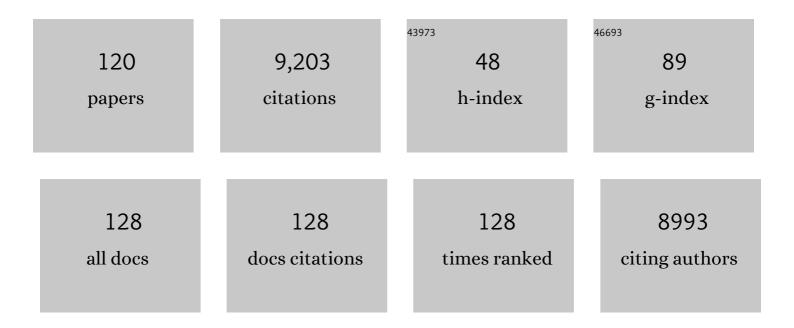
## Anders Götherström

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/625871/publications.pdf Version: 2024-02-01



ANDERS  $C\tilde{\Delta}$  THERSTRATE

#	Article	IF	CITATIONS
1	Molecular analysis of Neanderthal DNA from the northern Caucasus. Nature, 2000, 404, 490-493.	13.7	508
2	Origins and Genetic Legacy of Neolithic Farmers and Hunter-Gatherers in Europe. Science, 2012, 336, 466-469.	6.0	507
3	Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. PLoS Genetics, 2014, 10, e1004254.	1.5	391
4	Accurate sex identification of ancient human remains using DNA shotgun sequencing. Journal of Archaeological Science, 2013, 40, 4477-4482.	1.2	337
5	Genomic Diversity and Admixture Differs for Stone-Age Scandinavian Foragers and Farmers. Science, 2014, 344, 747-750.	6.0	315
6	DNA from Pre-Clovis Human Coprolites in Oregon, North America. Science, 2008, 320, 786-789.	6.0	283
7	Ancient Wolf Genome Reveals an Early Divergence of Domestic Dog Ancestors and Admixture into High-Latitude Breeds. Current Biology, 2015, 25, 1515-1519.	1.8	270
8	The genetic prehistory of the New World Arctic. Science, 2014, 345, 1255832.	6.0	264
9	Complete Genomes Reveal Signatures of Demographic and Genetic Declines in the Woolly Mammoth. Current Biology, 2015, 25, 1395-1400.	1.8	263
10	Ancient genomes link early farmers from Atapuerca in Spain to modern-day Basques. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11917-11922.	3.3	255
11	Whole-Genome Shotgun Sequencing of Mitochondria from Ancient Hair Shafts. Science, 2007, 317, 1927-1930.	6.0	220
12	Ancient DNA Reveals Lack of Continuity between Neolithic Hunter-Gatherers and Contemporary Scandinavians. Current Biology, 2009, 19, 1758-1762.	1.8	217
13	Paleo-Eskimo mtDNA Genome Reveals Matrilineal Discontinuity in Greenland. Science, 2008, 320, 1787-1789.	6.0	184
14	Million-year-old DNA sheds light on the genomic history of mammoths. Nature, 2021, 591, 265-269.	13.7	179
15	Population genomics of Mesolithic Scandinavia: Investigating early postglacial migration routes and high-latitude adaptation. PLoS Biology, 2018, 16, e2003703.	2.6	174
16	The Demographic Development of the First Farmers in Anatolia. Current Biology, 2016, 26, 2659-2666.	1.8	163
17	Origins and genetic legacy of prehistoric dogs. Science, 2020, 370, 557-564.	6.0	152
18	Cattle domestication in the Near East was followed by hybridization with aurochs bulls in Europe. Proceedings of the Royal Society B: Biological Sciences, 2005, 272, 2345-2351.	1.2	151

