

Whole-Genome Sequencing and Social-Network Analysis

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Bacterial epidemiology and biology - lessons from genome sequencing. <i>Genome Biology</i> , 2011, 12, 230.	9.6	72
2	A role for systems epidemiology in tuberculosis research. <i>Trends in Microbiology</i> , 2011, 19, 492-500.	7.7	71
3	Comparative Genomics of <i>Vibrio cholerae</i> from Haiti, Asia, and Africa. <i>Emerging Infectious Diseases</i> , 2011, 17, 2113-21.	4.3	136
4	Introduction to bioinformatics: sequencing technology. <i>Asia Pacific Allergy</i> , 2011, 1, 93-97.	1.3	0
5	Clonal Population of <i>Mycobacterium tuberculosis</i> Strains Reside within Multiple Lung Cavities. <i>PLoS ONE</i> , 2011, 6, e24770.	2.5	18
6	Tuberculosis: an unpredictable long-standing human companion still in need of rapid diagnostic tests. <i>Clinical Microbiology and Infection</i> , 2011, 17, 799.	6.0	0
7	Identification of <i>Salmonella enterica</i> species- and subgroup-specific genomic regions using Panseq 2.0. <i>Infection, Genetics and Evolution</i> , 2011, 11, 2151-2161.	2.3	10
8	Everything at once: Comparative analysis of the genomes of bacterial pathogens. <i>Veterinary Microbiology</i> , 2011, 153, 13-26.	1.9	12
9	Population Genetics of <i>Vibrio cholerae</i> from Nepal in 2010: Evidence on the Origin of the Haitian Outbreak. <i>MBio</i> , 2011, 2, e00157-11.	4.1	268
10	Microbial Genomics and Infectious Diseases. <i>New England Journal of Medicine</i> , 2011, 365, 347-357.	27.0	156
11	Difficulty accessing crack pipes and crack pipe sharing among people who use drugs in Vancouver, Canada. <i>Substance Abuse Treatment, Prevention, and Policy</i> , 2011, 6, 34.	2.2	21
12	Modelling the performance of isoniazid preventive therapy for reducing tuberculosis in HIV endemic settings: the effects of network structure. <i>Journal of the Royal Society Interface</i> , 2011, 8, 1510-1520.	3.4	16
13	Clinical Manifestations, Diagnosis, and Treatment of <i>Mycobacterium haemophilum</i> Infections. <i>Clinical Microbiology Reviews</i> , 2011, 24, 701-717.	13.6	127
14	The Changing Burden of Infectious Disease in Europe. <i>Science Translational Medicine</i> , 2011, 3, 103cm30.	12.4	15
15	Bacterial Genomics in Infectious Disease and the Clinical Pathology Laboratory. <i>Archives of Pathology and Laboratory Medicine</i> , 2012, 136, 1414-1422.	2.5	34
16	Insights from Genomics into Bacterial Pathogen Populations. <i>PLoS Pathogens</i> , 2012, 8, e1002874.	4.7	87
17	Routine Use of Microbial Whole Genome Sequencing in Diagnostic and Public Health Microbiology. <i>PLoS Pathogens</i> , 2012, 8, e1002824.	4.7	450
18	Whole Genome Sequencing Reveals Local Transmission Patterns of <i>Mycobacterium bovis</i> in Sympatric Cattle and Badger Populations. <i>PLoS Pathogens</i> , 2012, 8, e1003008.	4.7	173

