

Hendrik N Poinar

List of Publications by Year in descending order

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Version: 2024-02-01

74
papers

10,382
citations

94433

37
h-index

71685

76
g-index

81
all docs

81
docs citations

81
times ranked

11458
citing authors

#	ARTICLE	IF	CITATIONS
1	Antibiotic resistance is ancient. <i>Nature</i> , 2011, 477, 457-461.	27.8	1,967
2	Genetic Analyses from Ancient DNA. <i>Annual Review of Genetics</i> , 2004, 38, 645-679.	7.6	1,084
3	Ancient DNA: Do It Right or Not at All. <i>Science</i> , 2000, 289, 1139-1139.	12.6	983
4	Ancient DNA. <i>Nature Reviews Genetics</i> , 2001, 2, 353-359.	16.3	774
5	A draft genome of <i>Yersinia pestis</i> from victims of the Black Death. <i>Nature</i> , 2011, 478, 506-510.	27.8	619
6	Metagenomics to Paleogenomics: Large-Scale Sequencing of Mammoth DNA. <i>Science</i> , 2006, 311, 392-394.	12.6	519
7	<i>Yersinia pestis</i> and the Plague of Justinian 541â€“543 AD: a genomic analysis. <i>Lancet Infectious Diseases</i> , 2014, 14, 319-326.	9.1	358
8	Complete Genomes Reveal Signatures of Demographic and Genetic Declines in the Woolly Mammoth. <i>Current Biology</i> , 2015, 25, 1395-1400.	3.9	263
9	Isolation of nucleic acids and cultures from fossil ice and permafrost. <i>Trends in Ecology and Evolution</i> , 2004, 19, 141-147.	8.7	231
10	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.	7.1	211
11	17th Century Variola Virus Reveals the Recent History of Smallpox. <i>Current Biology</i> , 2016, 26, 3407-3412.	3.9	197
12	Shotgun Mitogenomics Provides a Reference Phylogenetic Framework and Timescale for Living Xenarthrans. <i>Molecular Biology and Evolution</i> , 2016, 33, 621-642.	8.9	167
13	Recharacterization of ancient DNA miscoding lesions: insights in the era of sequencing-by-synthesis. <i>Nucleic Acids Research</i> , 2006, 35, 1-10.	14.5	166
14	A comprehensive genomic history of extinct and living elephants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2566-E2574.	7.1	142
15	Ancient Whole Genome Enrichment Using Baits Built from Modern DNA. <i>Molecular Biology and Evolution</i> , 2014, 31, 1292-1294.	8.9	141
16	Eighteenth century <i>Yersinia pestis</i> genomes reveal the long-term persistence of an historical plague focus. <i>ELife</i> , 2016, 5, e12994.	6.0	139
17	New insights from old bones: DNA preservation and degradation in permafrost preserved mammoth remains. <i>Nucleic Acids Research</i> , 2009, 37, 3215-3229.	14.5	137
18	Second-Pandemic Strain of <i>Vibrio cholerae</i> from the Philadelphia Cholera Outbreak of 1849. <i>New England Journal of Medicine</i> , 2014, 370, 334-340.	27.0	134

