

Torsten Gärtner

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

4,224
citations

236612

25
h-index

223531

46
g-index

58
all docs

58
docs citations

58
times ranked

6837
citing authors

#	ARTICLE	IF	CITATIONS
1	Multidisciplinary investigation reveals an individual of West African origin buried in a Portuguese Mesolithic shell midden four centuries ago. <i>Journal of Archaeological Science: Reports</i> , 2022, 42, 103370.	0.2	3
2	Bioarchaeological evidence of one of the earliest Islamic burials in the Levant. <i>Communications Biology</i> , 2022, 5, .	2.0	3
3	Ancient DNA from a 2700-year-old goitered gazelle (<i>Gazella subgutturosa</i>) supports gazelle hunting in Iron Age Central Asia. <i>Royal Society Open Science</i> , 2022, 9, .	1.1	1
4	Mobility patterns in inland southwestern Sweden during the Neolithic and Early Bronze Age. <i>Archaeological and Anthropological Sciences</i> , 2021, 13, 1.	0.7	11
5	Disentangling adaptation from drift in bottlenecked and reintroduced populations of Alpine ibex. <i>Molecular Ecology Resources</i> , 2021, 21, 2350-2363.	2.2	8
6	Variable kinship patterns in Neolithic Anatolia revealed by ancient genomes. <i>Current Biology</i> , 2021, 31, 2455-2468.e18.	1.8	47
7	Genome of PeÅŸtera Muierii skull shows high diversity and low mutational load in pre-glacial Europe. <i>Current Biology</i> , 2021, 31, 2973-2983.e9.	1.8	18
8	Human population dynamics and <i>Yersinia pestis</i> in ancient northeast Asia. <i>Science Advances</i> , 2021, 7, .	4.7	32
9	Archaeogenetic analysis of Neolithic sheep from Anatolia suggests a complex demographic history since domestication. <i>Communications Biology</i> , 2021, 4, 1279.	2.0	16
10	Khoe-San Genomes Reveal Unique Variation and Confirm the Deepest Population Divergence in Homo sapiens. <i>Molecular Biology and Evolution</i> , 2020, 37, 2944-2954.	3.5	60
11	Robust genome-wide ancestry inference for heterogeneous datasets: illustrated using the 1,000 genome project with 3D facial images. <i>Scientific Reports</i> , 2020, 10, 11850.	1.6	7
12	The Neolithic Pitted Ware culture foragers were culturally but not genetically influenced by the Battle Axe culture herders. <i>American Journal of Physical Anthropology</i> , 2020, 172, 638-649.	2.1	20
13	The presence and impact of reference bias on population genomic studies of prehistoric human populations. <i>PLoS Genetics</i> , 2019, 15, e1008302.	1.5	137
14	The genomic ancestry of the Scandinavian Battle Axe Culture people and their relation to the broader Corded Ware horizon. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191528.	1.2	35
15	Copy number determination of the gene for the human pancreatic polypeptide receptor NPY4R using read depth analysis and droplet digital PCR. <i>BMC Biotechnology</i> , 2019, 19, 31.	1.7	4
16	Genetic data and radiocarbon dating question Plovers Lake as a Middle Stone Age hominin-bearing site. <i>Journal of Human Evolution</i> , 2019, 131, 203-209.	1.3	4
17	Viking warrior women? Reassessing Birka chamber grave Bj.581. <i>Antiquity</i> , 2019, 93, 181-198.	0.5	31
18	Four millennia of Iberian biomolecular prehistory illustrate the impact of prehistoric migrations at the far end of Eurasia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3428-3433.	3.3	96

