# Team Microbe Presentation Script

## General intro and Team intro

Hello everyone,

Today, we are thrilled to share with you the journey of our project, an adventure into the microscopic world where we battled against one of the most formidable foes: tuberculosis (TB). Our story begins with a challenge that has plagued humanity for centuries and has only grown more daunting with time.

But first, we are team Microbe:

I am Eya from Tunisia, the Docking Lead in this project and this is…

Treasure from Nigeria, the Presentation Lead,

Zeina from Palestine, Visualisation lead,

Wanzya from Zambia, Visualisation lead

And Britney from Cameroon, Project lead.

Without further ado, this is our project.

## Introduction

Today, we are excited to share our recent project on docking inhibitors into beta-lactamase to combat TB. As we know, TB remains one of the most challenging infectious diseases, and with the rise of antibiotic resistance, traditional antibiotics are becoming less effective. This has led us to explore alternative approaches, such as docking inhibitors, to enhance the efficacy of treatment.

## Why Antibiotics Alone Aren't Enough

Antibiotics have been the cornerstone of TB treatment for decades. However, the bacterium Mycobacterium tuberculosis has become increasingly resistant, rendering many antibiotics ineffective. The bacterium’s ability to evolve and develop resistance mechanisms, such as the production of beta-lactamase, an enzyme that breaks down beta-lactam antibiotics, necessitates a different approach.  
This growing specificity and resistance demand innovative strategies to tackle TB.

## The Role of Inhibitors

In our project, we focused on docking inhibitors to beta-lactamase, an enzyme produced by M. tuberculosis that confers resistance to beta-lactam antibiotics. An inhibitor in this case is a protein that goes into the active site of the enzyme [beta-lactamase] and stops it from destroying the beta-lactam by inactivating it.By inhibiting this enzyme, we aim to restore the efficacy of beta-lactam antibiotics against TB.

## Our Approach

We examined two specific inhibitors: Avibactam and Vaborbactam. These inhibitors have shown promise in inhibiting beta-lactamase in other bacterial species. However, when we docked these inhibitors on the B chain of beta-lactamase from M. tuberculosis, the results were not as expected.

## Challenges and Insights

Despite promising studies from 2012 and 2010 that suggested successful inhibition, our docking experiments using a 2020 model did not perform as well. This discrepancy led us to delve deeper into the structure and dynamics of the beta-lactamase enzyme in TB.

## Successful Docking with Ceftriaxone

Interestingly, when we docked Ceftriaxone, a third-generation cephalosporin antibiotic, we observed successful binding. This finding is significant as it suggests that while some inhibitors may not perform well, others like Ceftriaxone could offer a viable solution.

# Conclusion

Our observations underscore the importance of continuously updating and refining our models and methods. The differences between our results and previous studies highlight the evolving nature of bacterial resistance and the need for ongoing research. Moving forward, we plan to:

1. Investigate the structural nuances that may have contributed to the varying efficacy of inhibitors.
2. Explore other potential inhibitors and antibiotics that could be docked effectively.

In conclusion, our project sheds light on the complexities of combating TB with inhibitors. While some inhibitors did not perform as anticipated, the success with Ceftriaxone opens new avenues for treatment strategies. We hope our findings contribute to the ongoing efforts to develop more effective treatments for TB and inspire further research in this critical area.

Thank you for your attention. We welcome any questions or feedback.