

*Supplementary Information for the manuscript*

**The paralogue of the intrinsically disordered nuclear protein 1 has a nuclear localization sequence that binds to human importin  $\alpha 3$**

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**SUPPLEMENTARY FIGURE LEGENDS**

**FIGURE S1: Binding of intact NUPR1L to Imp $\alpha 3$  monitored by spectroscopic techniques:** (A) Fluorescence spectrum obtained by excitation at 295 nm of the complex between Imp $\alpha 3$  and intact NUPR1L, and addition spectrum obtained by the sum of the spectra of both isolated macromolecules. (B) Far-UV CD spectrum of the complex between Imp $\alpha 3$  and NUPR1L and the addition spectrum obtained by the sum of the spectra of both isolated macromolecules. (C) Thermal denaturations of Imp $\alpha 3$  in the presence and absence of NUPR1L followed by the changes in ellipticity at 222 nm. The data on the y-axis has been scaled up. All experiments were carried out in phosphate buffer (50 mM, pH 7.0).

**FIGURE S2: Structural features of isolated NLS-NUPR1L as monitored by fluorescence:** The spectrum of NLS-NUPR1L after excitation at 280 nm. Spectrum was acquired in phosphate buffer (50 mM, pH 7.0) at 298 K.

**FIGURE S3: Binding of NLS-NUPR1L to  $\Delta$ Imp $\alpha 3$  as monitored by changes in the fluorescence and CD spectra:** (A) Changes occurring upon binding of NLS-NUPR1L to  $\Delta$ Imp $\alpha 3$  as monitored by far-UV CD. (B) Changes in fluorescence spectra upon addition of NLS-NUPR1L to  $\Delta$ Imp $\alpha 3$ , after excitation at 280 nm. (C) Thermal denaturations followed by

ellipticity at 222 nm (far-UV CD) of isolated  $\Delta$ Imp $\alpha$ 3 and its complex with NLS-NUPR1L. Experiments were acquired in phosphate buffer (50 mM, pH 7.0) at 298 K.

**FIGURE S4: Binding of NLS-NUPR1L to Imp $\alpha$ 3 as monitored by changes in the fluorescence and CD spectra:** (A) Changes occurring upon binding of NLS-NUPR1L to Imp $\alpha$ 3 as monitored by far-UV CD. (B) Changes in fluorescence spectra upon addition of NLS-NUPR1L to Imp $\alpha$ 3, after excitation at 280 nm. (C) Thermal denaturations followed by ellipticity at 222 nm (far-UV CD) of isolated Imp $\alpha$ 3 and its complex with NLS-NUPR1L. The data on the y-axis has been scaled up. Experiments were acquired in phosphate buffer (50 mM, pH 7.0) at 298 K.

Fig. S1 (Neira et al.)

