

# Mattias Jakobsson

## List of Publications by Year in descending order

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Version: 2024-02-01

122  
papers

21,240  
citations

38660

50  
h-index

16127

124  
g-index

140  
all docs

140  
docs citations

140  
times ranked

24583  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenomic Modifications in Modern and Ancient Genomes. <i>Genes</i> , 2022, 13, 178.	1.0	7
2	Episodes of Diversification and Isolation in Island Southeast Asian and Near Oceanian Male Lineages. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9
3	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
4	An empirical evaluation of genotype imputation of ancient DNA. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	18
5	Bioarchaeological evidence of one of the earliest Islamic burials in the Levant. <i>Communications Biology</i> , 2022, 5, .	2.0	3
6	Taste perception and lifestyle: insights from phenotype and genome data among Africans and Asians. <i>European Journal of Human Genetics</i> , 2021, 29, 325-337.	1.4	10
7	The deep population history in Africa. <i>Human Molecular Genetics</i> , 2021, 30, R2-R10.	1.4	15
8	Later Stone Age human hair from Vaalkrans Shelter, Cape Floristic Region of South Africa, reveals genetic affinity to Khoe groups. <i>American Journal of Physical Anthropology</i> , 2021, 174, 701-713.	2.1	3
9	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
10	Estimating divergence times from DNA sequences. <i>Genetics</i> , 2021, 217, .	1.2	14
11	The Genetic Variation of Lactase Persistence Alleles in Sudan and South Sudan. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	4
12	Multiple migrations to the Philippines during the last 50,000 years. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	50
13	Genomic insights into population history and biological adaptation in Oceania. <i>Nature</i> , 2021, 592, 583-589.	13.7	100
14	Human origins in Southern African palaeo-wetlands? Strong claims from weak evidence. <i>Journal of Archaeological Science</i> , 2021, 130, 105374.	1.2	9
15	Variable kinship patterns in Neolithic Anatolia revealed by ancient genomes. <i>Current Biology</i> , 2021, 31, 2455-2468.e18.	1.8	47
16	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
17	Maternal genetic origin of the late and final Neolithic human populations from presentâ€day Poland. <i>American Journal of Physical Anthropology</i> , 2021, 176, 223-236.	2.1	3
18	Philippine Ayta possess the highest level of Denisovan ancestry in the world. <i>Current Biology</i> , 2021, 31, 4219-4230.e10.	1.8	37

