**Research questions:**

1. Can we via ML/deeplearning models predict signal peptides in *Aspergillus Oryzae*?
   1. How does the model capture the most important features of the signal peptides?
   2. How does the models perform? We could use deeploc to see if it predicts the same as SignalP and if both can capture actual secreting signal peptides.
2. Can we predict novel signal peptides generated from these models?
   1. Discuss what can ML do? What are the limitations etc.
   2. How can we use ML models to answer complex biological questions?
3. Can we use the ML/deeplearning models for diverse signal peptide prediction?
   1. How does the model perform at predicting signal peptides between *Aspergillus sp.*?
   2. Can we the model a specie-specific signal peptide structures/pattern which can be summarized in a list to act as an intial template to construct optimal peptides between similar species? Is there a specific pattern in the first place?
4. Can we outperform the optimal signal peptide design of the nature?
   1. How do the predicted signal peptides perform compared to the currently existing most optimal singnal peptide?
   2. Compare predicted and determined peptides to discuss which feature changes (length, AA composition, position, peptide structure) had an influence on the peptide activity.
5. Can we identify signal peptide structures for different target functions?
   1. How does the model separate signal peptides depending on the function of the signal peptides?