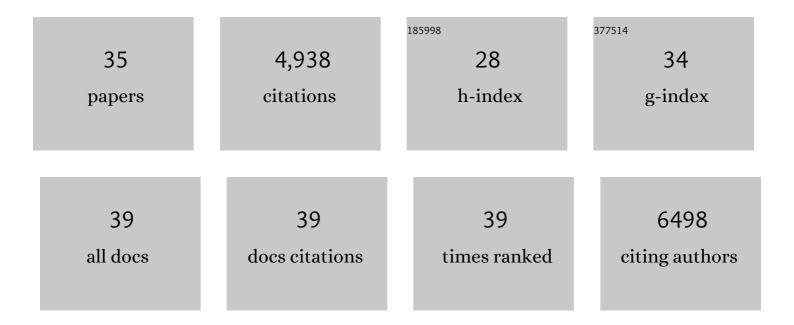
J VÃ-ctor Moreno-Mayar

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6086302/publications.pdf

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#	Article	IF	CITATIONS
1	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. Science, 2011, 334, 94-98.	6.0	675
2	Genomic evidence for the Pleistocene and recent population history of Native Americans. Science, 2015, 349, aab3884.	6.0	449
3	A genomic history of Aboriginal Australia. Nature, 2016, 538, 207-214.	13.7	439
4	137 ancient human genomes from across the Eurasian steppes. Nature, 2018, 557, 369-374.	13.7	325
5	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. Nature, 2018, 553, 203-207.	13.7	304
6	The prehistoric peopling of Southeast Asia. Science, 2018, 361, 88-92.	6.0	291
7	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. Science, 2018, 360, .	6.0	262
8	The ancestry and affiliations of Kennewick Man. Nature, 2015, 523, 455-458.	13.7	241
9	Early human dispersals within the Americas. Science, 2018, 362, .	6.0	230
10	Bacterial natural transformation by highly fragmented and damaged DNA. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19860-19865.	3.3	170
11	Population genomics of the Viking world. Nature, 2020, 585, 390-396.	13.7	143
12	Ancient genomics. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130387.	1.8	142
13	Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny. Nature, 2019, 574, 103-107.	13.7	135
14	Genome Sequence of a 5,310-Year-Old Maize Cob Provides Insights into the Early Stages of Maize Domestication. Current Biology, 2016, 26, 3195-3201.	1.8	130
15	Genome-wide ancestry of 17th-century enslaved Africans from the Caribbean. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3669-3673.	3.3	110
16	Application and comparison of large-scale solution-based DNA capture-enrichment methods on ancient DNA. Scientific Reports, 2011, 1, 74.	1.6	106
17	Recent Diversification of a Marine Genus (Tursiops spp.) Tracks Habitat Preference and Environmental Change. Systematic Biology, 2013, 62, 865-877.	2.7	84
18	Ancient Biomolecules and Evolutionary Inference. Annual Review of Biochemistry, 2018, 87, 1029-1060.	5.0	76

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19	Human Disease Variation in the Light of Population Genomics. Cell, 2019, 177, 115-131.	13.5	75
20	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. Current Biology, 2014, 24, R1035-R1037.	1.8	73
21	Origins and genetic legacies of the Caribbean Taino. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2341-2346.	3.3	64
22	Native American gene flow into Polynesia predating Easter Island settlement. Nature, 2020, 583, 572-577.	13.7	64
23	Genome-wide Ancestry Patterns in Rapanui Suggest Pre-European Admixture with Native Americans. Current Biology, 2014, 24, 2518-2525.	1.8	50
24	Genome-wide Ancestry and Demographic History of African-Descendant Maroon Communities from French Guiana and Suriname. American Journal of Human Genetics, 2017, 101, 725-736.	2.6	50
25	The limits and potential of paleogenomic techniques for reconstructing grapevine domestication. Journal of Archaeological Science, 2016, 72, 57-70.	1.2	43
26	The genomic history of the Aegean palatial civilizations. Cell, 2021, 184, 2565-2586.e21.	13.5	43
27	<i>bammds:</i> a tool for assessing the ancestry of low-depth whole-genome data using multidimensional scaling (MDS). Bioinformatics, 2014, 30, 2962-2964.	1.8	40
28	Speciation and demographic history of Atlantic eels (Anguilla anguilla and A. rostrata) revealed by mitogenome sequencing. Heredity, 2014, 113, 432-442.	1.2	38
29	Genetic diversity among pandemic 2009 influenza viruses isolated from a transmission chain. Virology Journal, 2013, 10, 116.	1.4	22
30	Revisiting the Kalahari debate in the highlands: ancient DNA provides new faunal identifications at Sehonghong, Lesotho. Azania, 2016, 51, 295-306.	0.4	18
31	A likelihood method for estimating present-day human contamination in ancient male samples using low-depth X-chromosome data. Bioinformatics, 2020, 36, 828-841.	1.8	14
32	Ancient Human Genomes and Environmental DNA from the Cement Attaching 2,000-Year-Old Head Lice Nits. Molecular Biology and Evolution, 2022, 39, .	3.5	10
33	Identifying a living great-grandson of the Lakota Sioux leader Tatanka Iyotake (Sitting Bull). Science Advances, 2021, 7, eabh2013.	4.7	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. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	Ο