

# Johannes Krause

## List of Publications by Year in descending order

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189  
papers

35,057  
citations

5876

81  
h-index

4535

171  
g-index

238  
all docs

238  
docs citations

238  
times ranked

21520  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Draft Sequence of the Neandertal Genome. <i>Science</i> , 2010, 328, 710-722.	6.0	3,588
2	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010, 468, 1053-1060.	13.7	1,537
3	Massive migration from the steppe was a source for Indo-European languages in Europe. <i>Nature</i> , 2015, 522, 207-211.	13.7	1,435
4	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014, 513, 409-413.	13.7	1,179
5	Genome-wide patterns of selection in 230 ancient Eurasians. <i>Nature</i> , 2015, 528, 499-503.	13.7	1,160
6	Genetic Analyses from Ancient DNA. <i>Annual Review of Genetics</i> , 2004, 38, 645-679.	3.2	1,084
7	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, 14616-14621.	3.3	799
8	Genomic insights into the origin of farming in the ancient Near East. <i>Nature</i> , 2016, 536, 419-424.	13.7	733
9	The genetic history of Ice Age Europe. <i>Nature</i> , 2016, 534, 200-205.	13.7	729
10	Analysis of one million base pairs of Neanderthal DNA. <i>Nature</i> , 2006, 444, 330-336.	13.7	671
11	The complete mitochondrial DNA genome of an unknown hominin from southern Siberia. <i>Nature</i> , 2010, 464, 894-897.	13.7	659
12	A draft genome of <i>Yersinia pestis</i> from victims of the Black Death. <i>Nature</i> , 2011, 478, 506-510.	13.7	619
13	Sequencing and Analysis of Neanderthal Genomic DNA. <i>Science</i> , 2006, 314, 1113-1118.	6.0	547
14	A Revised Timescale for Human Evolution Based on Ancient Mitochondrial Genomes. <i>Current Biology</i> , 2013, 23, 553-559.	1.8	540
15	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. <i>Nature</i> , 2014, 514, 494-497.	13.7	506
16	A Complete Neandertal Mitochondrial Genome Sequence Determined by High-Throughput Sequencing. <i>Cell</i> , 2008, 134, 416-426.	13.5	503
17	The Beaker phenomenon and the genomic transformation of northwest Europe. <i>Nature</i> , 2018, 555, 190-196.	13.7	503
18	The Derived FOXP2 Variant of Modern Humans Was Shared with Neandertals. <i>Current Biology</i> , 2007, 17, 1908-1912.	1.8	487

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19	The genomic history of southeastern Europe. <i>Nature</i> , 2018, 555, 197-203.	13.7	479
20	Genomics and the challenging translation into conservation practice. <i>Trends in Ecology and Evolution</i> , 2015, 30, 78-87.	4.2	469
21	Targeted Retrieval and Analysis of Five Neandertal mtDNA Genomes. <i>Science</i> , 2009, 325, 318-321.	6.0	456
22	Complete Mitochondrial Genomes of Ancient Canids Suggest a European Origin of Domestic Dogs. <i>Science</i> , 2013, 342, 871-874.	6.0	438
23	Temporal Patterns of Nucleotide Misincorporations and DNA Fragmentation in Ancient DNA. <i>PLoS ONE</i> , 2012, 7, e34131.	1.1	428
24	Removal of deaminated cytosines and detection of in vivo methylation in ancient DNA. <i>Nucleic Acids Research</i> , 2010, 38, e87-e87.	6.5	362
25	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, 2229-2234.	3.3	349
26	The rise and fall of the <i>Phytophthora infestans</i> lineage that triggered the Irish potato famine. <i>ELife</i> , 2013, 2, e00731.	2.8	339
27	Genome-Wide Comparison of Medieval and Modern <i>Mycobacterium leprae</i> . <i>Science</i> , 2013, 341, 179-183.	6.0	313
28	Reconstructing Prehistoric African Population Structure. <i>Cell</i> , 2017, 171, 59-71.e21.	13.5	308
29	EAGER: efficient ancient genome reconstruction. <i>Genome Biology</i> , 2016, 17, 60.	3.8	305
30	Neanderthals in central Asia and Siberia. <i>Nature</i> , 2007, 449, 902-904.	13.7	293
31	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, 827-833.	1.8	277
32	Genomic insights into the peopling of the Southwest Pacific. <i>Nature</i> , 2016, 538, 510-513.	13.7	262
33	Mitochondrial genomes reveal an explosive radiation of extinct and extant bears near the Miocene-Pliocene boundary. <i>BMC Evolutionary Biology</i> , 2008, 8, 220.	3.2	261
34	Reconstructing the Deep Population History of Central and South America. <i>Cell</i> , 2018, 175, 1185-1197.e22.	13.5	259
35	Targeted Investigation of the Neandertal Genome by Array-Based Sequence Capture. <i>Science</i> , 2010, 328, 723-725.	6.0	255
36	A Complete mtDNA Genome of an Early Modern Human from Kostenki, Russia. <i>Current Biology</i> , 2010, 20, 231-236.	1.8	252

