

Kay PrÃ¼fer

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

20,409
citations

76326

40
h-index

128289

60
g-index

67
all docs

67
docs citations

67
times ranked

17635
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic and dietary discontinuities during the Mesolithic and Neolithic in Sicily. <i>IScience</i> , 2022, 25, 104244.	4.1	11
2	Population Genetics and Signatures of Selection in Early Neolithic European Farmers. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	16
3	A genome sequence from a modern human skull over 45,000 years old from Zlatá ½ kÁ~Á in Czechia. <i>Nature Ecology and Evolution</i> , 2021, 5, 820-825.	7.8	69
4	Genome of a middle Holocene hunter-gatherer from Wallacea. <i>Nature</i> , 2021, 596, 543-547.	27.8	35
5	Ten millennia of hepatitis B virus evolution. <i>Science</i> , 2021, 374, 182-188.	12.6	64
6	A high-coverage Neandertal genome from Chagyrskaya Cave. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15132-15136.	7.1	176
7	Multiple Genomic Events Altering Hominin SIGLEC Biology and Innate Immunity Predated the Common Ancestor of Humans and Archaic Hominins. <i>Genome Biology and Evolution</i> , 2020, 12, 1040-1050.	2.5	14
8	Presentâ€Day DNA Contamination in Ancient DNA Datasets. <i>BioEssays</i> , 2020, 42, e2000081.	2.5	31
9	A genetic analysis of the Gibraltar Neanderthals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15610-15615.	7.1	30
10	Nuclear DNA from two early Neanderthals reveals 80,000 years of genetic continuity in Europe. <i>Science Advances</i> , 2019, 5, eaaw5873.	10.3	52
11	Reconstructing the genetic history of late Neanderthals. <i>Nature</i> , 2018, 555, 652-656.	27.8	197
12	Turning Vice into Virtue: Using Batch-Effects to Detect Errors in Large Genomic Data Sets. <i>Genome Biology and Evolution</i> , 2018, 10, 2697-2708.	2.5	7
13	Quantifying and reducing spurious alignments for the analysis of ultra-short ancient DNA sequences. <i>BMC Biology</i> , 2018, 16, 121.	3.8	41
14	snpAD: an ancient DNA genotype caller. <i>Bioinformatics</i> , 2018, 34, 4165-4171.	4.1	52
15	The genome of the offspring of a Neanderthal mother and a Denisovan father. <i>Nature</i> , 2018, 561, 113-116.	27.8	323
16	Functional implications of Neandertal introgression in modern humans. <i>Genome Biology</i> , 2017, 18, 61.	8.8	81
17	Neandertal and Denisovan DNA from Pleistocene sediments. <i>Science</i> , 2017, 356, 605-608.	12.6	329
18	A high-coverage Neandertal genome from Vindija Cave in Croatia. <i>Science</i> , 2017, 358, 655-658.	12.6	501

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19	A fourth Denisovan individual. <i>Science Advances</i> , 2017, 3, e1700186.	10.3	74
20	Detecting ancient positive selection in humans using extended lineage sorting. <i>Genome Research</i> , 2017, 27, 1563-1572.	5.5	99
21	Better support for a small effective population size of Neandertals and a long shared history of Neandertals and Denisovans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10256-E10257.	7.1	19
22	Using the Neandertal genome to study the evolution of small insertions and deletions in modern humans. <i>BMC Evolutionary Biology</i> , 2017, 17, 179.	3.2	14
23	ABAEEnrichment: an R package to test for gene set expression enrichment in the adult and developing human brain. <i>Bioinformatics</i> , 2016, 32, 3201-3203.	4.1	43
24	Natural Selection in the Great Apes. <i>Molecular Biology and Evolution</i> , 2016, 33, 3268-3283.	8.9	70
25	Nuclear DNA sequences from the Middle Pleistocene Sima de los Huesos hominins. <i>Nature</i> , 2016, 531, 504-507.	27.8	436
26	Contesting the presence of wheat in the British Isles 8,000 years ago by assessing ancient DNA authenticity from low-coverage data. <i>ELife</i> , 2015, 4, .	6.0	31
27	Extreme selective sweeps independently targeted the X chromosomes of the great apes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6413-6418.	7.1	75
28	Nuclear and mitochondrial DNA sequences from two Denisovan individuals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15696-15700.	7.1	154
29	Comment on "Late Pleistocene human skeleton and mtDNA link Paleoamericans and modern Native Americans". <i>Science</i> , 2015, 347, 835-835.	12.6	21
30	Human-specific gene <i>ARHGAP11B</i> promotes basal progenitor amplification and neocortex expansion. <i>Science</i> , 2015, 347, 1465-1470.	12.6	487
31	Kiwi genome provides insights into evolution of a nocturnal lifestyle. <i>Genome Biology</i> , 2015, 16, 147.	8.8	68
32	An early modern human from Romania with a recent Neanderthal ancestor. <i>Nature</i> , 2015, 524, 216-219.	27.8	633
33	Lineage-Specific Changes in Biomarkers in Great Apes and Humans. <i>PLoS ONE</i> , 2015, 10, e0134548.	2.5	7
34	Reconstructing the DNA Methylation Maps of the Neandertal and the Denisovan. <i>Science</i> , 2014, 344, 523-527.	12.6	188
35	Neanderthal ancestry drives evolution of lipid catabolism in contemporary Europeans. <i>Nature Communications</i> , 2014, 5, 3584.	12.8	70
36	The complete genome sequence of a Neanderthal from the Altai Mountains. <i>Nature</i> , 2014, 505, 43-49.	27.8	1,830

