

Real-time, portable genome sequencing for Ebola surve

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Use of Unamplified RNA/cDNAâ€“Hybrid Nanopore Sequencing for Rapid Detection and Characterization of RNA Viruses. <i>Emerging Infectious Diseases</i> , 2016, 22, 1448-1451.	2.0	36
2	Microreact: visualizing and sharing data for genomic epidemiology and phylogeography. <i>Microbial Genomics</i> , 2016, 2, e000093.	1.0	470
3	Unusual Ebola Virus Chain of Transmission, Conakry, Guinea, 2014â€“2015. <i>Emerging Infectious Diseases</i> , 2016, 22, 2149-2152.	2.0	21
4	Tracking Strains in the Microbiome: Insights from Metagenomics and Models. <i>Frontiers in Microbiology</i> , 2016, 7, 712.	1.5	44
5	Rapid Detection Strategies for the Global Threat of Zika Virus: Current State, New Hypotheses, and Limitations. <i>Frontiers in Microbiology</i> , 2016, 7, 1685.	1.5	32
6	Integrated Computational Approach for Virtual Hit Identification against Ebola Viral Proteins VP35 and VP40. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1748.	1.8	37
7	Advances in the Microbiome: Applications to Clostridium difficile Infection. <i>Journal of Clinical Medicine</i> , 2016, 5, 83.	1.0	23
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20	Coming of age: ten years of next-generation sequencing technologies. <i>Nature Reviews Genetics</i> , 2016, 17, 333-351.	7.7	3,160
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