

Wolfgang Haak

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115
papers

10,301
citations

47
h-index

101
g-index

124
ext. papers

13,272
ext. citations

16.6
avg, IF

5.21
L-index

#	Paper	IF	Citations
115	Massive migration from the steppe was a source for Indo-European languages in Europe. <i>Nature</i> , 2015 , 522, 207-11	50.4	968
114	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014 , 513, 409-13	50.4	812
113	Genome-wide patterns of selection in 230 ancient Eurasians. <i>Nature</i> , 2015 , 528, 499-503	50.4	774
112	The genetic history of Ice Age Europe. <i>Nature</i> , 2016 , 534, 200-5	50.4	473
111	Ancient DNA from the first European farmers in 7500-year-old Neolithic sites. <i>Science</i> , 2005 , 310, 1016-8	33.3	376
110	Sequencing ancient calcified dental plaque shows changes in oral microbiota with dietary shifts of the Neolithic and Industrial revolutions. <i>Nature Genetics</i> , 2013 , 45, 450-5, 455e1	36.3	366
109	Genetic discontinuity between local hunter-gatherers and central Europe's first farmers. <i>Science</i> , 2009 , 326, 137-40	33.3	356
108	Absence of the lactase-persistence-associated allele in early Neolithic Europeans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 3736-41	11.5	307
107	The Beaker phenomenon and the genomic transformation of northwest Europe. <i>Nature</i> , 2018 , 555, 190-106	50.4	293
106	The genomic history of southeastern Europe. <i>Nature</i> , 2018 , 555, 197-203	50.4	287
105	Ancient DNA from European early neolithic farmers reveals their near eastern affinities. <i>PLoS Biology</i> , 2010 , 8, e1000536	9.7	286
104	Neanderthal behaviour, diet, and disease inferred from ancient DNA in dental calculus. <i>Nature</i> , 2017 , 544, 357-361	50.4	263
103	Ancient DNA reveals key stages in the formation of central European mitochondrial genetic diversity. <i>Science</i> , 2013 , 342, 257-61	33.3	237
102	Ancient mitochondrial DNA provides high-resolution time scale of the peopling of the Americas. <i>Science Advances</i> , 2016 , 2, e1501385	14.3	211
101	Pleistocene Mitochondrial Genomes Suggest a Single Major Dispersal of Non-Africans and a Late Glacial Population Turnover in Europe. <i>Current Biology</i> , 2016 , 26, 827-33	6.3	208
100	Ancient DNA, Strontium isotopes, and osteological analyses shed light on social and kinship organization of the Later Stone Age. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 18226-31	11.5	207
99	Parallel palaeogenomic transects reveal complex genetic history of early European farmers. <i>Nature</i> , 2017 , 551, 368-372	50.4	194

98	The genomic history of the Iberian Peninsula over the past 8000 years. <i>Science</i> , 2019 , 363, 1230-1234	33.3	186
97	Reconstructing the Deep Population History of Central and South America. <i>Cell</i> , 2018 , 175, 1185-1197.e23	26.2	143
96	Neolithic mitochondrial haplogroup H genomes and the genetic origins of Europeans. <i>Nature Communications</i> , 2013 , 4, 1764	17.4	141
95	Aboriginal mitogenomes reveal 50,000 years of regionalism in Australia. <i>Nature</i> , 2017 , 544, 180-184	50.4	122
94	Survival and recovery of DNA from ancient teeth and bones. <i>Journal of Archaeological Science</i> , 2011 , 38, 956-964	2.9	114
93	Parallel evolution of genes and languages in the Caucasus region. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2905-20	8.3	107
92	Iron Age and Anglo-Saxon genomes from East England reveal British migration history. <i>Nature Communications</i> , 2016 , 7, 10408	17.4	100
91	Tracing the genetic origin of Europe's first farmers reveals insights into their social organization. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015 , 282,	4.4	97
90	Kinship-based social inequality in Bronze Age Europe. <i>Science</i> , 2019 , 366, 731-734	33.3	97
89	The genetic prehistory of the Baltic Sea region. <i>Nature Communications</i> , 2018 , 9, 442	17.4	96
88	Ancient Egyptian mummy genomes suggest an increase of Sub-Saharan African ancestry in post-Roman periods. <i>Nature Communications</i> , 2017 , 8, 15694	17.4	91
87	From the field to the laboratory: Controlling DNA contamination in human ancient DNA research in the high-throughput sequencing era. <i>Science and Technology of Archaeological Research</i> , 2017 , 3, 1-14	1.2	83
86	Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations. <i>Science</i> , 2018 , 360, 548-552	33.3	83
85	The Stone Age Plague and Its Persistence in Eurasia. <i>Current Biology</i> , 2017 , 27, 3683-3691.e8	6.3	81
84	Geographic population structure analysis of worldwide human populations infers their biogeographical origins. <i>Nature Communications</i> , 2014 , 5, 3513	17.4	78
83	DNA capture and next-generation sequencing can recover whole mitochondrial genomes from highly degraded samples for human identification. <i>Investigative Genetics</i> , 2013 , 4, 26		78
82	A mitochondrial revelation of early human migrations to the Tibetan Plateau before and after the last glacial maximum. <i>American Journal of Physical Anthropology</i> , 2010 , 143, 555-69	2.5	77
81	The genetic history of admixture across inner Eurasia. <i>Nature Ecology and Evolution</i> , 2019 , 3, 966-976	12.3	69