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19	Intraspecific phylogenetic analysis of Siberian woolly mammoths using complete mitochondrial genomes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8327-8332.	3.3	149
20	Extensive Human DNA Contamination in Extracts from Ancient Dog Bones and Teeth. Molecular Biology and Evolution, 2005, 22, 2040-2047.	3.5	137
21	Ancient DNA reveals lack of postglacial habitat tracking in the arctic fox. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6726-6729.	3.3	137
22	Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny. Nature, 2019, 574, 103-107.	13.7	135
23	Partial genomic survival of cave bears in living brown bears. Nature Ecology and Evolution, 2018, 2, 1563-1570.	3.4	132
24	Molecular phylogeny of the extinct cave lion Panthera leo spelaea. Molecular Phylogenetics and Evolution, 2004, 30, 841-849.	1.2	131
25	Staying out in the cold: glacial refugia and mitochondrial DNA phylogeography in ancient European brown bears. Molecular Ecology, 2007, 16, 5140-5148.	2.0	130
26	More on Contamination: The Use of Asymmetric Molecular Behavior to Identify Authentic Ancient Human DNA. Molecular Biology and Evolution, 2007, 24, 998-1004.	3.5	114
27	Genomic Evidence Establishes Anatolia as the Source of the European Neolithic Gene Pool. Current Biology, 2016, 26, 270-275.	1.8	111
28	Prehistoric contacts over the Straits of Gibraltar indicated by genetic analysis of Iberian Bronze Age cattle. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 8431-8435.	3.3	109
29	The mitochondrial genome sequence of the Tasmanian tiger ( <i>Thylacinus cynocephalus</i> ). Genome Research, 2009, 19, 213-220.	2.4	102
30	Ancient pigs reveal a near-complete genomic turnover following their introduction to Europe. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17231-17238.	3.3	101
31	Four millennia of Iberian biomolecular prehistory illustrate the impact of prehistoric migrations at the far end of Eurasia. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3428-3433.	3.3	96
32	Carnivore conservation in practice: replicated management actions on a large spatial scale. Journal of Applied Ecology, 2013, 50, 59-67.	1.9	93
33	"The wet and the wild followed by the dry and the tame―– or did they occur at the same time? Diet in Mesolithic – Neolithic southern Sweden. Antiquity, 2004, 78, 23-33.	0.5	90
34	Surprising migration and population size dynamics in ancient Iberian brown bears (Ursus arctos). Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 5123-5128.	3.3	86
35	Partial Genetic Turnover in Neandertals: Continuity in the East and Population Replacement in the West. Molecular Biology and Evolution, 2012, 29, 1893-1897.	3.5	82
36	Megalithic tombs in western and northern Neolithic Europe were linked to a kindred society. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 9469-9474.	3.3	81

