SSEAPS

A two-fold project to identify the ammino-acid content of a peptide from experimental data.

As things stand, a known bacterium is matched with a known peptide are tested to see when they exhibit an interaction. The idea is to streamline the user-experience.

Identify peptides by breaking them up at convenient locations, individually solving the structures, and then putting them together. The goal is to increase the maximum length of the fragments from ~10 to >20.

Getting the mass-spec data and parsing the data is the current problem the team is facing.