

Supporting Information

Interactions between the Intrinsically Disordered Regions of hnRNP-A2 and TDP-43 Accelerate TDP-43's Conformational Transition

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Table S1. The secondary structure population (%) derived from CD measurement using BeStSel.

	Time (h) ^a	1:0 ^b	1:1	1:3	1:5
α ^c	0.5	4.9 ± 0.30	4.5 ± 0.72	1.9 ± 0.74	1.3 ± 0.56
	4	4.8 ± 1.34	3.3 ± 1.26	1.8 ± 0.55	1.4 ± 0.53
	7	4.7 ± 1.47	0.8 ± 1.3	1.2 ± 0.50	1.6 ± 0.26
	10	0.63 ± 0.78	0 ± 0	0.3 ± 0.10	0.9 ± 0.78
β ^d	0.5	32.5 ± 0.38	31.6 ± 1.08	33.9 ± 0.50	32.7 ± 1.13
	4	33.3 ± 1.82	34.4 ± 2.21	34.5 ± 0.66	34.0 ± 0.55
	7	33.9 ± 2.16	38.1 ± 2.10	35.6 ± 0.76	34.9 ± 0.36
	10	39.7 ± 1.59	41.0 ± 0.11	35.2 ± 0.99	33.8 ± 1.48

^a The incubation time before CD measurements; ^b The TDP-43:hnRNP-A2 ratio; ^c α -helical population (%); ^d Antiparallel β -sheet population.

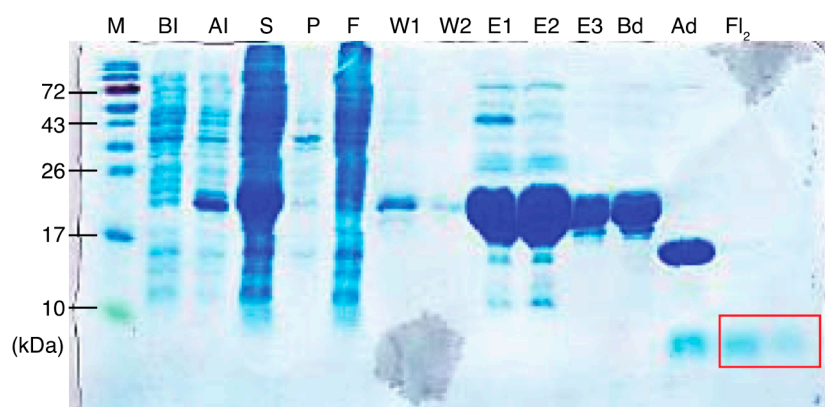


Figure S1. The SDS-PAGE showing different stages of the purification of hnRNP-A2^{288–341}. M: protein size marker; BI/AI: before/after IPTG induction; S/P: supernatant/pellet of the lysed cell; F/W/E: flow-through/wash-through/elution of the first IMAC purification; Bd/Ad: before/after enzyme digestion; Fl2: second flow through the IMAC column. The purified hnRNP-A2^{288–341} is indicated with the red box.