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37	Ancient genomes revisit the ancestry of domestic and Przewalski's horses. <i>Science</i> , 2018, 360, 111-114.	6.0	241
38	Genomic Sequencing of Pleistocene Cave Bears. <i>Science</i> , 2005, 309, 597-599.	6.0	221
39	<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.	3.4	218
40	Genomic insights into the formation of human populations in East Asia. <i>Nature</i> , 2021, 591, 413-419.	13.7	216
41	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.	3.3	211
42	Deeply divergent archaic mitochondrial genome provides lower time boundary for African gene flow into Neanderthals. <i>Nature Communications</i> , 2017, 8, 16046.	5.8	211
43	Next-Generation Museomics Disentangles One of the Largest Primate Radiations. <i>Systematic Biology</i> , 2013, 62, 539-554.	2.7	204
44	Genetic origins of the Minoans and Mycenaeans. <i>Nature</i> , 2017, 548, 214-218.	13.7	203
45	The 5300-year-old <i>Helicobacter pylori</i> genome of the Iceman. <i>Science</i> , 2016, 351, 162-165.	6.0	200
46	Reconstructing the genetic history of late Neanderthals. <i>Nature</i> , 2018, 555, 652-656.	13.7	197
47	Ancient pathogen genomics as an emerging tool for infectious disease research. <i>Nature Reviews Genetics</i> , 2019, 20, 323-340.	7.7	195
48	Multiplex amplification of the mammoth mitochondrial genome and the evolution of Elephantidae. <i>Nature</i> , 2006, 439, 724-727.	13.7	194
49	Kinship-based social inequality in Bronze Age Europe. <i>Science</i> , 2019, 366, 731-734.	6.0	175
50	Learning about human population history from ancient and modern genomes. <i>Nature Reviews Genetics</i> , 2011, 12, 603-614.	7.7	172
51	The Neandertal genome and ancient DNA authenticity. <i>EMBO Journal</i> , 2009, 28, 2494-2502.	3.5	170
52	Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. <i>Science</i> , 2017, 357, 512-515.	6.0	169
53	The genetic prehistory of the Baltic Sea region. <i>Nature Communications</i> , 2018, 9, 442.	5.8	151
54	A Robust Framework for Microbial Archaeology. <i>Annual Review of Genomics and Human Genetics</i> , 2017, 18, 321-356.	2.5	144

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55	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, 874-881.	5.1	142
56	Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations. <i>Science</i> , 2018, 360, 548-552.	6.0	142
57	The origins and spread of domestic horses from the Western Eurasian steppes. <i>Nature</i> , 2021, 598, 634-640.	13.7	142
58	Eighteenth century <i>Yersinia pestis</i> genomes reveal the long-term persistence of an historical plague focus. <i>ELife</i> , 2016, 5, e12994.	2.8	139
59	Origin of modern syphilis and emergence of a pandemic <i>Treponema pallidum</i> cluster. <i>Nature Microbiology</i> , 2017, 2, 16245.	5.9	138
60	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.	3.3	136
61	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.	3.3	135
62	The genetic history of admixture across inner Eurasia. <i>Nature Ecology and Evolution</i> , 2019, 3, 966-976.	3.4	135
63	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, 4459-4464.	3.3	134
64	Ancient genomes from northern China suggest links between subsistence changes and human migration. <i>Nature Communications</i> , 2020, 11, 2700.	5.8	133
65	Ancient DNA analysis. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	133
66	Ancient Egyptian mummy genomes suggest an increase of Sub-Saharan African ancestry in post-Roman periods. <i>Nature Communications</i> , 2017, 8, 15694.	5.8	131
67	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, 10346-10353.	1.5	127
68	The Stone Age Plague and Its Persistence in Eurasia. <i>Current Biology</i> , 2017, 27, 3683-3691.e8.	1.8	125
69	A Dynamic 6,000-Year Genetic History of Eurasia's Eastern Steppe. <i>Cell</i> , 2020, 183, 890-904.e29.	13.5	124
70	Analysis of 3800-year-old <i>Yersinia pestis</i> genomes suggests Bronze Age origin for bubonic plague. <i>Nature Communications</i> , 2018, 9, 2234.	5.8	123
71	Genomic analysis of 6,000-year-old cultivated grain illuminates the domestication history of barley. <i>Nature Genetics</i> , 2016, 48, 1089-1093.	9.4	122
72	Palaeo-Eskimo genetic ancestry and the peopling of Chukotka and North America. <i>Nature</i> , 2019, 570, 236-240.	13.7	118