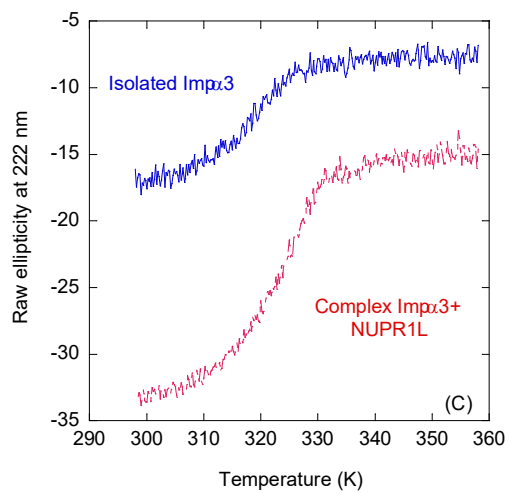
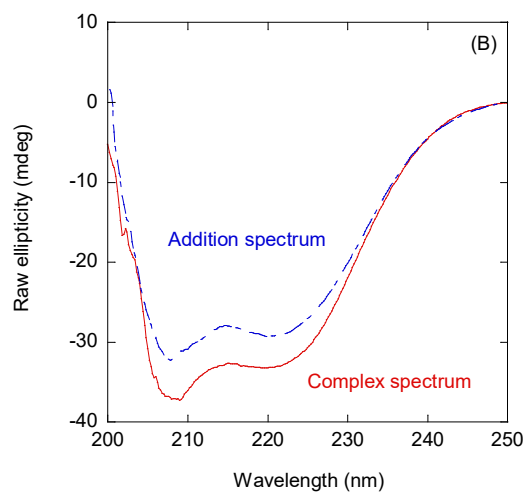
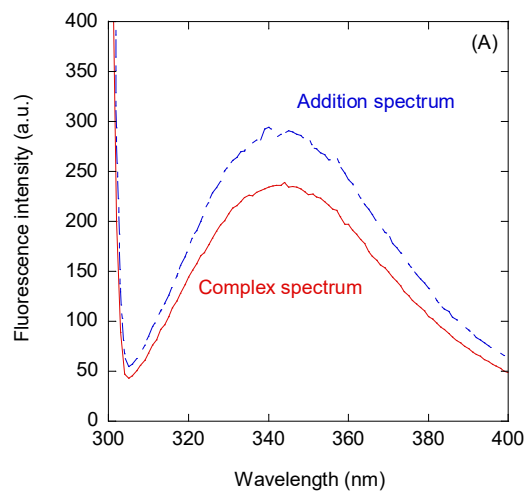


Fig. S2 (Neira et al.)

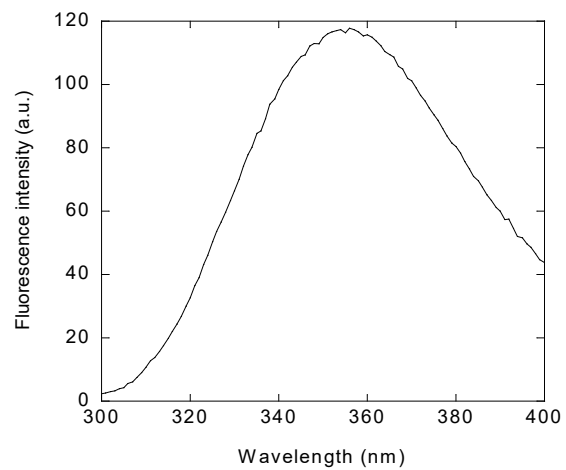


Fig. S3 (Neira et al.)

