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Next-generation sequencing to investigate antimicrobial resistance

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Propositions

accompanying the dissertation

Next-generation Sequencing to Investigate Antimicrobial Resistance A One-Health Perspective

by

Giuseppe Fleres

1. Standard culture methods combined with WGS allow the identification of unique bacterial clones in the hospital environment. (This thesis)
2. cgSNP analysis of WGS-data reveals the persistence of colistin-resistant bacterial clones in the drains of high-risk hospital units. (This thesis)
3. The hospital water environment can act as a reservoir of last-resort antibiotic resistance genes and resistant bacteria (This thesis)
4. Shotgun Metagenomics can be used for hospital tap-water AMR surveillance and provides unbiased information on the microbial and ARGs composition (This thesis)
5. The implementation of NGS in One-Health surveillance is critical to identifying AMR reservoirs and preventing their further spread (This thesis)
6. Combining short- and long-read sequencing can help to resolve MGE-carrying ARGs (This thesis)
7. Metagenomic assembly enables the exploration of the genomic context of antibiotic resistance genes (This thesis)
8. Science knows no country, because knowledge belongs to humanity, and is the torch that illuminates the world. (Louis Pasteur)