

Neolithic and medieval virus genomes reveal complex e

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Ancient Pathogens Through Human History: A Paleogenomic Perspective. <i>Population Genomics</i> , 2018, , 115-138.	0.2	5
2	The Role of aDNA in Understanding the Coevolutionary Patterns of Human Sexually Transmitted Infections. <i>Genes</i> , 2018, 9, 317.	1.0	17
3	Human biology and ancient DNA: exploring disease, domestication and movement. <i>Annals of Human Biology</i> , 2019, 46, 95-98.	0.4	5
4	Paleomicrobiology: Diagnosis and Evolution of Ancient Pathogens. <i>Annual Review of Microbiology</i> , 2019, 73, 639-666.	2.9	36
5	Reconstruction of the spatial and temporal dynamics of hepatitis B virus genotype D in the Americas. <i>PLoS ONE</i> , 2019, 14, e0220342.	1.1	22
6	Infectious diseases and Neolithic transformations: Evaluating biological and archaeological proxies in the German loess zone between 5500 and 2500 BCE. <i>Holocene</i> , 2019, 29, 1545-1557.	0.9	19
7	The concept of socio-environmental transformations in prehistoric and archaic societies in the Holocene: An introduction to the special issue. <i>Holocene</i> , 2019, 29, 1517-1530.	0.9	12
8	Ancient DNA in the Study of Ancient Disease. , 2019, , 183-210.		14
10	Possible European Origin of Circulating Varicella Zoster Virus Strains. <i>Journal of Infectious Diseases</i> , 2020, 221, 1286-1294.	1.9	13
11	Ancient pathogen genomics as an emerging tool for infectious disease research. <i>Nature Reviews Genetics</i> , 2019, 20, 323-340.	7.7	195
12	Mode and tempo of human hepatitis virus evolution. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1384-1395.	1.9	7
13	A 5700 year-old human genome and oral microbiome from chewed birch pitch. <i>Nature Communications</i> , 2019, 10, 5520.	5.8	61
14	Evolutionary biology of human hepatitis viruses. <i>Journal of Hepatology</i> , 2019, 70, 501-520.	1.8	50
15	Prisoners of war – host adaptation and its constraints on virus evolution. <i>Nature Reviews Microbiology</i> , 2019, 17, 321-328.	13.6	117
16	Recent Out-of-Africa Migration of Human Herpes Simplex Viruses. <i>Molecular Biology and Evolution</i> , 2020, 37, 1259-1271.	3.5	22
17	We Are All Africans: A Highly Personal Migratory View of the History of Hepatitis B. <i>Clinical Liver Disease</i> , 2020, 16, 24-33.	1.0	1
18	The Recovery, Interpretation and Use of Ancient Pathogen Genomes. <i>Current Biology</i> , 2020, 30, R1215-R1231.	1.8	33
19	Excavating new facts from ancient Hepatitis B virus sequences. <i>Virology</i> , 2020, 549, 89-99.	1.1	7

