This directory contains raw data and code for the survival score and protein mass calculation. It’s contents are as follows:

* Folders
  + dataset\_houser\_et\_al
    - Raw data for the houser et al. datasets, a document with further details and explanations is in the folder
  + dataset hui\_et\_al
    - Raw data for the hui et al. datasets, a document with further details and explanations is in the folder
  + dataset schmidt\_et\_al
    - Raw data for the schmidt et al. datasets, a document with further details and explanations is in the folder
  + GO analyses
    - Results of the enrichment analyses
  + Mapping
    - protid2gene.tsv
      * mapping from uniprot identifiers to gene names
    - gene\_name\_infos.tsv
      * maps descriptive names to genes
    - gene2abundance.tsv
      * The mass estimates from Li et al. (2014) used in this study
* Files
  + Code
    - write\_merged\_ztables.ipynb
      * jupyter notebook that goes through the dataset\_ folders and calculates zvalues for each perturbation
    - write\_carls\_table.ipynb
      * jupyter notebook that takes the zvalues and writes and overview table including the survival score
    - merge\_per\_dataset.py
      * python file with helper classes