

# Hendrik N Poinar

## List of Publications by Citations

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

72  
papers

7,902  
citations

34  
h-index

81  
g-index

81  
ext. papers

9,329  
ext. citations

11.2  
avg, IF

5.52  
L-index

#	Paper	IF	Citations
72	Antibiotic resistance is ancient. <i>Nature</i> , <b>2011</b> , 477, 457-61	50.4	1438
71	Genetic analyses from ancient DNA. <i>Annual Review of Genetics</i> , <b>2004</b> , 38, 645-79	14.5	904
70	Ancient DNA: do it right or not at all. <i>Science</i> , <b>2000</b> , 289, 1139	33.3	826
69	Ancient DNA. <i>Nature Reviews Genetics</i> , <b>2001</b> , 2, 353-9	30.1	667
68	A draft genome of <i>Yersinia pestis</i> from victims of the Black Death. <i>Nature</i> , <b>2011</b> , 478, 506-10	50.4	463
67	Metagenomics to paleogenomics: large-scale sequencing of mammoth DNA. <i>Science</i> , <b>2006</b> , 311, 392-4	33.3	435
66	<i>Yersinia pestis</i> and the plague of Justinian 541-543 AD: a genomic analysis. <i>Lancet Infectious Diseases</i> , <b>2014</b> , 14, 319-26	25.5	263
65	Isolation of nucleic acids and cultures from fossil ice and permafrost. <i>Trends in Ecology and Evolution</i> , <b>2004</b> , 19, 141-7	10.9	203
64	Complete genomes reveal signatures of demographic and genetic declines in the woolly mammoth. <i>Current Biology</i> , <b>2015</b> , 25, 1395-400	6.3	177
63	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> , <b>2011</b> , 108, E746-52	11.5	169
62	Recharacterization of ancient DNA miscoding lesions: insights in the era of sequencing-by-synthesis. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, 1-10	20.1	136
61	17 Century Variola Virus Reveals the Recent History of Smallpox. <i>Current Biology</i> , <b>2016</b> , 26, 3407-3412	6.3	118
60	Ancient whole genome enrichment using baits built from modern DNA. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 1292-4	8.3	110
59	Nuclear gene sequences from a late pleistocene sloth coprolite. <i>Current Biology</i> , <b>2003</b> , 13, 1150-2	6.3	108
58	Ancient DNA from lake sediments: bridging the gap between paleoecology and genetics. <i>BMC Evolutionary Biology</i> , <b>2011</b> , 11, 30	3	107
57	New insights from old bones: DNA preservation and degradation in permafrost preserved mammoth remains. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, 3215-29	20.1	106
56	Shotgun Mitogenomics Provides a Reference Phylogenetic Framework and Timescale for Living Xenarthrans. <i>Molecular Biology and Evolution</i> , <b>2016</b> , 33, 621-42	8.3	105

