Johannes Krause

List of Publications by Year in Descending Order

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	Geographically dispersed zoonotic tuberculosis in pre-contact South American human populations.. *Nature Communications*, **2022**, 13, 1195	17.4	0
211	The well-preserved Late Neolithic dolmen burial of Oberbipp, Switzerland. Construction, use, and post-depositional processes. *Journal of Archaeological Science: Reports*, **2022**, 42, 103397	0.7	
210	Stone Age genomes shed light on the early evolution, diversity, and ecology of plague.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119, e2116722119	11.5	3
209	Genomic and dietary discontinuities during the Mesolithic and Neolithic in Sicily.. *IScience*, **2022**, 25, 104244	6.1	0
208	Palaeogenomic analysis of black rat (Rattus rattus) reveals multiple European introductions associated with human economic history.. *Nature Communications*, **2022**, 13, 2399	17.4	1
207	Genomic transformation and social organization during the Copper Age-Bronze Age transition in southern Iberia. *Science Advances*, **2021**, 7, eabi7038	14.3	3
206	Mycobacterium leprae diversity and population dynamics in medieval Europe from novel ancient genomes. *BMC Biology*, **2021**, 19, 220	7.3	0
205	Ten millennia of hepatitis B virus evolution. *Science*, **2021**, 374, 182-188	33.3	7
204	Ethics of DNA research on human remains: five globally applicable guidelines. *Nature*, **2021**, 599, 41-46	50.4	9
203	The origins and spread of domestic horses from the Western Eurasian steppes. *Nature*, **2021**, 598, 634-640	50.4	24
202	The genomic origins of the Bronze Age Tarim Basin mummies. *Nature*, **2021**, 599, 256-261	50.4	14
201	Ancient genomic time transect from the Central Asian Steppe unravels the history of the Scythians. *Science Advances*, **2021**, 7,	14.3	11
200	A genome sequence from a modern human skull over 45,000 years old from Zlatý kůň in Czechia. *Nature Ecology and Evolution*, **2021**, 5, 820-825	12.3	18
199	Analysis of Genomic DNA from Medieval Plague Victims Suggests Long-Term Effect of Yersinia pestis on Human Immunity Genes. *Molecular Biology and Evolution*, **2021**, 38, 4059-4076	8.3	4
198	Mass burial genomics reveals outbreak of enteric paratyphoid fever in the Late Medieval trade city Lübeck. *IScience*, **2021**, 24, 102419	6.1	3
197	The evolution and changing ecology of the African hominid oral microbiome. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	20
196	Human mobility at Tell Atchana (Alalakh), Hatay, Turkey during the 2nd millennium BC: Integration of isotopic and genomic evidence. *PLoS ONE*, **2021**, 16, e0241883	3.7	1

195	Using Y-chromosome capture enrichment to resolve haplogroup H2 shows new evidence for a two-path Neolithic expansion to Western Europe. *Scientific Reports*, **2021**, 11, 15005	4.9	5
194	Genome-wide study of a Neolithic Wartberg grave community reveals distinct HLA variation and hunter-gatherer ancestry. *Communications Biology*, **2021**, 4, 113	6.7	5
193	Ancient DNA analysis. *Nature Reviews Methods Primers*, **2021**, 1,		21
192	Genomic insights into the formation of human populations in East Asia. *Nature*, **2021**, 591, 413-419	50.4	62
191	Dynamic changes in genomic and social structures in third millennium BCE central Europe. *Science Advances*, **2021**, 7,	14.3	3
190	Genome of a middle Holocene hunter-gatherer from Wallacea. *Nature*, **2021**, 596, 543-547	50.4	7
189	Genome-wide autosomal, mtDNA, and Y chromosome analysis of King Bela III of the Hungarian Arpad dynasty. *Scientific Reports*, **2021**, 11, 19210	4.9	0
188	Insights into human history from the first decade of ancient human genomics. *Science*, **2021**, 373, 1479-1484	3[illegible]	7
187	The origin and legacy of the Etruscans through a 2000-year archeogenomic time transect. *Science Advances*, **2021**, 7, eabi7673	14.3	3
186	Performance and automation of ancient DNA capture with RNA hyRAD probes. *Molecular Ecology Resources*, **2021**,	8.4	1
185	A 3,000-year-old, basal S. enterica lineage from Bronze Age Xinjiang suggests spread along the Proto-Silk Road. *PLoS Pathogens*, **2021**, 17, e1009886	7.6	1
184	A Dynamic 6,000-Year Genetic History of Eurasia's Eastern Steppe. *Cell*, **2020**, 183, 890-904.e29	56.2	48
183	Comparison of target enrichment strategies for ancient pathogen DNA. *BioTechniques*, **2020**, 69, 455-459	2.5	3
182	A Paleogenomic Reconstruction of the Deep Population History of the Andes. *Cell*, **2020**, 181, 1131-1145.e21	36.1	33
181	Ancient genomes from northern China suggest links between subsistence changes and human migration. *Nature Communications*, **2020**, 11, 2700	17.4	53
180	Origin and Health Status of First-Generation Africans from Early Colonial Mexico. *Current Biology*, **2020**, 30, 2078-2091.e11	6.3	16
179	Ancient genome-wide DNA from France highlights the complexity of interactions between Mesolithic hunter-gatherers and Neolithic farmers. *Science Advances*, **2020**, 6, eaaz5344	14.3	41
178	Ancient genomes reveal complex patterns of population movement, interaction, and replacement in sub-Saharan Africa. *Science Advances*, **2020**, 6, eaaz0183	14.3	29