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73	The rate and potential relevance of new mutations in a colonizing plant lineage. <i>PLoS Genetics</i> , 2018, 14, e1007155.	1.5	116
74	Phylogeography of the second plague pandemic revealed through analysis of historical <i>Yersinia pestis</i> genomes. <i>Nature Communications</i> , 2019, 10, 4470.	5.8	113
75	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.	5.8	113
76	Understanding 6th-century barbarian social organization and migration through paleogenomics. <i>Nature Communications</i> , 2018, 9, 3547.	5.8	111
77	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.	3.5	109
78	Temporal patterns of damage and decay kinetics of DNA retrieved from plant herbarium specimens. <i>Royal Society Open Science</i> , 2016, 3, 160239.	1.1	108
79	From micrograms to picograms: quantitative PCR reduces the material demands of high-throughput sequencing. <i>Nucleic Acids Research</i> , 2008, 36, e5-e5.	6.5	105
80	Neolithic and medieval virus genomes reveal complex evolution of hepatitis B. <i>ELife</i> , 2018, 7, .	2.8	101
81	Ancient <i>Yersinia pestis</i> 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.	3.3	100
82	Ancient genomes reveal a high diversity of <i>Mycobacterium leprae</i> in medieval Europe. <i>PLoS Pathogens</i> , 2018, 14, e1006997.	2.1	98
83	Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia. <i>Nature Communications</i> , 2020, 11, 939.	5.8	96
84	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.	4.7	92
85	A Molecular Approach to the Sexing of the Triple Burial at the Upper Paleolithic Site of Doln-Vstonic. <i>PLoS ONE</i> , 2016, 11, e0163019.	1.1	92
86	Language continuity despite population replacement in Remote Oceania. <i>Nature Ecology and Evolution</i> , 2018, 2, 731-740.	3.4	91
87	Mining Metagenomic Data Sets for Ancient DNA: Recommended Protocols for Authentication. <i>Trends in Genetics</i> , 2017, 33, 508-520.	2.9	90
88	Survival of Late Pleistocene Hunter-Gatherer Ancestry in the Iberian Peninsula. <i>Current Biology</i> , 2019, 29, 1169-1177.e7.	1.8	90
89	Differential preservation of endogenous human and microbial DNA in dental calculus and dentin. <i>Scientific Reports</i> , 2018, 8, 9822.	1.6	88
90	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe. <i>Nature Communications</i> , 2018, 9, 5018.	5.8	86

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91	Genomic History of Neolithic to Bronze Age Anatolia, Northern Levant, and Southern Caucasus. <i>Cell</i> , 2020, 181, 1158-1175.e28.	13.5	86
92	Early cave art and ancient DNA record the origin of European bison. <i>Nature Communications</i> , 2016, 7, 13158.	5.8	81
93	Multiplex amplification of ancient DNA. <i>Nature Protocols</i> , 2006, 1, 720-728.	5.5	78
94	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.	1.6	74
95	Late Pleistocene human genome suggests a local origin for the first farmers of central Anatolia. <i>Nature Communications</i> , 2019, 10, 1218.	5.8	74
96	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, .	3.3	74
97	Mining Herbaria for Plant Pathogen Genomes: Back to the Future. <i>PLoS Pathogens</i> , 2014, 10, e1004028.	2.1	72
98	Emergence of human-adapted <i>Salmonella enterica</i> is linked to the Neolithization process. <i>Nature Ecology and Evolution</i> , 2020, 4, 324-333.	3.4	72
99	Paleolithic to Bronze Age Siberians Reveal Connections with First Americans and across Eurasia. <i>Cell</i> , 2020, 181, 1232-1245.e20.	13.5	71
100	Neandertal cannibalism and Neandertal bones used as tools in Northern Europe. <i>Scientific Reports</i> , 2016, 6, 29005.	1.6	70
101	Ancient DNA suggests modern wolves trace their origin to a Late Pleistocene expansion from Beringia. <i>Molecular Ecology</i> , 2020, 29, 1596-1610.	2.0	70
102	Reconciling material cultures in archaeology with genetic data: The nomenclature of clusters emerging from archaeogenomic analysis. <i>Scientific Reports</i> , 2018, 8, 13003.	1.6	69
103	A Paleogenomic Reconstruction of the Deep Population History of the Andes. <i>Cell</i> , 2020, 181, 1131-1145.e21.	13.5	69
104	A genome sequence from a modern human skull over 45,000 years old from Zlatá Koruna in Czechia. <i>Nature Ecology and Evolution</i> , 2021, 5, 820-825.	3.4	69
105	Mitochondrial DNA of an Iberian Neandertal suggests a population affinity with other European Neandertals. <i>Current Biology</i> , 2006, 16, R629-R630.	1.8	68
106	HOPS: automated detection and authentication of pathogen DNA in archaeological remains. <i>Genome Biology</i> , 2019, 20, 280.	3.8	67
107	The genomic origins of the Bronze Age Tarim Basin mummies. <i>Nature</i> , 2021, 599, 256-261.	13.7	65
108	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.	1.8	64

