

# **FUNCTIONAL and TECHNICAL REQUIREMENTS** **DOCUMENT**

Title:

predict activity of short antimicrobial peptides

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## 1. General information

predict activity of short antimicrobial peptides.

I will be building a machine learning model to predict antimicrobial peptides

### 1.1. Purpose

Antimicrobial resistance is an urgent and global health problem as existing drugs are becoming ineffective against the treatment of antimicrobial infections.

### 1.2. Scope

Particularly, we will be retrieving 2 datasets consisting of antimicrobial peptides (positive set) and non-antimicrobial peptides (negative set). Then, I will be computing some peptide features to quantitatively describe peptides followed by model building and finally model interpretation where we shed light on the key important features important for predicting antimicrobial peptides.

## 2. Acronyms and/or definitions

<b>Conda</b>	In which we install packages like python, Our working Environments
<b>Pfeature</b>	Pfeature allow us to compute properties of Amino Acid which will be crucial to Quantify the Molecular properties of peptides
<b>Jupyter Notebook/ Colab</b>	
<b>CD-Hit from bioconda</b>	A library allows us to fit or out any Redundancy in Peptide Sequence, meaning that peptide that are Much Similar will be removed, So We will get non-redundant and a unique sub set of Peptides that will be using in Molecular sequence
<b>Pandas</b>	It's data-frame for viewing Visualization
<b>Python</b>	For Programing
<b>Random Forest classifier</b>	modeling
<b>Matplotlip</b>	Graph visualization

### 3. Project Overview

I will be computing some peptide features to quantitatively describe peptides followed by model building

Functional Requirements and user Impact

Calculate Features Using P features

Featuring most to least featured amino acid

Data Resource:

A research paper