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19	Ancient DNA from lake sediments: Bridging the gap between paleoecology and genetics. BMC Evolutionary Biology, 2011, 11, 30.	3.2	126
20	Nuclear Gene Sequences from a Late Pleistocene Sloth Coprolite. Current Biology, 2003, 13, 1150-1152.	3.9	115
21	Out of America: Ancient DNA Evidence for a New World Origin of Late Quaternary Woolly Mammoths. Current Biology, 2008, 18, 1320-1326.	3.9	110
22	Comparison of methods in the recovery of nucleic acids from archival formalin-fixed paraffin-embedded autopsy tissues. Analytical Biochemistry, 2010, 400, 110-117.	2.4	104
23	The hygiene hypothesis, the COVID pandemic, and consequences for the human microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	100
24	Ancient Mitogenomes Reveal the Evolutionary History and Biogeography of Sloths. Current Biology, 2019, 29, 2031-2042.e6.	3.9	99
25	Plasmodium falciparum malaria in 1 st –2 nd century CE southern Italy. Current Biology, 2016, 26, R1220-R1222.	3.9	94
26	The phylogenetic affinities of the extinct glyptodonts. Current Biology, 2016, 26, R155-R156.	3.9	83
27	A quantitative approach to detect and overcome PCR inhibition in ancient DNA extracts. BioTechniques, 2009, 47, 941-949.	1.8	80
28	The Justinianic Plague: An inconsequential pandemic?. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25546-25554.	7.1	73
29	The paradox of HBV evolution as revealed from a 16th century mummy. PLoS Pathogens, 2018, 14, e1006750.	4.7	66
30	Capturing the Resistome: a Targeted Capture Method To Reveal Antibiotic Resistance Determinants in Metagenomes. Antimicrobial Agents and Chemotherapy, 2019, 64, .	3.2	63
31	A novel method for collection and preservation of faeces for genetic studies. Molecular Ecology Notes, 2004, 4, 761-764.	1.7	62
32	Comment on “eDNA from Pre-Clovis Human Coprolites in Oregon, North America” Science, 2009, 325, 148-148.	12.6	62
33	Complete Columbian mammoth mitogenome suggests interbreeding with woolly mammoths. Genome Biology, 2011, 12, R51.	9.6	56
34	Mammuthus Population Dynamics in Late Pleistocene North America: Divergence, Phylogeography, and Introgression. Frontiers in Ecology and Evolution, 2016, 4, .	2.2	56
35	Ancient pathogen DNA in archaeological samples detected with a Microbial Detection Array. Scientific Reports, 2014, 4, 4245.	3.3	48
36	A molecular portrait of maternal sepsis from Byzantine Troy. ELife, 2017, 6, .	6.0	46

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37	Optimizing extraction and targeted capture of ancient environmental DNA for reconstructing past environments using the PalaeoChip Arctic-1.0 bait-set. <i>Quaternary Research</i> , 2021, 99, 305-328.	1.7	46
38	Quantitative PCR as a predictor of aligned ancient DNA read counts following targeted enrichment. <i>BioTechniques</i> , 2013, 55, 300-9.	1.8	39
39	The evolutionary and phylogeographic history of woolly mammoths: a comprehensive mitogenomic analysis. <i>Scientific Reports</i> , 2017, 7, 44585.	3.3	39
40	Complete mitochondrial genomes of living and extinct pigeons revise the timing of the columbiform radiation. <i>BMC Evolutionary Biology</i> , 2016, 16, 230.	3.2	38
41	Time Dependency of Molecular Rates in Ancient DNA Data Sets, A Sampling Artifact?. <i>Systematic Biology</i> , 2009, 58, 348-360.	5.6	37
42	Collapse of the mammoth-steppe in central Yukon as revealed by ancient environmental DNA. <i>Nature Communications</i> , 2021, 12, 7120.	12.8	37
43	The Recovery, Interpretation and Use of Ancient Pathogen Genomes. <i>Current Biology</i> , 2020, 30, R1215-R1231.	3.9	33
44	Herald waves of cholera in nineteenth century London. <i>Journal of the Royal Society Interface</i> , 2011, 8, 756-760.	3.4	32
45	A preliminary analysis of the DNA and diet of the extinct Beothuk: A systematic approach to ancient human DNA. <i>American Journal of Physical Anthropology</i> , 2007, 132, 594-604.	2.1	30
46	Quantitative Assessment of the Sensitivity of Various Commercial Reverse Transcriptases Based on Armored HIV RNA. <i>PLoS ONE</i> , 2010, 5, e13931.	2.5	26
47	Ancient DNA and the tropics: a rodent's tale. <i>Biology Letters</i> , 2014, 10, 20140224.	2.3	26
48	Ancient human genomics: the methodology behind reconstructing evolutionary pathways. <i>Journal of Human Evolution</i> , 2015, 79, 21-34.	2.6	22
49	The origins and genomic diversity of American Civil War Era smallpox vaccine strains. <i>Genome Biology</i> , 2020, 21, 175.	8.8	22
50	Shifting Climates, Foods, and Diseases: The Human Microbiome through Evolution. <i>BioEssays</i> , 2019, 41, e1900034.	2.5	21
51	Surveying the repair of ancient DNA from bones via high-throughput sequencing. <i>BioTechniques</i> , 2015, 59, 19-25.	1.8	18
52	Genetic Discontinuity between the Maritime Archaic and Beothuk Populations in Newfoundland, Canada. <i>Current Biology</i> , 2017, 27, 3149-3156.e11.	3.9	17
53	<i>Mylodon darwini</i> DNA sequences from ancient fecal hair shafts. <i>Annals of Anatomy</i> , 2012, 194, 26-30.	1.9	16
54	A Single Amino Acid Change in the Response Regulator PhoP, Acquired during <i>Yersinia pestis</i> Evolution, Affects PhoP Target Gene Transcription and Polymyxin B Susceptibility. <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	16

