

## Protein interaction network with a 3D resolution

A protein interaction network contains information on which proteins interact with each other (Figure 1). However, information on *how* a pair of proteins interact (3D structure of a protein-protein complex) is typically absent. This additional 3D information layer is crucial to distinguish the interactors competing for the same binding interface from those interaction partners that could potentially bind together into multimeric structures.

In this project, we will explore the yeast protein interaction network in 3D using bioinformatics tools. We will take a closer look into 3D structures of protein-protein complexes to identify residues and domains that form interaction interfaces. We will next predict which interactors of any given protein are potential competitors or collaborators (i.e., whether they are binding the same or different sites) and rebuild a protein interaction network using this information. Finally, we may explore whether protein position within a network is predictive of its fitness contribution, as well as computationally build higher order structures (e.g., protein trimers).

For this project, we are looking for a student interested in bioinformatics and analysis of 3D protein structures.

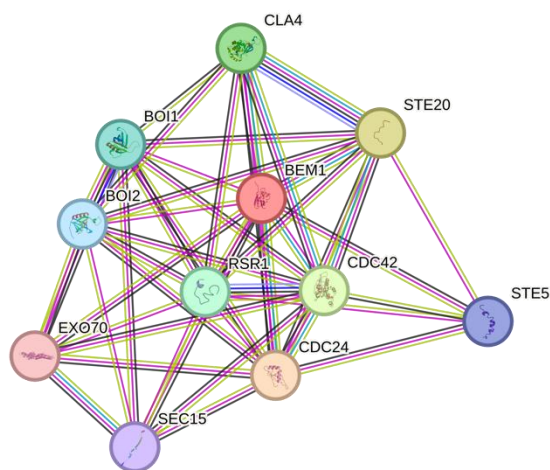


Figure 1. An example of a protein interaction network: Bem1 protein and its first shell of interactors (STRING database).

This project is a collaboration between Šoštarić and Laan groups. To learn more about this topic, you can contact: Nikolina Šoštarić, n.sostaric [at] tudelft [dot] nl, 58.F1.250