. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	10
33	Identifying a living great-grandson of the Lakota Sioux leader Tatanka Iyotake (Sitting Bull). <i>Science Advances</i> , 2021, 7, eabh2013.	10.3	5
34	Early Peopling of the Americas. , 2021, , 32-44.		2
35	FrAnTK: a Frequency-based Analysis ToolKit for efficient exploration of allele sharing patterns in present-day and ancient genomic datasets. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	0