Supplementary information

The unique proline-rich domain regulates the chaperone function of AIPL1

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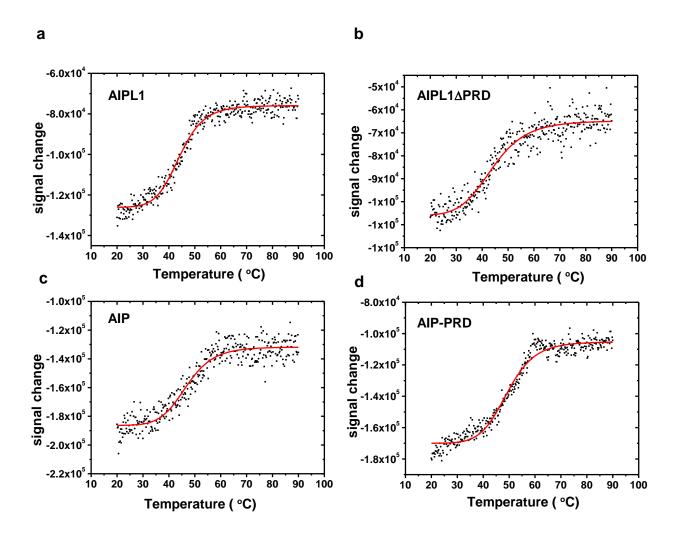
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Supplementary Fig. 1: Thermal stability of AIP, AIPL1 and their variants

To assess the stability of the different proteins, temperature-induced unfolding experiments were performed (a-d). Temperature-induced unfolding was monitored by far UV-CD spectroscopy at a fixed wavelength with a heating rate of 20 °C/h. Data were fitted to a Boltzmann function to obtain transition midpoints.



Supplementary Fig. 2: The proline-rich domain is a negative regulator of Hsp90 interaction.

- a. Determination of the affinity of AIP to Hsp90 by SPR. The K_D of AIP to hHsp90 was calculated to be 2.28 μ M based on injections with different concentration of AIP onto a human Hsp90-coated CM5 chip
- b. Determination of the affinity of AIP-PRD to Hsp90 by SPR. The K_D of AIP-PRD to hHsp90 was calculated to be 6.88 μ M based on injections with different concentrations of AIP-PRD onto a human Hsp90-coated CM5 chip.
- c. Determination of the affinity of AIPL1 to Hsp90 by SPR. The K_D of AIPL1 to hHsp90 was calculated to be 2.60 μ M based on injections with different concentration of AIPL1 onto a human Hsp90-coated CM5 chip
- d. Determination of the affinity of AIPL1 Δ PRD to Hsp90 by SPR. The K_D of AIPL1 Δ PRD to hHsp90 was calculated to be 0.89 μ M based on injections with different concentrations of AIPL1 Δ PRD onto a human Hsp90-coated CM5 chip.

