Matthias Meyer

List of Publications by Year
in descending order

104	30,049	23567 58	34986 98
papers	citations	h-index	g-index

115	115	115	19570
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Integrated multidisciplinary ecological analysis from the Uluzzian settlement at the Uluzzo C Rock Shelter, southâ€eastern Italy. Journal of Quaternary Science, 2022, 37, 235-256.	2.1	7
2	The earliest Denisovans and their cultural adaptation. Nature Ecology and Evolution, 2022, 6, 28-35.	7.8	19
3	Ancient DNA Methods Improve Forensic DNA Profiling of Korean War and World War II Unknowns. Genes, 2022, 13, 129.	2.4	22
4	Microstratigraphic preservation of ancient faunal and hominin DNA in Pleistocene cave sediments. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	41
5	African climate and geomorphology drive evolution and ghost introgression in sable antelope. Molecular Ecology, 2022, 31, 2968-2984.	3.9	8
6	Quantifying and reducing crossâ€contamination in singleâ€and multiplex hybridization capture of ancient DNA. Molecular Ecology Resources, 2022, 22, 2196-2207.	4.8	9
7	Ancient genomes from the last three millennia support multiple human dispersals into Wallacea. Nature Ecology and Evolution, 2022, 6, 1024-1034.	7.8	15
8	Point-of-care bulk testing for SARS-CoV-2 by combining hybridization capture with improved colorimetric LAMP. Nature Communications, 2021, 12, 1467.	12.8	81
9	Reevaluating the timing of Neanderthal disappearance in Northwest Europe. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	43
10	Unearthing Neanderthal population history using nuclear and mitochondrial DNA from cave sediments. Science, 2021, 372, .	12.6	86
11	Initial Upper Palaeolithic humans in Europe had recent Neanderthal ancestry. Nature, 2021, 592, 253-257.	27.8	119
12	Pleistocene sediment DNA reveals hominin and faunal turnovers at Denisova Cave. Nature, 2021, 595, 399-403.	27.8	67
13	Reply to Van Peer: Direct radiocarbon dating and ancient genomic analysis reveal the true age of the Neanderthals at Spy Cave. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	1
14	A method for the temperature-controlled extraction of DNA from ancient bones. BioTechniques, 2021, 71, 382-386.	1.8	6
15	Ancient DNA from Guam and the peopling of the Pacific. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	25
16	Developmental Systems Drift and the Drivers of Sex Chromosome Evolution. Molecular Biology and Evolution, 2020, 37, 799-810.	8.9	25
17	A late Neanderthal tooth from northeastern Italy. Journal of Human Evolution, 2020, 147, 102867.	2.6	14
18	Reconstructing double-stranded DNA fragments on a single-molecule level reveals patterns of degradation in ancient samples. Genome Research, 2020, 30, 1449-1457.	5.5	7

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19	Mitogenomics of macaques (Macaca) across Wallace's Line in the context of modern human dispersals. Journal of Human Evolution, 2020, 146, 102852.	2.6	18
20	A systematic investigation of human DNA preservation in medieval skeletons. Scientific Reports, 2020, 10, 18225.	3.3	39
21	Denisovan DNA in Late Pleistocene sediments from Baishiya Karst Cave on the Tibetan Plateau. Science, 2020, 370, 584-587.	12.6	129
22	Denisovan ancestry and population history of early East Asians. Science, 2020, 370, 579-583.	12.6	57
23	The evolutionary history of Neanderthal and Denisovan Y chromosomes. Science, 2020, 369, 1653-1656.	12.6	90
24	Pluridisciplinary evidence for burial for the La Ferrassie 8 Neandertal child. Scientific Reports, 2020, 10, 21230.	3.3	30
25	Initial Upper Palaeolithic Homo sapiens from Bacho Kiro Cave, Bulgaria. Nature, 2020, 581, 299-302.	27.8	188
26	A high-coverage Neandertal genome from Chagyrskaya Cave. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15132-15136.	7.1	176
27	Manual and automated preparation of single-stranded DNA libraries for the sequencing of DNA from ancient biological remains and other sources of highly degraded DNA. Nature Protocols, 2020, 15, 2279-2300.	12.0	101
28	Mining ancient microbiomes using selective enrichment of damaged DNA molecules. BMC Genomics, 2020, 21, 432.	2.8	6
29	Emergence of human-adapted Salmonella enterica is linked to the Neolithization process. Nature Ecology and Evolution, 2020, 4, 324-333.	7.8	72
30	Hybridization ddRADâ€sequencing for population genomics of nonmodel plants using highly degraded historical specimen DNA. Molecular Ecology Resources, 2020, 20, 1228-1247.	4.8	19
31	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. PLoS ONE, 2020, 15, e0244824.	2.5	12
32	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
33	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
34	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
35	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
36	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0