177	Genomic insights into the early peopling of the Caribbean. *Science*, **2020**, 369, 456-460	33.3	21
176	An ancient view on host pathogen interaction across time and space. *Current Opinion in Immunology* , **2020**, 65, 65-69	7.8	1
175	Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia. *Nature Communications*, **2020**, 11, 939	17.4	42
174	Emergence of human-adapted Salmonella enterica is linked to the Neolithization process. *Nature Ecology and Evolution*, **2020**, 4, 324-333	12.3	36
173	Paleolithic to Bronze Age Siberians Reveal Connections with First Americans and across Eurasia. *Cell*, **2020**, 181, 1232-1245.e20	56.2	33
172	Genomic History of Neolithic to Bronze Age Anatolia, Northern Levant, and Southern Caucasus. *Cell* , **2020**, 181, 1158-1175.e28	56.2	29
171	Ancient DNA suggests modern wolves trace their origin to a Late Pleistocene expansion from Beringia. *Molecular Ecology*, **2020**, 29, 1596-1610	5.7	33
170	'TB or not TB': the conundrum of pre-European contact tuberculosis in the Pacific. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2020**, 375, 20190583	5.8	3
169	Identification of African swine fever virus-like elements in the soft tick genome provides insights into the virus' evolution. *BMC Biology*, **2020**, 18, 136	7.3	14
168	The immunogenetic diversity of the HLA system in Mexico correlates with underlying population genetic structure. *Human Immunology*, **2020**, 81, 461-474	2.3	32
167	Ancient Bacterial Genomes Reveal a High Diversity of Treponema pallidum Strains in Early Modern Europe. *Current Biology*, **2020**, 30, 3788-3803.e10	6.3	21
166	A systematic investigation of human DNA preservation in medieval skeletons. *Scientific Reports*, **2020**, 10, 18225	4.9	13
165	2000-year-old pathogen genomes reconstructed from metagenomic analysis of Egyptian mummified individuals. *BMC Biology*, **2020**, 18, 108	7.3	16
164	Crops vs. animals: regional differences in subsistence strategies of Swiss Neolithic farmers revealed by stable isotopes. *Archaeological and Anthropological Sciences*, **2020**, 12, 1	1.8	2
163	Ancient genomes reveal social and genetic structure of Late Neolithic Switzerland. *Nature Communications*, **2020**, 11, 1915	17.4	18
162	A58 Epidemic dynamics of ancient disease outbreaks. *Virus Evolution*, **2019**, 5,	3.7	78
161	Multiple Radiocarbon Dating of Human remains: Clarifying the Chronology and Sequences of Burials in the late Neolithic Dolmen of Oberbipp (Switzerland). *Radiocarbon*, **2019**, 61, 1697-1709	4.6	3
160	Phylogeography of the second plague pandemic revealed through analysis of historical Yersinia pestis genomes. *Nature Communications*, **2019**, 10, 4470	17.4	55

