

Johannes Krause

List of Publications by Citations

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212
papers

23,834
citations

70
h-index

153
g-index

238
ext. papers

30,550
ext. citations

18.3
avg, IF

6.26
L-index

#	Paper	IF	Citations
212	A draft sequence of the Neandertal genome. <i>Science</i> , 2010 , 328, 710-722	33.3	2599
211	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010 , 468, 1053-60	50.4	1169
210	Massive migration from the steppe was a source for Indo-European languages in Europe. <i>Nature</i> , 2015 , 522, 207-11	50.4	968
209	Genetic analyses from ancient DNA. <i>Annual Review of Genetics</i> , 2004 , 38, 645-79	14.5	904
208	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014 , 513, 409-13	50.4	812
207	Genome-wide patterns of selection in 230 ancient Eurasians. <i>Nature</i> , 2015 , 528, 499-503	50.4	774
206	Patterns of damage in genomic DNA sequences from a Neandertal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 14616-21	11.5	610
205	The complete mitochondrial DNA genome of an unknown hominin from southern Siberia. <i>Nature</i> , 2010 , 464, 894-7	50.4	521
204	Analysis of one million base pairs of Neanderthal DNA. <i>Nature</i> , 2006 , 444, 330-6	50.4	511
203	Genomic insights into the origin of farming in the ancient Near East. <i>Nature</i> , 2016 , 536, 419-24	50.4	485
202	The genetic history of Ice Age Europe. <i>Nature</i> , 2016 , 534, 200-5	50.4	473
201	A draft genome of <i>Yersinia pestis</i> from victims of the Black Death. <i>Nature</i> , 2011 , 478, 506-10	50.4	463
200	Sequencing and analysis of Neanderthal genomic DNA. <i>Science</i> , 2006 , 314, 1113-8	33.3	415
199	A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. <i>Cell</i> , 2008 , 134, 416-26	56.2	405
198	A revised timescale for human evolution based on ancient mitochondrial genomes. <i>Current Biology</i> , 2013 , 23, 553-559	6.3	387
197	Targeted retrieval and analysis of five Neandertal mtDNA genomes. <i>Science</i> , 2009 , 325, 318-21	33.3	387
196	The derived FOXP2 variant of modern humans was shared with Neandertals. <i>Current Biology</i> , 2007 , 17, 1908-12	6.3	376

195	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. <i>Nature</i> , 2014 , 514, 494-7	50.4	358
194	Genomics and the challenging translation into conservation practice. <i>Trends in Ecology and Evolution</i> , 2015 , 30, 78-87	10.9	335
193	Complete mitochondrial genomes of ancient canids suggest a European origin of domestic dogs. <i>Science</i> , 2013 , 342, 871-4	33.3	328
192	Temporal patterns of nucleotide misincorporations and DNA fragmentation in ancient DNA. <i>PLoS ONE</i> , 2012 , 7, e34131	3.7	325
191	The Beaker phenomenon and the genomic transformation of northwest Europe. <i>Nature</i> , 2018 , 555, 190-196	50.4	293
190	The genomic history of southeastern Europe. <i>Nature</i> , 2018 , 555, 197-203	50.4	287
189	Removal of deaminated cytosines and detection of in vivo methylation in ancient DNA. <i>Nucleic Acids Research</i> , 2010 , 38, e87	20.1	283
188	The rise and fall of the <i>Phytophthora infestans</i> lineage that triggered the Irish potato famine. <i>ELife</i> , 2013 , 2, e00731	8.9	246
187	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
186	Neanderthals in central Asia and Siberia. <i>Nature</i> , 2007 , 449, 902-4	50.4	243
185	Genome-wide comparison of medieval and modern <i>Mycobacterium leprae</i> . <i>Science</i> , 2013 , 341, 179-83	33.3	240
184	Targeted investigation of the Neandertal genome by array-based sequence capture. <i>Science</i> , 2010 , 328, 723-5	33.3	224
183	A complete mtDNA genome of an early modern human from Kostenki, Russia. <i>Current Biology</i> , 2010 , 20, 231-6	6.3	213
182	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
181	Mitochondrial genomes reveal an explosive radiation of extinct and extant bears near the Miocene-Pliocene boundary. <i>BMC Evolutionary Biology</i> , 2008 , 8, 220	3	207
180	Reconstructing Prehistoric African Population Structure. <i>Cell</i> , 2017 , 171, 59-71.e21	56.2	201
179	EAGER: efficient ancient genome reconstruction. <i>Genome Biology</i> , 2016 , 17, 60	18.3	195
178	Genomic sequencing of Pleistocene cave bears. <i>Science</i> , 2005 , 309, 597-9	33.3	191