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55	Resolving the phylogenetic position of Darwin's extinct ground sloth (<i>Mylodon darwini</i>) using mitogenomic and nuclear exon data. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180214.	2.6	16
56	Genetic resiliency and the Black Death: No apparent loss of mitogenomic diversity due to the Black Death in medieval London and Denmark. <i>American Journal of Physical Anthropology</i> , 2019, 169, 240-252.	2.1	15
57	Molecular identification of paleofeces from Bechan Cave, southeastern Utah, USA. <i>Quaternary International</i> , 2017, 443, 140-146.	1.5	14
58	A Black Death mass grave at Thornton Abbey: the discovery and examination of a fourteenth-century rural catastrophe. <i>Antiquity</i> , 2020, 94, 179-196.	1.0	14
59	Comment: Characterization of Two Historic Smallpox Specimens from a Czech Museum. <i>Viruses</i> , 2017, 9, 276.	3.3	13
60	A multi-faceted anthropological and genomic approach to framing <i>Plasmodium falciparum</i> malaria in Imperial period central-southern Italy (1st–4th c. CE). <i>Journal of Anthropological Archaeology</i> , 2018, 49, 210-224.	1.6	13
61	Pleistocene mitogenomes reconstructed from the environmental DNA of permafrost sediments. <i>Current Biology</i> , 2022, 32, 851-860.e7.	3.9	13
62	Acceleration of plague outbreaks in the second pandemic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27703-27711.	7.1	12
63	Adaptation in a Fibronectin Binding Autolysin of <i>Staphylococcus saprophyticus</i> . <i>MSphere</i> , 2017, 2, .	2.9	9
64	Ancient Roman mitochondrial genomes and isotopes reveal relationships and geographic origins at the local and pan-Mediterranean scales. <i>Journal of Archaeological Science: Reports</i> , 2018, 20, 200-209.	0.5	9
65	American mastodon mitochondrial genomes suggest multiple dispersal events in response to Pleistocene climate oscillations. <i>Nature Communications</i> , 2020, 11, 4048.	12.8	9
66	Response to Comment on "Whole-Genome Shotgun Sequencing of Mitochondria from Ancient Hair Shafts". <i>Science</i> , 2008, 322, 857-857.	12.6	6
67	Ancient Pathogens Through Human History: A Paleogenomic Perspective. <i>Population Genomics</i> , 2018, , 115-138.	0.5	5
68	Human ectoparasite transmission of the plague during the Second Pandemic is only weakly supported by proposed mathematical models. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E7892-E7893.	7.1	5
69	<i>Yersinia pestis</i> and the three plague pandemics—Authors' reply. <i>Lancet Infectious Diseases</i> , The, 2014, 14, 919.	9.1	4
70	Estimation of Gene Insertion/Deletion Rates with Missing Data. <i>Genetics</i> , 2016, 204, 513-529.	2.9	3
71	Dorset Pre-Inuit and Beothuk foodways in Newfoundland, ca. AD 500-1829. <i>PLoS ONE</i> , 2019, 14, e0210187.	2.5	3
72	Probe design for simultaneous, targeted capture of diverse metagenomic targets. <i>Cell Reports Methods</i> , 2021, 1, 100069.	2.9	3

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73	Response to Brinkmann et al. "Re-assembly of 19th century smallpox vaccine genomes reveals the contemporaneous use of horsepox and horsepox-related viruses in the United States". Genome Biology, 2020, 21, 287.	8.8	2
74	A 16th century Escherichia coli draft genome associated with an opportunistic bile infection. Communications Biology, 2022, 5, .	4.4	2