159	Nuclear DNA from two early Neandertals reveals 80,000 years of genetic continuity in Europe. *Science Advances*, **2019**, 5, eaaw5873	14.3	31
158	Ancient genomes from across Western Europe reveal early diversification during the First Pandemic (541-750). *Proceedings of the National Academy of Sciences of the United States of America* , **2019**, 116, 12363-12372	11.5	56
157	Palaeo-Eskimo genetic ancestry and the peopling of Chukotka and North America. *Nature*, **2019**, 570, 236-240	50.4	53
156	Who lived on the Swiss Plateau around 3300 BCE? Analyses of commingled human skeletal remains from the dolmen of Oberbipp. *International Journal of Osteoarchaeology*, **2019**, 29, 786-796	1.1	4
155	The genetic history of admixture across inner Eurasia. *Nature Ecology and Evolution*, **2019**, 3, 966-976	12.3	69
154	Late Pleistocene human genome suggests a local origin for the first farmers of central Anatolia. *Nature Communications*, **2019**, 10, 1218	17.4	40
153	Survival of Late Pleistocene Hunter-Gatherer Ancestry in the Iberian Peninsula. *Current Biology*, **2019**, 29, 1169-1177.e7	6.3	48
152	Stable isotopes reveal patterns of diet and mobility in the last Neandertals and first modern humans in Europe. *Scientific Reports*, **2019**, 9, 4433	4.9	42
151	Response to ‘Ancient DNA and its contribution to understanding the human history of the Pacific Islands’ (Bedford et´al. 2018). *Archaeology in Oceania*, **2019**, 54, 57-61	0.7	1
150	Ancient pathogen genomics as an´emerging tool for infectious disease´research. *Nature Reviews Genetics*, **2019**, 20, 323-340	30.1	76
149	Large-scale mitogenomic analysis of the phylogeography of the Late Pleistocene cave bear. *Scientific Reports*, **2019**, 9, 10700	4.9	45
148	Paleomicrobiology: Diagnosis and Evolution of Ancient Pathogens. *Annual Review of Microbiology*, **2019**, 73, 639-666	17.5	20
147	Ancient Genomes Reveal Yamnaya-Related Ancestry and a Potential Source of Indo-European Speakers in Iron Age Tianshan. *Current Biology*, **2019**, 29, 2526-2532.e4	6.3	37
146	Ancient DNA sheds light on the genetic origins of early Iron Age Philistines. *Science Advances*, **2019**, 5, eaax0061	14.3	34
145	Kinship-based social inequality in Bronze Age Europe. *Science*, **2019**, 366, 731-734	33.3	97
144	Ancient human genome-wide data from a 3000-year interval in the Caucasus corresponds with eco-geographic regions. *Nature Communications*, **2019**, 10, 590	17.4	55
143	Human mitochondrial DNA lineages in Iron-Age Fennoscandia suggest incipient admixture and eastern introduction of farming-related maternal ancestry. *Scientific Reports*, **2019**, 9, 16883	4.9	9
142	Jenaer Erklärung – Das Konzept der Rasse ist das Ergebnis von Rassismus und nicht dessen Voraussetzung. *Biologie in Unserer Zeit*, **2019**, 49, 399-402	0.1	5