80	Ancient DNA reveals prehistoric gene-flow from siberia in the complex human population history of North East Europe. <i>PLoS Genetics</i> , 2013 , 9, e1003296	6	66
79	Early cave art and ancient DNA record the origin of European bison. <i>Nature Communications</i> , 2016 , 7, 13158	17.4	63
78	Human paleogenetics of Europe--the known knowns and the known unknowns. <i>Journal of Human Evolution</i> , 2015 , 79, 73-92	3.1	62
77	An updated tree of Y-chromosome Haplogroup O and revised phylogenetic positions of mutations P164 and PK4. <i>European Journal of Human Genetics</i> , 2011 , 19, 1013-5	5.3	62
76	Genetic Heritage of the Balto-Slavic Speaking Populations: A Synthesis of Autosomal, Mitochondrial and Y-Chromosomal Data. <i>PLoS ONE</i> , 2015 , 10, e0135820	3.7	58
75	Human migration through bottlenecks from Southeast Asia into East Asia during Last Glacial Maximum revealed by Y chromosomes. <i>PLoS ONE</i> , 2011 , 6, e24282	3.7	58
74	Ancient human genome-wide data from a 3000-year interval in the Caucasus corresponds with eco-geographic regions. <i>Nature Communications</i> , 2019 , 10, 590	17.4	55
73	Uniparental markers in Italy reveal a sex-biased genetic structure and different historical strata. <i>PLoS ONE</i> , 2013 , 8, e65441	3.7	54
72	Climate change underlies global demographic, genetic, and cultural transitions in pre-Columbian southern Peru. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 9443-8	11.5	53
71	Survival of Late Pleistocene Hunter-Gatherer Ancestry in the Iberian Peninsula. <i>Current Biology</i> , 2019 , 29, 1169-1177.e7	6.3	48
70	A Dynamic 6,000-Year Genetic History of Eurasia's Eastern Steppe. <i>Cell</i> , 2020 , 183, 890-904.e29	56.2	48
69	The Basque paradigm: genetic evidence of a maternal continuity in the Franco-Cantabrian region since pre-Neolithic times. <i>American Journal of Human Genetics</i> , 2012 , 90, 486-93	11	47
68	Y-chromosome analysis reveals genetic divergence and new founding native lineages in Athapaskan- and Eskimoan-speaking populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 8471-6	11.5	44
67	The GenoChip: a new tool for genetic anthropology. <i>Genome Biology and Evolution</i> , 2013 , 5, 1021-31	3.9	44
66	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe. <i>Nature Communications</i> , 2018 , 9, 5018	17.4	43
65	Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia. <i>Nature Communications</i> , 2020 , 11, 939	17.4	42
64	The Eulau eulogy: Bioarchaeological interpretation of lethal violence in Corded Ware multiple burials from Saxony-Anhalt, Germany. <i>Journal of Anthropological Archaeology</i> , 2009 , 28, 412-423	1.9	42
63	Ancient genome-wide DNA from France highlights the complexity of interactions between Mesolithic hunter-gatherers and Neolithic farmers. <i>Science Advances</i> , 2020 , 6, eaaz5344	14.3	41