177	Genomic insights into the peopling of the Southwest Pacific. <i>Nature</i> , 2016 , 538, 510-513	50.4	180
176	Targeted enrichment of ancient pathogens yielding the pPCP1 plasmid of <i>Yersinia pestis</i> from victims of the Black Death. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, E746-52	11.5	169
175	Multiplex amplification of the mammoth mitochondrial genome and the evolution of Elephantidae. <i>Nature</i> , 2006 , 439, 724-7	50.4	167
174	Next-generation museomics disentangles one of the largest primate radiations. <i>Systematic Biology</i> , 2013 , 62, 539-54	8.4	161
173	Ancient genomes revisit the ancestry of domestic and Przewalski's horses. <i>Science</i> , 2018 , 360, 111-114	33.3	153
172	The 5300-year-old <i>Helicobacter pylori</i> genome of the Iceman. <i>Science</i> , 2016 , 351, 162-165	33.3	152
171	Reconstructing the Deep Population History of Central and South America. <i>Cell</i> , 2018 , 175, 1185-1197.e27	36.2	143
170	Reconstructing the genetic history of late Neanderthals. <i>Nature</i> , 2018 , 555, 652-656	50.4	138
169	Deeply divergent archaic mitochondrial genome provides lower time boundary for African gene flow into Neanderthals. <i>Nature Communications</i> , 2017 , 8, 16046	17.4	132
168	Learning about human population history from ancient and modern genomes. <i>Nature Reviews Genetics</i> , 2011 , 12, 603-14	30.1	127
167	<i>Salmonella enterica</i> genomes from victims of a major sixteenth-century epidemic in Mexico. <i>Nature Ecology and Evolution</i> , 2018 , 2, 520-528	12.3	124
166	The Neandertal genome and ancient DNA authenticity. <i>EMBO Journal</i> , 2009 , 28, 2494-502	13	118
165	Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. <i>Science</i> , 2017 , 357, 512-515	33.3	110
164	Genetic origins of the Minoans and Mycenaeans. <i>Nature</i> , 2017 , 548, 214-218	50.4	108
163	Virus progeny of murine cytomegalovirus bacterial artificial chromosome pSM3fr show reduced growth in salivary Glands due to a fixed mutation of MCK-2. <i>Journal of Virology</i> , 2011 , 85, 10346-53	6.6	102
162	Eighteenth century <i>Yersinia pestis</i> genomes reveal the long-term persistence of an historical plague focus. <i>ELife</i> , 2016 , 5, e12994	8.9	101
161	From micrograms to picograms: quantitative PCR reduces the material demands of high-throughput sequencing. <i>Nucleic Acids Research</i> , 2008 , 36, e5	20.1	100
160	Insight into the evolution and origin of leprosy bacilli from the genome sequence of <i>Mycobacterium lepromatosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 4459-64	11.5	99

