



Sphinx Bio Take Home Challenge

Feel free to use any language/libraries/frameworks that you are comfortable with.

Background

As an engineer at Sphinx, you will be building software for scientists. In this challenge, you will build an example full-stack application intended to help scientists design an experiment.

A common task for a scientist is to design an experiment using an **assay plate**. A plate is a rectangular object composed of wells (see this example: <https://www.biorad.com/en-us/product/384-well-pcr-plates?ID=OCH4UM15>). Each well contains a set of reagents used for the experiment. More formally:



Plates are a fixed array that conforms to one of two dimensions:

- 384-well plates (24 x 16)
- 96-well plates (12 x 8)

Plates can be indexed by a numerical row and column pair (row, col).

Each well can contain some combination of the following:

- Reagent
 - A string starting with 'R' and followed by numbers
- Antibody
 - A sequence of amino acids (https://en.wikipedia.org/wiki/Amino_acid) between 20 and 40 amino acids long
- Concentration
 - A floating point number
 - Only valid if there is also a antibody in the well

Problem Description

For this challenge, we'd like you to build a web application that allows a user to design an experiment by creating a plate and filling out information about the contents of the wells.

Concretely, a user should be able to:

- Create a new plate
- Add information to an empty well
- View information in an existing well
- Edit information in an existing well
- Delete a plate

Most biotech companies these days also have a computational team with data scientists and software engineers who write code. You should also expose a set of API endpoints that would allow users to do each of these actions programmatically.

Please send a zipped archive or a link to a private Github repo shared with me (@nlarusstone) containing all of your code.