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37	Identifying species from pieces of faeces. Conservation Genetics, 2004, 5, 109-111.	0.8	78
38	Ancient genomes suggest the eastern Pontic-Caspian steppe as the source of western Iron Age nomads. Science Advances, 2018, 4, eaat4457.	4.7	76
39	Comparing the survival of osteocalcin and mtDNA in archaeological bone from four European sites. Journal of Archaeological Science, 2008, 35, 1756-1764.	1.2	73
40	High frequency of lactose intolerance in a prehistoric hunter-gatherer population in northern Europe. BMC Evolutionary Biology, 2010, 10, 89.	3.2	73
41	A female Viking warrior confirmed by genomics. American Journal of Physical Anthropology, 2017, 164, 853-860.	2.1	69
42	Y-chromosome diversity in Sweden – A long-time perspective. European Journal of Human Genetics, 2006, 14, 963-970.	1.4	65
43	Ancient mitochondrial DNA from the northern fringe of the Neolithic farming expansion in Europe sheds light on the dispersion process. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130373.	1.8	65
44	Genomic Analyses of Pre-European Conquest Human Remains from the Canary Islands Reveal Close Affinity to Modern North Africans. Current Biology, 2017, 27, 3396-3402.e5.	1.8	62
45	Estimation of Population Divergence Times from Non-Overlapping Genomic Sequences: Examples from Dogs and Wolves. Molecular Biology and Evolution, 2011, 28, 1505-1517.	3.5	61
46	Ancient DNA sequences point to a large loss of mitochondrial genetic diversity in the saiga antelope ( <i>Saiga tatarica</i> ) since the Pleistocene. Molecular Ecology, 2010, 19, 4863-4875.	2.0	59
47	Ancient DNA reveals traces of Iberian Neolithic and Bronze Age lineages in modern Iberian horses. Molecular Ecology, 2010, 19, 64-78.	2.0	56
48	Population genomics of grey wolves and wolf-like canids in North America. PLoS Genetics, 2018, 14, e1007745.	1.5	54
49	Genome-Based Sexing Provides Clues about Behavior and Social Structure in the Woolly Mammoth. Current Biology, 2017, 27, 3505-3510.e3.	1.8	53
50	Direct Estimates of Natural Selection in Iberia Indicate Calcium Absorption Was Not the Only Driver of Lactase Persistence in Europe. Molecular Biology and Evolution, 2014, 31, 975-983.	3.5	52
51	Slaves as burial gifts in Viking Age Norway? Evidence from stable isotope and ancient DNA analyses. Journal of Archaeological Science, 2014, 41, 533-540.	1.2	51
52	Is the endangered Fennoscandian arctic fox (Alopex lagopus) population genetically isolated?. Biological Conservation, 2002, 105, 171-178.	1.9	50
53	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. Cell, 2021, 184, 4874-4885.e16.	13.5	49
54	Variable kinship patterns in Neolithic Anatolia revealed by ancient genomes. Current Biology, 2021, 31, 2455-2468.e18.	1.8	47

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55	Population Demography and Genetic Diversity in the Pleistocene Cave Lion. Open Quaternary, 2015, 1, 4.	0.5	44
56	Genomic and Strontium Isotope Variation Reveal Immigration Patterns in a Viking Age Town. Current Biology, 2018, 28, 2730-2738.e10.	1.8	44
57	Pre-extinction Demographic Stability and Genomic Signatures of Adaptation in the Woolly Rhinoceros. Current Biology, 2020, 30, 3871-3879.e7.	1.8	41
58	Fishing for ancient DNA. Forensic Science International: Genetics, 2008, 2, 104-107.	1.6	39
59	The evolutionary and phylogeographic history of woolly mammoths: a comprehensive mitogenomic analysis. Scientific Reports, 2017, 7, 44585.	1.6	39
60	Specialized sledge dogs accompanied Inuit dispersal across the North American Arctic. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191929.	1.2	38
61	The genomic ancestry of the Scandinavian Battle Axe Culture people and their relation to the broader Corded Ware horizon. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191528.	1.2	35
62	A DNA test for sex identification in cattle confirms osteometric results. Journal of Archaeological Science, 2008, 35, 942-946.	1.2	34
63	Response to Comment by Poinar <i>et al</i> . on "DNA from Pre-Clovis Human Coprolites in Oregon, North America― Science, 2009, 325, 148-148.	6.0	34
64	Inbreeding depression in a critically endangered carnivore. Molecular Ecology, 2016, 25, 3309-3318.	2.0	34
65	Molecular and osteometric sexing of cattle metacarpals: a case study from 15th century AD Beja, Portugal. Journal of Archaeological Science, 2012, 39, 1445-1454.	1.2	32
66	Ancient DNA from mastics solidifies connection between material culture and genetics of mesolithic hunter–gatherers in Scandinavia. Communications Biology, 2019, 2, 185.	2.0	32
67	Human population dynamics and <i>Yersinia pestis</i> in ancient northeast Asia. Science Advances, 2021, 7, .	4.7	32
68	Detection of farm fox and hybrid genotypes among wild arctic foxes in Scandinavia. Conservation Genetics, 2006, 6, 885-894.	0.8	31
69	Viking warrior women? Reassessing Birka chamber grave Bj.581. Antiquity, 2019, 93, 181-198.	0.5	31
70	Temporal fluctuations of Y-chromosomal variation in Bos taurus. Biology Letters, 2008, 4, 752-754.	1.0	30
71	50,000 years of genetic uniformity in the critically endangered Iberian lynx. Molecular Ecology, 2011, 20, 3785-3795.	2.0	30
72	Ancient horse genomes reveal the timing and extent of dispersals across the Bering Land Bridge. Molecular Ecology, 2021, 30, 6144-6161.	2.0	30

