

Mattias Jakobsson

List of Publications by Citations

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128
papers

15,569
citations

45
h-index

124
g-index

140
ext. papers

19,102
ext. citations

9.4
avg, IF

6.83
L-index

#	Paper	IF	Citations
128	CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure. <i>Bioinformatics</i> , 2007 , 23, 1801-6	7.2	4312
127	Clumpak: a program for identifying clustering modes and packaging population structure inferences across K. <i>Molecular Ecology Resources</i> , 2015 , 15, 1179-91	8.4	1526
126	The pattern of polymorphism in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2005 , 3, e196	9.7	764
125	Genotype, haplotype and copy-number variation in worldwide human populations. <i>Nature</i> , 2008 , 451, 998-1003	50.4	662
124	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014 , 505, 87-91	50.4	581
123	ADZE: a rarefaction approach for counting alleles private to combinations of populations. <i>Bioinformatics</i> , 2008 , 24, 2498-504	7.2	505
122	Origins and genetic legacy of Neolithic farmers and hunter-gatherers in Europe. <i>Science</i> , 2012 , 336, 466-9	33.3	410
121	A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. <i>Nature Genetics</i> , 2006 , 38, 1251-60	36.3	406
120	Genetic variation and population structure in native Americans. <i>PLoS Genetics</i> , 2007 , 3, e185	6	392
119	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014 , 506, 225-9	50.4	357
118	Tracing the peopling of the world through genomics. <i>Nature</i> , 2017 , 541, 302-310	50.4	338
117	POPULATION GENETICS. Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015 , 349, aab3884	33.3	317
116	Genomic variation in seven Khoe-San groups reveals adaptation and complex African history. <i>Science</i> , 2012 , 338, 374-9	33.3	286
115	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, 2229-34	11.5	244
114	Genomic diversity and admixture differs for Stone-Age Scandinavian foragers and farmers. <i>Science</i> , 2014 , 344, 747-50	33.3	232
113	Southern African ancient genomes estimate modern human divergence to 350,000 to 260,000 years ago. <i>Science</i> , 2017 , 358, 652-655	33.3	223
112	Accurate sex identification of ancient human remains using DNA shotgun sequencing. <i>Journal of Archaeological Science</i> , 2013 , 40, 4477-4482	2.9	212

111	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014 , 345, 1255832	33.3	204
110	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, 11917-22	11.5	171
109	Demographic history of european populations of Arabidopsis thaliana. <i>PLoS Genetics</i> , 2008 , 4, e10000756		150
108	The relationship between F(ST) and the frequency of the most frequent allele. <i>Genetics</i> , 2013 , 193, 515-28		145
107	Out of Africa: modern human origins special feature: 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, 16057-62	11.5	124
106	Archaic human ancestry in East Asia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 18301-6	11.5	113
105	The Demographic Development of the First Farmers in Anatolia. <i>Current Biology</i> , 2016 , 26, 2659-2666	6.3	112
104	A unique recent origin of the allotetraploid species Arabidopsis suecica: Evidence from nuclear DNA markers. <i>Molecular Biology and Evolution</i> , 2006 , 23, 1217-31	8.3	109
103	Population genomics of Mesolithic Scandinavia: Investigating early postglacial migration routes and high-latitude adaptation. <i>PLoS Biology</i> , 2018 , 16, e2003703	9.7	107
102	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	5.7	100
101	The origin and evolution of maize in the Southwestern United States. <i>Nature Plants</i> , 2015 , 1, 14003	11.5	99
100	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, 7485-90	11.5	97
99	Human adaptation to arsenic-rich environments. <i>Molecular Biology and Evolution</i> , 2015 , 32, 1544-55	8.3	95
98	Genomic Evidence Establishes Anatolia as the Source of the European Neolithic Gene Pool. <i>Current Biology</i> , 2016 , 26, 270-275	6.3	89
97	Estimating genetic kin relationships in prehistoric populations. <i>PLoS ONE</i> , 2018 , 13, e0195491	3.7	89
96	Comparing spatial maps of human population-genetic variation using Procrustes analysis. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2010 , 9, Article 13	1.2	84
95	Lactase persistence alleles reveal partial East African ancestry of southern African Khoe pastoralists. <i>Current Biology</i> , 2014 , 24, 852-8	6.3	83
94	Nonlinear dynamics of nonsynonymous (dN) and synonymous (dS) substitution rates affects inference of selection. <i>Genome Biology and Evolution</i> , 2009 , 1, 308-19	3.9	75