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19	Evolution of cytokine production capacity in ancient and modern European populations. <i>ELife</i> , 2021, 10, .	2.8	15
20	Human population dynamics and <i>Yersinia pestis</i> in ancient northeast Asia. <i>Science Advances</i> , 2021, 7, .	4.7	32
21	Comparison of sequencing data processing pipelines and application to underrepresented African human populations. <i>BMC Bioinformatics</i> , 2021, 22, 488.	1.2	5
22	Y-Chromosome Variation in Southern African Khoe-San Populations Based on Whole-Genome Sequences. <i>Genome Biology and Evolution</i> , 2020, 12, 1031-1039.	1.1	6
23	Khoe-San Genomes Reveal Unique Variation and Confirm the Deepest Population Divergence in <i>Homo sapiens</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 2944-2954.	3.5	60
24	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
25	Illuminating Genetic Mysteries of the Dead Sea Scrolls. <i>Cell</i> , 2020, 181, 1218-1231.e27.	13.5	10
26	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
27	Mitochondrial genomes from Bronze Age Poland reveal genetic continuity from the Late Neolithic and additional genetic affinities with the steppe populations. <i>American Journal of Physical Anthropology</i> , 2020, 172, 176-188.	2.1	12
28	Genetic Affinities among Southern Africa Hunter-Gatherers and the Impact of Admixing Farmer and Herder Populations. <i>Molecular Biology and Evolution</i> , 2019, 36, 1849-1861.	3.5	21
29	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
30	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
31	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
32	Megalithic tombs in western and northern Neolithic Europe were linked to a kindred society. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9469-9474.	3.3	81
33	Viking warrior women? Reassessing Birka chamber grave Bj.581. <i>Antiquity</i> , 2019, 93, 181-198.	0.5	31
34	McSwan: A joint site frequency spectrum method to detect and date selective sweeps across multiple population genomes. <i>Molecular Ecology Resources</i> , 2019, 19, 283-295.	2.2	13
35	Tales of Human Migration, Admixture, and Selection in Africa. <i>Annual Review of Genomics and Human Genetics</i> , 2018, 19, 405-428.	2.5	78
36	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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37	New insights on cultural dualism and population structure in the Middle Neolithic Funnel Beaker culture on the island of Gotland. <i>Journal of Archaeological Science: Reports</i> , 2018, 17, 325-334.	0.2	10
38	Ancient human DNA: How sequencing the genome of a boy from Ballito Bay changed human history. <i>South African Journal of Science</i> , 2018, 114, 3.	0.3	5
39	Ancient genomes suggest the eastern Pontic-Caspian steppe as the source of western Iron Age nomads. <i>Science Advances</i> , 2018, 4, eaat4457.	4.7	76
40	Patterns of variation in cis-regulatory regions: examining evidence of purifying selection. <i>BMC Genomics</i> , 2018, 19, 95.	1.2	8
41	The stone cist conundrum: A multidisciplinary approach to investigate Late Neolithic/Early Bronze Age population demography on the island of Gotland. <i>Journal of Archaeological Science: Reports</i> , 2018, 20, 324-337.	0.2	4
42	Mitochondrial genomes reveal an east to west cline of steppe ancestry in Corded Ware populations. <i>Scientific Reports</i> , 2018, 8, 11603.	1.6	30
43	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
44	Estimating genetic kin relationships in prehistoric populations. <i>PLoS ONE</i> , 2018, 13, e0195491.	1.1	187
45	Investigating Holocene human population history in North Asia using ancient mitogenomes. <i>Scientific Reports</i> , 2018, 8, 8969.	1.6	15
46	Population genomics of Mesolithic Scandinavia: Investigating early postglacial migration routes and high-latitude adaptation. <i>PLoS Biology</i> , 2018, 16, e2003703.	2.6	174
47	Tracing the peopling of the world through genomics. <i>Nature</i> , 2017, 541, 302-310.	13.7	562
48	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
49	Adaptation to infectious disease exposure in indigenous Southern African populations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170226.	1.2	13
50	Late Danubian mitochondrial genomes shed light into the Neolithisation of Central Europe in the 5th millennium BC. <i>BMC Evolutionary Biology</i> , 2017, 17, 80.	3.2	13
51	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
52	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
53	A female Viking warrior confirmed by genomics. <i>American Journal of Physical Anthropology</i> , 2017, 164, 853-860.	2.1	69
54	Investigating kinship of Neolithic post-LBK human remains from Krusza Zamkowa, Poland using ancient DNA. <i>Forensic Science International: Genetics</i> , 2017, 26, 30-39.	1.6	26

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55	Northeast African genomic variation shaped by the continuity of indigenous groups and Eurasian migrations. <i>PLoS Genetics</i> , 2017, 13, e1006976.	1.5	45
56	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
57	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
58	The Demographic Development of the First Farmers in Anatolia. <i>Current Biology</i> , 2016, 26, 2659-2666.	1.8	163
59	The disappearing San of southeastern Africa and their genetic affinities. <i>Human Genetics</i> , 2016, 135, 1365-1373.	1.8	22
60	The mitogenome of a 35,000-year-old <i>Homo sapiens</i> from Europe supports a Palaeolithic back-migration to Africa. <i>Scientific Reports</i> , 2016, 6, 25501.	1.6	22
61	Inferring Past Effective Population Size from Distributions of Coalescent Times. <i>Genetics</i> , 2016, 204, 1191-1206.	1.2	28
62	Long-term genetic stability and a high-altitude East Asian origin for the peoples of the high valleys of the Himalayan arc. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7485-7490.	3.3	151
63	Genomic Evidence Establishes Anatolia as the Source of the European Neolithic Gene Pool. <i>Current Biology</i> , 2016, 26, 270-275.	1.8	111
64	The origin and evolution of maize in the Southwestern United States. <i>Nature Plants</i> , 2015, 1, 14003.	4.7	138
65	<sc>Clumpak</sc>: a program for identifying clustering modes and packaging population structure inferences across <i>K</i>. <i>Molecular Ecology Resources</i> , 2015, 15, 1179-1191.	2.2	2,411
66	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	6.0	449
67	Human Adaptation to Arsenic-Rich Environments. <i>Molecular Biology and Evolution</i> , 2015, 32, 1544-1555.	3.5	113
68	HaploPOP: a software that improves population assignment by combining markers into haplotypes. <i>BMC Bioinformatics</i> , 2015, 16, 242.	1.2	8
69	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
70	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.	1.8	65
71	Anthropological Description of Skeletal Material from the Dniester Barrowcemetery Complex, Yampil Region, Vinnitsa Oblast (Ukraine). <i>Baltic-Pontic Studies</i> , 2015, 20, 293-336.	0.0	1
72	Private haplotypes can reveal local adaptation. <i>BMC Genetics</i> , 2014, 15, 61.	2.7	26

