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* You should state whether an appropriate sample size was computed when the study was being designed
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* You should report how often each experiment was performed
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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
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* Include model definition files including the full list of parameters used
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Please indicate the figures or tables for which source data files have been provided:

We have provided the source data files used for generation of the volcano plot depicting differences in protein abundances in YFP-SLIM4X and YFP-Ctrl pulldowns in Figure 6B (Figure 6-source data 2) and the source data files for calculation of distances for peptide structures retrieved from PDB (Figure 7-figure supplement 1-source data 1 and 4). We have included all the relevant PyMOL sessions for figure 7.