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109	Ancient DNA sheds light on the genetic origins of early Iron Age Philistines. <i>Science Advances</i> , 2019, 5, eaax0061.	4.7	64
110	Ten millennia of hepatitis B virus evolution. <i>Science</i> , 2021, 374, 182-188.	6.0	64
111	Complete Mitochondrial Genomes Reveal Neolithic Expansion into Europe. <i>PLoS ONE</i> , 2012, 7, e32473.	1.1	61
112	<i>Mycobacterium leprae</i> genomes from a British medieval leprosy hospital: towards understanding an ancient epidemic. <i>BMC Genomics</i> , 2014, 15, 270.	1.2	60
113	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.	1.6	60
114	Historic <i>Treponema pallidum</i> genomes from Colonial Mexico retrieved from archaeological remains. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006447.	1.3	58
115	The source of the Black Death in fourteenth-century central Eurasia. <i>Nature</i> , 2022, 606, 718-724.	13.7	58
116	Large-scale mitogenomic analysis of the phylogeography of the Late Pleistocene cave bear. <i>Scientific Reports</i> , 2019, 9, 10700.	1.6	57
117	Ancient genomes reveal complex patterns of population movement, interaction, and replacement in sub-Saharan Africa. <i>Science Advances</i> , 2020, 6, eaaz0183.	4.7	56
118	Genetic characterization of the ABO blood group in Neandertals. <i>BMC Evolutionary Biology</i> , 2008, 8, 342.	3.2	53
119	Reconstructing Asian faunal introductions to eastern Africa from multi-proxy biomolecular and archaeological datasets. <i>PLoS ONE</i> , 2017, 12, e0182565.	1.1	53
120	Nuclear DNA from two early Neandertals reveals 80,000 years of genetic continuity in Europe. <i>Science Advances</i> , 2019, 5, eaaw5873.	4.7	52
121	Linkage Disequilibrium Extends Across Putative Selected Sites in <i>FOXP2</i> . <i>Molecular Biology and Evolution</i> , 2009, 26, 2181-2184.	3.5	51
122	Ancient genomes reveal social and genetic structure of Late Neolithic Switzerland. <i>Nature Communications</i> , 2020, 11, 1915.	5.8	50
123	Ethics of DNA research on human remains: five globally applicable guidelines. <i>Nature</i> , 2021, 599, 41-46.	13.7	49
124	Ratio of mitochondrial to nuclear DNA affects contamination estimates in ancient DNA analysis. <i>Scientific Reports</i> , 2018, 8, 14075.	1.6	48
125	Grey wolf genomic history reveals a dual ancestry of dogs. <i>Nature</i> , 2022, 607, 313-320.	13.7	48
126	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.	1.8	47