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20	Long-term evolution of hepatitis B virus genotype F: Strong association between viral diversification and the prehistoric settlement of Central and South America. <i>Journal of Viral Hepatitis</i> , 2020, 27, 620-630.	1.0	17
21	Variola virus genome sequenced from an eighteenth-century museum specimen supports the recent origin of smallpox. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190572.	1.8	24
22	2000-year-old pathogen genomes reconstructed from metagenomic analysis of Egyptian mummified individuals. <i>BMC Biology</i> , 2020, 18, 108.	1.7	29
23	A near full-length HIV-1 genome from 1966 recovered from formalin-fixed paraffin-embedded tissue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12222-12229.	3.3	31
24	Origin and Health Status of First-Generation Africans from Early Colonial Mexico. <i>Current Biology</i> , 2020, 30, 2078-2091.e11.	1.8	34
25	The evolution and clinical impact of hepatitis B virus genome diversity. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2020, 17, 618-634.	8.2	107
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29	The landscape of persistent human DNA viruses in femoral bone. <i>Forensic Science International: Genetics</i> , 2020, 48, 102353.	1.6	17
30	Genome-wide study of a Neolithic Wartberg grave community reveals distinct HLA variation and hunter-gatherer ancestry. <i>Communications Biology</i> , 2021, 4, 113.	2.0	20
31	Quantitative analysis of the splice variants expressed by the major hepatitis B virus genotypes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	16
32	Analysis of Hepatitis B Virus Genotype D in Greenland Suggests the Presence of a Novel Quasi-Subgenotype. <i>Frontiers in Microbiology</i> , 2020, 11, 602296.	1.5	5
34	Reproducible, portable, and efficient ancient genome reconstruction with nf-core/eager. <i>PeerJ</i> , 2021, 9, e10947.	0.9	43
35	Examining Natural History through the Lens of Palaeogenomics. <i>Trends in Ecology and Evolution</i> , 2021, 36, 258-267.	4.2	26
38	Paleogenomics of the prehistory of Europe: human migrations, domestication and disease. <i>Annals of Human Biology</i> , 2021, 48, 179-190.	0.4	20
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43	A 5,000-year-old hunter-gatherer already plagued by <i>Yersinia pestis</i> . <i>Cell Reports</i> , 2021, 35, 109278.	2.9	42
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46	Hepatitis B Virus DNA Integration, Chronic Infections and Hepatocellular Carcinoma. <i>Microorganisms</i> , 2021, 9, 1787.	1.6	29
47	Ancient viral genomes reveal introduction of human pathogenic viruses into Mexico during the transatlantic slave trade. <i>ELife</i> , 2021, 10, .	2.8	23
48	Metagenomic analysis of ancient dental calculus reveals unexplored diversity of oral archaeal <i>Methanobrevibacter</i> . <i>Microbiome</i> , 2021, 9, 197.	4.9	18
50	Unravelling the history of hepatitis B virus genotypes A and D infection using a full-genome phylogenetic and phylogeographic approach. <i>ELife</i> , 2018, 7, .	2.8	28
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64	Malignancy in three medieval Polish osteological collections. <i>Journal of Archaeological Science: Reports</i> , 2021, 40, 103246.	0.2	1
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69	Benchmarking metagenomics classifiers on ancient viral DNA: a simulation study. <i>PeerJ</i> , 2022, 10, e12784.	0.9	4
70	A Theoretical Analysis of Taxonomic Binning Accuracy. <i>Molecular Ecology Resources</i> , 2022, , .	2.2	0

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71	In vitro investigation of HBV clinical isolates from Chinese patients reveals that genotype C isolates possess higher infectivity than genotype B isolates. <i>Virologica Sinica</i> , 2022, 37, 398-407.	1.2	3
72	Genotype E: The neglected genotype of hepatitis B virus. <i>World Journal of Hepatology</i> , 2021, 13, 1875-1891.	0.8	11
73	Metagenomic analysis reveals mixed <i>Mycobacterium tuberculosis</i> infection in a 18th century Hungarian midwife. <i>Tuberculosis</i> , 2022, , 102181.	0.8	3
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75	Disease-causing human viruses: novelty and legacy. <i>Trends in Microbiology</i> , 2022, 30, 1232-1242.	3.5	5
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79	Advances in multi-omics research on viral hepatitis. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	16
80	Smallpox's antiquity in doubt. <i>Journal of Roman Archaeology</i> , 2022, 35, 897-913.	0.1	16
81	Historic and Prehistoric Epidemics: An Overview of Sources Available for the Study of Ancient Pathogens. <i>Epidemiologia</i> , 2022, 3, 443-464.	1.1	2
82	Pathogen genomics study of an early medieval community in Germany reveals extensive co-infections. <i>Genome Biology</i> , 2022, 23, .	3.8	6
83	Phylogeography of hepatitis B virus: The role of Portugal in the early dissemination of HBV worldwide. <i>PLoS ONE</i> , 2022, 17, e0276618.	1.1	0
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