159	Kinship-based social inequality in Bronze Age Europe. <i>Science</i> , 2019 , 366, 731-734	33.3	97
158	The genetic prehistory of the Baltic Sea region. <i>Nature Communications</i> , 2018 , 9, 442	17.4	96
157	Genomic analysis of 6,000-year-old cultivated grain illuminates the domestication history of barley. <i>Nature Genetics</i> , 2016 , 48, 1089-93	36.3	95
156	A Robust Framework for Microbial Archaeology. <i>Annual Review of Genomics and Human Genetics</i> , 2017 , 18, 321-356	9.7	92
155	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
154	Historical <i>Y. pestis</i> Genomes Reveal the European Black Death as the Source of Ancient and Modern Plague Pandemics. <i>Cell Host and Microbe</i> , 2016 , 19, 874-81	23.4	90
153	Female exogamy and gene pool diversification at the transition from the Final Neolithic to the Early Bronze Age in central Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 10083-10088	11.5	86
152	A High-Coverage <i>Yersinia pestis</i> Genome from a Sixth-Century Justinianic Plague Victim. <i>Molecular Biology and Evolution</i> , 2016 , 33, 2911-2923	8.3	85
151	Bronze Age population dynamics and the rise of dairy pastoralism on the eastern Eurasian steppe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E11248-E11255	11.5	84
150	Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations. <i>Science</i> , 2018 , 360, 548-552	33.3	83
149	Origin of modern syphilis and emergence of a pandemic <i>Treponema pallidum</i> cluster. <i>Nature Microbiology</i> , 2016 , 2, 16245	26.6	81
148	The Stone Age Plague and Its Persistence in Eurasia. <i>Current Biology</i> , 2017 , 27, 3683-3691.e8	6.3	81
147	A58 Epidemic dynamics of ancient disease outbreaks. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
146	Ancient pathogen genomics as an emerging tool for infectious disease research. <i>Nature Reviews Genetics</i> , 2019 , 20, 323-340	30.1	76
145	Analysis of 3800-year-old <i>Yersinia pestis</i> genomes suggests Bronze Age origin for bubonic plague. <i>Nature Communications</i> , 2018 , 9, 2234	17.4	72
144	Multiplex amplification of ancient DNA. <i>Nature Protocols</i> , 2006 , 1, 720-8	18.8	71
143	Ancient genomes reveal a high diversity of <i>Mycobacterium leprae</i> in medieval Europe. <i>PLoS Pathogens</i> , 2018 , 14, e1006997	7.6	70
142	The genetic history of admixture across inner Eurasia. <i>Nature Ecology and Evolution</i> , 2019 , 3, 966-976	12.3	69

141	The rate and potential relevance of new mutations in a colonizing plant lineage. <i>PLoS Genetics</i> , 2018 , 14, e1007155	6	65
140	Early cave art and ancient DNA record the origin of European bison. <i>Nature Communications</i> , 2016 , 7, 13158	17.4	63
139	Mitochondrial DNA of an Iberian Neandertal suggests a population affinity with other European Neandertals. <i>Current Biology</i> , 2006 , 16, R629-30	6.3	63
138	Temporal patterns of damage and decay kinetics of DNA retrieved from plant herbarium specimens. <i>Royal Society Open Science</i> , 2016 , 3, 160239	3.3	62
137	Genomic insights into the formation of human populations in East Asia. <i>Nature</i> , 2021 , 591, 413-419	50.4	62
136	Neandertal cannibalism and Neandertal bones used as tools in Northern Europe. <i>Scientific Reports</i> , 2016 , 6, 29005	4.9	59
135	Mining Metagenomic Data Sets for Ancient DNA: Recommended Protocols for Authentication. <i>Trends in Genetics</i> , 2017 , 33, 508-520	8.5	59
134	Neolithic and medieval virus genomes reveal complex evolution of hepatitis B. <i>ELife</i> , 2018 , 7,	8.9	59
133	Understanding 6th-century barbarian social organization and migration through paleogenomics. <i>Nature Communications</i> , 2018 , 9, 3547	17.4	57
132	Ancient genomes from across Western Europe reveal early diversification during the First Pandemic (541-750). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 12363-12372	11.5	56
131	Phylogeography of the second plague pandemic revealed through analysis of historical <i>Yersinia pestis</i> genomes. <i>Nature Communications</i> , 2019 , 10, 4470	17.4	55
130	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
129	Differential preservation of endogenous human and microbial DNA in dental calculus and dentin. <i>Scientific Reports</i> , 2018 , 8, 9822	4.9	55
128	Palaeo-Eskimo genetic ancestry and the peopling of Chukotka and North America. <i>Nature</i> , 2019 , 570, 236-240	50.4	53
127	Ancient genomes from northern China suggest links between subsistence changes and human migration. <i>Nature Communications</i> , 2020 , 11, 2700	17.4	53
126	Effect of X-ray irradiation on ancient DNA in sub-fossil bones - Guidelines for safe X-ray imaging. <i>Scientific Reports</i> , 2016 , 6, 32969	4.9	52
125	MALT: Fast alignment and analysis of metagenomic DNA sequence data applied to the Tyrolean Iceman		51
124	Language continuity despite population replacement in Remote Oceania. <i>Nature Ecology and Evolution</i> , 2018 , 2, 731-740	12.3	50

