Mattias Jakobsson

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1360719/publications.pdf

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	CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure. Bioinformatics, 2007, 23, 1801-1806.	1.8	5,408
2	<scp>Clumpak</scp>: a program for identifying clustering modes and packaging population structure inferences across <i>K</i>. Molecular Ecology Resources, 2015, 15, 1179-1191.	2.2	2,411
3	The Pattern of Polymorphism in Arabidopsis thaliana. PLoS Biology, 2005, 3, e196.	2.6	895
4	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. Nature, 2014, 505, 87-91.	13.7	821
5	Genotype, haplotype and copy-number variation in worldwide human populations. Nature, 2008, 451, 998-1003.	13.7	780
6	ADZE: a rarefaction approach for counting alleles private to combinations of populations. Bioinformatics, 2008, 24, 2498-2504.	1.8	666
7	Tracing the peopling of the world through genomics. Nature, 2017, 541, 302-310.	13.7	562
8	Origins and Genetic Legacy of Neolithic Farmers and Hunter-Gatherers in Europe. Science, 2012, 336, 466-469.	6.0	507
9	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. Nature, 2014, 506, 225-229.	13.7	500
10	A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. Nature Genetics, 2006, 38, 1251-1260.	9.4	474
11	Genetic Variation and Population Structure in Native Americans. PLoS Genetics, 2007, 3, e185.	1.5	454
12	Genomic evidence for the Pleistocene and recent population history of Native Americans. Science, 2015, 349, aab3884.	6.0	449
13	Genomic Variation in Seven Khoe-San Groups Reveals Adaptation and Complex African History. Science, 2012, 338, 374-379.	6.0	364
14	Southern African ancient genomes estimate modern human divergence to 350,000 to 260,000 years ago. Science, 2017, 358, 652-655.	6.0	351
15	Separating endogenous ancient DNA from modern day contamination in a Siberian Neandertal. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2229-2234.	3.3	349
16	Accurate sex identification of ancient human remains using DNA shotgun sequencing. Journal of Archaeological Science, 2013, 40, 4477-4482.	1.2	337
17	Genomic Diversity and Admixture Differs for Stone-Age Scandinavian Foragers and Farmers. Science, 2014, 344, 747-750.	6.0	315
18	The genetic prehistory of the New World Arctic. Science, 2014, 345, 1255832.	6.0	264

#	ARTICLE	IF	CITATIONS
19	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
20	The Relationship Between <i>F</i>ST and the Frequency of the Most Frequent Allele. Genetics, 2013, 193, 515-528.	1.2	212
21	Estimating genetic kin relationships in prehistoric populations. PLoS ONE, 2018, 13, e0195491.	1.1	187
22	Demographic History of European Populations of Arabidopsis thaliana. PLoS Genetics, 2008, 4, e1000075.	1.5	182
23	Population genomics of Mesolithic Scandinavia: Investigating early postglacial migration routes and high-latitude adaptation. PLoS Biology, 2018, 16, e2003703.	2.6	174
24	The Demographic Development of the First Farmers in Anatolia. Current Biology, 2016, 26, 2659-2666.	1.8	163
25	Explaining worldwide patterns of human genetic variation using a coalescent-based serial founder model of migration outward from Africa. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16057-16062.	3.3	161
26	Long-term genetic stability and a high-altitude East Asian origin for the peoples of the high valleys of the Himalayan arc. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7485-7490.	3.3	151
27	Joint analysis of demography and selection in population genetics: where do we stand and where could we go?. Molecular Ecology, 2012, 21, 28-44.	2.0	138
28	The origin and evolution of maize in the Southwestern United States. Nature Plants, 2015, 1, 14003.	4.7	138
29	Archaic human ancestry in East Asia. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18301-18306.	3.3	135
30	A Unique Recent Origin of the Allotetraploid Species Arabidopsis suecica: Evidence from Nuclear DNA Markers. Molecular Biology and Evolution, 2006, 23, 1217-1231.	3.5	119
31	Human Adaptation to Arsenic-Rich Environments. Molecular Biology and Evolution, 2015, 32, 1544-1555.	3.5	113
32	Lactase Persistence Alleles Reveal Partial East African Ancestry of Southern African Khoe Pastoralists. Current Biology, 2014, 24, 852-858.	1.8	111
33	Genomic Evidence Establishes Anatolia as the Source of the European Neolithic Gene Pool. Current Biology, 2016, 26, 270-275.	1.8	111
34	Comparing Spatial Maps of Human Population-Genetic Variation Using Procrustes Analysis. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article 13.	0.2	103
35	Genomic insights into population history and biological adaptation in Oceania. Nature, 2021, 592, 583-589.	13.7	100
36	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

