

Rui Martiniano

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

29
papers

1,613
citations

16
h-index

33
g-index

33
ext. papers

2,236
ext. citations

14.3
avg, IF

3.74
L-index

#	Paper	IF	Citations
29	Placing ancient DNA sequences into reference phylogenies.. <i>Molecular Biology and Evolution</i> , 2022 ,	8.3	3
28	Ancient DNA at the edge of the world: Continental immigration and the persistence of Neolithic male lineages in Bronze Age Orkney.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	2
27	Biomolecular insights into North African-related ancestry, mobility and diet in eleventh-century Al-Andalus. <i>Scientific Reports</i> , 2021 , 11, 18121	4.9	0
26	Removing reference bias and improving indel calling in ancient DNA data analysis by mapping to a sequence variation graph. <i>Genome Biology</i> , 2020 , 21, 250	18.3	9
25	Population genomics of the Viking world. <i>Nature</i> , 2020 , 585, 390-396	50.4	35
24	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , 2019 , 570, 182-188	50.4	137
23	A Transient Pulse of Genetic Admixture from the Crusaders in the Near East Identified from Ancient Genome Sequences. <i>American Journal of Human Genetics</i> , 2019 , 104, 977-984	11	20
22	Ancient genomes indicate population replacement in Early Neolithic Britain. <i>Nature Ecology and Evolution</i> , 2019 , 3, 765-771	12.3	82
21	Response to Glem. <i>American Journal of Human Genetics</i> , 2018 , 102, 331	11	1
20	Dose-dependent expression of claudin-5 is a modifying factor in schizophrenia. <i>Molecular Psychiatry</i> , 2018 , 23, 2156-2166	15.1	87
19	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , 2018 , 360,	33.3	162
18	Insular Celtic population structure and genomic footprints of migration. <i>PLoS Genetics</i> , 2018 , 14, e1007162		17
17	The Eastern side of the Westernmost Europeans: Insights from subclades within Y-chromosome haplogroup J-M304. <i>American Journal of Human Biology</i> , 2018 , 30, e23082	2.7	1
16	Continuity and Admixture in the Last Five Millennia of Levantine History from Ancient Canaanite and Present-Day Lebanese Genome Sequences. <i>American Journal of Human Genetics</i> , 2017 , 101, 274-282 ¹¹		60
15	The population genomics of archaeological transition in west Iberia: Investigation of ancient substructure using imputation and haplotype-based methods. <i>PLoS Genetics</i> , 2017 , 13, e1006852	6	66
14	Early Neolithic genomes from the eastern Fertile Crescent. <i>Science</i> , 2016 , 353, 499-503	33.3	153
13	Early farmers from across Europe directly descended from Neolithic Aegeans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 6886-91	11.5	255

12	Genomic signals of migration and continuity in Britain before the Anglo-Saxons. <i>Nature Communications</i> , 2016 , 7, 10326	17.4	70
11	Neolithic and Bronze Age migration to Ireland and establishment of the insular Atlantic genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 368-73	11.5	149
10	Detection of novel germline mutations for breast cancer in non-BRCA1/2 families. <i>FEBS Journal</i> , 2015 , 282, 3424-37	5.7	31
9	Upper Palaeolithic genomes reveal deep roots of modern Eurasians. <i>Nature Communications</i> , 2015 , 6, 8912	17.4	229
8	Genetic evidence of African slavery at the beginning of the trans-Atlantic slave trade. <i>Scientific Reports</i> , 2014 , 4, 5994	4.9	17
7	Y-chromosome diversity in central Portugal reveals signatures of ancient maritime expansions. <i>Anthropologischer Anzeiger</i> , 2013 , 70, 355-67	0.6	3
6	Early farmers from across Europe directly descended from Neolithic Aegeans		10
5	The population genomics of archaeological transition in west Iberia: Investigation of ancient substructure using imputation and haplotype-based methods		1
4	Placing ancient DNA sequences into reference phylogenies		2
3	Insular Celtic population structure and genomic footprints of migration		1
2	The population history of northeastern Siberia since the Pleistocene		1
1	Removing reference bias and improving indel calling in ancient DNA data analysis by mapping to a sequence variation graph		5