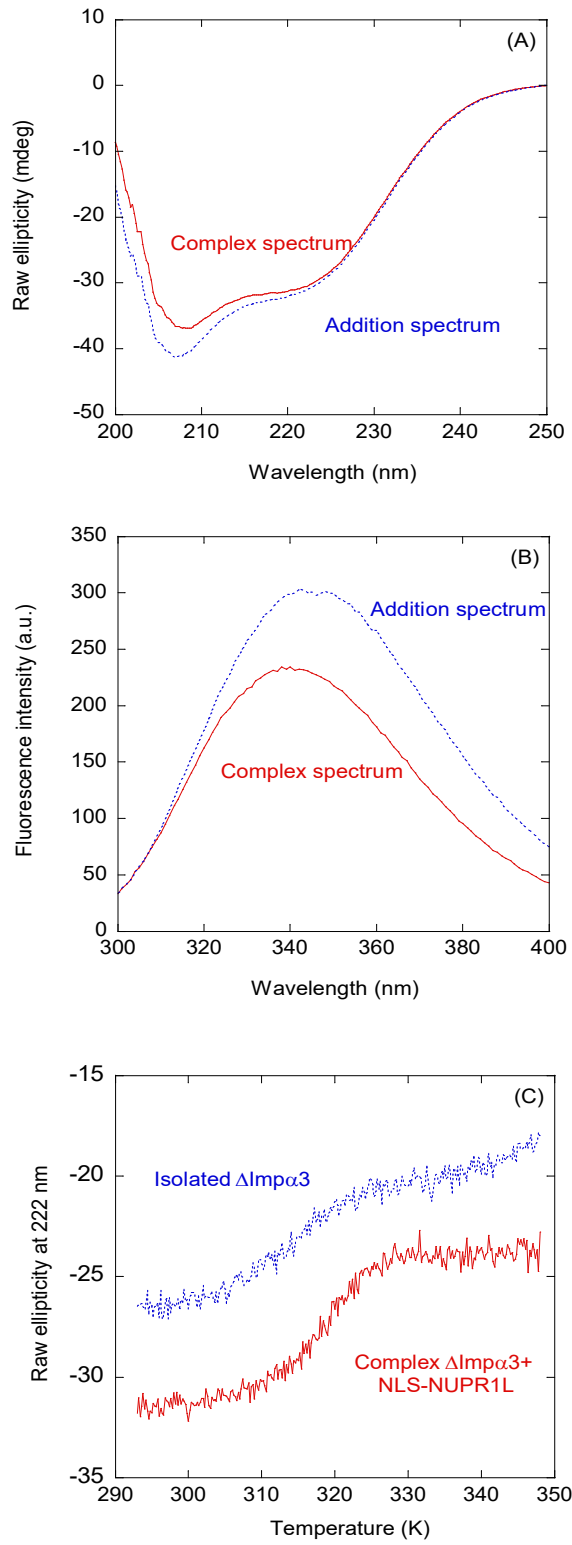
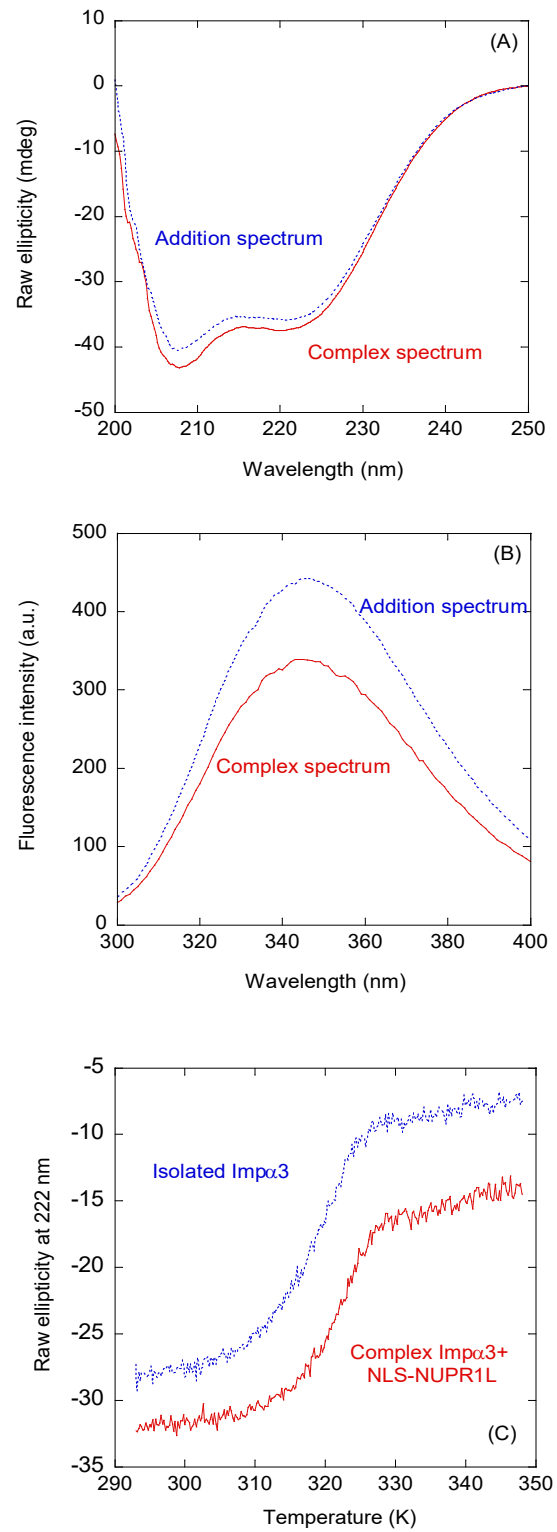


Fig. S4 (Neira et al.)