123	Mining herbaria for plant pathogen genomes: back to the future. <i>PLoS Pathogens</i> , 2014 , 10, e1004028	7.6	50
122	<i>Mycobacterium leprae</i> genomes from a British medieval leprosy hospital: towards understanding an ancient epidemic. <i>BMC Genomics</i> , 2014 , 15, 270	4.5	49
121	Complete mitochondrial genomes reveal neolithic expansion into Europe. <i>PLoS ONE</i> , 2012 , 7, e32473	3.7	49
120	Survival of Late Pleistocene Hunter-Gatherer Ancestry in the Iberian Peninsula. <i>Current Biology</i> , 2019 , 29, 1169-1177.e7	6.3	48
119	A Dynamic 6,000-Year Genetic History of Eurasia's Eastern Steppe. <i>Cell</i> , 2020 , 183, 890-904.e29	56.2	48
118	Large-scale mitogenomic analysis of the phylogeography of the Late Pleistocene cave bear. <i>Scientific Reports</i> , 2019 , 9, 10700	4.9	45
117	Genetic characterization of the ABO blood group in Neandertals. <i>BMC Evolutionary Biology</i> , 2008 , 8, 3423		45
116	A Molecular Approach to the Sexing of the Triple Burial at the Upper Paleolithic Site of Dolní Věstonice. <i>PLoS ONE</i> , 2016 , 11, e0163019	3.7	44
115	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe. <i>Nature Communications</i> , 2018 , 9, 5018	17.4	43
114	Stable isotopes reveal patterns of diet and mobility in the last Neandertals and first modern humans in Europe. <i>Scientific Reports</i> , 2019 , 9, 4433	4.9	42
113	Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia. <i>Nature Communications</i> , 2020 , 11, 939	17.4	42
112	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
111	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
110	Historic <i>Treponema pallidum</i> genomes from Colonial Mexico retrieved from archaeological remains. <i>PLoS Neglected Tropical Diseases</i> , 2018 , 12, e0006447	4.8	37
109	Ancient Genomes Reveal Yamnaya-Related Ancestry and a Potential Source of Indo-European Speakers in Iron Age Tianshan. <i>Current Biology</i> , 2019 , 29, 2526-2532.e4	6.3	37
108	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
107	Reconciling material cultures in archaeology with genetic data: The nomenclature of clusters emerging from archaeogenomic analysis. <i>Scientific Reports</i> , 2018 , 8, 13003	4.9	36
106	Reconstructing Asian faunal introductions to eastern Africa from multi-proxy biomolecular and archaeological datasets. <i>PLoS ONE</i> , 2017 , 12, e0182565	3.7	34

105	Ancient DNA sheds light on the genetic origins of early Iron Age Philistines. <i>Science Advances</i> , 2019 , 5, eaax0061	14.3	34
104	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
103	HOPS: automated detection and authentication of pathogen DNA in archaeological remains. <i>Genome Biology</i> , 2019 , 20, 280	18.3	34
102	Parallel detection of ancient pathogens via array-based DNA capture. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015 , 370, 20130375	5.8	33
101	A Paleogenomic Reconstruction of the Deep Population History of the Andes. <i>Cell</i> , 2020 , 181, 1131-1145.621	56.2	33
100	Linkage disequilibrium extends across putative selected sites in FOXP2. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2181-4	8.3	33
99	Paleolithic to Bronze Age Siberians Reveal Connections with First Americans and across Eurasia. <i>Cell</i> , 2020 , 181, 1232-1245.e20	56.2	33
98	Ancient DNA suggests modern wolves trace their origin to a Late Pleistocene expansion from Beringia. <i>Molecular Ecology</i> , 2020 , 29, 1596-1610	5.7	33
97	The immunogenetic diversity of the HLA system in Mexico correlates with underlying population genetic structure. <i>Human Immunology</i> , 2020 , 81, 461-474	2.3	32
96	Nuclear DNA from two early Neandertals reveals 80,000 years of genetic continuity in Europe. <i>Science Advances</i> , 2019 , 5, eaaw5873	14.3	31
95	Nonhuman primates across sub-Saharan Africa are infected with the yaws bacterium <i>Treponema pallidum</i> subsp. <i>pertenue</i> . <i>Emerging Microbes and Infections</i> , 2018 , 7, 157	18.9	30
94	Ancient genomes reveal complex patterns of population movement, interaction, and replacement in sub-Saharan Africa. <i>Science Advances</i> , 2020 , 6, eaaz0183	14.3	29
93	Genomic History of Neolithic to Bronze Age Anatolia, Northern Levant, and Southern Caucasus. <i>Cell</i> , 2020 , 181, 1158-1175.e28	56.2	29
92	<i>Yersinia pestis</i> : new evidence for an old infection. <i>PLoS ONE</i> , 2012 , 7, e49803	3.7	28
91	Rewriting the Central European Early Bronze Age Chronology: Evidence from Large-Scale Radiocarbon Dating. <i>PLoS ONE</i> , 2015 , 10, e0139705	3.7	27
90	Ratio of mitochondrial to nuclear DNA affects contamination estimates in ancient DNA analysis. <i>Scientific Reports</i> , 2018 , 8, 14075	4.9	25
89	Central European Woolly Mammoth Population Dynamics: Insights from Late Pleistocene Mitochondrial Genomes. <i>Scientific Reports</i> , 2017 , 7, 17714	4.9	24
88	The origins and spread of domestic horses from the Western Eurasian steppes. <i>Nature</i> , 2021 , 598, 634-640.4	50.4	24

