

## CED : « Engineering Sciences and Techniques »

# THESIS DEFENSE

## « ICHRAK BENAMRI »

CANDIDATE FOR DOCTOR SCIENCES AND TECHNIQUES

« Bioinformatics Approaches to Explore the Genetic Causes of Chlamydiae Resistance to Antibiotics »

<b>Date :</b>	<b>Saturday 22 July 2023</b>
<b>Time :</b>	<b>10 am</b>
<b>Location :</b>	<b>Conference Hall, ENSA - Tangier</b>

### Committee Members

Pr. Hassan BADIR	ENSA - Tangier	Chair
Pr. Rachida FISSOUNE	ENSA - Tangier	Reviewer
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## ABSTRACT

Bioinformatics studies provided fundamental methods of modeling a biological living cell system and docking proteins that enabled scientists to discover effective drug strategies to combat the problem of antibiotic resistance in different micrograms, such as Chlamydiae which is our research topic.

Chlamydiae are intracellular bacteria responsible for redoubtable diseases in both human and animals. The commonly used drugs against Chlamydiae infections are antibiotics. However, the misuse of antimicrobial agents have resulted in an increase in the appearance of bacterial drug resistance, this phenomenon represents a growing public health problem worldwide.

The main goal of this research project is to apply bioinformatics approaches to explore the genetic causes of Chlamydiae infections and the problematic related to their resistance to antibiotics. Our methodology based on three steps: i) A literature search to explore the genes and mutations associated to the antibiotic resistance, ii) The development of a database which enable gathering the retrieved genes and mutations shown to be associated to Chlamydiae resistance to antibiotics, iii) The in silico analysis of all the retrieved genes' variants encoded proteins to identify the functional and structural related effects of the mutations, and consequently their impact on the bacteria sensitivity to antibiotics.

The results revealed that the retrieved variations could affect the proteins' functionalities, structures and their interactions with other proteins, which can impact the bacteria mechanisms of sensitivity to antibiotics. The developed database and the in silico analysis results would be a friendly useful resource to a deeper drug exploration and drug design for precision medicine, enabling curbing the Chlamydiae strains resistance issues.

**Keywords:** Chlamydia, Bacteria, Antibiotic Resistance, Gene, Protein, Mutation, Database, In silico Analysis, Bioinformatics.

