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Supplementary Information:

Affinity adsorbents for proline-rich peptide sequences: a new role for WW domains

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Figure S1

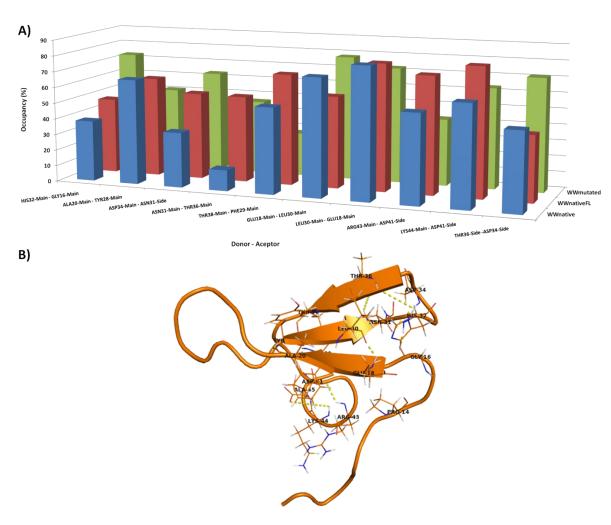


Figure S1. Hydrogen Bond Analysis over the time of simulation: **A)** Most prevalent Hydrogen Bonds Interactions in hYAP65_WWnative, hYAP65_WWnativeFL and hYAP65_WWmutated. **B)** Representation in hYAP65_WWmutated of the interactions described in A), (figure produced using PyMol Software).

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Figure S2

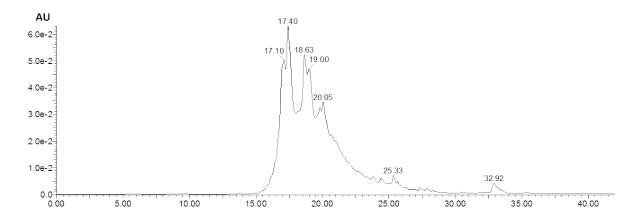


Figure S2. HPLC chromatogram of the hYAP65_WWmutated standard method (linear gradient from 10% to 90% solvent B over 25min with a flow rate of 10ml/min (solvent A: water/TFA, 99.9:0.1 v/v) and solvent B: acetonitrile/water/TFA, 90:9.9:0.1 v/v)).

Figure S3

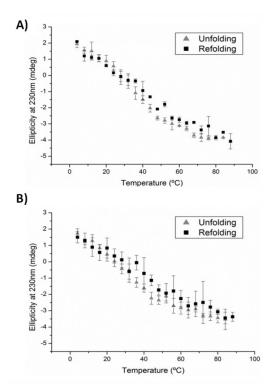


Figure S3. Circular Dichroism studies: unfolding and refolding curves between 4 and 88 °C. A) hYAP65_WWmutated_SCR and B) hYAP65_WWmutated_PP. The unfolding state is reversible for both peptides.