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73	DNA analysis on fox faeces and competition induced niche shifts. Molecular Ecology, 2004, 13, 2389-2392.	2.0	29
74	Corded Ware cultural complexity uncovered using genomic and isotopic analysis from south-eastern Poland. Scientific Reports, 2020, 10, 6885.	1.6	29
75	Typing single polymorphic nucleotides in mitochondrial DNA as a way to access Middle Pleistocene DNA. Biology Letters, 2006, 2, 601-603.	1.0	28
76	Arctic fox <i>Vulpes lagopus</i> population structure: circumpolar patterns and processes. Oikos, 2011, 120, 873-885.	1.2	28
77	Recovery of DNA from Footprints in the Snow. Canadian Field-Naturalist, 2007, 121, 321.	0.0	26
78	Archaeogenomic analysis of the first steps of Neolithization in Anatolia and the Aegean. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20172064.	1.2	26
79	Mitochondrial DNA variation in the Viking age population of Norway. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130384.	1.8	25
80	Diverse origin of mitochondrial lineages in Iron Age Black Sea Scythians. Scientific Reports, 2017, 7, 43950.	1.6	24
81	Barking up the wrong tree: Modern northern European dogs fail to explain their origin. BMC Evolutionary Biology, 2008, 8, 71.	3.2	22
82	The Neolithic Pitted Ware culture foragers were culturally but not genetically influenced by the Battle Axe culture herders. American Journal of Physical Anthropology, 2020, 172, 638-649.	2.1	20
83	African and Asian leopards are highly differentiated at the genomic level. Current Biology, 2021, 31, 1872-1882.e5.	1.8	20
84	Human inbreeding has decreased in time through the Holocene. Current Biology, 2021, 31, 3925-3934.e8.	1.8	20
85	Modern Siberian dog ancestry was shaped by several thousand years of Eurasian-wide trade and human dispersal. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	19
86	The curious case of the Mesolithic Iberian dogs: An archaeogenetic study. Journal of Archaeological Science, 2019, 105, 116-129.	1.2	18
87	The genetic origin of Huns, Avars, and conquering Hungarians. Current Biology, 2022, 32, 2858-2870.e7.	1.8	18
88	Not just old but old and cold?. Nature, 2001, 410, 772-772.	13.7	17
89	Archaeogenetic analysis of Neolithic sheep from Anatolia suggests a complex demographic history since domestication. Communications Biology, 2021, 4, 1279.	2.0	16
90	Further developments in molecular sex assignment: a blind test of 18th and 19th century human skeletons. Journal of Archaeological Science, 2011, 38, 1326-1330.	1.2	15