55	Second-pandemic strain of <i>Vibrio cholerae</i> from the Philadelphia cholera outbreak of 1849. <i>New England Journal of Medicine</i> , <b>2014</b> , 370, 334-40	59.2	104
54	Eighteenth century <i>Yersinia pestis</i> genomes reveal the long-term persistence of an historical plague focus. <i>ELife</i> , <b>2016</b> , 5, e12994	8.9	101
53	Out of America: ancient DNA evidence for a new world origin of late quaternary woolly mammoths. <i>Current Biology</i> , <b>2008</b> , 18, 1320-6	6.3	98
52	Comparison of methods in the recovery of nucleic acids from archival formalin-fixed paraffin-embedded autopsy tissues. <i>Analytical Biochemistry</i> , <b>2010</b> , 400, 110-7	3.1	89
51	A comprehensive genomic history of extinct and living elephants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, E2566-E2574	11.5	86
50	A quantitative approach to detect and overcome PCR inhibition in ancient DNA extracts. <i>BioTechniques</i> , <b>2009</b> , 47, 941-9	2.5	69
49	<i>Plasmodium falciparum</i> malaria in 1-2 century CE southern Italy. <i>Current Biology</i> , <b>2016</b> , 26, R1220-R1222	6.3	64
48	The phylogenetic affinities of the extinct glyptodonts. <i>Current Biology</i> , <b>2016</b> , 26, R155-6	6.3	57
47	A novel method for collection and preservation of faeces for genetic studies. <i>Molecular Ecology Notes</i> , <b>2004</b> , 4, 761-764		56
46	The paradox of HBV evolution as revealed from a 16th century mummy. <i>PLoS Pathogens</i> , <b>2018</b> , 14, e1006760	6.3	53
45	Ancient Mitogenomes Reveal the Evolutionary History and Biogeography of Sloths. <i>Current Biology</i> , <b>2019</b> , 29, 2031-2042.e6	6.3	52
44	Complete Columbian mammoth mitogenome suggests interbreeding with woolly mammoths. <i>Genome Biology</i> , <b>2011</b> , 12, R51	18.3	49
43	The hygiene hypothesis, the COVID pandemic, and consequences for the human microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	45
42	The Justinianic Plague: An inconsequential pandemic?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 25546-25554	11.5	44
41	Comment on "DNA from pre-Clovis human coprolites in Oregon, North America". <i>Science</i> , <b>2009</b> , 325, 148; author reply 148	33.3	42
40	Ancient pathogen DNA in archaeological samples detected with a Microbial Detection Array. <i>Scientific Reports</i> , <b>2014</b> , 4, 4245	4.9	38
39	Time dependency of molecular rates in ancient DNA data sets, a sampling artifact?. <i>Systematic Biology</i> , <b>2009</b> , 58, 348-60	8.4	36
38	The evolutionary and phylogeographic history of woolly mammoths: a comprehensive mitogenomic analysis. <i>Scientific Reports</i> , <b>2017</b> , 7, 44585	4.9	34

37	Quantitative PCR as a predictor of aligned ancient DNA read counts following targeted enrichment. <i>BioTechniques</i> , <b>2013</b> , 55, 300-9	2.5	33
36	Mammuthus Population Dynamics in Late Pleistocene North America: Divergence, Phylogeography, and Introgression. <i>Frontiers in Ecology and Evolution</i> , <b>2016</b> , 4,	3.7	32
35	Capturing the Resistome: a Targeted Capture Method To Reveal Antibiotic Resistance Determinants in Metagenomes. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2019</b> , 64,	5.9	29
34	A molecular portrait of maternal sepsis from Byzantine Troy. <i>ELife</i> , <b>2017</b> , 6,	8.9	26
33	Herald waves of cholera in nineteenth century London. <i>Journal of the Royal Society Interface</i> , <b>2011</b> , 8, 756-60	4.1	26
32	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> , <b>2007</b> , 132, 594-604	2.5	26
31	Complete mitochondrial genomes of living and extinct pigeons revise the timing of the columbiform radiation. <i>BMC Evolutionary Biology</i> , <b>2016</b> , 16, 230	3	25
30	Quantitative assessment of the sensitivity of various commercial reverse transcriptases based on armored HIV RNA. <i>PLoS ONE</i> , <b>2010</b> , 5, e13931	3.7	23
29	Ancient DNA and the tropics: a rodent's tale. <i>Biology Letters</i> , <b>2014</b> , 10,	3.6	19
28	Ancient human genomics: the methodology behind reconstructing evolutionary pathways. <i>Journal of Human Evolution</i> , <b>2015</b> , 79, 21-34	3.1	18
27	Myiodon darwinii DNA sequences from ancient fecal hair shafts. <i>Annals of Anatomy</i> , <b>2012</b> , 194, 26-30	2.9	16
26	Genetic Discontinuity between the Maritime Archaic and Beothuk Populations in Newfoundland, Canada. <i>Current Biology</i> , <b>2017</b> , 27, 3149-3156.e11	6.3	15
25	Surveying the repair of ancient DNA from bones via high-throughput sequencing. <i>BioTechniques</i> , <b>2015</b> , 59, 19-25	2.5	12
24	A Single Amino Acid Change in the Response Regulator PhoP, Acquired during Yersinia pestis Evolution, Affects PhoP Target Gene Transcription and Polymyxin B Susceptibility. <i>Journal of Bacteriology</i> , <b>2018</b> , 200,	3.5	11
23	Resolving the phylogenetic position of Darwin's extinct ground sloth () using mitogenomic and nuclear exon data. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2018</b> , 285,	4.4	11
22	The origins and genomic diversity of American Civil War Era smallpox vaccine strains. <i>Genome Biology</i> , <b>2020</b> , 21, 175	18.3	10
21	A multi-faceted anthropological and genomic approach to framing Plasmodium falciparum malaria in Imperial period central-southern Italy (1st-4th c. CE). <i>Journal of Anthropological Archaeology</i> , <b>2018</b> , 49, 210-224	1.9	9
20	Comment: Characterization of Two Historic Smallpox Specimens from a Czech Museum. <i>Viruses</i> , <b>2017</b> , 9,	6.2	9

