

Figure S1.

Venn diagram showing overlap between our dataset including all hits compared to proteins identified in the literature (29, 35).

Figure S2.

Results of *in vitro* binding assay showing specific binding of INO80E to the SUMO2 trimer. BLM, a known SUMO2 trimer binding protein (34), is shown as a positive control.

Figure S3.

Results of *in vivo* binding assay for INO80 and TFPT. HCT116 cells were co-transfected with an N-terminal fragment of INO80 (1-406), SUMO2 and TFPT. FLAG-tagged INO80 was then immunoprecipitated, and immunoblotted with anti-V5, to detect both the SUMO2-modified and unmodified forms of TFPT.

Figure S4.

This figure graphically illustrates all 21 of the network motifs that were generated in this study. Different types of protein interactions are shown with either solid, dashed, or dotted lines. SUMO-binding and SUMOylation interactions were identified in this study (this manuscript and Uzoma et al. (submitted)). Protein-protein interactions are based on data gathered from the literature and publicly available databases. For specific proteins contained within these network motifs, see **Data Set S3**.

Data Set S1. This data set lists all the SUMO-binding proteins identified in this study with the corresponding SUMO probe that was used to identify the protein, the official gene symbol, and the Life Technologies Ultimate ORF collection clone ID.

Data Set S2. This data set includes the union of all SUMO-modified proteins identified in this study, including proteins modified by either SUMO1 or SUMO2, or both, and described in Uzoma et al (submitted). Proteins are identified by official gene symbol and Life Technologies Ultimate ORF collection clone ID.

Data Set S3. This data set includes most of the protein networks identified in this study. Networks are listed by class number and each network includes between two and five edges. A graphical illustration of each class is shown in Supplemental Figure 4 with a selection of classes shown in Figure 3. Each edge for each network is described in the form *protein_X_protein*, in which the single letter 'X' indicates the type of interaction between the two proteins in the edge. The types of interactions are described as follows:
'L' = an interaction identified in this study: one of the two proteins is SUMO-modified, the other protein is the relevant SUMO paralog (SUMO1 or SUMO2)
'I' = the two proteins are known to interact with each other based on data gathered from the literature and publicly available databases
'B' = an interaction identified in this study: one of the two proteins is a SUMO-binding protein, the other protein is the relevant SUMO paralog (SUMO1 or SUMO2)