141	HOPS: automated detection and authentication of pathogen DNA in archaeological remains. *Genome Biology*, **2019**, 20, 280	18.3	34
140	The Beaker phenomenon and the genomic transformation of northwest Europe. *Nature*, **2018**, 555, 190-196	50.4	293
139	The genomic history of southeastern Europe. *Nature*, **2018**, 555, 197-203	50.4	287
138	Ancient genomes revisit the ancestry of domestic and Przewalski's horses. *Science*, **2018**, 360, 111-114	33.3	153
137	Language continuity despite population replacement in Remote Oceania. *Nature Ecology and Evolution*, **2018**, 2, 731-740	12.3	50
136	The genetic prehistory of the Baltic Sea region. *Nature Communications*, **2018**, 9, 442	17.4	96
135	Inferring genetic origins and phenotypic traits of George Bähr, the architect of the Dresden Frauenkirche. *Scientific Reports*, **2018**, 8, 2115	4.9	6
134	Salmonella enterica genomes from victims of a major sixteenth-century epidemic in Mexico. *Nature Ecology and Evolution*, **2018**, 2, 520-528	12.3	124
133	Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations. *Science*, **2018**, 360, 548-552	33.3	83
132	Reconstructing the genetic history of late Neanderthals. *Nature*, **2018**, 555, 652-656	50.4	138
131	Historic Treponema pallidum genomes from Colonial Mexico retrieved from archaeological remains. *PLoS Neglected Tropical Diseases*, **2018**, 12, e0006447	4.8	37
130	Genetic diversity of the HLA system in human populations from the Sierra (Andean), Oriente (Amazonian) and Costa (Coastal) regions of Ecuador. *Human Immunology*, **2018**, 79, 639-650	2.3	5
129	Analysis of 3800-year-old Yersinia pestis genomes suggests Bronze Age origin for bubonic plague. *Nature Communications*, **2018**, 9, 2234	17.4	72
128	Ancient genomes reveal a high diversity of Mycobacterium leprae in medieval Europe. *PLoS Pathogens*, **2018**, 14, e1006997	7.6	70
127	The rate and potential relevance of new mutations in a colonizing plant lineage. *PLoS Genetics*, **2018**, 14, e1007155	6	65
126	Neolithic and medieval virus genomes reveal complex evolution of hepatitis B. *ELife*, **2018**, 7,	8.9	59
125	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe. *Nature Communications*, **2018**, 9, 5018	17.4	43
124	Bronze Age population dynamics and the rise of dairy pastoralism on the eastern Eurasian steppe. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E11248-E11255	11.5	84

123	Reconstructing the Deep Population History of Central and South America. *Cell*, **2018**, 175, 1185-1197.e22	56.2	143
122	Ratio of mitochondrial to nuclear DNA affects contamination estimates in ancient DNA analysis. *Scientific Reports*, **2018**, 8, 14075	4.9	25
121	Nonhuman primates across sub-Saharan Africa are infected with the yaws bacterium Treponema pallidum subsp. pertenue. *Emerging Microbes and Infections*, **2018**, 7, 157	18.9	30
120	Ancient genome-wide analyses infer kinship structure in an Early Medieval Alemannic graveyard. *Science Advances*, **2018**, 4, eaao1262	14.3	12
119	Understanding 6th-century barbarian social organization and migration through paleogenomics. *Nature Communications*, **2018**, 9, 3547	17.4	57
118	Reconciling material cultures in archaeology with genetic data: The nomenclature of clusters emerging from archaeogenomic analysis. *Scientific Reports*, **2018**, 8, 13003	4.9	36
117	Differential preservation of endogenous human and microbial DNA in dental calculus and dentin. *Scientific Reports*, **2018**, 8, 9822	4.9	55
116	Genetic structure of Tibetan populations in Gansu revealed by forensic STR loci. *Scientific Reports*, **2017**, 7, 41195	4.9	11
115	A Robust Framework for Microbial Archaeology. *Annual Review of Genomics and Human Genetics*, **2017**, 18, 321-356	9.7	92
114	Ancient Egyptian mummy genomes suggest an increase of Sub-Saharan African ancestry in post-Roman periods. *Nature Communications*, **2017**, 8, 15694	17.4	91
113	Reconstructing Prehistoric African Population Structure. *Cell*, **2017**, 171, 59-71.e21	56.2	201
112	Reconstructing Asian faunal introductions to eastern Africa from multi-proxy biomolecular and archaeological datasets. *PLoS ONE*, **2017**, 12, e0182565	3.7	34
111	The Beaker Phenomenon and the Genomic Transformation of Northwest Europe **2017**,		11
110	Female exogamy and gene pool diversification at the transition from the Final Neolithic to the Early Bronze Age in central Europe. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 10083-10088	11.5	86
109	Genetic origins of the Minoans and Mycenaeans. *Nature*, **2017**, 548, 214-218	50.4	108
108	Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. *Science*, **2017**, 357, 512-515	33.3	110
107	The maternal genetic make-up of the Iberian Peninsula between the Neolithic and the Early Bronze Age. *Scientific Reports*, **2017**, 7, 15644	4.9	34
106	The Stone Age Plague and Its Persistence in Eurasia. *Current Biology*, **2017**, 27, 3683-3691.e8	6.3	81