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37	The genomic landscape of Neanderthal ancestry in present-day humans. <i>Nature</i> , 2014, 507, 354-357.	27.8	877
38	Genome sequence of a 45,000-year-old modern human from western Siberia. <i>Nature</i> , 2014, 514, 445-449.	27.8	856
39	Ancient humans and the origin of modern humans. <i>Current Opinion in Genetics and Development</i> , 2014, 29, 133-138.	3.3	26
40	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014, 513, 409-413.	27.8	1,179
41	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	27.8	768
42	Reply to Gibb and Hills: Divergence times, generation lengths and mutation rates in great apes and humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E612-E612.	7.1	3
43	A New Isolation with Migration Model along Complete Genomes Infers Very Different Divergence Processes among Closely Related Great Ape Species. <i>PLoS Genetics</i> , 2012, 8, e1003125.	3.5	102
44	Impact of ontology evolution on functional analyses. <i>Bioinformatics</i> , 2012, 28, 2671-2677.	4.1	33
45	Transcription Factors Are Targeted by Differentially Expressed miRNAs in Primates. <i>Genome Biology and Evolution</i> , 2012, 4, 552-564.	2.5	30
46	Generation times in wild chimpanzees and gorillas suggest earlier divergence times in great ape and human evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15716-15721.	7.1	499
47	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. <i>Science</i> , 2012, 338, 222-226.	12.6	1,695
48	The bonobo genome compared with the chimpanzee and human genomes. <i>Nature</i> , 2012, 486, 527-531.	27.8	445
49	Bonobos Fall within the Genomic Variation of Chimpanzees. <i>PLoS ONE</i> , 2011, 6, e21605.	2.5	57
50	A Draft Sequence of the Neandertal Genome. <i>Science</i> , 2010, 328, 710-722.	12.6	3,588
51	Computational challenges in the analysis of ancient DNA. <i>Genome Biology</i> , 2010, 11, R47.	9.6	135
52	Ontologies in Biology. , 2010, , 347-371.		3
53	The Neandertal genome and ancient DNA authenticity. <i>EMBO Journal</i> , 2009, 28, 2494-2502.	7.8	170
54	A Complete Neandertal Mitochondrial Genome Sequence Determined by High-Throughput Sequencing. <i>Cell</i> , 2008, 134, 416-426.	28.9	503

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55	PatMaN: rapid alignment of short sequences to large databases. <i>Bioinformatics</i> , 2008, 24, 1530-1531.	4.1	193
56	Targeted high-throughput sequencing of tagged nucleic acid samples. <i>Nucleic Acids Research</i> , 2007, 35, e97.	14.5	171
57	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.	7.1	799
58	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	12.6	1,283
59	Neanderthals in central Asia and Siberia. <i>Nature</i> , 2007, 449, 902-904.	27.8	293
60	FUNC: a package for detecting significant associations between gene sets and ontological annotations. <i>BMC Bioinformatics</i> , 2007, 8, 41.	2.6	180
61	Why do human diversity levels vary at a megabase scale?. <i>Genome Research</i> , 2005, 15, 1222-1231.	5.5	156