

READ.ME

This Zenodo entry contains information related to the publication: Temporal control of acute protein aggregate turnover by UBE3C and NRF1-dependent proteasomal pathways.

1) The HTML files of python notebook scripts used for analysis agDD and NRF1 images. There are two different scripts: 1) agDD_low_vs_high_count.html and 2) NRF1_levels.html These were used to analyze data plotted in Fig 3B,C and Fig. 5D,E, respectively.

2) In addition, this contains a READ.ME file containing parameters for proteomic analysis of purified proteasomes from RPN13 mutant cell lines.

The .xlsx Dataset S1 spreadsheet is proteomic analysis of purified proteasomes analyzed as described in the associated READ.ME file. Raw data can be found at ProteomeXChange with the identifier PXD055227.

3) Finally, the deposit includes a detailed Key Resource Table for all of the reagents and resources used and generated in this study.