62	Late Pleistocene human genome suggests a local origin for the first farmers of central Anatolia. <i>Nature Communications</i> , 2019 , 10, 1218	17.4	40
61	Y-chromosome and mtDNA genetics reveal significant contrasts in affinities of modern Middle Eastern populations with European and African populations. <i>PLoS ONE</i> , 2013 , 8, e54616	3.7	39
60	Influences of history, geography, and religion on genetic structure: the Maronites in Lebanon. <i>European Journal of Human Genetics</i> , 2011 , 19, 334-40	5.3	37
59	Emergence of human-adapted <i>Salmonella enterica</i> is linked to the Neolithization process. <i>Nature Ecology and Evolution</i> , 2020 , 4, 324-333	12.3	36
58	Afghanistan's ethnic groups share a Y-chromosomal heritage structured by historical events. <i>PLoS ONE</i> , 2012 , 7, e34288	3.7	35
57	The maternal genetic make-up of the Iberian Peninsula between the Neolithic and the Early Bronze Age. <i>Scientific Reports</i> , 2017 , 7, 15644	4.9	34
56	A new subhaplogroup of native American Y-Chromosomes from the Andes. <i>American Journal of Physical Anthropology</i> , 2011 , 146, 553-9	2.5	34
55	Population differentiation of southern Indian male lineages correlates with agricultural expansions predating the caste system. <i>PLoS ONE</i> , 2012 , 7, e50269	3.7	34
54	A Re-Appraisal of the Early Andean Human Remains from Lauricocha in Peru. <i>PLoS ONE</i> , 2015 , 10, e0127141	3.7	34
53	A Paleogenomic Reconstruction of the Deep Population History of the Andes. <i>Cell</i> , 2020 , 181, 1131-1145.e21	5.2	33
52	Evidence of pre-Roman tribal genetic structure in Basques from uniparentally inherited markers. <i>Molecular Biology and Evolution</i> , 2012 , 29, 2211-22	8.3	32
51	Clan, language, and migration history has shaped genetic diversity in Haida and Tlingit populations from Southeast Alaska. <i>American Journal of Physical Anthropology</i> , 2012 , 148, 422-35	2.5	30
50	Genomic History of Neolithic to Bronze Age Anatolia, Northern Levant, and Southern Caucasus. <i>Cell</i> , 2020 , 181, 1158-1175.e28	56.2	29
49	Genetic diversity in Puerto Rico and its implications for the peopling of the Island and the West Indies. <i>American Journal of Physical Anthropology</i> , 2014 , 155, 352-68	2.5	28
48	Aboriginal Australian mitochondrial genome variation - an increased understanding of population antiquity and diversity. <i>Scientific Reports</i> , 2017 , 7, 43041	4.9	26
47	From cheek swabs to consensus sequences: an A to Z protocol for high-throughput DNA sequencing of complete human mitochondrial genomes. <i>BMC Genomics</i> , 2014 , 15, 68	4.5	25
46	Recombination gives a new insight in the effective population size and the history of the old world human populations. <i>Molecular Biology and Evolution</i> , 2012 , 29, 25-30	8.3	24
45	The origins and spread of domestic horses from the Western Eurasian steppes. <i>Nature</i> , 2021 , 598, 634-640.4	30.4	24