87	Genomic insights into the early peopling of the Caribbean. <i>Science</i> , 2020 , 369, 456-460	33.3	21
86	Ancient Bacterial Genomes Reveal a High Diversity of <i>Treponema pallidum</i> Strains in Early Modern Europe. <i>Current Biology</i> , 2020 , 30, 3788-3803.e10	6.3	21
85	Ancient DNA analysis. <i>Nature Reviews Methods Primers</i> , 2021 , 1,		21
84	Paleomicrobiology: Diagnosis and Evolution of Ancient Pathogens. <i>Annual Review of Microbiology</i> , 2019 , 73, 639-666	17.5	20
83	Mitochondrial Genomes of Giant Deers Suggest their Late Survival in Central Europe. <i>Scientific Reports</i> , 2015 , 5, 10853	4.9	20
82	The evolution and changing ecology of the African hominid oral microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	20
81	A genome sequence from a modern human skull over 45,000 years old from Zlatý kůň in Czechia. <i>Nature Ecology and Evolution</i> , 2021 , 5, 820-825	12.3	18
80	Genetic Time Travel. <i>Genetics</i> , 2016 , 203, 9-12	4	18
79	Tools for opening new chapters in the book of <i>Treponema pallidum</i> evolutionary history. <i>Clinical Microbiology and Infection</i> , 2016 , 22, 916-921	9.5	18
78	Ancient genomes reveal social and genetic structure of Late Neolithic Switzerland. <i>Nature Communications</i> , 2020 , 11, 1915	17.4	18
77	Functional analysis of human and chimpanzee promoters. <i>Genome Biology</i> , 2005 , 6, R57	18.3	17
76	Origin and Health Status of First-Generation Africans from Early Colonial Mexico. <i>Current Biology</i> , 2020 , 30, 2078-2091.e11	6.3	16
75	Primer extension capture: targeted sequence retrieval from heavily degraded DNA sources. <i>Journal of Visualized Experiments</i> , 2009 , 1573	1.6	16
74	2000-year-old pathogen genomes reconstructed from metagenomic analysis of Egyptian mummified individuals. <i>BMC Biology</i> , 2020 , 18, 108	7.3	16
73	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
72	Screening ancient tuberculosis with qPCR: challenges and opportunities. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015 , 370, 20130622	5.8	14
71	The genomic origins of the Bronze Age Tarim Basin mummies. <i>Nature</i> , 2021 , 599, 256-261	50.4	14
70	The Genomic Formation of Human Populations in East Asia		14