105	Deeply divergent archaic mitochondrial genome provides lower time boundary for African gene flow into Neanderthals. *Nature Communications*, **2017**, 8, 16046	17.4	132
104	Mining Metagenomic Data Sets for Ancient DNA: Recommended Protocols for Authentication. *Trends in Genetics*, **2017**, 33, 508-520	8.5	59
103	Central European Woolly Mammoth Population Dynamics: Insights from Late Pleistocene Mitochondrial Genomes. *Scientific Reports*, **2017**, 7, 17714	4.9	24
102	Origin of modern syphilis and emergence of a pandemic Treponema pallidum cluster. *Nature Microbiology*, **2016**, 2, 16245	26.6	81
101	A High-Coverage Yersinia pestis Genome from a Sixth-Century Justinianic Plague Victim. *Molecular Biology and Evolution*, **2016**, 33, 2911-2923	8.3	85
100	Genomic insights into the origin of farming in the ancient Near East. *Nature*, **2016**, 536, 419-24	50.4	485
99	Genomic analysis of 6,000-year-old cultivated grain illuminates the domestication history of barley. *Nature Genetics*, **2016**, 48, 1089-93	36.3	95
98	Neandertal cannibalism and Neandertal bones used as tools in Northern Europe. *Scientific Reports*, **2016**, 6, 29005	4.9	59
97	Early cave art and ancient DNA record the origin of European bison. *Nature Communications*, **2016**, 7, 13158	17.4	63
96	Temporal patterns of damage and decay kinetics of DNA retrieved from plant herbarium specimens. *Royal Society Open Science*, **2016**, 3, 160239	3.3	62
95	Historical Y.´pestis Genomes Reveal the European Black Death as the Source of Ancient and Modern Plague Pandemics. *Cell Host and Microbe*, **2016**, 19, 874-81	23.4	90
94	Pleistocene Mitochondrial Genomes Suggest a Single Major Dispersal of Non-Africans and a Late Glacial Population Turnover in Europe. *Current Biology*, **2016**, 26, 557-561	6.3	15
93	EAGER: efficient ancient genome reconstruction. *Genome Biology*, **2016**, 17, 60	18.3	195
92	Pleistocene Mitochondrial Genomes Suggest a Single Major Dispersal of Non-Africans and a Late Glacial Population Turnover in Europe. *Current Biology*, **2016**, 26, 827-33	6.3	208
91	The 5300-year-old Helicobacter pylori genome of the Iceman. *Science*, **2016**, 351, 162-165	33.3	152
90	A Molecular Approach to the Sexing of the Triple Burial at the Upper Paleolithic Site of Doln Vstonice. *PLoS ONE*, **2016**, 11, e0163019	3.7	44
89	Eighteenth century Yersinia pestis genomes reveal the long-term persistence of an historical plague focus. *ELife*, **2016**, 5, e12994	8.9	101
88	Effect of X-ray irradiation on ancient DNA in sub-fossil bones - Guidelines for safe X-ray imaging. *Scientific Reports*, **2016**, 6, 32969	4.9	52

