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Core Genome Multilocus Sequence Typing Scheme for Improved Characterization and Epidemiological Surveillance of Pathogenic *Brucella*

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Journal of Clinical Microbiology, , , .

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4	Whole-genome sequencing (WGS) analysis of <i>Brucella suis</i> biovar 2 isolated from domestic pigs in Egypt for epidemiological and genetic diversity tracing. 2022 , 109637		0
3	Epidemiological Investigation of Hospital Transmission of <i>Corynebacterium striatum</i> Infection by Core Genome Multilocus Sequence Typing Approach.		0
2	First record of the human infection of <i>Brucella melitensis</i> in Kyrgyzstan: evidence from whole-genome sequencing-based analysis. 2022 , 11,		0
1	<i>Brucella abortus</i> in Kazakhstan, population structure and comparison with worldwide genetic diversity. 14,		0