

Krause Johannes

List of Publications by Citations

Source: <https://exaly.com/author-pdf/227254/krause-johannes-publications-by-citations.pdf>

Version: 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

193
papers

23,424
citations

69
h-index

152
g-index

213
ext. papers

29,998
ext. citations

18.9
avg, IF

6.2
L-index

#	Paper	IF	Citations
193	A draft sequence of the Neandertal genome. <i>Science</i> , 2010 , 328, 710-722	33.3	2599
192	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010 , 468, 1053-60	50.4	1169
191	Massive migration from the steppe was a source for Indo-European languages in Europe. <i>Nature</i> , 2015 , 522, 207-11	50.4	968
190	Genetic analyses from ancient DNA. <i>Annual Review of Genetics</i> , 2004 , 38, 645-79	14.5	904
189	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014 , 513, 409-13	50.4	812
188	Genome-wide patterns of selection in 230 ancient Eurasians. <i>Nature</i> , 2015 , 528, 499-503	50.4	774
187	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
186	The complete mitochondrial DNA genome of an unknown hominin from southern Siberia. <i>Nature</i> , 2010 , 464, 894-7	50.4	521
185	Analysis of one million base pairs of Neanderthal DNA. <i>Nature</i> , 2006 , 444, 330-6	50.4	511
184	Genomic insights into the origin of farming in the ancient Near East. <i>Nature</i> , 2016 , 536, 419-24	50.4	485
183	The genetic history of Ice Age Europe. <i>Nature</i> , 2016 , 534, 200-5	50.4	473
182	A draft genome of <i>Yersinia pestis</i> from victims of the Black Death. <i>Nature</i> , 2011 , 478, 506-10	50.4	463
181	Sequencing and analysis of Neanderthal genomic DNA. <i>Science</i> , 2006 , 314, 1113-8	33.3	415
180	A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. <i>Cell</i> , 2008 , 134, 416-26	56.2	405
179	A revised timescale for human evolution based on ancient mitochondrial genomes. <i>Current Biology</i> , 2013 , 23, 553-559	6.3	387
178	Targeted retrieval and analysis of five Neandertal mtDNA genomes. <i>Science</i> , 2009 , 325, 318-21	33.3	387
177	The derived FOXP2 variant of modern humans was shared with Neandertals. <i>Current Biology</i> , 2007 , 17, 1908-12	6.3	376

176	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. <i>Nature</i> , 2014 , 514, 494-7	50.4	358
175	Genomics and the challenging translation into conservation practice. <i>Trends in Ecology and Evolution</i> , 2015 , 30, 78-87	10.9	335
174	Complete mitochondrial genomes of ancient canids suggest a European origin of domestic dogs. <i>Science</i> , 2013 , 342, 871-4	33.3	328
173	Temporal patterns of nucleotide misincorporations and DNA fragmentation in ancient DNA. <i>PLoS ONE</i> , 2012 , 7, e34131	3.7	325
172	The Beaker phenomenon and the genomic transformation of northwest Europe. <i>Nature</i> , 2018 , 555, 190-196	10.4	293
171	The genomic history of southeastern Europe. <i>Nature</i> , 2018 , 555, 197-203	50.4	287
170	Removal of deaminated cytosines and detection of in vivo methylation in ancient DNA. <i>Nucleic Acids Research</i> , 2010 , 38, e87	20.1	283
169	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
168	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
167	Neanderthals in central Asia and Siberia. <i>Nature</i> , 2007 , 449, 902-4	50.4	243
166	Genome-wide comparison of medieval and modern <i>Mycobacterium leprae</i> . <i>Science</i> , 2013 , 341, 179-83	33.3	240
165	Targeted investigation of the Neandertal genome by array-based sequence capture. <i>Science</i> , 2010 , 328, 723-5	33.3	224
164	A complete mtDNA genome of an early modern human from Kostenki, Russia. <i>Current Biology</i> , 2010 , 20, 231-6	6.3	213
163	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
162	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
161	Reconstructing Prehistoric African Population Structure. <i>Cell</i> , 2017 , 171, 59-71.e21	56.2	201
160	EAGER: efficient ancient genome reconstruction. <i>Genome Biology</i> , 2016 , 17, 60	18.3	195
159	Genomic sequencing of Pleistocene cave bears. <i>Science</i> , 2005 , 309, 597-9	33.3	191