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73	Genetic variation reveals large-scale population expansion and migration during the expansion of Bantu-speaking peoples. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20141448.	1.2	92
74	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014, 506, 225-229.	13.7	500
75	Genomic Diversity and Admixture Differs for Stone-Age Scandinavian Foragers and Farmers. <i>Science</i> , 2014, 344, 747-750.	6.0	315
76	Lactase Persistence Alleles Reveal Partial East African Ancestry of Southern African Khoe Pastoralists. <i>Current Biology</i> , 2014, 24, 852-858.	1.8	111
77	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.	3.3	349
78	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014, 505, 87-91.	13.7	821
79	Investigating Population History Using Temporal Genetic Differentiation. <i>Molecular Biology and Evolution</i> , 2014, 31, 2516-2527.	3.5	50
80	Assessing the Maximum Contribution from Ancient Populations. <i>Molecular Biology and Evolution</i> , 2014, 31, 1248-1260.	3.5	13
81	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014, 345, 1255-1262.	6.0	264
82	Accurate sex identification of ancient human remains using DNA shotgun sequencing. <i>Journal of Archaeological Science</i> , 2013, 40, 4477-4482.	1.2	337
83	Inferring population size changes with sequence and SNP data: lessons from human bottlenecks. <i>Heredity</i> , 2013, 110, 409-419.	1.2	84
84	Stronger signal of recent selection for lactase persistence in Maasai than in Europeans. <i>European Journal of Human Genetics</i> , 2013, 21, 550-553.	1.4	34
85	Anisotropic Isolation by Distance: The Main Orientations of Human Genetic Differentiation. <i>Molecular Biology and Evolution</i> , 2013, 30, 513-525.	3.5	35
86	The Relationship Between $F_{ST}$ and the Frequency of the Most Frequent Allele. <i>Genetics</i> , 2013, 193, 515-528.	1.2	212
87	Possible Positive Selection for an Arsenic-Protective Haplotype in Humans. <i>Environmental Health Perspectives</i> , 2013, 121, 53-58.	2.8	44
88	Resequencing Data Provide No Evidence for a Human Bottleneck in Africa during the Penultimate Glacial Period. <i>Molecular Biology and Evolution</i> , 2012, 29, 1851-1860.	3.5	43
89	Combining Markers into Haplotypes Can Improve Population Structure Inference. <i>Genetics</i> , 2012, 190, 159-174.	1.2	42
90	Genetic variation of 15 autosomal STR loci in various populations from southern Africa. <i>Forensic Science International: Genetics</i> , 2012, 6, e20-e21.	1.6	6

