**Minutes from meeting 2023.09.20**

* We discussed the function of the C-terminal domain. It blocks the active site with a “placeholder” residue and is cleaved off in the active enzyme.
  + How about the short fungal ones? Is the latent enzyme active?
* Question: Should we blast with the whole sequence or only pfam domain?

Decision: We try both for one of the long fungal ones and see what the difference is.

* Question: If we only blast with the pfam domain, we maybe don’t need to blast all seeds?

Decision: We’ll try to blast all and see whether they find different things

* In the clustering we will probably use the full-lengths sequences, but we can also try clustering only based on the pfam domain
* We will look at the conserved residues in each cluster. For example look at differences in the “placeholder” amino acids (as in Aguilera paper)
* We will look at all domains of life, but focus mostly on fungal/bacteria
* We’ll see if we find laccases when blasting
* We should include an O-aminophenol oxidase as seed
* Activity can be divided into the following categories:
  + Tyrosinases (mono- and di-phenolase activity)
    - 0 methoxylations
    - 1 methoxylations
    - 2 methoxylations
  + Catechol oxidases (diphenolase activity)
  + O-Aminophenol oxidases (nitrosation)
  + Hemocyanins
* We could investigate the co-occurrence between laccases and POPs

**Ida tasks:** Complete seed table with Caio. Read Aguilera paper again. Try blasting a long fungal PPO with and without C-terminal domain, and look at the difference. Work on project description.

**Jane tasks:** Work on project description.