87	The genetic history of Ice Age Europe. *Nature*, **2016**, 534, 200-5	50.4	473
86	Genetic Time Travel. *Genetics*, **2016**, 203, 9-12	4	18
85	Genomic insights into the peopling of the Southwest Pacific. *Nature*, **2016**, 538, 510-513	50.4	180
84	Tools for opening new chapters in the book of Treponema pallidum evolutionary history. *Clinical Microbiology and Infection*, **2016**, 22, 916-921	9.5	18
83	Massive migration from the steppe was a source for Indo-European languages in Europe. *Nature*, **2015**, 522, 207-11	50.4	968
82	Insight into the evolution and origin of leprosy bacilli from the genome sequence of Mycobacterium lepromatosis. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 4459-64	11.5	99
81	Genome-wide patterns of selection in 230 ancient Eurasians. *Nature*, **2015**, 528, 499-503	50.4	774
80	Genomics and the challenging translation into conservation practice. *Trends in Ecology and Evolution*, **2015**, 30, 78-87	10.9	335
79	Parallel detection of ancient pathogens via array-based DNA capture. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2015**, 370, 20130375	5.8	33
78	Screening ancient tuberculosis with qPCR: challenges and opportunities. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2015**, 370, 20130622	5.8	14
77	Mitochondrial Genomes of Giant Deers Suggest their Late Survival in Central Europe. *Scientific Reports*, **2015**, 5, 10853	4.9	20
76	Rewriting the Central European Early Bronze Age Chronology: Evidence from Large-Scale Radiocarbon Dating. *PLoS ONE*, **2015**, 10, e0139705	3.7	27
75	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, 2229-34	11.5	244
74	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. *Nature*, **2014**, 514, 494-7	50.4	358
73	Ancient human genomes suggest three ancestral populations for present-day Europeans. *Nature*, **2014**, 513, 409-13	50.4	812
72	Mycobacterium leprae genomes from a British medieval leprosy hospital: towards understanding an ancient epidemic. *BMC Genomics*, **2014**, 15, 270	4.5	49
71	Mining herbaria for plant pathogen genomes: back to the future. *PLoS Pathogens*, **2014**, 10, e1004028	7.6	50
70	Genomic correlates of atherosclerosis in ancient humans. *Global Heart*, **2014**, 9, 203-9	2.9	14

69	Complete mitochondrial genomes of ancient canids suggest a European origin of domestic dogs. *Science*, **2013**, 342, 871-4	33.3	328
68	A revised timescale for human evolution based on ancient mitochondrial genomes. *Current Biology*, **2013**, 23, 553-559	6.3	387
67	Genome-wide comparison of medieval and modern Mycobacterium leprae. *Science*, **2013**, 341, 179-83	33.3	240
66	Ancient human migrations **2013**, 45-64		
65	Next-generation museomics disentangles one of the largest primate radiations. *Systematic Biology*, **2013**, 62, 539-54	8.4	161
64	The rise and fall of the Phytophthora infestans lineage that triggered the Irish potato famine. *ELife*, **2013**, 2, e00731	8.9	246
63	Complete mitochondrial genomes reveal neolithic expansion into Europe. *PLoS ONE*, **2012**, 7, e32473	3.7	49
62	Yersinia pestis: new evidence for an old infection. *PLoS ONE*, **2012**, 7, e49803	3.7	28
61	Temporal patterns of nucleotide misincorporations and DNA fragmentation in ancient DNA. *PLoS ONE*, **2012**, 7, e34131	3.7	325
60	Learning about human population history from ancient and modern genomes. *Nature Reviews Genetics*, **2011**, 12, 603-14	30.1	127
59	A draft genome of Yersinia pestis from victims of the Black Death. *Nature*, **2011**, 478, 506-10	50.4	463
58	Targeted enrichment of ancient pathogens yielding the pPCP1 plasmid of Yersinia pestis from victims of the Black Death. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, E746-52	11.5	169
57	Virus progeny of murine cytomegalovirus bacterial artificial chromosome pSM3fr show reduced growth in salivary Glands due to a fixed mutation of MCK-2. *Journal of Virology*, **2011**, 85, 10346-53	6.6	102
56	The complete mitochondrial DNA genome of an unknown hominin from southern Siberia. *Nature*, **2010**, 464, 894-7	50.4	521
55	Genetic history of an archaic hominin group from Denisova Cave in Siberia. *Nature*, **2010**, 468, 1053-60	50.4	1169
54	Removal of deaminated cytosines and detection of in vivo methylation in ancient DNA. *Nucleic Acids Research*, **2010**, 38, e87	20.1	283
53	Targeted investigation of the Neandertal genome by array-based sequence capture. *Science*, **2010**, 328, 723-5	33.3	224
52	A draft sequence of the Neandertal genome. *Science*, **2010**, 328, 710-722	33.3	2599