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19	Genomic and Strontium Isotope Variation Reveal Immigration Patterns in a Viking Age Town. <i>Current Biology</i> , 2018, 28, 2730-2738.e10.	1.8	44
20	Estimating genetic kin relationships in prehistoric populations. <i>PLoS ONE</i> , 2018, 13, e0195491.	1.1	187
21	Population genomics of Mesolithic Scandinavia: Investigating early postglacial migration routes and high-latitude adaptation. <i>PLoS Biology</i> , 2018, 16, e2003703.	2.6	174
22	Ancient X chromosomes reveal contrasting sex bias in Neolithic and Bronze Age Eurasian migrations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2657-2662.	3.3	94
23	Genomic Analyses of Pre-European Conquest Human Remains from the Canary Islands Reveal Close Affinity to Modern North Africans. <i>Current Biology</i> , 2017, 27, 3396-3402.e5.	1.8	62
24	Southern African ancient genomes estimate modern human divergence to 350,000 to 260,000 years ago. <i>Science</i> , 2017, 358, 652-655.	6.0	351
25	A female Viking warrior confirmed by genomics. <i>American Journal of Physical Anthropology</i> , 2017, 164, 853-860.	2.1	69
26	Northeast African genomic variation shaped by the continuity of indigenous groups and Eurasian migrations. <i>PLoS Genetics</i> , 2017, 13, e1006976.	1.5	45
27	Reply to Lazaridis and Reich: Robust model-based inference of male-biased admixture during Bronze Age migration from the Pontic-Caspian Steppe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3875-E3877.	3.3	11
28	Genomic and phenotypic differentiation of <i>Arabidopsis thaliana</i> along altitudinal gradients in the North Italian Alps. <i>Molecular Ecology</i> , 2016, 25, 3574-3592.	2.0	47
29	Genes mirror migrations and cultures in prehistoric Europe – a population genomic perspective. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 115-123.	1.5	40
30	The Demographic Development of the First Farmers in Anatolia. <i>Current Biology</i> , 2016, 26, 2659-2666.	1.8	163
31	Inferring Past Effective Population Size from Distributions of Coalescent Times. <i>Genetics</i> , 2016, 204, 1191-1206.	1.2	28
32	Genomic Evidence Establishes Anatolia as the Source of the European Neolithic Gene Pool. <i>Current Biology</i> , 2016, 26, 270-275.	1.8	111
33	Genome-wide association studies in elite varieties of German winter barley using single-marker and haplotype-based methods. <i>Plant Breeding</i> , 2015, 134, 28-39.	1.0	59
34	Ancient genomes link early farmers from Atapuerca in Spain to modern-day Basques. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11917-11922.	3.3	255
35	Water yam (<i>Dioscorea alata</i> L.) diversity pattern in Brazil: an analysis with SSR and morphological markers. <i>Genetic Resources and Crop Evolution</i> , 2014, 61, 611-624.	0.8	20
36	Genomic Diversity and Admixture Differs for Stone-Age Scandinavian Foragers and Farmers. <i>Science</i> , 2014, 344, 747-750.	6.0	315

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37	Robust Identification of Local Adaptation from Allele Frequencies. <i>Genetics</i> , 2013, 195, 205-220.	1.2	518
38	Mutational Bias and Gene Conversion Affect the Intraspecific Nitrogen Stoichiometry of the <i>Arabidopsis thaliana</i> Transcriptome. <i>Molecular Biology and Evolution</i> , 2013, 30, 561-568.	3.5	11
39	Islands and streams: clusters and gene flow in wild barley populations from the Levant. <i>Molecular Ecology</i> , 2012, 21, 1115-1129.	2.0	47
40	Whole-genome sequencing of multiple <i>Arabidopsis thaliana</i> populations. <i>Nature Genetics</i> , 2011, 43, 956-963.	9.4	910
41	phenosim - A software to simulate phenotypes for testing in genome-wide association studies. <i>BMC Bioinformatics</i> , 2011, 12, 265.	1.2	18
42	Improved haplotype-based detection of ongoing selective sweeps towards an application in <i>Arabidopsis thaliana</i> . <i>BMC Research Notes</i> , 2011, 4, 232.	0.6	11
43	Where in the Genome Are Significant Single Nucleotide Polymorphisms from Genome-Wide Association Studies Located?. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 507-512.	1.0	10
44	Deleterious amino acid polymorphisms in <i>Arabidopsis thaliana</i> and rice. <i>Theoretical and Applied Genetics</i> , 2010, 121, 157-168.	1.8	39
45	Single feature polymorphism (SFP)-based selective sweep identification and association mapping of growth-related metabolic traits in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2010, 11, 188.	1.2	11
46	Analysis of <i>Arabidopsis</i> natural variation in biomass accumulation and metabolism. <i>New Biotechnology</i> , 2009, 25, S307.	2.4	2
47	Be careful when studying selection based on polygenic score overdispersion. <i>Peer Community in Evolutionary Biology</i> , 0, , .	0.0	0