

ReadMe

The files contain the codes for the computational analysis. The sequence of the code is also indicated by the file names. For example "1-libraries_needed" represents the code to be run first and the description is followed by "-".

The input files needed are raw data for 12x library(raw count , byaa, bynuc) for both replicates in folder 12_x.

The dataset for 12x degron library for all the replicates in other_datasets. Input data also includes data for capping and saturation mutagenesis.

Yeast dataset for mapping yeast C terminome to MPS yeast Cterminome is taken from Uniprot and is in yeast_prot.csv.