51	A complete mtDNA genome of an early modern human from Kostenki, Russia. *Current Biology*, **2010**, 20, 231-6	6.3	213
50	Linkage disequilibrium extends across putative selected sites in FOXP2. *Molecular Biology and Evolution*, **2009**, 26, 2181-4	8.3	33
49	The Neandertal genome and ancient DNA authenticity. *EMBO Journal*, **2009**, 28, 2494-502	13	118
48	Targeted retrieval and analysis of five Neandertal mtDNA genomes. *Science*, **2009**, 325, 318-21	33.3	387
47	Primer extension capture: targeted sequence retrieval from heavily degraded DNA sources. *Journal of Visualized Experiments*, **2009**, 1573	1.6	16
46	Mitochondrial genomes reveal an explosive radiation of extinct and extant bears near the Miocene-Pliocene boundary. *BMC Evolutionary Biology*, **2008**, 8, 220	3	207
45	Genetic characterization of the ABO blood group in Neandertals. *BMC Evolutionary Biology*, **2008**, 8, 342	3	45
44	A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. *Cell*, **2008**, 134, 416-26	56.2	405
43	From micrograms to picograms: quantitative PCR reduces the material demands of high-throughput sequencing. *Nucleic Acids Research*, **2008**, 36, e5	20.1	100
42	Patterns of damage in genomic DNA sequences from a Neandertal. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 14616-21	11.5	610
41	Neanderthals in central Asia and Siberia. *Nature*, **2007**, 449, 902-4	50.4	243
40	The derived FOXP2 variant of modern humans was shared with Neandertals. *Current Biology*, **2007**, 17, 1908-12	6.3	376
39	Mitochondrial DNA of an Iberian Neandertal suggests a population affinity with other European Neandertals. *Current Biology*, **2006**, 16, R629-30	6.3	63
38	Sequencing and analysis of Neanderthal genomic DNA. *Science*, **2006**, 314, 1113-8	33.3	415
37	Multiplex amplification of the mammoth mitochondrial genome and the evolution of Elephantidae. *Nature*, **2006**, 439, 724-7	50.4	167
36	Multiplex amplification of ancient DNA. *Nature Protocols*, **2006**, 1, 720-8	18.8	71
35	Analysis of one million base pairs of Neanderthal DNA. *Nature*, **2006**, 444, 330-6	50.4	511
34	Genomic sequencing of Pleistocene cave bears. *Science*, **2005**, 309, 597-9	33.3	191

33	Functional analysis of human and chimpanzee promoters. *Genome Biology*, **2005**, 6, R57	18.3	17
32	Genetic analyses from ancient DNA. *Annual Review of Genetics*, **2004**, 38, 645-79	14.5	904
31	Patterns of Transformation from the Final Neolithic to the Early Bronze Age:241-261		2
30	Correction: The rise and fall of the Phytophthora infestans lineage that triggered the Irish potato famine. *ELife*,2,	8.9	5
29	AncientYersinia pestisgenomes from across Western Europe reveal early diversification during the First Pandemic (541–750)		2
28	HOPS: Automated detection and authentication of pathogen DNA in archaeological remains		1
27	The rate and potential relevance of new mutations in a colonizing plant lineage		1
26	MALT: Fast alignment and analysis of metagenomic DNA sequence data applied to the Tyrolean Iceman		51
25	The genetic structure of the world's first farmers		2
24	Na-Dene populations descend from the Paleo-Eskimo migration into America		3
23	The Stone Age Plague: 1000 years of Persistence in Eurasia		3
22	Salmonella entericagenomes recovered from victims of a major 16th century epidemic in Mexico		11
21	African nonhuman primates are infected with the yaws bacterium Treponema pallidum subsp. pertenue		4
20	The Genomic History Of Southeastern Europe		4
19	African swine fever virus-like integrated elements in a soft tick genome – an ancient virus vector arms race?		1
18	Genomic and dietary transitions during the Mesolithic and Early Neolithic in Sicily		6
17	The Genomic Formation of Human Populations in East Asia		14
16	A dynamic 6,000-year genetic history of Eurasia's Eastern Steppe		3

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14	The genomic formation of First American ancestors in East and Northeast Asia		6
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12	Understanding 6th-Century Barbarian Social Organization and Migration through Paleogenomics		1
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