

## 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 the 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.

The yeast dataset for mapping yeast C terminome to MPS yeast Cterminome is taken from UniProt dataset, with the filter to take Swiss-Prot reviewed Saccharomyces cerevisiae yeast proteins, downloaded on 3/07/2023. Additional data on Das1 substrate ORF type (Verified, Uncharacterized and Dubious) and corresponding Gene Ontology is taken from SGD least mine under the list “ALL\_Verified\_Uncharacterized\_Dubious\_ORFs” for 6611 genes, downloaded on 3/07/2023.

The dataset for the code is in the folder

<https://figshare.com/account/items/23621646/edit> . Before using the code the dataset has to be decompressed.