#	ARTICLE	IF	CITATIONS
37	Nonlinear Dynamics of Nonsynonymous (dN) and Synonymous (dS) Substitution Rates Affects Inference of Selection. Genome Biology and Evolution, 2009, 1, 308-319.	1.1	95
38	Ancient X chromosomes reveal contrasting sex bias in Neolithic and Bronze Age Eurasian migrations. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2657-2662.	3.3	94
39	Genetic variation reveals large-scale population expansion and migration during the expansion of Bantu-speaking peoples. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20141448.	1.2	92
40	Inferring population size changes with sequence and SNP data: lessons from human bottlenecks. Heredity, 2013, 110, 409-419.	1.2	84
41	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
42	Tales of Human Migration, Admixture, and Selection in Africa. Annual Review of Genomics and Human Genetics, 2018, 19, 405-428.	2.5	78
43	Ancient genomes suggest the eastern Pontic-Caspian steppe as the source of western Iron Age nomads. Science Advances, 2018, 4, eaat4457.	4.7	76
44	Haplotypic Background of a Private Allele at High Frequency in the Americas. Molecular Biology and Evolution, 2009, 26, 995-1016.	3.5	74
45	High frequency of lactose intolerance in a prehistoric hunter-gatherer population in northern Europe. BMC Evolutionary Biology, 2010, 10, 89.	3.2	73
46	A female Viking warrior confirmed by genomics. American Journal of Physical Anthropology, 2017, 164, 853-860.	2.1	69
47	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
48	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
49	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
50	Deep Divergences of Human Gene Trees and Models of Human Origins. Molecular Biology and Evolution, 2011, 28, 889-898.	3.5	60
51	Khoe-San Genomes Reveal Unique Variation and Confirm the Deepest Population Divergence in Homo sapiens. Molecular Biology and Evolution, 2020, 37, 2944-2954.	3.5	60
52	Evolution of chloroplast mononucleotide microsatellites in Arabidopsis thaliana. Theoretical and Applied Genetics, 2006, 114, 223-235.	1.8	59
53	Sequence determinants of human microsatellite variability. BMC Genomics, 2009, 10, 612.	1.2	56
54	Investigating Population History Using Temporal Genetic Differentiation. Molecular Biology and Evolution, 2014, 31, 2516-2527.	3.5	50

#	ARTICLE	IF	CITATIONS
55	Multiple migrations to the Philippines during the last 50,000 years. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	50
56	Variable kinship patterns in Neolithic Anatolia revealed by ancient genomes. Current Biology, 2021, 31, 2455-2468.e18.	1.8	47
57	Northeast African genomic variation shaped by the continuity of indigenous groups and Eurasian migrations. PLoS Genetics, 2017, 13, e1006976.	1.5	45
58	Possible Positive Selection for an Arsenic-Protective Haplotype in Humans. Environmental Health Perspectives, 2013, 121, 53-58.	2.8	44
59	Genomic and Strontium Isotope Variation Reveal Immigration Patterns in a Viking Age Town. Current Biology, 2018, 28, 2730-2738.e10.	1.8	44
60	Resequencing Data Provide No Evidence for a Human Bottleneck in Africa during the Penultimate Glacial Period. Molecular Biology and Evolution, 2012, 29, 1851-1860.	3.5	43
61	Combining Markers into Haplotypes Can Improve Population Structure Inference. Genetics, 2012, 190, 159-174.	1.2	42
62	Estimating demographic parameters from large-scale population genomic data using Approximate Bayesian Computation. BMC Genetics, 2012, 13, 22.	2.7	40
63	Genes mirror migrations and cultures in prehistoric Europe â€" a population genomic perspective. Current Opinion in Genetics and Development, 2016, 41, 115-123.	1.5	40
64	Haplotype variation and genotype imputation in African populations. Genetic Epidemiology, 2011, 35, 766-780.	0.6	39
65	Philippine Ayta possess the highest level of Denisovan ancestry in the world. Current Biology, 2021, 31, 4219-4230.e10.	1.8	37
66	Microsatellite genotyping reveals endâ€Pleistocene decline in mammoth autosomal genetic variation. Molecular Ecology, 2012, 21, 3391-3402.	2.0	36
67	Anisotropic Isolation by Distance: The Main Orientations of Human Genetic Differentiation. Molecular Biology and Evolution, 2013, 30, 513-525.	3.5	35
68	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
69	Stronger signal of recent selection for lactase persistence in Maasai than in Europeans. European Journal of Human Genetics, 2013, 21, 550-553.	1.4	34
70	Genetic variation and population structure of Sudanese populations as indicated by 15 Identifiler sequence-tagged repeat (STR) loci. Investigative Genetics, 2011, 2, 12.	3.3	33
71	Human population dynamics and <i>Yersinia pestis</i> in ancient northeast Asia. Science Advances, 2021, 7, .	4.7	32
72	Using Population Mixtures to Optimize the Utility of Genomic Databases: Linkage Disequilibrium and Association Study Design in India. Annals of Human Genetics, 2008, 72, 535-546.	0.3	31

