

Mattias Jakobsson

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	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
127	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	0.7	0
126	An empirical evaluation of genotype imputation of ancient DNA.. <i>G3: Genes, Genomes, Genetics</i> , 2022 ,	3.2	1
125	Comparison of sequencing data processing pipelines and application to underrepresented African human populations. <i>BMC Bioinformatics</i> , 2021 , 22, 488	3.6	2
124	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
123	Estimating divergence times from DNA sequences. <i>Genetics</i> , 2021 , 217,	4	4
122	The Genetic Variation of Lactase Persistence Alleles in Sudan and South Sudan. <i>Genome Biology and Evolution</i> , 2021 , 13,	3.9	1
121	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
120	Genomic insights into population history and biological adaptation in Oceania. <i>Nature</i> , 2021 , 592, 583-589	30.4	26
119	Human origins in Southern African palaeo-wetlands? Strong claims from weak evidence. <i>Journal of Archaeological Science</i> , 2021 , 130, 105374	2.9	3
118	Variable kinship patterns in Neolithic Anatolia revealed by ancient genomes. <i>Current Biology</i> , 2021 , 31, 2455-2468.e18	6.3	9
117	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
116	Maternal genetic origin of the late and final Neolithic human populations from present-day Poland. <i>American Journal of Physical Anthropology</i> , 2021 , 176, 223-236	2.5	0
115	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
114	The deep population history in Africa. <i>Human Molecular Genetics</i> , 2021 , 30, R2-R10	5.6	8
113	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
112	Philippine Ayta possess the highest level of Denisovan ancestry in the world. <i>Current Biology</i> , 2021 , 31, 4219-4230.e10	6.3	11

111	Evolution of cytokine production capacity in ancient and modern European populations. <i>ELife</i> , 2021 , 10,	8.9	7
110	Analysis of Population Structure 2021 , 47-68		
109	Human population dynamics and in ancient northeast Asia. <i>Science Advances</i> , 2021 , 7,	14.3	11
108	Illuminating Genetic Mysteries of the Dead Sea Scrolls. <i>Cell</i> , 2020 , 181, 1218-1231.e27	56.2	5
107	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
106	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
105	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
104	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
103	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
102	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
101	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
100	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
99	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
98	Viking warrior women? Reassessing Birka chamber grave Bj.581. <i>Antiquity</i> , 2019 , 93, 181-198	1	23
97	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
96	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
95	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
94	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

93	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
92	Estimating genetic kin relationships in prehistoric populations. <i>PLoS ONE</i> , 2018 , 13, e0195491	3.7	89
91	Investigating Holocene human population history in North Asia using ancient mitogenomes. <i>Scientific Reports</i> , 2018 , 8, 8969	4.9	10
90	Population genomics of Mesolithic Scandinavia: Investigating early postglacial migration routes and high-latitude adaptation. <i>PLoS Biology</i> , 2018 , 16, e2003703	9.7	107
89	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
88	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
87	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
86	Patterns of variation in cis-regulatory regions: examining evidence of purifying selection. <i>BMC Genomics</i> , 2018 , 19, 95	4.5	5
85	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
84	Tracing the peopling of the world through genomics. <i>Nature</i> , 2017 , 541, 302-310	50.4	338
83	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
82	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
81	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
80	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
79	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
78	Northeast African genomic variation shaped by the continuity of indigenous groups and Eurasian migrations. <i>PLoS Genetics</i> , 2017 , 13, e1006976	6	32
77	A female Viking warrior confirmed by genomics. <i>American Journal of Physical Anthropology</i> , 2017 , 164, 853-860	2.5	43
76	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

75	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
74	The disappearing San of southeastern Africa and their genetic affinities. <i>Human Genetics</i> , 2016 , 135, 1365-1373	13.7	17
73	The mitogenome of a 35,000-year-old Homo sapiens from Europe supports a Palaeolithic back-migration to Africa. <i>Scientific Reports</i> , 2016 , 6, 25501	4.9	16
72	Inferring Past Effective Population Size from Distributions of Coalescent Times. <i>Genetics</i> , 2016 , 204, 1191-1206	4	19
71	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
70	Genomic Evidence Establishes Anatolia as the Source of the European Neolithic Gene Pool. <i>Current Biology</i> , 2016 , 26, 270-275	6.3	89
69	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
68	The Demographic Development of the First Farmers in Anatolia. <i>Current Biology</i> , 2016 , 26, 2659-2666	6.3	112
67	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
66	POPULATION GENETICS. Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015 , 349, aab3884	33.3	317
65	Human adaptation to arsenic-rich environments. <i>Molecular Biology and Evolution</i> , 2015 , 32, 1544-55	8.3	95
64	HaploPOP: a software that improves population assignment by combining markers into haplotypes. <i>BMC Bioinformatics</i> , 2015 , 16, 242	3.6	5
63	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
62	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
61	The origin and evolution of maize in the Southwestern United States. <i>Nature Plants</i> , 2015 , 1, 14003	11.5	99
60	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
59	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
58	Genomic diversity and admixture differs for Stone-Age Scandinavian foragers and farmers. <i>Science</i> , 2014 , 344, 747-50	33.3	232