158	Genomic insights into the peopling of the Southwest Pacific. <i>Nature</i> , 2016 , 538, 510-513	50.4	180
157	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
156	Multiplex amplification of the mammoth mitochondrial genome and the evolution of Elephantidae. <i>Nature</i> , 2006 , 439, 724-7	50.4	167
155	Next-generation museomics disentangles one of the largest primate radiations. <i>Systematic Biology</i> , 2013 , 62, 539-54	8.4	161
154	Ancient genomes revisit the ancestry of domestic and Przewalski's horses. <i>Science</i> , 2018 , 360, 111-114	33.3	153
153	The 5300-year-old <i>Helicobacter pylori</i> genome of the Iceman. <i>Science</i> , 2016 , 351, 162-165	33.3	152
152	Reconstructing the Deep Population History of Central and South America. <i>Cell</i> , 2018 , 175, 1185-1197.e27	36.2	143
151	Reconstructing the genetic history of late Neanderthals. <i>Nature</i> , 2018 , 555, 652-656	50.4	138
150	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
149	Learning about human population history from ancient and modern genomes. <i>Nature Reviews Genetics</i> , 2011 , 12, 603-14	30.1	127
148	<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
147	The Neandertal genome and ancient DNA authenticity. <i>EMBO Journal</i> , 2009 , 28, 2494-502	13	118
146	Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. <i>Science</i> , 2017 , 357, 512-515	33.3	110
145	Genetic origins of the Minoans and Mycenaeans. <i>Nature</i> , 2017 , 548, 214-218	50.4	108
144	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
143	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
142	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
141	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

140	Kinship-based social inequality in Bronze Age Europe. <i>Science</i> , 2019 , 366, 731-734	33.3	97
139	The genetic prehistory of the Baltic Sea region. <i>Nature Communications</i> , 2018 , 9, 442	17.4	96
138	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
137	A Robust Framework for Microbial Archaeology. <i>Annual Review of Genomics and Human Genetics</i> , 2017 , 18, 321-356	9.7	92
136	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
135	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
134	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
133	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
132	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
131	Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations. <i>Science</i> , 2018 , 360, 548-552	33.3	83
130	The Stone Age Plague and Its Persistence in Eurasia. <i>Current Biology</i> , 2017 , 27, 3683-3691.e8	6.3	81
129	A58 Epidemic dynamics of ancient disease outbreaks. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
128	Ancient pathogen genomics as an emerging tool for infectious disease research. <i>Nature Reviews Genetics</i> , 2019 , 20, 323-340	30.1	76
127	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
126	Multiplex amplification of ancient DNA. <i>Nature Protocols</i> , 2006 , 1, 720-8	18.8	71
125	Ancient genomes reveal a high diversity of <i>Mycobacterium leprae</i> in medieval Europe. <i>PLoS Pathogens</i> , 2018 , 14, e1006997	7.6	70
124	The genetic history of admixture across inner Eurasia. <i>Nature Ecology and Evolution</i> , 2019 , 3, 966-976	12.3	69
123	The rate and potential relevance of new mutations in a colonizing plant lineage. <i>PLoS Genetics</i> , 2018 , 14, e1007155	6	65

122	Early cave art and ancient DNA record the origin of European bison. <i>Nature Communications</i> , 2016 , 7, 13158	17.4	63
121	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
120	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
119	Genomic insights into the formation of human populations in East Asia. <i>Nature</i> , 2021 , 591, 413-419	50.4	62
118	Neandertal cannibalism and Neandertal bones used as tools in Northern Europe. <i>Scientific Reports</i> , 2016 , 6, 29005	4.9	59
117	Mining Metagenomic Data Sets for Ancient DNA: Recommended Protocols for Authentication. <i>Trends in Genetics</i> , 2017 , 33, 508-520	8.5	59
116	Neolithic and medieval virus genomes reveal complex evolution of hepatitis B. <i>ELife</i> , 2018 , 7,	8.9	59
115	Understanding 6th-century barbarian social organization and migration through paleogenomics. <i>Nature Communications</i> , 2018 , 9, 3547	17.4	57
114	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
113	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
112	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
111	Differential preservation of endogenous human and microbial DNA in dental calculus and dentin. <i>Scientific Reports</i> , 2018 , 8, 9822	4.9	55
110	Palaeo-Eskimo genetic ancestry and the peopling of Chukotka and North America. <i>Nature</i> , 2019 , 570, 236-240	50.4	53
109	Ancient genomes from northern China suggest links between subsistence changes and human migration. <i>Nature Communications</i> , 2020 , 11, 2700	17.4	53
108	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
107	MALT: Fast alignment and analysis of metagenomic DNA sequence data applied to the Tyrolean Iceman		51
106	Language continuity despite population replacement in Remote Oceania. <i>Nature Ecology and Evolution</i> , 2018 , 2, 731-740	12.3	50
105	Mining herbaria for plant pathogen genomes: back to the future. <i>PLoS Pathogens</i> , 2014 , 10, e1004028	7.6	50