93	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	11.5	69
92	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,	4.4	66
91	High frequency of lactose intolerance in a prehistoric hunter-gatherer population in northern Europe. <i>BMC Evolutionary Biology</i> , 2010 , 10, 89	3	60
90	Inferring population size changes with sequence and SNP data: lessons from human bottlenecks. <i>Heredity</i> , 2013 , 110, 409-19	3.6	56
89	Deep divergences of human gene trees and models of human origins. <i>Molecular Biology and Evolution</i> , 2011 , 28, 889-98	8.3	53
88	Tales of Human Migration, Admixture, and Selection in Africa. <i>Annual Review of Genomics and Human Genetics</i> , 2018 , 19, 405-428	9.7	51
87	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	11.5	51
86	Estimation of population divergence times from non-overlapping genomic sequences: examples from dogs and wolves. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1505-17	8.3	50
85	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	5.8	48
84	Haplotypic background of a private allele at high frequency in the Americas. <i>Molecular Biology and Evolution</i> , 2009 , 26, 995-1016	8.3	48
83	A female Viking warrior confirmed by genomics. <i>American Journal of Physical Anthropology</i> , 2017 , 164, 853-860	2.5	43
82	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	11.5	41
81	Possible positive selection for an arsenic-protective haplotype in humans. <i>Environmental Health Perspectives</i> , 2013 , 121, 53-8	8.4	40
80	Evolution of chloroplast mononucleotide microsatellites in <i>Arabidopsis thaliana</i> . <i>Theoretical and Applied Genetics</i> , 2007 , 114, 223-35	6	37
79	Ancient genomes suggest the eastern Pontic-Caspian steppe as the source of western Iron Age nomads. <i>Science Advances</i> , 2018 , 4, eaat4457	14.3	37
78	Sequence determinants of human microsatellite variability. <i>BMC Genomics</i> , 2009 , 10, 612	4.5	36
77	Investigating population history using temporal genetic differentiation. <i>Molecular Biology and Evolution</i> , 2014 , 31, 2516-27	8.3	34
76	Microsatellite genotyping reveals end-Pleistocene decline in mammoth autosomal genetic variation. <i>Molecular Ecology</i> , 2012 , 21, 3391-402	5.7	34

75	Resequencing data provide no evidence for a human bottleneck in Africa during the penultimate glacial period. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1851-60	8.3	33
74	Genes mirror migrations and cultures in prehistoric Europe-a population genomic perspective. <i>Current Opinion in Genetics and Development</i> , 2016 , 41, 115-123	4.9	33
73	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	6.3	32
72	Northeast African genomic variation shaped by the continuity of indigenous groups and Eurasian migrations. <i>PLoS Genetics</i> , 2017 , 13, e1006976	6	32
71	Estimating demographic parameters from large-scale population genomic data using Approximate Bayesian Computation. <i>BMC Genetics</i> , 2012 , 13, 22	2.6	32
70	Haplotype variation and genotype imputation in African populations. <i>Genetic Epidemiology</i> , 2011 , 35, 766-80	2.6	31
69	Combining markers into haplotypes can improve population structure inference. <i>Genetics</i> , 2012 , 190, 159-74	4	31
68	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	8.3	28
67	Genomic and Strontium Isotope Variation Reveal Immigration Patterns in a Viking Age Town. <i>Current Biology</i> , 2018 , 28, 2730-2738.e10	6.3	27
66	Stronger signal of recent selection for lactase persistence in Maasai than in Europeans. <i>European Journal of Human Genetics</i> , 2013 , 21, 550-3	5.3	27
65	Anisotropic isolation by distance: the main orientations of human genetic differentiation. <i>Molecular Biology and Evolution</i> , 2013 , 30, 513-25	8.3	27
64	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, 535-46	2.2	27
63	Genomic insights into population history and biological adaptation in Oceania. <i>Nature</i> , 2021 , 592, 583-589	9.4	26
62	Viking warrior women? Reassessing Birka chamber grave Bj.581. <i>Antiquity</i> , 2019 , 93, 181-198	1	23
61	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		22
60	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	4.3	21
59	Private haplotypes can reveal local adaptation. <i>BMC Genetics</i> , 2014 , 15, 61	2.6	20
58	Inferring Past Effective Population Size From Distributions of Coalescent Times. <i>Genetics</i> , 2016 , 204, 1191-1206	4	19

57	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, 104-21	2.3	18
56	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,	11.5	18
55	The disappearing San of southeastern Africa and their genetic affinities. <i>Human Genetics</i> , 2016 , 135, 1366-1373	4.3	17
54	Mitochondrial genomes reveal an east to west cline of steppe ancestry in Corded Ware populations. <i>Scientific Reports</i> , 2018 , 8, 11603	4.9	17
53	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	4.4	17
52	Population genetic nature of copy number variation. <i>Methods in Molecular Biology</i> , 2012 , 838, 209-23	1.4	17
51	Mode of reproduction in <i>Arabidopsis suecica</i> . <i>Hereditas</i> , 2004 , 141, 313-7	2.4	17
50	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	4.9	16
49	The relationship between homozygosity and the frequency of the most frequent allele. <i>Genetics</i> , 2008 , 179, 2027-36	4	16
48	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	8.3	15
47	Ancient genomes from southern Africa pushes modern human divergence beyond 260,000 years ago		13
46	Late Danubian mitochondrial genomes shed light into the Neolithisation of Central Europe in the 5 millennium BC. <i>BMC Evolutionary Biology</i> , 2017 , 17, 80	3	12
45	Adaptation to infectious disease exposure in indigenous Southern African populations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017 , 284,	4.4	11
44	Assessing the maximum contribution from ancient populations. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1248-60	8.3	11
43	Philippine Ayta possess the highest level of Denisovan ancestry in the world. <i>Current Biology</i> , 2021 , 31, 4219-4230.e10	6.3	11
42	Human population dynamics and in ancient northeast Asia. <i>Science Advances</i> , 2021 , 7,	14.3	11
41	Investigating Holocene human population history in North Asia using ancient mitogenomes. <i>Scientific Reports</i> , 2018 , 8, 8969	4.9	10
40	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	11.5	10