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127	Dynamic changes in genomic and social structures in third millennium BCE central Europe. <i>Science Advances</i> , 2021, 7, .	4.7	46
128	The maternal genetic make-up of the Iberian Peninsula between the Neolithic and the Early Bronze Age. <i>Scientific Reports</i> , 2017, 7, 15644.	1.6	44
129	Genomic insights into the early peopling of the Caribbean. <i>Science</i> , 2020, 369, 456-460.	6.0	44
130	The origin and legacy of the Etruscans through a 2000-year archeogenomic time transect. <i>Science Advances</i> , 2021, 7, eabi7673.	4.7	44
131	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, 1-4.	3.0	41
132	Insights into human history from the first decade of ancient human genomics. <i>Science</i> , 2021, 373, 1479-1484.	6.0	41
133	The immunogenetic diversity of the HLA system in Mexico correlates with underlying population genetic structure. <i>Human Immunology</i> , 2020, 81, 461-474.	1.2	39
134	A systematic investigation of human DNA preservation in medieval skeletons. <i>Scientific Reports</i> , 2020, 10, 18225.	1.6	39
135	Ancient genomic time transect from the Central Asian Steppe unravels the history of the Scythians. <i>Science Advances</i> , 2021, 7, .	4.7	39
136	Genomic transformation and social organization during the Copper Age–Bronze Age transition in southern Iberia. <i>Science Advances</i> , 2021, 7, eabi7038.	4.7	39
137	Parallel detection of ancient pathogens via array-based DNA capture. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130375.	1.8	38
138	Paleomicrobiology: Diagnosis and Evolution of Ancient Pathogens. <i>Annual Review of Microbiology</i> , 2019, 73, 639-666.	2.9	36
139	Genome of a middle Holocene hunter-gatherer from Wallacea. <i>Nature</i> , 2021, 596, 543-547.	13.7	35
140	Rewriting the Central European Early Bronze Age Chronology: Evidence from Large-Scale Radiocarbon Dating. <i>PLoS ONE</i> , 2015, 10, e0139705.	1.1	34
141	Origin and Health Status of First-Generation Africans from Early Colonial Mexico. <i>Current Biology</i> , 2020, 30, 2078-2091.e11.	1.8	34
142	<i>Yersinia pestis</i> : New Evidence for an Old Infection. <i>PLoS ONE</i> , 2012, 7, e49803.	1.1	33
143	Stone Age <i>Yersinia pestis</i> 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.	3.3	31
144	Central European Woolly Mammoth Population Dynamics: Insights from Late Pleistocene Mitochondrial Genomes. <i>Scientific Reports</i> , 2017, 7, 17714.	1.6	30

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145	2000-year-old pathogen genomes reconstructed from metagenomic analysis of Egyptian mummified individuals. <i>BMC Biology</i> , 2020, 18, 108.	1.7	29
146	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.	3.5	29
147	Mitochondrial Genomes of Giant Deers Suggest their Late Survival in Central Europe. <i>Scientific Reports</i> , 2015, 5, 10853.	1.6	28
148	Ancient genome-wide analyses infer kinship structure in an Early Medieval Alemannic graveyard. <i>Science Advances</i> , 2018, 4, eaao1262.	4.7	28
149	Identification of African swine fever virus-like elements in the soft tick genome provides insights into the virus's evolution. <i>BMC Biology</i> , 2020, 18, 136.	1.7	28
150	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.	2.8	26
151	Ancient genomes reveal origin and rapid trans-Eurasian migration of 7th century Avar elites. <i>Cell</i> , 2022, 185, 1402-1413.e21.	13.5	26
152	Genetic Time Travel. <i>Genetics</i> , 2016, 203, 9-12.	1.2	23
153	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.	1.6	23
154	Primer Extension Capture: Targeted Sequence Retrieval from Heavily Degraded DNA Sources. <i>Journal of Visualized Experiments</i> , 2009, , 1573.	0.2	22
155	Geographically dispersed zoonotic tuberculosis in pre-contact South American human populations. <i>Nature Communications</i> , 2022, 13, 1195.	5.8	22
156	Emergence and intensification of dairying in the Caucasus and Eurasian steppes. <i>Nature Ecology and Evolution</i> , 2022, 6, 813-822.	3.4	22
157	Screening ancient tuberculosis with qPCR: challenges and opportunities. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130622.	1.8	21
158	Genomic Correlates of Atherosclerosis in Ancient Humans. <i>Global Heart</i> , 2014, 9, 203.	0.9	20
159	Genome-wide study of a Neolithic Wartberg grave community reveals distinct HLA variation and hunter-gatherer ancestry. <i>Communications Biology</i> , 2021, 4, 113.	2.0	20
160	Functional analysis of human and chimpanzee promoters. <i>Genome Biology</i> , 2005, 6, R57.	13.9	19
161	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.	1.8	17
162	Comparison of target enrichment strategies for ancient pathogen DNA. <i>BioTechniques</i> , 2020, 69, 455-459.	0.8	17

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163	Population Genetics and Signatures of Selection in Early Neolithic European Farmers. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	16
164	Ancient genomes from the last three millennia support multiple human dispersals into Wallacea. <i>Nature Ecology and Evolution</i> , 2022, 6, 1024-1034.	3.4	15
165	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.	1.6	14
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