

Supporting Information

Aromatic residues link binding and function of intrinsically disordered proteins

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Table S1. PDB entries of protein-protein complexes used in this study.

1a3b	1a81	1apm	1axc
1cee	1cmk	1cqt	1dev
1dow	1dpj	1dt7	1ee5
1ej4	1emu	1fqj	1fv1
1g3j	1h26	1h2k	1h8b
1hv2	1i7x	1i8h	1iwq
1j2j	1j2x	1jd5	1jsu
1kdx	1kil	1l8c	1lm8
1mv0	1mxl	1nx1	1o9a
1ozs	1p16	1p22	1p4b
1p4q	1pq1	1q68	1r1r
1rf8	1rp3	1sb0	1sqk
1sqq	1t08	1tba	1tce
1th1	1un0	1wkw	1xtg
1ycq	1ymh	1zoq	2a6q
2auh	2b3g	2b3g	2c1t
2clt	2cly	2fym	2gl7
2gsi	2iv8	2ivz	2o8a
2oq1	2pg1	2phe	3b71
4htc			

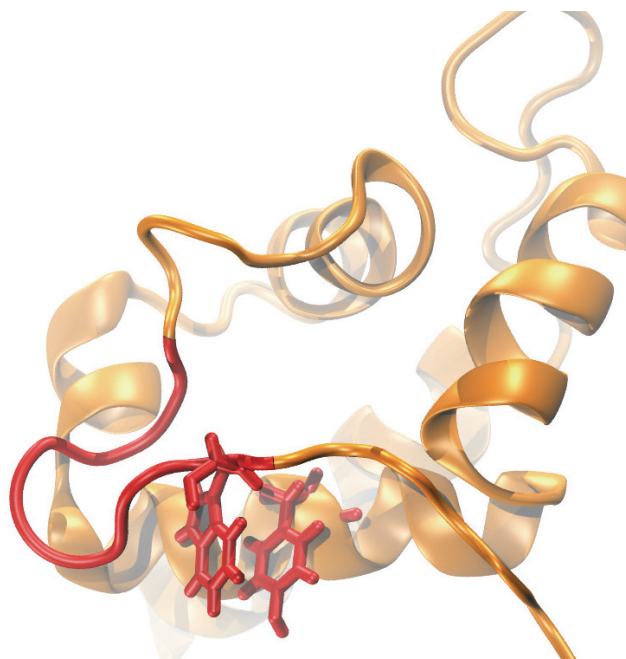


Figure S1. Three-dimensional structure of the autoinhibited WASP. The segment of the hairpin formed by residues Gly251-Leu262 is shown in red, and residues Trp252 and Tyr279 are represented by sticks.

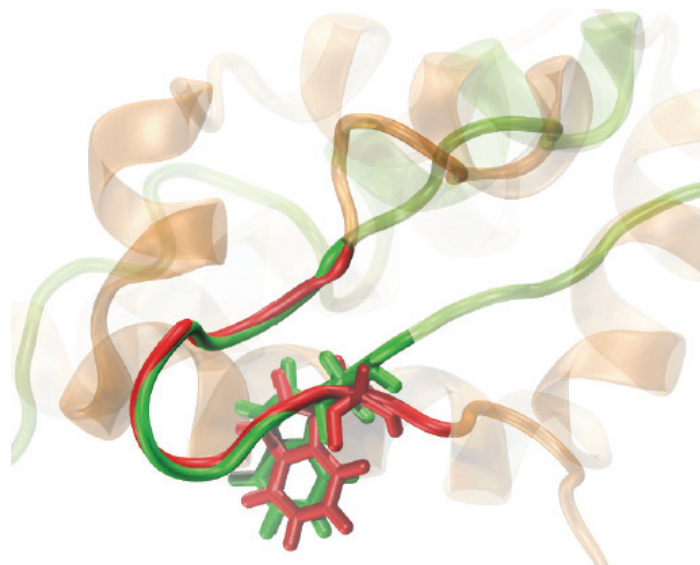


Figure S2. Structural comparison between the region Trp252-Asp259 of Cdc42-bound (green) and autoinhibited (orange) WASP. Alignment was performed by superimposing the backbone atoms of the region Trp252-Asp259 of the two conformational ensembles of WASP. The region Trp252-Asp259 is shown in green and red for Cdc42-bound and autoinhibited WASP, respectively. Trp252 is represented by sticks.