Supporting information for publication

Polylysine is a Proteostasis Network-Engaging Structural Determinant

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- **Figure S-1**

  Length distribution of the poly-D-lysine peptide mix.

- **Figure S-2**

  LFQ protein intensities correlate strongly between independent biological repetitions.

- **Figure S-3**

  PL interactors are weakly, yet significantly aggregation-prone.

- **Figure S-4**

  Interactome of the PL-tagged model protein in yeast is enriched in members from the proteostasis network.

- **Figure S-5**

  Proteasome is enriched in the interactome of the PL-tagged model protein in yeast.

- **Figure S-6**

  PL-tagged model protein forms SDS-insoluble aggregates.

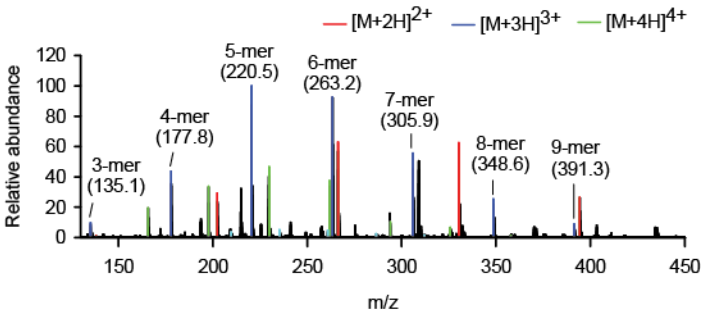
- **Supplementary references**

- **Table S-1**

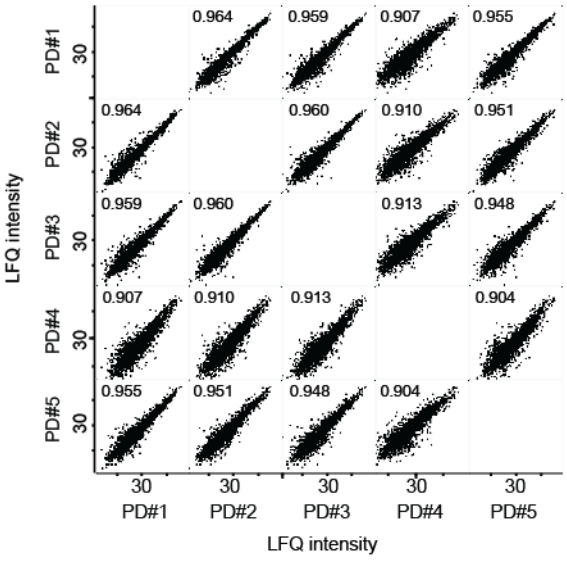
  MaxLFQ quantitative data and identifiers.

- **Table S-2**

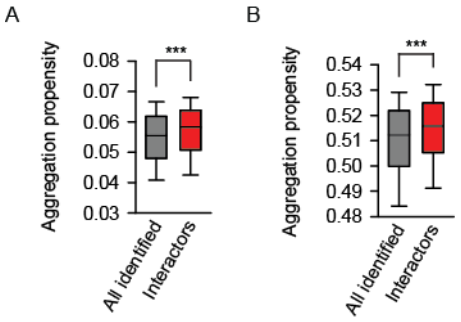
  List of PL interactors and identifiers.



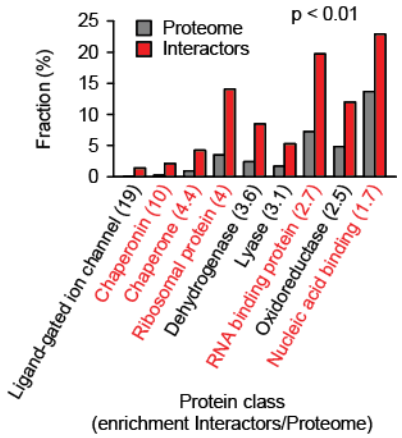
Supplementary figure S-1: Length distribution of the poly-D-lysine peptide mix. The mix used to block lysate proteins from interaction with poly-L-lysine agarose was analyzed by mass spectrometry. The corresponding m/z values are shown in brackets.



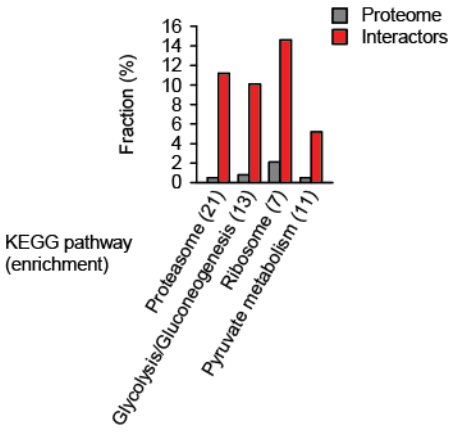
Supplementary figure S-2: LFQ protein intensities correlate strongly between independent biological repetitions. PD, pulldown. The values in individual dot plots represent the squared Pearson correlation coefficient.



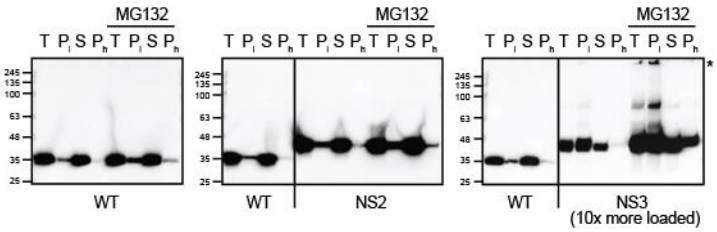
Supplementary figure S-3: PL interactors are weakly, yet significantly aggregation-prone. The statistical significance of the difference between the distribution of the aggregation propensity according to the TANGO (A) and Zyggregator (B) predictors of all identified proteins (grey) and of the interactors (red) was estimated using Mann-Whitney test; ***p>0.001.



Supplementary figure S-4: Interactome of the PL-tagged model protein in yeast[1] is enriched in members from the proteostasis network. Significant hits ($p<0.01$) of the PANTHER over-represention test sorted according to the enrichment factor which is indicated in the brackets. Red labels, protein classes found enriched in the PL interactome in this study.



Supplementary figure S-5: Proteasome is enriched in the interactome of the PL-tagged model protein in yeast[1]**.** KEGG analysis identifies proteasome as the most enriched biochemical pathway in yeast (p=5.62E-38).



Supplementary figure S-6: PL-tagged model protein forms SDS-insoluble aggregates. Solubility analysis of the wild-type and read-through variants, overexposed western blots from Figure 7c. Asterisk indicated SDS-insoluble fraction of NS3.

Supplementary references

(1) Defenouillère, Q.; Namane, A.; Mouaikel, J.; Jacquier, A.; Fromont-Racine, M. The Ribosome-Bound Quality Control Complex Remains Associated to Aberrant Peptides during Their Proteasomal Targeting and Interacts with Tom1 to Limit Protein Aggregation. *Mol. Biol. Cell* **2017**, *28* (9), 1165–1176.