

SUPPLEMENTARY MATERIAL

**CW-PRED: Prediction of C-terminal cell-wall sorting
signals in Bacteria and Archaea**

JUCHMME (Java Utility for Class Hidden Markov Models and Extensions) is a publicly available tool for biological sequence analysis.

The software can be downloaded from:

1. Github: <https://github.com/pbagos/juchmme>
2. <http://www.compgen.org/tools/juchmme>

The CWPRED HMM-based method can be used to predict the C-terminal sorting signals of Archaea, Gram-positive and Gram-negative bacteria.

This example shows how parameter testing with JUCHMME works for each organism class. We recommend to run the last 60 amino acids of the input sequence to increase the accuracy of prediction.

Running

```
java hmm/Juchmme -a ../tables/A_ALPXTG_MYMODEL -e ../tables/E_ALPXTG_MYMODEL -  
c ../conf/conf.cwpred_archaea -m ../models/ cwpred_archaea.mdl -f <filename>
```

```
java hmm/Juchmme -a ../tables/A_PLPXTG_MYMODEL -e ../tables/E_PLPXTG_MYMODEL -  
c ../conf/conf.cwpred_positive -m ../models/ cwpred_positive.mdl -f <filename>
```

```
java hmm/Juchmme -a ../tables/A_NLPXTG_MYMODEL -e ../tables/E_NLPXTG_MYMODEL -  
c ../conf/conf.cwpred_negative -m ../models/ cwpred_negative.mdl -f <filename>
```