#	Article	IF	Citations
73	Viking warrior women? Reassessing Birka chamber grave Bj.581. Antiquity, 2019, 93, 181-198.	0.5	31
74	Mitochondrial genomes reveal an east to west cline of steppe ancestry in Corded Ware populations. Scientific Reports, 2018, 8, 11603.	1.6	30
75	Inferring Past Effective Population Size from Distributions of Coalescent Times. Genetics, 2016, 204, 1191-1206.	1.2	28
76	Private haplotypes can reveal local adaptation. BMC Genetics, 2014, 15, 61.	2.7	26
77	Investigating kinship of Neolithic post-LBK human remains from Krusza Zamkowa, Poland using ancient DNA. Forensic Science International: Genetics, 2017, 26, 30-39.	1.6	26
78	The disappearing San of southeastern Africa and their genetic affinities. Human Genetics, 2016, 135, 1365-1373.	1.8	22
79	The mitogenome of a 35,000-year-old Homo sapiens from Europe supports a Palaeolithic back-migration to Africa. Scientific Reports, 2016, 6, 25501.	1.6	22
80	Mode of reproduction in Arabidopsis suecica. Hereditas, 2005, 141, 313-317.	0.5	21
81	The evolutionary history of the common chloroplast genome of Arabidopsis thaliana and A. suecica. Journal of Evolutionary Biology, 2007, 20, 104-121.	0.8	21
82	Population Genetic Nature of Copy Number Variation. Methods in Molecular Biology, 2012, 838, 209-223.	0.4	21
83	Genetic Affinities among Southern Africa Hunter-Gatherers and the Impact of Admixing Farmer and Herder Populations. Molecular Biology and Evolution, 2019, 36, 1849-1861.	3.5	21
84	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
85	The Relationship Between Homozygosity and the Frequency of the Most Frequent Allele. Genetics, 2008, 179, 2027-2036.	1.2	19
86	Genome of PeÅŸtera Muierii skull shows high diversity and low mutational load in pre-glacial Europe. Current Biology, 2021, 31, 2973-2983.e9.	1.8	18
87	An empirical evaluation of genotype imputation of ancient DNA. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	18
88	Investigating Holocene human population history in North Asia using ancient mitogenomes. Scientific Reports, 2018, 8, 8969.	1.6	15
89	The deep population history in Africa. Human Molecular Genetics, 2021, 30, R2-R10.	1.4	15
90	Evolution of cytokine production capacity in ancient and modern European populations. ELife, 2021, 10, .	2.8	15