104	Mycobacterium leprae genomes from a British medieval leprosy hospital: towards understanding an ancient epidemic. <i>BMC Genomics</i> , 2014 , 15, 270	4.5	49
103	Complete mitochondrial genomes reveal neolithic expansion into Europe. <i>PLoS ONE</i> , 2012 , 7, e32473	3.7	49
102	Survival of Late Pleistocene Hunter-Gatherer Ancestry in the Iberian Peninsula. <i>Current Biology</i> , 2019 , 29, 1169-1177.e7	6.3	48
101	A Dynamic 6,000-Year Genetic History of Eurasia's Eastern Steppe. <i>Cell</i> , 2020 , 183, 890-904.e29	56.2	48
100	Genetic characterization of the ABO blood group in Neandertals. <i>BMC Evolutionary Biology</i> , 2008 , 8, 3423		45
99	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
98	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe. <i>Nature Communications</i> , 2018 , 9, 5018	17.4	43
97	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
96	Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia. <i>Nature Communications</i> , 2020 , 11, 939	17.4	42
95	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
94	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
93	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
92	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
91	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
90	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
89	Ancient DNA sheds light on the genetic origins of early Iron Age Philistines. <i>Science Advances</i> , 2019 , 5, eaax0061	14.3	34
88	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
87	HOPS: automated detection and authentication of pathogen DNA in archaeological remains. <i>Genome Biology</i> , 2019 , 20, 280	18.3	34

86	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
85	A Paleogenomic Reconstruction of the Deep Population History of the Andes. <i>Cell</i> , 2020 , 181, 1131-1145.e21	56.2	33
84	Linkage disequilibrium extends across putative selected sites in FOXP2. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2181-4	8.3	33
83	Paleolithic to Bronze Age Siberians Reveal Connections with First Americans and across Eurasia. <i>Cell</i> , 2020 , 181, 1232-1245.e20	56.2	33
82	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
81	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
80	Genomic History of Neolithic to Bronze Age Anatolia, Northern Levant, and Southern Caucasus. <i>Cell</i> , 2020 , 181, 1158-1175.e28	56.2	29
79	<i>Yersinia pestis</i> : new evidence for an old infection. <i>PLoS ONE</i> , 2012 , 7, e49803	3.7	28
78	Rewriting the Central European Early Bronze Age Chronology: Evidence from Large-Scale Radiocarbon Dating. <i>PLoS ONE</i> , 2015 , 10, e0139705	3.7	27
77	Ratio of mitochondrial to nuclear DNA affects contamination estimates in ancient DNA analysis. <i>Scientific Reports</i> , 2018 , 8, 14075	4.9	25
76	Central European Woolly Mammoth Population Dynamics: Insights from Late Pleistocene Mitochondrial Genomes. <i>Scientific Reports</i> , 2017 , 7, 17714	4.9	24
75	The origins and spread of domestic horses from the Western Eurasian steppes. <i>Nature</i> , 2021 , 598, 634-640.	50.4	24
74	Genomic insights into the early peopling of the Caribbean. <i>Science</i> , 2020 , 369, 456-460	33.3	21
73	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
72	Ancient DNA analysis. <i>Nature Reviews Methods Primers</i> , 2021 , 1,		21
71	Paleomicrobiology: Diagnosis and Evolution of Ancient Pathogens. <i>Annual Review of Microbiology</i> , 2019 , 73, 639-666	17.5	20
70	Mitochondrial Genomes of Giant Deers Suggest their Late Survival in Central Europe. <i>Scientific Reports</i> , 2015 , 5, 10853	4.9	20
69	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

