Introduction

Materials and Methods

* Cell culture, strains
* Absorption measurements + normalization and confidence interval
* WB
* In depth analysis of DESeq (bei Ute’s paper schauen, wie sie es gemacht hat) + warum man welchen tool benutzt hat
  + GO enrichement analysis (function + parameter (LFC, padj) used) + cite!
  + Other bioinformatical analyses (parameters used)
  + Anno file (Phillipp): paper proteogenomics zitieren
* AlphaFold Multimer and ColabFold (parameters used,) + cite!
* FISH (tbd)

Results

* Phenotypical changes of Δrbp1 mutants and RBP1 complementants under cold shock
  + Peaks nennen und erklären, warum es 2 chlorophyll peaks gibt
* In depth analysis of DESeq2 dataset
  + Venn diagrams
  + GO enrichement analysis
* Protein interaction modelling using AlphaFold Multimer
* FISH (tbd)

Discussion