44	The Genetic History of Peruvian Quechua-Lamistas and Chankas: Uniparental DNA Patterns among Autochthonous Amazonian and Andean Populations. <i>Annals of Human Genetics</i> , 2016 , 80, 88-101	2.2	22
43	Molecular evidence of HLA-B27 in a historical case of ankylosing spondylitis. <i>Arthritis and Rheumatism</i> , 2005 , 52, 3318-9		19
42	Ancient genomes reveal social and genetic structure of Late Neolithic Switzerland. <i>Nature Communications</i> , 2020 , 11, 1915	17.4	18
41	Pleistocene Mitochondrial Genomes Suggest a Single Major Dispersal of Non-Africans and a Late Glacial Population Turnover in Europe. <i>Current Biology</i> , 2016 , 26, 557-561	6.3	15
40	Mitochondrial genome sequencing in Mesolithic North East Europe Unearths a new sub-clade within the broadly distributed human haplogroup C1. <i>PLoS ONE</i> , 2014 , 9, e87612	3.7	15
39	AmericaPlex26: a SNaPshot multiplex system for genotyping the main human mitochondrial founder lineages of the Americas. <i>PLoS ONE</i> , 2014 , 9, e93292	3.7	14
38	A new method to reconstruct recombination events at a genomic scale. <i>PLoS Computational Biology</i> , 2010 , 6, e1001010	5	13
37	Genetic heritage and native identity of the Seaconke Wampanoag tribe of Massachusetts. <i>American Journal of Physical Anthropology</i> , 2010 , 142, 579-89	2.5	13
36	A systematic investigation of human DNA preservation in medieval skeletons. <i>Scientific Reports</i> , 2020 , 10, 18225	4.9	13
35	The Beaker Phenomenon and the Genomic Transformation of Northwest Europe 2017 ,		11
34	Comment on "Ancient DNA from the first European farmers in 7500-year-old Neolithic sites". <i>Science</i> , 2006 , 312, 1875; author reply 1875	33.3	11
33	Discussion: Are the Origins of Indo-European Languages Explained by the Migration of the Yamnaya Culture to the West?. <i>European Journal of Archaeology</i> , 2018 , 21, 3-17	0.7	10
32	Mitochondrial origin of the matrilineal Mosuo people in China. <i>Mitochondrial DNA</i> , 2012 , 23, 13-9		10
31	Ancient DNA Analysis Suggests Negligible Impact of the Wari Empire Expansion in Peru's Central Coast during the Middle Horizon. <i>PLoS ONE</i> , 2016 , 11, e0155508	3.7	10
30	The genetic prehistory of the Greater Caucasus		10
29	Ethics of DNA research on human remains: five globally applicable guidelines. <i>Nature</i> , 2021 , 599, 41-46	50.4	9
28	Human mitochondrial DNA lineages in Iron-Age Fennoscandia suggest incipient admixture and eastern introduction of farming-related maternal ancestry. <i>Scientific Reports</i> , 2019 , 9, 16883	4.9	9
27	Ten millennia of hepatitis B virus evolution. <i>Science</i> , 2021 , 374, 182-188	33.3	7

26	Parallel paleogenomic transects reveal complex genetic history of early European farmers		7
25	Positive selection on mitochondrial M7 lineages among the Gelong people in Hainan. <i>Journal of Human Genetics</i> , 2011 , 56, 253-6	4.3	6
24	Genomic and dietary transitions during the Mesolithic and Early Neolithic in Sicily		6
23	Emblems and spaces of power during the Argaric Bronze Age at La Almoloya, Murcia. <i>Antiquity</i> , 2021 , 95, 329-348	1	6
22	Tracing the genetic origin of Europe's first farmers reveals insights into their social organization		5
21	Population history from the Neolithic to present on the Mediterranean island of Sardinia: An ancient DNA perspective		5
20	Predicting skeletal stature using ancient DNA		5
19	Using Y-chromosome capture enrichment to resolve haplogroup H2 shows new evidence for a two-path Neolithic expansion to Western Europe. <i>Scientific Reports</i> , 2021 , 11, 15005	4.9	5
18	The Genomic History Of Southeastern Europe		4
17	ABO genotyping by PCR-RFLP and cloning and sequencing. <i>Anthropologischer Anzeiger</i> , 2004 , 62, 397-410.6		3
16	Genomic transformation and social organization during the Copper Age-Bronze Age transition in southern Iberia. <i>Science Advances</i> , 2021 , 7, eabi7038	14.3	3
15	The Stone Age Plague: 1000 years of Persistence in Eurasia		3
14	A dynamic 6,000-year genetic history of Eurasia's Eastern Steppe		3
13	Characterizing the genetic history of admixture across inner Eurasia		3
12	Dynamic changes in genomic and social structures in third millennium BCE central Europe. <i>Science Advances</i> , 2021 , 7,	14.3	3
11	The origin and legacy of the Etruscans through a 2000-year archeogenomic time transect. <i>Science Advances</i> , 2021 , 7, eabi7673	14.3	3
10	Stone Age genomes shed light on the early evolution, diversity, and ecology of plague.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2116722119	11.5	3
9	A-Z of ancient DNA protocols for shotgun Illumina Next Generation Sequencing v1		2

- 8 Predicting skeletal stature using ancient DNA. *American Journal of Biological Anthropology*, 2
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- 2 Ancient DNA gives new insights into a Norman Neolithic monumental cemetery dedicated to male elites.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119, e2120786119^{11.5} 0
- 1 Stephen Shennan. 2018. *The first farmers of Europe: an evolutionary perspective*. Cambridge: Cambridge University Press; 978-1-108-43521-5 £24.99.. *Antiquity*, **2019**, 93, 1683-1684 1