## SUPPLEMENTARY TABLE

Table ST1: Chemical shifts ( $\delta$ , ppm from TSP) of NLSp8L wild-type in aqueous solution (pH 7.2, 283 K)<sup>a</sup>

	NH	H $_{\alpha}$	H $_{\beta 2}$	H $_{\beta 3}$	H $_{\gamma 2}$	H $_{\gamma 3}$	H $_{\delta 2}$	H $_{\delta 3}$	H $_{\epsilon}$	H $_{\zeta}$
Ac-Arg51		4.32 (-0.09)	1.80							
Thr52	8.19	4.24 (-0.10)	4.07		1.05 (Me)					
Arg53	8.55	4.30 (-0.07)	1.80		1.57					
Arg54	8.54	4.29 (-0.03)	1.80							
Glu55	8.43	4.26 (0.00)	2.07		2.42					
Gln56	8.48	4.32 (0.03)	2.07		2.37					
Ala57	8.31	4.28 (-0.01)	1.37 (Me)							
Leu58	8.17	4.32 (-0.02)	1.63		1.60		0.90 (Me)			
Arg59	8.55	4.35 (-0.09)	1.80							
Thr60	8.31	4.37 (0.08)	4.23		1.21 (Me)					
Asn61 (c)	8.32	4.67 (0.02)	2.65		6.94; 7.59					
Asn61 (t)	8.60	4.70 (0.05)	2.80							
Trp62 (c)	8.23	4.71 (-0.26)	3.06; 3.34		10.12 (NH); 7.22 (2H); 7.52 (7H); 7.15 (5H) 7.20 (6H); 7.69 (4H)					
Trp62 (t)	8.28	4.60 (-0.37)	3.12; 3.41		10.27 (NH); 7.25 (2H); 7.54 (7H); 7.15 (5H) 7.20 (6H), 7.61 (4H)					
Pro63 (c)		4.65 (0.36)	1.95		2.24		3.52; 3.78			
Pro63 (t)		4.50 (0.21)	2.03		2.30		3.70; 3.88			

Ala64 (c)	8.28	4.50 (0.08)	1.37 (Me)		
Ala64 (t)		4.59 (0.17)	1.35 (Me)		
Pro65		4.43 (-0.04)	1.95	2.25	3.64; 3.77
Gly66	8.66	3.98 (0.03)			
Gly67	8.42	3.93 (-0.04)			
His68	8.06	4.63 (-0.02)	3.14	7.17 (C4H); 8.29 (C2H)	
Glu69	8.60	4.23 (-0.04)	1.96	2.25	
Arg70	8.53	4.24 (-0.07)	1.95		
Lys71	8.51	4.25 (-0.09)	1.90		
Val72	8.33	4.08 (0.01)	2.03	0.96 (Me)	
Ala73	8.51	4.28 (-0.03)	1.37 (Me)		
Gln74-am	8.42	4.24 (-0.05)	2.03	2.32	

<sup>a</sup> The (c) and (t) indicate the cis and trans conformations. For the H<sub>α</sub> proton column, the value within parenthesis is the conformational shift ( $\delta_{\text{res}} - \delta_{\text{rc}}$ ), where  $\delta_{\text{res}}$  is the chemical shift of such proton for the corresponding residue. The random-coil values for the sequence,  $\delta_{\text{rc}}$ , were obtained from: [https://spin.niddk.nih.gov/bax/nmrserver/Poulsen\\_rc\\_CS/](https://spin.niddk.nih.gov/bax/nmrserver/Poulsen_rc_CS/).