



# St. Jude BioHackathon

## **Title**

A web-based molecular profiler capable of matching ChIP data based on similarity to established profiles

## **Category**

Processing Pipelines And Methods

## **Challenge**

A system to enter a ChIP molecular profile into an interface that will then search a profile repository for the best matches to recognize similarity of the input profile to well-annotated profiles (identify cell type). This could be done by peak overlap, signal similarity, etc.

## **Benefit**

It would help researchers recognize similarities between their data and well-known cell types.

## **Helpful Tools, Packages, or Software**

Packages performing similar functions for single cell RNA-seq data include SingleR and AUCell. The ReMap database and R package may be helpful for acquiring test data:  
<https://remap.univ-amu.fr/>

## **Test Data**

Encode, ReMap