

Pontus Skoglund

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

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81900

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all docs

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docs citations

72
times ranked

10756
citing authors

#	ARTICLE	IF	CITATIONS
1	Grey wolf genomic history reveals a dual ancestry of dogs. <i>Nature</i> , 2022, 607, 313-320.	27.8	48
2	Origins of modern human ancestry. <i>Nature</i> , 2021, 590, 229-237.	27.8	166
3	Ancient DNA analysis. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	21.2	133
4	Million-year-old DNA sheds light on the genomic history of mammoths. <i>Nature</i> , 2021, 591, 265-269.	27.8	179
5	Initial Upper Palaeolithic humans in Europe had recent Neanderthal ancestry. <i>Nature</i> , 2021, 592, 253-257.	27.8	119
6	Inferring Population Histories for Ancient Genomes Using Genome-Wide Genealogies. <i>Molecular Biology and Evolution</i> , 2021, 38, 3497-3511.	8.9	33
7	Genome-scale sequencing and analysis of human, wolf, and bison DNA from 25,000-year-old sediment. <i>Current Biology</i> , 2021, 31, 3564-3574.e9.	3.9	34
8	Ethics of DNA research on human remains: five globally applicable guidelines. <i>Nature</i> , 2021, 599, 41-46.	27.8	49
9	Comment on "A global environmental crisis 42,000 years ago" <i>Science</i> , 2021, 374, eabi8330.	12.6	3
10	Origins and genetic legacy of prehistoric dogs. <i>Science</i> , 2020, 370, 557-564.	12.6	152
11	A Paleogenomic Reconstruction of the Deep Population History of the Andes. <i>Cell</i> , 2020, 181, 1131-1145.e21.	28.9	69
12	A high-coverage Neandertal genome from Chagyrskaya Cave. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15132-15136.	7.1	176
13	Insights into human genetic variation and population history from 929 diverse genomes. <i>Science</i> , 2020, 367, .	12.6	534
14	Arctic-adapted dogs emerged at the Pleistocene-Holocene transition. <i>Science</i> , 2020, 368, 1495-1499.	12.6	60
15	An Ancient Baboon Genome Demonstrates Long-Term Population Continuity in Southern Africa. <i>Genome Biology and Evolution</i> , 2020, 12, 407-412.	2.5	13
16	Genomic Approaches Reveal an Endemic Subpopulation of Gray Wolves in Southern China. <i>IScience</i> , 2019, 20, 110-118.	4.1	6
17	Palaeo-Eskimo genetic ancestry and the peopling of Chukotka and North America. <i>Nature</i> , 2019, 570, 236-240.	27.8	118
18	Revisiting ancient DNA insights into the human history of the Pacific Islands. <i>Archaeology in Oceania</i> , 2019, 54, 53-56.	0.7	3

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19	Global Phylogeographic and Admixture Patterns in Grey Wolves and Genetic Legacy of An Ancient Siberian Lineage. <i>Scientific Reports</i> , 2019, 9, 17328.	3.3	26
20	Northwest passage to Scandinavia. <i>Nature Ecology and Evolution</i> , 2018, 2, 593-594.	7.8	1
21	Population Turnover in Remote Oceania Shortly after Initial Settlement. <i>Current Biology</i> , 2018, 28, 1157-1165.e7.	3.9	91
22	Ancient Genomics of Modern Humans: The First Decade. <i>Annual Review of Genomics and Human Genetics</i> , 2018, 19, 381-404.	6.2	161
23	No evidence for unknown archaic ancestry in South Asia. <i>Nature Genetics</i> , 2018, 50, 632-633.	21.4	7
24	Reconstructing the genetic history of late Neanderthals. <i>Nature</i> , 2018, 555, 652-656.	27.8	197
25	Reconstructing the Deep Population History of Central and South America. <i>Cell</i> , 2018, 175, 1185-1197.e22.	28.9	259
26	Genes reveal traces of common recent demographic history for most of the Uralic-speaking populations. <i>Genome Biology</i> , 2018, 19, 139.	8.8	67
27	Biological Sexing of a 4000-Year-Old Egyptian Mummy Head to Assess the Potential of Nuclear DNA Recovery from the Most Damaged and Limited Forensic Specimens. <i>Genes</i> , 2018, 9, 135.	2.4	39
28	Archaeogenomic evidence reveals prehistoric matrilineal dynasty. <i>Nature Communications</i> , 2017, 8, 14115.	12.8	210
29	Adaptation to infectious disease exposure in indigenous Southern African populations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170226.	2.6	13
30	A high-coverage Neandertal genome from Vindija Cave in Croatia. <i>Science</i> , 2017, 358, 655-658.	12.6	501
31	Reconstructing Prehistoric African Population Structure. <i>Cell</i> , 2017, 171, 59-71.e21.	28.9	308
32	Genetic Ancestry of Rapanui before and after European Contact. <i>Current Biology</i> , 2017, 27, 3209-3215.e6.	3.9	25
33	Mitogenome evolution in the last surviving woolly mammoth population reveals neutral and functional consequences of small population size. <i>Evolution Letters</i> , 2017, 1, 292-303.	3.3	22
34	The genetic history of Ice Age Europe. <i>Nature</i> , 2016, 534, 200-205.	27.8	729
35	Genomic insights into the peopling of the Southwest Pacific. <i>Nature</i> , 2016, 538, 510-513.	27.8	262
36	A genomic view of the peopling of the Americas. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 27-35.	3.3	103