57	Lactase persistence alleles reveal partial East African ancestry of southern African Khoe pastoralists. <i>Current Biology</i> , 2014 , 24, 852-8	6.3	83
56	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
55	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014 , 505, 87-91	50.4	581
54	Investigating population history using temporal genetic differentiation. <i>Molecular Biology and Evolution</i> , 2014 , 31, 2516-27	8.3	34
53	Assessing the maximum contribution from ancient populations. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1248-60	8.3	11
52	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014 , 345, 1255832	33.3	204
51	Private haplotypes can reveal local adaptation. <i>BMC Genetics</i> , 2014 , 15, 61	2.6	20
50	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
49	Accurate sex identification of ancient human remains using DNA shotgun sequencing. <i>Journal of Archaeological Science</i> , 2013 , 40, 4477-4482	2.9	212
48	Inferring population size changes with sequence and SNP data: lessons from human bottlenecks. <i>Heredity</i> , 2013 , 110, 409-19	3.6	56
47	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
46	Anisotropic isolation by distance: the main orientations of human genetic differentiation. <i>Molecular Biology and Evolution</i> , 2013 , 30, 513-25	8.3	27
45	The relationship between F_{ST} and the frequency of the most frequent allele. <i>Genetics</i> , 2013 , 193, 515-28	28	145
44	Possible positive selection for an arsenic-protective haplotype in humans. <i>Environmental Health Perspectives</i> , 2013 , 121, 53-8	8.4	40
43	Microsatellite genotyping reveals end-Pleistocene decline in mammoth autosomal genetic variation. <i>Molecular Ecology</i> , 2012 , 21, 3391-402	5.7	34
42	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
41	Genomic variation in seven Khoe-San groups reveals adaptation and complex African history. <i>Science</i> , 2012 , 338, 374-9	33.3	286
40	Estimating demographic parameters from large-scale population genomic data using Approximate Bayesian Computation. <i>BMC Genetics</i> , 2012 , 13, 22	2.6	32

39	Origins and genetic legacy of Neolithic farmers and hunter-gatherers in Europe. <i>Science</i> , 2012 , 336, 466-93,3	410
38	Population genetic nature of copy number variation. <i>Methods in Molecular Biology</i> , 2012 , 838, 209-23	1.4 17
37	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
36	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
35	Combining markers into haplotypes can improve population structure inference. <i>Genetics</i> , 2012 , 190, 159-74	4 31
34	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
33	Haplotype variation and genotype imputation in African populations. <i>Genetic Epidemiology</i> , 2011 , 35, 766-80	2.6 31
32	Deep divergences of human gene trees and models of human origins. <i>Molecular Biology and Evolution</i> , 2011 , 28, 889-98	8.3 53
31	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
30	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
29	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
28	High frequency of lactose intolerance in a prehistoric hunter-gatherer population in northern Europe. <i>BMC Evolutionary Biology</i> , 2010 , 10, 89	3 60
27	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
26	COMPASS: a program for generating serial samples under an infinite sites model. <i>Bioinformatics</i> , 2009 , 25, 2845-7	7.2 9
25	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
24	Sequence determinants of human microsatellite variability. <i>BMC Genomics</i> , 2009 , 10, 612	4.5 36
23	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
22	Genotype, haplotype and copy-number variation in worldwide human populations. <i>Nature</i> , 2008 , 451, 998-1003	50.4 662

21	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
20	Demographic history of european populations of Arabidopsis thaliana. <i>PLoS Genetics</i> , 2008 , 4, e10000756		150
19	ADZE: a rarefaction approach for counting alleles private to combinations of populations. <i>Bioinformatics</i> , 2008 , 24, 2498-504	7.2	505
18	The relationship between homozygosity and the frequency of the most frequent allele. <i>Genetics</i> , 2008 , 179, 2027-36	4	16
17	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
16	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
15	The evolutionary history of the common chloroplast genome of Arabidopsis thaliana and A. suecica. <i>Journal of Evolutionary Biology</i> , 2007 , 20, 104-21	2.3	18
14	Evolution of chloroplast mononucleotide microsatellites in Arabidopsis thaliana. <i>Theoretical and Applied Genetics</i> , 2007 , 114, 223-35	6	37
13	Genetic variation and population structure in native Americans. <i>PLoS Genetics</i> , 2007 , 3, e185	6	392
12	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
11	A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. <i>Nature Genetics</i> , 2006 , 38, 1251-60	36.3	406
10	The pattern of polymorphism in Arabidopsis thaliana. <i>PLoS Biology</i> , 2005 , 3, e196	9.7	764
9	Mode of reproduction in Arabidopsis suecica. <i>Hereditas</i> , 2004 , 141, 313-7	2.4	17
8	Ancient DNA of Rickettsia felis and Toxoplasma gondii implicated in the death of a hunter-gatherer boy from South Africa, 2,000 years ago		2
7	Familial migration of the Neolithic contrasts massive male migration during Bronze Age in Europe inferred from ancient X chromosomes		3
6	Estimating Genetic Kin Relationships in Prehistoric Populations		5
5	Ancient genomes from southern Africa pushes modern human divergence beyond 260,000 years ago		13
4	Genomics of Mesolithic Scandinavia reveal colonization routes and high-latitude adaptation		2

3	The genetic variation of lactase persistence alleles in northeast Africa	1
2	Bioarchaeological analysis of one of the earliest Islamic burials in the Levant	2
1	Robust Genome-Wide Ancestry Inference for Heterogeneous Datasets and Ancestry Facial Imaging based on the 1000 Genomes Project	5