

Genome-Wide Comparison of Medieval and Modern <i>

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Insights into ancient leprosy and tuberculosis using metagenomics. Trends in Microbiology, 2013, 21, 448-450.	7.7	15
2	Back to the Future!. Nature Reviews Microbiology, 2013, 11, 600-600.	28.6	0
3	Whole-genome sequencing in bacteriology: state of the art. Infection and Drug Resistance, 2013, 6, 115.	2.7	33
4	Mycobacterium Species Related to <i>M. leprae</i> and <i>M. lepromatosis</i> from Cows with Bovine Nodular Thelitis. Emerging Infectious Diseases, 2014, 20, 2111-2114.	4.3	18
5	Genome-wide re-sequencing of multidrug-resistant <i>Mycobacterium leprae</i> Airaku-3. Clinical Microbiology and Infection, 2014, 20, O619-O622.	6.0	18
6	Diagnostic metagenomics: potential applications to bacterial, viral and parasitic infections. Parasitology, 2014, 141, 1856-1862.	1.5	102
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8	On the Age of Leprosy. PLoS Neglected Tropical Diseases, 2014, 8, e2544.	3.0	55
9	Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome. Genome Research, 2014, 24, 454-466.	5.5	161
10	Recovery of a Medieval <i>Brucella melitensis</i> Genome Using Shotgun Metagenomics. MBio, 2014, 5, e01337-14.	4.1	67
11	A glimpse into the past and predictions for the future: the molecular evolution of the tuberculosis agent. Molecular Microbiology, 2014, 93, 835-852.	2.5	76
12	Analysis of the Leprosy Agents <i>Mycobacterium leprae</i> and <i>Mycobacterium lepromatosis</i> in Four Countries. American Journal of Clinical Pathology, 2014, 142, 524-532.	0.7	40
13	Shotgun microbial profiling of fossil remains. Molecular Ecology, 2014, 23, 1780-1798.	3.9	55
14	Genotyping of ancient <i>Mycobacterium tuberculosis</i> strains reveals historic genetic diversity. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20133236.	2.6	43
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16	A Paleogenomic Perspective on Evolution and Gene Function: New Insights from Ancient DNA. Science, 2014, 343, 1236573.	12.6	197
17	<i>Yersinia pestis</i> and the Plague of Justinian 541–543 AD: a genomic analysis. Lancet Infectious Diseases, The, 2014, 14, 319-326.	9.1	358
18	NOD2 and CCDC122-LACC1 genes are associated with leprosy susceptibility in Brazilians. Human Genetics, 2014, 133, 1525-1532.	3.8	48

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20	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
21	Ancient-Pathogen Genomics: Coming of Age?. <i>MBio</i> , 2014, 5, e01676-14.	4.1	5
22	<i>Mycobacterium leprae</i> genomes from a British medieval leprosy hospital: towards understanding an ancient epidemic. <i>BMC Genomics</i> , 2014, 15, 270.	2.8	60
23	Biological and social implications of a medieval burial from Cyprus for understanding leprosy in the past. <i>International Journal of Paleopathology</i> , 2014, 4, 17-24.	1.4	13
25	Correspondence. <i>Retina</i> , 2014, 34, 1022.	1.7	0
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31	Comparative performance of two whole-genome capture methodologies on ancient <i>scp</i> DNA libraries. <i>Methods in Ecology and Evolution</i> , 2015, 6, 725-734.	5.2	43
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35	Ancient pathogen genomics: insights into timing and adaptation. <i>Journal of Human Evolution</i> , 2015, 79, 137-149.	2.6	60
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40	Draft Genome Sequence of New Leprosy Agent <i>Mycobacterium lepromatosis</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	19
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