iGEM Advisor's Meeting
4/17/12

Project Proposals Round 2

Resveratrol Metabolite Blocks Apidogenesis

- Why aren't we just producing lots of resveratrol and putting it in the body? The body will naturally change it into piceatannol for us. Response: Does it happen in the necessary quantity and concentration? We want to make these molecules more stable and more soluble in the body.
- Resveratrol is widely regarded as a wonderful compound to extend life and help health. It's widely researched and popular, but there is much controversy about it still.
- How are we going to make this more soluble? Add groups to the non-active sites of the molecule. Groups increase solubility, like halogenation.
- Do these modifications change the molecule itself? Well we can run computational tests on that. We can also biologically make resveratrol derivatives and test them like a pharmaceutical company.
    - Beyond looking a solubility, computational testing might not be of much help. You really need to synthesize libraries of the molecule and test them.
- Need to look into P450 enzymes. But we want to stay away from protein engineering. We can buy and test a range of enzymes though.
- Computational side? The molecule docking technology to do simple hydrogen bond analysis is free, but for the more complex and detailed information we need an expert. Courtney will consult with one person in her lab who has experience in this area.
    - The computation sounds like it is beyond the scope of the summer.
    - Our best bet in terms of time is to just make a few analogs and test them.

Microbial Expression and

- PUF works with only 8 base pairs of recognition.
- Where should the PUF binding site go? Let's test a bunch of models with it in various places to see which is the most effective (via visibility of YFP).
- Need to clearly understand the PUF mechanism. This ensures that it is binding to a specific RNA sequences and not just the PolyA tail.
- Applications: the PUF library is obvious and useful, but could also use PUF as a scaffolding tool in the style of zinc fingers.
- How about engineering different kinds of PUF? First need to make sure it works in prokaryotes, then test the first type of PUF and optimize where the binding site should be. Then and only then we should look at making different versions of PUF and starting the library.
- For this to work at all, it is necessary to make really sure that PUF works in E. coli.
    - It is possible to make this work with cDNA. Are we sure that we can get the cDNA from UNC?

- It is a small protein. It might be easier to just synthesize it rather than clone it. We should definitely start with cDNA.