

SUPPLEMENTARY MATERIAL

Figure legends:

Supplementary figure 1: HSQC spectrum with assignment of the SUMO2 backbone amine groups

Supplementary figure 2: *A* SUMO1 titrations with 0-100 μ l of PIAS short, *B* SUMO1 titration with 0-100 μ l of TTRAP *C* SUMO1 titration with 0-100 μ l of PIAS *D* SUMO1 titration with 0-100 μ l of pPIAS *E* SUMO2 titration with 0-100 μ l of PIAS short *F* SUMO2 titration with 0-100 μ l of TTRAP *G* SUMO2 titration with 0-100 μ l PIAS *H* SUMO2 titration with 0-100 μ l of pPIAS

Supplementary figure 3: Peptides corresponding to the SIM of PIAS detected by MALDI fingerprinting on immunoprecipitated PIAS from mammalian cells (HEK 293T). The position of these peptides in PIAS sequence is given in the second column, their expected mass with and without phosphorylation in the third and fourth column. Since the signal was very weak, only masses with which two isotopic masses could be associated were retained. The mass measured for the peptide with no, one or two isotopes are referred to as m, m+1 and m+2. The annotations “well62_b_003” refer to the well on the MALDI plate in which the measurement was made, and the serial number of the measurement.