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37	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
38	A genetic analysis of the Gibraltar Neanderthals. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15610-15615.	7.1	30
39	An Ancient Harappan Genome Lacks Ancestry from Steppe Pastoralists or Iranian Farmers. Cell, 2019, 179, 729-735.e10.	28.9	62
40	The formation of human populations in South and Central Asia. Science, 2019, 365, .	12.6	383
41	Xenopus fraseri: Mr. Fraser, where did your frog come from?. PLoS ONE, 2019, 14, e0220892.	2.5	24
42	Compound-specific radiocarbon dating and mitochondrial DNA analysis of the Pleistocene hominin from Salkhit Mongolia. Nature Communications, 2019, 10, 274.	12.8	39
43	Age estimates for hominin fossils and the onset of the Upper Palaeolithic at Denisova Cave. Nature, 2019, 565, 640-644.	27.8	137
44	Nuclear DNA from two early Neandertals reveals 80,000 years of genetic continuity in Europe. Science Advances, 2019, 5, eaaw5873.	10.3	52
45	Pretreatment: Removing DNA Contamination from Ancient Bones and Teeth Using Sodium Hypochlorite and Phosphate. Methods in Molecular Biology, 2019, 1963, 15-19.	0.9	9
46	Extraction of Highly Degraded DNA from Ancient Bones and Teeth. Methods in Molecular Biology, 2019, 1963, 25-29.	0.9	32
47	A Method for Single-Stranded Ancient DNA Library Preparation. Methods in Molecular Biology, 2019, 1963, 75-83.	0.9	15
48	A combined method for DNA analysis and radiocarbon dating from a single sample. Scientific Reports, 2018, 8, 4127.	3.3	42
49	Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations. Science, 2018, 360, 548-552.	12.6	142
50	Reconstructing the genetic history of late Neanderthals. Nature, 2018, 555, 652-656.	27.8	197
51	The impact of endogenous content, replicates and pooling on genome capture from faecal samples. Molecular Ecology Resources, 2018, 18, 319-333.	4.8	33
52	Quantifying and reducing spurious alignments for the analysis of ultra-short ancient DNA sequences. BMC Biology, 2018, 16, 121.	3.8	41
53	Historical biogeography of the leopard (Panthera pardus) and its extinct Eurasian populations. BMC Evolutionary Biology, 2018, 18, 156.	3.2	16
54	Extraction of highly degraded DNA from ancient bones, teeth and sediments for high-throughput sequencing. Nature Protocols, 2018, 13, 2447-2461.	12.0	193

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55	The genome of the offspring of a Neanderthal mother and a Denisovan father. Nature, 2018, 561, 113-116.	27.8	323
56	Extending the spectrum of DNA sequences retrieved from ancient bones and teeth. Genome Research, 2017, 27, 1230-1237.	5.5	111
57	Direct radiocarbon dating and DNA analysis of the Darra-i-Kur (Afghanistan) human temporal bone. Journal of Human Evolution, 2017, 107, 86-93.	2.6	19
58	Neandertal and Denisovan DNA from Pleistocene sediments. Science, 2017, 356, 605-608.	12.6	329
59	Single-stranded DNA library preparation from highly degraded DNA usingT4DNA ligase. Nucleic Acids Research, 2017, 45, gkx033.	14.5	198
60	Fossil and genomic evidence constrains the timing of bison arrival in North America. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3457-3462.	7.1	84
61	A high-coverage Neandertal genome from Vindija Cave in Croatia. Science, 2017, 358, 655-658.	12.6	501
62	Reconstructing Prehistoric African Population Structure. Cell, 2017, 171, 59-71.e21.	28.9	308
63	40,000-Year-Old Individual from Asia Provides Insight into Early Population Structure in Eurasia. Current Biology, 2017, 27, 3202-3208.e9.	3.9	191
64	A fourth Denisovan individual. Science Advances, 2017, 3, e1700186.	10.3	74
65	Palaeogenomes of Eurasian straight-tusked elephants challenge the current view of elephant evolution. ELife, 2017, 6, .	6.0	50
66	The genetic history of Ice Age Europe. Nature, 2016, 534, 200-205.	27.8	729
67	Palaeoproteomic evidence identifies archaic hominins associated with the ChÃ¢telperronian at the Grotte du Renne. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 11162-11167.	7.1	251
68	Identification of a new hominin bone from Denisova Cave, Siberia using collagen fingerprinting and mitochondrial DNA analysis. Scientific Reports, 2016, 6, 23559.	3.3	144
69	Direct radiocarbon dating and genetic analyses on the purported Neanderthal mandible from the Monti Lessini (Italy). Scientific Reports, 2016, 6, 29144.	3.3	16
70	Ancient gene flow from early modern humans into Eastern Neanderthals. Nature, 2016, 530, 429-433.	27.8	392
71	Nuclear DNA sequences from the Middle Pleistocene Sima de los Huesos hominins. Nature, 2016, 531, 504-507.	27.8	436
72	Mammalian mitochondrial capture, a tool for rapid screening of DNA preservation in faunal and undiagnostic remains, and its application to Middle Pleistocene specimens from Qesem Cave (Israel). Quaternary International, 2016, 398, 210-218.	1.5	31