69	Identification of African swine fever virus-like elements in the soft tick genome provides insights into the virus' evolution. <i>BMC Biology</i> , 2020 , 18, 136	7.3	14
68	Genomic correlates of atherosclerosis in ancient humans. <i>Global Heart</i> , 2014 , 9, 203-9	2.9	14
67	A systematic investigation of human DNA preservation in medieval skeletons. <i>Scientific Reports</i> , 2020 , 10, 18225	4.9	13
66	Ancient genome-wide analyses infer kinship structure in an Early Medieval Alemannic graveyard. <i>Science Advances</i> , 2018 , 4, eaao1262	14.3	12
65	Genetic structure of Tibetan populations in Gansu revealed by forensic STR loci. <i>Scientific Reports</i> , 2017 , 7, 41195	4.9	11
64	The Beaker Phenomenon and the Genomic Transformation of Northwest Europe 2017 ,		11
63	Salmonella entericagenomes recovered from victims of a major 16th century epidemic in Mexico		11
62	Ancient genomic time transect from the Central Asian Steppe unravels the history of the Scythians. <i>Science Advances</i> , 2021 , 7,	14.3	11
61	Paleo-Eskimo genetic legacy across North America		10
60	The genetic prehistory of the Greater Caucasus		10
59	Ethics of DNA research on human remains: five globally applicable guidelines. <i>Nature</i> , 2021 , 599, 41-46	50.4	9
58	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
57	Ten millennia of hepatitis B virus evolution. <i>Science</i> , 2021 , 374, 182-188	33.3	7
56	Genome of a middle Holocene hunter-gatherer from Wallacea. <i>Nature</i> , 2021 , 596, 543-547	50.4	7
55	Insights into human history from the first decade of ancient human genomics. <i>Science</i> , 2021 , 373, 1479-1484	50.4	7
54	Inferring genetic origins and phenotypic traits of George Bähr, the architect of the Dresden Frauenkirche. <i>Scientific Reports</i> , 2018 , 8, 2115	4.9	6
53	Genomic and dietary transitions during the Mesolithic and Early Neolithic in Sicily		6
52	The genomic formation of First American ancestors in East and Northeast Asia		6

51	Genetic diversity of the HLA system in human populations from the Sierra (Andean), Oriente (Amazonian) and Costa (Coastal) regions of Ecuador. <i>Human Immunology</i> , 2018 , 79, 639-650	2.3	5
50	Correction: The rise and fall of the <i>Phytophthora infestans</i> lineage that triggered the Irish potato famine. <i>ELife</i> , 2,	8.9	5
49	Population history from the Neolithic to present on the Mediterranean island of Sardinia: An ancient DNA perspective		5
48	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
47	Jenaer Erklärung Das Konzept der Rasse ist das Ergebnis von Rassismus und nicht dessen Voraussetzung. <i>Biologie in Unserer Zeit</i> , 2019 , 49, 399-402	0.1	5
46	Genome-wide study of a Neolithic Wartberg grave community reveals distinct HLA variation and hunter-gatherer ancestry. <i>Communications Biology</i> , 2021 , 4, 113	6.7	5
45	Who lived on the Swiss Plateau around 3300 BCE? Analyses of commingled human skeletal remains from the dolmen of Oberbipp. <i>International Journal of Osteoarchaeology</i> , 2019 , 29, 786-796	1.1	4
44	African nonhuman primates are infected with the yaws bacterium <i>Treponema pallidum</i> subsp. <i>pertenue</i>		4
43	The Genomic History Of Southeastern Europe		4
42	A phylogeography of the second plague pandemic revealed through the analysis of historical <i>Y. pestis</i> genomes		4
41	Ancient <i>Yersinia pestis</i> genomes provide no evidence for the origins or spread of the Justinianic Plague		4
40	Analysis of Genomic DNA from Medieval Plague Victims Suggests Long-Term Effect of <i>Yersinia pestis</i> on Human Immunity Genes. <i>Molecular Biology and Evolution</i> , 2021 , 38, 4059-4076	8.3	4
39	Multiple Radiocarbon Dating of Human remains: Clarifying the Chronology and Sequences of Burials in the late Neolithic Dolmen of Oberbipp (Switzerland). <i>Radiocarbon</i> , 2019 , 61, 1697-1709	4.6	3
38	Comparison of target enrichment strategies for ancient pathogen DNA. <i>BioTechniques</i> , 2020 , 69, 455-459.5		3
37	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
36	Na-Dene populations descend from the Paleo-Eskimo migration into America		3
35	The Stone Age Plague: 1000 years of Persistence in Eurasia		3
34	A dynamic 6,000-year genetic history of Eurasia's Eastern Steppe		3