39	COMPASS: a program for generating serial samples under an infinite sites model. <i>Bioinformatics</i> , 2009 , 25, 2845-7	7.2	9
38	Variable kinship patterns in Neolithic Anatolia revealed by ancient genomes. <i>Current Biology</i> , 2021 , 31, 2455-2468.e18	6.3	9
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	0.7	9
36	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	2.5	8
35	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	2.5	8
34	The deep population history in Africa. <i>Human Molecular Genetics</i> , 2021 , 30, R2-R10	5.6	8
33	Evolution of cytokine production capacity in ancient and modern European populations. <i>ELife</i> , 2021 , 10,	8.9	7
32	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	8.4	6
31	HaploPOP: a software that improves population assignment by combining markers into haplotypes. <i>BMC Bioinformatics</i> , 2015 , 16, 242	3.6	5
30	Illuminating Genetic Mysteries of the Dead Sea Scrolls. <i>Cell</i> , 2020 , 181, 1218-1231.e27	56.2	5
29	Genetic variation of 15 autosomal STR loci in various populations from southern Africa. <i>Forensic Science International: Genetics</i> , 2012 , 6, e20-1	4.3	5
28	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, 502-23	1.2	5
27	Estimating Genetic Kin Relationships in Prehistoric Populations		5
26	Robust Genome-Wide Ancestry Inference for Heterogeneous Datasets and Ancestry Facial Imaging based on the 1000 Genomes Project		5
25	Patterns of variation in cis-regulatory regions: examining evidence of purifying selection. <i>BMC Genomics</i> , 2018 , 19, 95	4.5	5
24	Y-Chromosome Variation in Southern African Khoe-San Populations Based on Whole-Genome Sequences. <i>Genome Biology and Evolution</i> , 2020 , 12, 1031-1039	3.9	4
23	Estimating divergence times from DNA sequences. <i>Genetics</i> , 2021 , 217,	4	4
22	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,	1.3	4

21	Familial migration of the Neolithic contrasts massive male migration during Bronze Age in Europe inferred from ancient X chromosomes		3
20	Mobility patterns in inland southwestern Sweden during the Neolithic and Early Bronze Age. <i>Archaeological and Anthropological Sciences</i> , 2021 , 13, 1	1.8	3
19	Human origins in Southern African palaeo-wetlands? Strong claims from weak evidence. <i>Journal of Archaeological Science</i> , 2021 , 130, 105374	2.9	3
18	Genome of Peñera Muierii skull shows high diversity and low mutational load in pre-glacial Europe. <i>Current Biology</i> , 2021 , 31, 2973-2983.e9	6.3	3
17	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	5.3	3
16	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	0.7	3
15	Ancient DNA of <i>Rickettsia felis</i> and <i>Toxoplasma gondii</i> implicated in the death of a hunter-gatherer boy from South Africa, 2,000 years ago		2
14	Comparison of sequencing data processing pipelines and application to underrepresented African human populations. <i>BMC Bioinformatics</i> , 2021 , 22, 488	3.6	2
13	Genomics of Mesolithic Scandinavia reveal colonization routes and high-latitude adaptation		2
12	Bioarchaeological analysis of one of the earliest Islamic burials in the Levant		2
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	4.9	2
10	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	2.5	2
9	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	3.5	1
8	The genetic variation of lactase persistence alleles in northeast Africa		1
7	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	1
6	The Genetic Variation of Lactase Persistence Alleles in Sudan and South Sudan. <i>Genome Biology and Evolution</i> , 2021 , 13,	3.9	1
5	Episodes of Diversification and Isolation in Island Southeast Asian and Near Oceanian Male Lineages.. <i>Molecular Biology and Evolution</i> , 2022 , 39,	8.3	1
4	An empirical evaluation of genotype imputation of ancient DNA.. <i>G3: Genes, Genomes, Genetics</i> , 2022 ,	3.2	1

- 3 Maternal genetic origin of the late and final Neolithic human populations from present-day Poland. *American Journal of Physical Anthropology*, **2021**, 176, 223-236 2.5 ○
- 2 Multidisciplinary investigation reveals an individual of West African origin buried in a Portuguese Mesolithic shell midden four centuries ago. *Journal of Archaeological Science: Reports*, **2022**, 42, 103370 ^{0.7} ○
- 1 Analysis of Population Structure **2021**, 47-68