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73	Reducing microbial and human contamination in DNA extractions from ancient bones and teeth. BioTechniques, 2015, 59, 87-93.	1.8	210
74	Long-Term Balancing Selection in LAD1 Maintains a Missense Trans-Species Polymorphism in Humans, Chimpanzees, and Bonobos. Molecular Biology and Evolution, 2015, 32, 1186-1196.	8.9	70
75	Comment on â€œLate Pleistocene human skeleton and mtDNA link Paleoamericans and modern Native Americansâ€. Science, 2015, 347, 835-835.	12.6	21
76	Massive migration from the steppe was a source for Indo-European languages in Europe. Nature, 2015, 522, 207-211.	27.8	1,435
77	An early modern human from Romania with a recent Neanderthal ancestor. Nature, 2015, 524, 216-219.	27.8	633
78	Patterns of coding variation in the complete exomes of three Neandertals. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6666-6671.	7.1	223
79	Illuminating the Base of the Annelid Tree Using Transcriptomics. Molecular Biology and Evolution, 2014, 31, 1391-1401.	8.9	268
80	The complete genome sequence of a Neanderthal from the Altai Mountains. Nature, 2014, 505, 43-49.	27.8	1,830
81	A mitochondrial genome sequence of a hominin from Sima de los Huesos. Nature, 2014, 505, 403-406.	27.8	434
82	Genome sequence of a 45,000-year-old modern human from western Siberia. Nature, 2014, 514, 445-449.	27.8	856
83	Selective enrichment of damaged DNA molecules for ancient genome sequencing. Genome Research, 2014, 24, 1543-1549.	5.5	93
84	Ancient human genomes suggest three ancestral populations for present-day Europeans. Nature, 2014, 513, 409-413.	27.8	1,179
85	Molecular Phylogeny, Biogeography, and Habitat Preference Evolution of Marsupials. Molecular Biology and Evolution, 2014, 31, 2322-2330.	8.9	189
86	Complete mitochondrial genome sequence of a Middle Pleistocene cave bear reconstructed from ultrashort DNA fragments. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15758-15763.	7.1	1,097
87	DNA analysis of an early modern human from Tianyuan Cave, China. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2223-2227.	7.1	484
88	Single-stranded DNA library preparation for the sequencing of ancient or damaged DNA. Nature Protocols, 2013, 8, 737-748.	12.0	448
89	Ancient DNA Damage. Cold Spring Harbor Perspectives in Biology, 2013, 5, a012567-a012567.	5.5	348
90	Double indexing overcomes inaccuracies in multiplex sequencing on the Illumina platform. Nucleic Acids Research, 2012, 40, e3-e3.	14.5	944

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91	Length and GC-biases during sequencing library amplification: A comparison of various polymerase-buffer systems with ancient and modern DNA sequencing libraries. BioTechniques, 2012, 52, 87-94.	1.8	292
92	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. Science, 2012, 338, 222-226.	12.6	1,695
93	A draft genome of Yersinia pestis from victims of the Black Death. Nature, 2011, 478, 506-510.	27.8	619
94	Targeted Investigation of the Neandertal Genome by Array-Based Sequence Capture. Science, 2010, 328, 723-725.	12.6	255
95	A Draft Sequence of the Neandertal Genome. Science, 2010, 328, 710-722.	12.6	3,588
96	Illumina Sequencing Library Preparation for Highly Multiplexed Target Capture and Sequencing. Cold Spring Harbor Protocols, 2010, 2010, pdb.prot5448.	0.3	1,690
97	Genetic history of an archaic hominin group from Denisova Cave in Siberia. Nature, 2010, 468, 1053-1060.	27.8	1,537
98	Genomic DNA Sequences from Mastodon and Woolly Mammoth Reveal Deep Speciation of Forest and Savanna Elephants. PLoS Biology, 2010, 8, e1000564.	5.6	162
99	Removal of deaminated cytosines and detection of in vivo methylation in ancient DNA. Nucleic Acids Research, 2010, 38, e87-e87.	14.5	362
100	Parallel tagged sequencing on the 454 platform. Nature Protocols, 2008, 3, 267-278.	12.0	289
101	A Complete Neandertal Mitochondrial Genome Sequence Determined by High-Throughput Sequencing. Cell, 2008, 134, 416-426.	28.9	503
102	From micrograms to picograms: quantitative PCR reduces the material demands of high-throughput sequencing. Nucleic Acids Research, 2008, 36, e5-e5.	14.5	105
103	Targeted high-throughput sequencing of tagged nucleic acid samples. Nucleic Acids Research, 2007, 35, e97.	14.5	171
104	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, 14616-14621.	7.1	799