#	ARTICLE	IF	CITATIONS
91	Estimating divergence times from DNA sequences. Genetics, 2021, 217, .	1.2	14
92	Assessing the Maximum Contribution from Ancient Populations. Molecular Biology and Evolution, 2014, 31, 1248-1260.	3.5	13
93	Adaptation to infectious disease exposure in indigenous Southern African populations. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170226.	1.2	13
94	Late Danubian mitochondrial genomes shed light into the Neolithisation of Central Europe in the 5th millennium BC. BMC Evolutionary Biology, 2017, 17, 80.	3.2	13
95	McSwan: A joint site frequency spectrum method to detect and date selective sweeps across multiple population genomes. Molecular Ecology Resources, 2019, 19, 283-295.	2.2	13
96	Mitochondrial genomes from Bronze Age Poland reveal genetic continuity from the Late Neolithic and additional genetic affinities with the steppe populations. American Journal of Physical Anthropology, 2020, 172, 176-188.	2.1	12
97	Mobility patterns in inland southwestern Sweden during the Neolithic and Early Bronze Age. Archaeological and Anthropological Sciences, 2021, 13, 1.	0.7	11
98	Reply to Lazaridis and Reich: Robust model-based inference of male-biased admixture during Bronze Age migration from the Pontic-Caspian Steppe. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3875-E3877.	3.3	11
99	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
100	Illuminating Genetic Mysteries of the Dead Sea Scrolls. Cell, 2020, 181, 1218-1231.e27.	13.5	10
101	Taste perception and lifestyle: insights from phenotype and genome data among Africans and Asians. European Journal of Human Genetics, 2021, 29, 325-337.	1.4	10
102	<i>COMPASS</i>: a program for generating serial samples under an infinite sites model. Bioinformatics, 2009, 25, 2845-2847.	1.8	9
103	Human origins in Southern African palaeo-wetlands? Strong claims from weak evidence. Journal of Archaeological Science, 2021, 130, 105374.	1.2	9
104	Episodes of Diversification and Isolation in Island Southeast Asian and Near Oceanian Male Lineages. Molecular Biology and Evolution, 2022, 39, .	3.5	9
105	HaploPOP: a software that improves population assignment by combining markers into haplotypes. BMC Bioinformatics, 2015, 16, 242.	1.2	8
106	Patterns of variation in cis-regulatory regions: examining evidence of purifying selection. BMC Genomics, 2018, 19, 95.	1.2	8
107	Robust genome-wide ancestry inference for heterogeneous datasets: illustrated using the 1,000 genome project with 3D facial images. Scientific Reports, 2020, 10, 11850.	1.6	7
108	Epigenomic Modifications in Modern and Ancient Genomes. Genes, 2022, 13, 178.	1.0	7

#	Article	IF	Citations
109	Genetic variation of 15 autosomal STR loci in various populations from southern Africa. Forensic Science International: Genetics, 2012, 6, e20-e21.	1.6	6
110	Y-Chromosome Variation in Southern African Khoe-San Populations Based on Whole-Genome Sequences. Genome Biology and Evolution, 2020, 12, 1031-1039.	1.1	6
111	The probability distribution under a population divergence model of the number of genetic founding lineages of a population or species. Theoretical Population Biology, 2007, 71, 502-523.	0.5	5
112	Ancient human DNA: How sequencing the genome of a boy from Ballito Bay changed human history. South African Journal of Science, 2018, 114, 3.	0.3	5
113	Comparison of sequencing data processing pipelines and application to underrepresented African human populations. BMC Bioinformatics, 2021, 22, 488.	1.2	5
114	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
115	Copy number determination of the gene for the human pancreatic polypeptide receptor NPY4R using read depth analysis and droplet digital PCR. BMC Biotechnology, 2019, 19, 31.	1.7	4
116	Genetic data and radiocarbon dating question Plovers Lake as a Middle Stone Age hominin-bearing site. Journal of Human Evolution, 2019, 131, 203-209.	1.3	4
117	The Genetic Variation of Lactase Persistence Alleles in Sudan and South Sudan. Genome Biology and Evolution, 2021, 13, .	1.1	4
118	Later Stone Age human hair from Vaalkrans Shelter, Cape Floristic Region of South Africa, reveals genetic affinity to Khoe groups. American Journal of Physical Anthropology, 2021, 174, 701-713.	2.1	3
119	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
120	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.	0.2	3
121	Bioarchaeological evidence of one of the earliest Islamic burials in the Levant. Communications Biology, 2022, 5, .	2.0	3
122	Anthropological Description of Skeletal Material from the Dniester Barrowcemetery Complex, Yampil Region, Vinnitsa Oblast (Ukraine). Baltic-Pontic Studies, 2015, 20, 293-336.	0.0	1