68	A genome sequence from a modern human skull over 45,000 years old from Zlatkūn Czechia. <i>Nature Ecology and Evolution</i> , 2021 , 5, 820-825	12.3	18
67	Genetic Time Travel. <i>Genetics</i> , 2016 , 203, 9-12	4	18
66	Ancient genomes reveal social and genetic structure of Late Neolithic Switzerland. <i>Nature Communications</i> , 2020 , 11, 1915	17.4	18
65	Functional analysis of human and chimpanzee promoters. <i>Genome Biology</i> , 2005 , 6, R57	18.3	17
64	Origin and Health Status of First-Generation Africans from Early Colonial Mexico. <i>Current Biology</i> , 2020 , 30, 2078-2091.e11	6.3	16
63	Primer extension capture: targeted sequence retrieval from heavily degraded DNA sources. <i>Journal of Visualized Experiments</i> , 2009 , 1573	1.6	16
62	2000-year-old pathogen genomes reconstructed from metagenomic analysis of Egyptian mummified individuals. <i>BMC Biology</i> , 2020 , 18, 108	7.3	16
61	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
60	The genomic origins of the Bronze Age Tarim Basin mummies. <i>Nature</i> , 2021 , 599, 256-261	50.4	14
59	The Genomic Formation of Human Populations in East Asia		14
58	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
57	Genomic correlates of atherosclerosis in ancient humans. <i>Global Heart</i> , 2014 , 9, 203-9	2.9	14
56	A systematic investigation of human DNA preservation in medieval skeletons. <i>Scientific Reports</i> , 2020 , 10, 18225	4.9	13
55	Ancient genome-wide analyses infer kinship structure in an Early Medieval Alemannic graveyard. <i>Science Advances</i> , 2018 , 4, eaao1262	14.3	12
54	Genetic structure of Tibetan populations in Gansu revealed by forensic STR loci. <i>Scientific Reports</i> , 2017 , 7, 41195	4.9	11
53	The Beaker Phenomenon and the Genomic Transformation of Northwest Europe 2017 ,		11
52	Salmonella entericagenomes recovered from victims of a major 16th century epidemic in Mexico		11
51	Ancient genomic time transect from the Central Asian Steppe unravels the history of the Scythians. <i>Science Advances</i> , 2021 , 7,	14.3	11

50	The genetic prehistory of the Greater Caucasus		10
49	Ethics of DNA research on human remains: five globally applicable guidelines. <i>Nature</i> , 2021 , 599, 41-46	50.4	9
48	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
47	Ten millennia of hepatitis B virus evolution. <i>Science</i> , 2021 , 374, 182-188	33.3	7
46	Genome of a middle Holocene hunter-gatherer from Wallacea. <i>Nature</i> , 2021 , 596, 543-547	50.4	7
45	Insights into human history from the first decade of ancient human genomics. <i>Science</i> , 2021 , 373, 1479-1484	33.3	7
44	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
43	Genomic and dietary transitions during the Mesolithic and Early Neolithic in Sicily		6
42	The genomic formation of First American ancestors in East and Northeast Asia		6
41	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
40	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
39	Population history from the Neolithic to present on the Mediterranean island of Sardinia: An ancient DNA perspective		5
38	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
37	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
36	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
35	The Genomic History Of Southeastern Europe		4
34	Ancient <i>Yersinia pestis</i> genomes provide no evidence for the origins or spread of the Justinianic Plague		4
33	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

32	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
31	Comparison of target enrichment strategies for ancient pathogen DNA. <i>BioTechniques</i> , 2020 , 69, 455-459.	5.5	3
30	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
29	The Stone Age Plague: 1000 years of Persistence in Eurasia		3
28	A dynamic 6,000-year genetic history of Eurasia's Eastern Steppe		3
27	Characterizing the genetic history of admixture across inner Eurasia		3
26	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
25	Dynamic changes in genomic and social structures in third millennium BCE central Europe. <i>Science Advances</i> , 2021 , 7,	14.3	3
24	The origin and legacy of the Etruscans through a 2000-year archeogenomic time transect. <i>Science Advances</i> , 2021 , 7, eabi7673	14.3	3
23	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
22	Ancient <i>Yersinia pestis</i> genomes from across Western Europe reveal early diversification during the First Pandemic (541-50)		2
21	The genetic structure of the world's first farmers		2
20	Ancient bacterial genomes reveal a formerly unknown diversity of <i>Treponema pallidum</i> strains in early modern Europe		2
19	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe		2
18	Late Pleistocene human genome suggests a local origin for the first farmers of central Anatolia		2
17	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
16	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
15	An ancient view on host pathogen interaction across time and space. <i>Current Opinion in Immunology</i> , 2020 , 65, 65-69	7.8	1

14	HOPS: Automated detection and authentication of pathogen DNA in archaeological remains		1
13	The rate and potential relevance of new mutations in a colonizing plant lineage		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
8	Palaeogenomic analysis of black rat (<i>Rattus rattus</i>) reveals multiple European introductions associated with human economic history.. <i>Nature Communications</i> , 2022 , 13, 2399	17.4	1
7	<i>Mycobacterium leprae</i> diversity and population dynamics in medieval Europe from novel ancient genomes. <i>BMC Biology</i> , 2021 , 19, 220	7.3	0
6	A Woman with a Sword? A 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	17.4	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	