19	Shifting Climates, Foods, and Diseases: The Human Microbiome through Evolution. <i>BioEssays</i> , <b>2019</b> , 41, e1900034	4.1	8
18	The Recovery, Interpretation and Use of Ancient Pathogen Genomes. <i>Current Biology</i> , <b>2020</b> , 30, R1215-R6231	3.1	8
17	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> , <b>2021</b> , 99, 305-328	1.9	8
16	A Black Death mass grave at Thornton Abbey: the discovery and examination of a fourteenth-century rural catastrophe. <i>Antiquity</i> , <b>2020</b> , 94, 179-196	1	7
15	Acceleration of plague outbreaks in the second pandemic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 27703-27711	11.5	7
14	Adaptation in a Fibronectin Binding Autolysin of. <i>MSphere</i> , <b>2017</b> , 2,	5	6
13	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> , <b>2018</b> , 20, 200-209	0.7	6
12	Molecular identification of paleofeces from Bechan Cave, southeastern Utah, USA. <i>Quaternary International</i> , <b>2017</b> , 443, 140-146	2	5
11	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> , <b>2019</b> , 169, 240-252	2.5	5
10	Comment on "Whole-genome shotgun sequencing of mitochondria from ancient hair shafts". <i>Science</i> , <b>2008</b> , 322, 857; author reply 857	33.3	5
9	Collapse of the mammoth-steppe in central Yukon as revealed by ancient environmental DNA. <i>Nature Communications</i> , <b>2021</b> , 12, 7120	17.4	4
8	American mastodon mitochondrial genomes suggest multiple dispersal events in response to Pleistocene climate oscillations. <i>Nature Communications</i> , <b>2020</b> , 11, 4048	17.4	4
7	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> , <b>2018</b> , 115, E7892-E7893	11.5	3
6	Yersinia pestis and the three plague pandemics--authorsReply. <i>Lancet Infectious Diseases, The</i> , <b>2014</b> , 14, 919	25.5	3
5	Ancient Pathogens Through Human History: A Paleogenomic Perspective. <i>Population Genomics</i> , <b>2018</b> , 115-138	1.4	3
4	Estimation of Gene Insertion/Deletion Rates with Missing Data. <i>Genetics</i> , <b>2016</b> , 204, 513-529	4	2
3	Dorset Pre-Inuit and Beothuk foodways in Newfoundland, ca. AD 500-1829. <i>PLoS ONE</i> , <b>2019</b> , 14, e0210187	1.7	2
2	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". <i>Genome Biology</i> , <b>2020</b> , 21, 287	18.3	0

- 1 Probe design for simultaneous, targeted capture of diverse metagenomic targets.. *Cell Reports Methods*, **2021**, 1, 100069