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37	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016, 538, 201-206.	27.8	1,216
38	The origin and evolution of maize in the Southwestern United States. <i>Nature Plants</i> , 2015, 1, 14003.	9.3	138
39	Ancient Wolf Genome Reveals an Early Divergence of Domestic Dog Ancestors and Admixture into High-Latitude Breeds. <i>Current Biology</i> , 2015, 25, 1515-1519.	3.9	270
40	Genetic evidence for two founding populations of the Americas. <i>Nature</i> , 2015, 525, 104-108.	27.8	348
41	An early modern human from Romania with a recent Neanderthal ancestor. <i>Nature</i> , 2015, 524, 216-219.	27.8	633
42	Complete Genomes Reveal Signatures of Demographic and Genetic Declines in the Woolly Mammoth. <i>Current Biology</i> , 2015, 25, 1395-1400.	3.9	263
43	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.	7.1	255
44	Mitochondrial DNA variation in the Viking age population of Norway. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130384.	4.0	25
45	Ancient mitochondrial DNA from the northern fringe of the Neolithic farming expansion in Europe sheds light on the dispersion process. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130373.	4.0	65
46	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014, 506, 225-229.	27.8	500
47	Genomic Diversity and Admixture Differs for Stone-Age Scandinavian Foragers and Farmers. <i>Science</i> , 2014, 344, 747-750.	12.6	315
48	Separating endogenous ancient DNA from modern day contamination in a Siberian Neandertal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2229-2234.	7.1	349
49	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014, 505, 87-91.	27.8	821
50	Investigating Population History Using Temporal Genetic Differentiation. <i>Molecular Biology and Evolution</i> , 2014, 31, 2516-2527.	8.9	50
51	Assessing the Maximum Contribution from Ancient Populations. <i>Molecular Biology and Evolution</i> , 2014, 31, 1248-1260.	8.9	13
52	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014, 345, 1255832.	12.6	264
53	Accurate sex identification of ancient human remains using DNA shotgun sequencing. <i>Journal of Archaeological Science</i> , 2013, 40, 4477-4482.	2.4	337
54	Stronger signal of recent selection for lactase persistence in Maasai than in Europeans. <i>European Journal of Human Genetics</i> , 2013, 21, 550-553.	2.8	34

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55	Genomic Variation in Seven Khoe-San Groups Reveals Adaptation and Complex African History. <i>Science</i> , 2012, 338, 374-379.	12.6	364
56	Origins and Genetic Legacy of Neolithic Farmers and Hunter-Gatherers in Europe. <i>Science</i> , 2012, 336, 466-469.	12.6	507
57	Microsatellite genotyping reveals endâ€Pleistocene decline in mammoth autosomal genetic variation. <i>Molecular Ecology</i> , 2012, 21, 3391-3402.	3.9	36
58	Vanishing native American dog lineages. <i>BMC Evolutionary Biology</i> , 2011, 11, 73.	3.2	31
59	Archaic human ancestry in East Asia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18301-18306.	7.1	135
60	Estimation of Population Divergence Times from Non-Overlapping Genomic Sequences: Examples from Dogs and Wolves. <i>Molecular Biology and Evolution</i> , 2011, 28, 1505-1517.	8.9	61
61	Sequence Polymorphism in Candidate Genes for Differences in Winter Plumage between Scottish and Scandinavian Willow Grouse (<i>Lagopus lagopus</i>). <i>PLoS ONE</i> , 2010, 5, e10334.	2.5	18