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91	Genomic Variation in Seven Khoe-San Groups Reveals Adaptation and Complex African History. <i>Science</i> , 2012, 338, 374-379.	6.0	364
92	Estimating demographic parameters from large-scale population genomic data using Approximate Bayesian Computation. <i>BMC Genetics</i> , 2012, 13, 22.	2.7	40
93	Origins and Genetic Legacy of Neolithic Farmers and Hunter-Gatherers in Europe. <i>Science</i> , 2012, 336, 466-469.	6.0	507
94	Population Genetic Nature of Copy Number Variation. <i>Methods in Molecular Biology</i> , 2012, 838, 209-223.	0.4	21
95	Joint analysis of demography and selection in population genetics: where do we stand and where could we go?. <i>Molecular Ecology</i> , 2012, 21, 28-44.	2.0	138
96	Microsatellite genotyping reveals end-Pleistocene decline in mammoth autosomal genetic variation. <i>Molecular Ecology</i> , 2012, 21, 3391-3402.	2.0	36
97	Genetic variation and population structure of Sudanese populations as indicated by 15 Identifier sequence-tagged repeat (STR) loci. <i>Investigative Genetics</i> , 2011, 2, 12.	3.3	33
98	Haplotype variation and genotype imputation in African populations. <i>Genetic Epidemiology</i> , 2011, 35, 766-780.	0.6	39
99	Deep Divergences of Human Gene Trees and Models of Human Origins. <i>Molecular Biology and Evolution</i> , 2011, 28, 889-898.	3.5	60
100	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.	3.3	135
101	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.	3.5	61
102	High frequency of lactose intolerance in a prehistoric hunter-gatherer population in northern Europe. <i>BMC Evolutionary Biology</i> , 2010, 10, 89.	3.2	73
103	Comparing Spatial Maps of Human Population-Genetic Variation Using Procrustes Analysis. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2010, 9, Article 13.	0.2	103
104	Nonlinear Dynamics of Nonsynonymous (dN) and Synonymous (dS) Substitution Rates Affects Inference of Selection. <i>Genome Biology and Evolution</i> , 2009, 1, 308-319.	1.1	95
105	<i>COMPASS</i> : a program for generating serial samples under an infinite sites model. <i>Bioinformatics</i> , 2009, 25, 2845-2847.	1.8	9
106	Explaining worldwide patterns of human genetic variation using a coalescent-based serial founder model of migration outward from Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16057-16062.	3.3	161
107	Sequence determinants of human microsatellite variability. <i>BMC Genomics</i> , 2009, 10, 612.	1.2	56
108	Haplotypic Background of a Private Allele at High Frequency in the Americas. <i>Molecular Biology and Evolution</i> , 2009, 26, 995-1016.	3.5	74

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109	Genotype, haplotype and copy-number variation in worldwide human populations. <i>Nature</i> , 2008, 451, 998-1003.	13.7	780
110	Using Population Mixtures to Optimize the Utility of Genomic Databases: Linkage Disequilibrium and Association Study Design in India. <i>Annals of Human Genetics</i> , 2008, 72, 535-546.	0.3	31
111	Demographic History of European Populations of <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2008, 4, e1000075.	1.5	182
112	ADZE: a rarefaction approach for counting alleles private to combinations of populations. <i>Bioinformatics</i> , 2008, 24, 2498-2504.	1.8	666
113	The Relationship Between Homozygosity and the Frequency of the Most Frequent Allele. <i>Genetics</i> , 2008, 179, 2027-2036.	1.2	19
114	Genetic Variation and Population Structure in Native Americans. <i>PLoS Genetics</i> , 2007, 3, e185.	1.5	454
115	CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure. <i>Bioinformatics</i> , 2007, 23, 1801-1806.	1.8	5,408
116	The probability distribution under a population divergence model of the number of genetic founding lineages of a population or species. <i>Theoretical Population Biology</i> , 2007, 71, 502-523.	0.5	5
117	The evolutionary history of the common chloroplast genome of <i>Arabidopsis thaliana</i> and <i>A. suecica</i> . <i>Journal of Evolutionary Biology</i> , 2007, 20, 104-121.	0.8	21
118	A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. <i>Nature Genetics</i> , 2006, 38, 1251-1260.	9.4	474
119	Evolution of chloroplast mononucleotide microsatellites in <i>Arabidopsis thaliana</i> . <i>Theoretical and Applied Genetics</i> , 2006, 114, 223-235.	1.8	59
120	A Unique Recent Origin of the Allotetraploid Species <i>Arabidopsis suecica</i> : Evidence from Nuclear DNA Markers. <i>Molecular Biology and Evolution</i> , 2006, 23, 1217-1231.	3.5	119
121	Mode of reproduction in <i>Arabidopsis suecica</i> . <i>Hereditas</i> , 2005, 141, 313-317.	0.5	21
122	The Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2005, 3, e196.	2.6	895