

Clio Der Sarkissian

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9246475/publications.pdf>

Version: 2024-02-01

33
papers

3,174
citations

257357

24
h-index

395590

33
g-index

34
all docs

34
docs citations

34
times ranked

5163
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of ancient and modern genomes by SNP detection and phylogenomic and metagenomic analysis using PALEOMIX. <i>Nature Protocols</i> , 2014, 9, 1056-1082.	5.5	403
2	Ancient and modern environmental DNA. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130383.	1.8	292
3	The Influence of Rate Heterogeneity among Sites on the Time Dependence of Molecular Rates. <i>Molecular Biology and Evolution</i> , 2012, 29, 3345-3358.	3.5	275
4	Prehistoric genomes reveal the genetic foundation and cost of horse domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5661-9.	3.3	260
5	Ancient genomic changes associated with domestication of the horse. <i>Science</i> , 2017, 356, 442-445.	6.0	185
6	Neolithic mitochondrial haplogroup H genomes and the genetic origins of Europeans. <i>Nature Communications</i> , 2013, 4, 1764.	5.8	180
7	Evolutionary Genomics and Conservation of the Endangered Przewalski's Horse. <i>Current Biology</i> , 2015, 25, 2577-2583.	1.8	161
8	Ancient genomics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130387.	1.8	142
9	The origins and spread of domestic horses from the Western Eurasian steppes. <i>Nature</i> , 2021, 598, 634-640.	13.7	142
10	Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E6889-97.	3.3	139
11	Ancient DNA analysis. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	133
12	Rodents of the Caribbean: origin and diversification of hutias unravelled by next-generation museomics. <i>Biology Letters</i> , 2014, 10, 20140266.	1.0	87
13	Ancient DNA Reveals Prehistoric Gene-Flow from Siberia in the Complex Human Population History of North East Europe. <i>PLoS Genetics</i> , 2013, 9, e1003296.	1.5	78
14	Combining bleach and mild predigestion improves ancient DNA recovery from bones. <i>Molecular Ecology Resources</i> , 2017, 17, 742-751.	2.2	77
15	Less effective selection leads to larger genomes. <i>Genome Research</i> , 2017, 27, 1016-1028.	2.4	75
16	Evolutionary Patterns and Processes: Lessons from Ancient DNA. <i>Systematic Biology</i> , 2017, 66, syw059.	2.7	73
17	Ancient DNA analysis identifies marine mollusc shells as new metagenomic archives of the past. <i>Molecular Ecology Resources</i> , 2017, 17, 835-853.	2.2	62
18	Pros and cons of methylation-based enrichment methods for ancient DNA. <i>Scientific Reports</i> , 2015, 5, 11826.	1.6	61

#	ARTICLE	IF	CITATIONS
19	The Evolutionary Origin and Genetic Makeup of Domestic Horses. <i>Genetics</i> , 2016, 204, 423-434.	1.2	61
20	Major transitions in human evolution revisited: A tribute to ancient DNA. <i>Journal of Human Evolution</i> , 2015, 79, 4-20.	1.3	37
21	Mitochondrial genomes reveal the extinct <i>Hippidion</i> as an outgroup to all living equids. <i>Biology Letters</i> , 2015, 11, 20141058.	1.0	36
22	metaBIT, an integrative and automated metagenomic pipeline for analysing microbial profiles from high-throughput sequencing shotgun data. <i>Molecular Ecology Resources</i> , 2016, 16, 1415-1427.	2.2	35
23	Mitochondrial Genome Sequencing in Mesolithic North East Europe Unearths a New Sub-Clade within the Broadly Distributed Human Haplogroup C1. <i>PLoS ONE</i> , 2014, 9, e87612.	1.1	34
24	Ancient horse genomes reveal the timing and extent of dispersals across the Bering Land Bridge. <i>Molecular Ecology</i> , 2021, 30, 6144-6161.	2.0	30
25	Unveiling the Ecological Applications of Ancient DNA From Mollusk Shells. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	29
26	Heterogeneous Hunter-Gatherer and Steppe-Related Ancestries in Late Neolithic and Bell Beaker Genomes from Present-Day France. <i>Current Biology</i> , 2021, 31, 1072-1083.e10.	1.8	20
27	No particular genomic features underpin the dramatic economic consequences of 17th century plague epidemics in Italy. <i>IScience</i> , 2021, 24, 102383.	1.9	13
28	<i>Vibrio tapetis</i> Displays an Original Type IV Secretion System in Strains Pathogenic for Bivalve Molluscs. <i>Frontiers in Microbiology</i> , 2018, 9, 227.	1.5	12
29	Ancient Metagenomic Studies: Considerations for the Wider Scientific Community. <i>MSystems</i> , 2021, 6, e0131521.	1.7	11
30	Assessing the predictive taxonomic power of the bony labyrinth 3D shape in horses, donkeys and their F1-hybrids. <i>Journal of Archaeological Science</i> , 2021, 131, 105383.	1.2	8
31	Historical management of equine resources in France from the Iron Age to the Modern Period. <i>Journal of Archaeological Science: Reports</i> , 2021, 40, 103250.	0.2	8
32	CASCADE: A Custom-Made Archiving System for the Conservation of Ancient DNA Experimental Data. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	4
33	Sex in the city: Uncovering sex-specific management of equine resources from prehistoric times to the Modern Period in France. <i>Journal of Archaeological Science: Reports</i> , 2022, 41, 103341.	0.2	1