33	Characterizing the genetic history of admixture across inner Eurasia		3
32	'TB or not TB': the conundrum of pre-European contact tuberculosis in the Pacific. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020 , 375, 20190583	5.8	3
31	Mass burial genomics reveals outbreak of enteric paratyphoid fever in the Late Medieval trade city Lübeck. <i>iScience</i> , 2021 , 24, 102419	6.1	3
30	Dynamic changes in genomic and social structures in third millennium BCE central Europe. <i>Science Advances</i> , 2021 , 7,	14.3	3
29	The origin and legacy of the Etruscans through a 2000-year archeogenomic time transect. <i>Science Advances</i> , 2021 , 7, eabi7673	14.3	3
28	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
27	Patterns of Transformation from the Final Neolithic to the Early Bronze Age:241-261		2
26	Ancient <i>Yersinia pestis</i> genomes from across Western Europe reveal early diversification during the First Pandemic (541-50)		2
25	The genetic structure of the world's first farmers		2
24	Ancient bacterial genomes reveal a formerly unknown diversity of <i>Treponema pallidum</i> strains in early modern Europe		2
23	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe		2
22	Modern wolves trace their origin to a late Pleistocene expansion from Beringia		2
21	Late Pleistocene human genome suggests a local origin for the first farmers of central Anatolia		2
20	Crops vs. animals: regional differences in subsistence strategies of Swiss Neolithic farmers revealed by stable isotopes. <i>Archaeological and Anthropological Sciences</i> , 2020 , 12, 1	1.8	2
19	Using Y-chromosome capture enrichment to resolve haplogroup H2 shows new evidence for a two-Path Neolithic expansion to Western Europe		2
18	Response to Ancient DNA and its contribution to understanding the human history of the Pacific Islands (Bedford et al. 2018). <i>Archaeology in Oceania</i> , 2019 , 54, 57-61	0.7	1
17	An ancient view on host pathogen interaction across time and space. <i>Current Opinion in Immunology</i> , 2020 , 65, 65-69	7.8	1
16	HOPS: Automated detection and authentication of pathogen DNA in archaeological remains		1

15	The rate and potential relevance of new mutations in a colonizing plant lineage		1
14	African swine fever virus-like integrated elements in a soft tick genome – An ancient virus vector arms race?		1
13	Understanding 6th-Century Barbarian Social Organization and Migration through Paleogenomics		1
12	Neolithic genomes reveal a distinct ancient HLA allele pool and population transformation in Europe		1
11	Human mobility at Tell Atchana (Alalakh), Hatay, Turkey during the 2nd millennium BC: Integration of isotopic and genomic evidence. <i>PLoS ONE</i> , 2021 , 16, e0241883	3.7	1
10	Performance and automation of ancient DNA capture with RNA hyRAD probes. <i>Molecular Ecology Resources</i> , 2021 ,	8.4	1
9	A 3,000-year-old, basal <i>S. enterica</i> lineage from Bronze Age Xinjiang suggests spread along the Proto-Silk Road. <i>PLoS Pathogens</i> , 2021 , 17, e1009886	7.6	1
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6	A Woman with a Sword? – Weapon Grave at Suontaka Vesitorninmäki, Finland. <i>European Journal of Archaeology</i> , 1-19	0.7	0
5	Genome-wide autosomal, mtDNA, and Y chromosome analysis of King Bela III of the Hungarian Arpad dynasty. <i>Scientific Reports</i> , 2021 , 11, 19210	4.9	0
4	Geographically dispersed zoonotic tuberculosis in pre-contact South American human populations.. <i>Nature Communications</i> , 2022 , 13, 1195	17.4	0
3	Genomic and dietary discontinuities during the Mesolithic and Neolithic in Sicily.. <i>iScience</i> , 2022 , 25, 104244	14.4	0
2	Ancient human migrations 2013 , 45-64		
1	The well-preserved Late Neolithic dolmen burial of Oberbipp, Switzerland. Construction, use, and post-depositional processes. <i>Journal of Archaeological Science: Reports</i> , 2022 , 42, 103397	0.7	