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19	Combination of Single Nucleotide Polymorphism and Variable-Number Tandem Repeats for Genotyping a Homogenous Population of Mycobacterium tuberculosis Beijing Strains in China. <i>Journal of Clinical Microbiology</i> , 2012, 50, 633-639.	3.9	35
20	Genomic epidemiology of the <i>Escherichia coli</i> O104:H4 outbreaks in Europe, 2011. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3065-3070.	7.1	262
21	Multidrug resistance after inappropriate tuberculosis treatment: a meta-analysis. <i>European Respiratory Journal</i> , 2012, 39, 1511-1519.	6.7	97
22	Spreading paths in partially observed social networks. <i>Physical Review E</i> , 2012, 85, 036106.	2.1	24
23	Modern contact investigation methods for enhancing tuberculosis control in Aboriginal communities. <i>International Journal of Circumpolar Health</i> , 2012, 71, 18643.	1.2	19
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25	The 2011 Garrod Lecture: From penicillin-binding proteins to molecular epidemiology. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 1578-1588.	3.0	13
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27	Transforming clinical microbiology with bacterial genome sequencing. <i>Nature Reviews Genetics</i> , 2012, 13, 601-612.	16.3	684
28	Full-Genome Dissection of an Epidemic of Severe Invasive Disease Caused by a Hypervirulent, Recently Emerged Clone of Group A Streptococcus. <i>American Journal of Pathology</i> , 2012, 180, 1522-1534.	3.8	70
29	High resolution clustering of <i>Salmonella enterica</i> serovar Montevideo strains using a next-generation sequencing approach. <i>BMC Genomics</i> , 2012, 13, 32.	2.8	140
30	Genomic variation in <i>Salmonella enterica</i> core genes for epidemiological typing. <i>BMC Genomics</i> , 2012, 13, 88.	2.8	76
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34	Genome sequencing in clinical microbiology. <i>Nature Biotechnology</i> , 2012, 30, 1068-1071.	17.5	37
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39	Phylogeographic variation in recombination rates within a global clone of methicillin-resistant Staphylococcus aureus. Genome Biology, 2012, 13, R126.	9.6	118
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54	Read and assembly metrics inconsequential for clinical utility of whole-genome sequencing in mapping outbreaks. Nature Biotechnology, 2013, 31, 592-594.	17.5	26

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55	The mutation rate of mycobacterial repetitive unit loci in strains of <i>M. tuberculosis</i> from cynomolgus macaque infection. <i>BMC Genomics</i> , 2013, 14, 145.	2.8	19
56	Inferring patient to patient transmission of <i>Mycobacterium tuberculosis</i> from whole genome sequencing data. <i>BMC Infectious Diseases</i> , 2013, 13, 110.	2.9	180
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67	LOST IN THE MAP. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 305-314.	2.3	78
68	Genomics and outbreak investigation: from sequence to consequence. <i>Genome Medicine</i> , 2013, 5, 36.	8.2	64
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89	Whole Genome Sequencing versus Traditional Genotyping for Investigation of a Mycobacterium tuberculosis Outbreak: A Longitudinal Molecular Epidemiological Study. <i>PLoS Medicine</i> , 2013, 10, e1001387.	8.4	425
90	Comparative Study of IS 6110 Restriction Fragment Length Polymorphism and Variable-Number Tandem-Repeat Typing of Mycobacterium tuberculosis Isolates in the Netherlands, Based on a 5-Year Nationwide Survey. <i>Journal of Clinical Microbiology</i> , 2013, 51, 1193-1198.	3.9	48

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92	Selected insights from application of whole-genome sequencing for outbreak investigations. <i>Current Opinion in Critical Care</i> , 2013, 19, 432-439.	3.2	45
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109	Carriage of Methicillin-Resistant <i>Staphylococcus aureus</i> by Wild Urban Norway Rats (<i>Rattus</i>) Tj ETQq1 1 0.784314 <small>255</small> / <small>46</small> <small>10</small> <small>TF</small>		

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110	Progenitor <i>Mycobacterium canettii</i> Clone Responsible for Lymph Node Tuberculosis Epidemic, Djibouti. <i>Emerging Infectious Diseases</i> , 2014, 20, 21-28.	4.3	62
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123	Classical and new assays for detecting drug resistance in tuberculosis. <i>Biomarkers in Medicine</i> , 2014, 8, 1105-1114.	1.4	6
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