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91	Investigating Holocene human population history in North Asia using ancient mitogenomes. Scientific Reports, 2018, 8, 8969.	1.6	15
92	Competitive mapping allows for the identification and exclusion of human DNA contamination in ancient faunal genomic datasets. BMC Genomics, 2020, 21, 844.	1.2	15
93	Integrating multi-taxon palaeogenomes and sedimentary ancient DNA to study past ecosystem dynamics. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20211252.	1.2	14
94	Typing Late Prehistoric Cows and Bulls—Osteology and Genetics of Cattle at the Eketorp Ringfort on the Ā–land Island in Sweden. PLoS ONE, 2011, 6, e20748.	1.1	14
95	Finding the founder of Stockholm – A kinship study based on Y-chromosomal, autosomal and mitochondrial DNA. Annals of Anatomy, 2012, 194, 138-145.	1.0	12
96	Consequences of past climate change and recent human persecution on mitogenomic diversity in the arctic fox. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20190212.	1.8	12
97	Phylogenetic placement and population structure of Indoâ€Pacific bottlenose dolphins ( <i>Tursiops) Tj ETQq1 1 431-448.</i>	1 0.784314 0.9	f rgBT /Overlo 11
98	Mobility patterns in inland southwestern Sweden during the Neolithic and Early Bronze Age. Archaeological and Anthropological Sciences, 2021, 13, 1.	0.7	11
99	Evolution, ecology and conservation—revisiting three decades of Arctic fox population genetic research. Polar Research, 2017, 36, 4.	1.6	10
100	New insights on cultural dualism and population structure in the Middle Neolithic Funnel Beaker culture on the island of Gotland. Journal of Archaeological Science: Reports, 2018, 17, 325-334.	0.2	10
101	A polar bear paleogenome reveals extensive ancient gene flow from polar bears into brown bears. Nature Ecology and Evolution, 2022, 6, 936-944.	3.4	10
102	Medieval remains from Lithuania indicate loss of a mitochondrial haplotype in Bison bonasus. Molecular Ecology, 2006, 15, 3083-3083.	2.0	9
103	Coat colour and sex identification in horses from Iron Age Sweden. Annals of Anatomy, 2012, 194, 82-87.	1.0	8
104	Population-level genotyping of coat colour polymorphism in woolly mammoth (Mammuthus) Tj ETQq0 0 0 rgBT	/Overlock	10 <sub>7</sub> Tf 50 222
105	Neolithic Hedgehogs (Erinaceus europaeus) from the Island of Gotland show early contacts with the Swedish mainland. Journal of Archaeological Science, 2012, 39, 229-233.	1.2	7
106	Ancient microRNA profiles of 14,300-yr-old canid samples confirm taxonomic origin and provide glimpses into tissue-specific gene regulation from the Pleistocene. Rna, 2021, 27, 324-334.	1.6	7
107	Cryptic Contamination and Phylogenetic Nonsense. PLoS ONE, 2008, 3, e2316.	1.1	7
108	Development and Optimization of a Silica Column-Based Extraction Protocol for Ancient DNA. Genes,	1.0	6

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109	Spatial variation in Arctic hare (Lepus arcticus) populations around the Hall Basin. Polar Biology, 2017, 40, 2113-2118.	O.5	5
110	Planned cull endangers Swedish wolf population. Science, 2022, 377, 162-162.	6.0	5
111	The stone cist conundrum: A multidisciplinary approach to investigate Late Neolithic/Early Bronze Age population demography on the island of Gotland. Journal of Archaeological Science: Reports, 2018, 20, 324-337.	0.2	4
112	Maternal genetic origin of the late and final Neolithic human populations from presentâ€day Poland. American Journal of Physical Anthropology, 2021, 176, 223-236.	2.1	3
113	Bioarchaeological evidence of one of the earliest Islamic burials in the Levant. Communications Biology, 2022, 5, .	2.0	3
114	The Jettbole Middle Neolithic Site on the Aland Islands Human Remains, Ancient dna and Pottery. European Journal of Archaeology, 2002, 5, 42-68.	0.3	2
115	A Study on Burrows-Wheeler Aligner's Performance Optimization for Ancient DNA Mapping. Lecture Notes in Networks and Systems, 2022, , 105-114.	0.5	1
116	Elucidating recent history by tracing genetic affinity of three 16th century miners from Sweden. Journal of Archaeological Science: Reports, 2018, 19, 651-657.	0.2	0
117	Related in death? A curious case of a foetus hidden in bishop Peder Winstrup's coffin in Lund, Sweden. Journal of Archaeological Science: Reports, 2021, 37, 102939.	0.2	0
118	Mammuthus sp. (Early and Middle Pleistocene Mammoths). Trends in Genetics, 2021, 37, 682-683.	2.9	0
119	The kÄkÄpÅ•(Strigops habroptilus). Trends in Genetics, 2022, , .	2.9	0
120	A multidisciplinary study of Iberian Chalcolithic dogs. Journal of Archaeological Science: Reports, 2022, 42, 103338.	0.2	0