

Supplementary information

Enhanced Stability of an Intrinsically Disordered Protein against Proteolytic Cleavage through Interactions with Silver Nanoparticles

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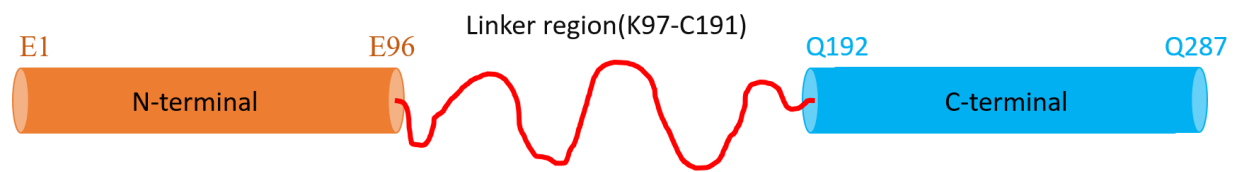
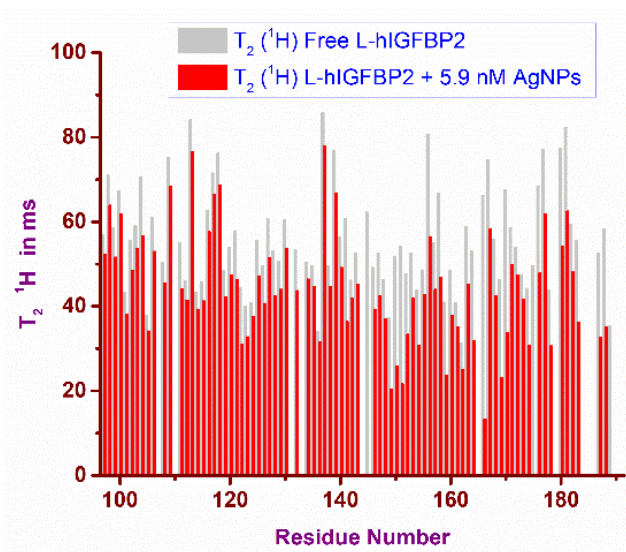
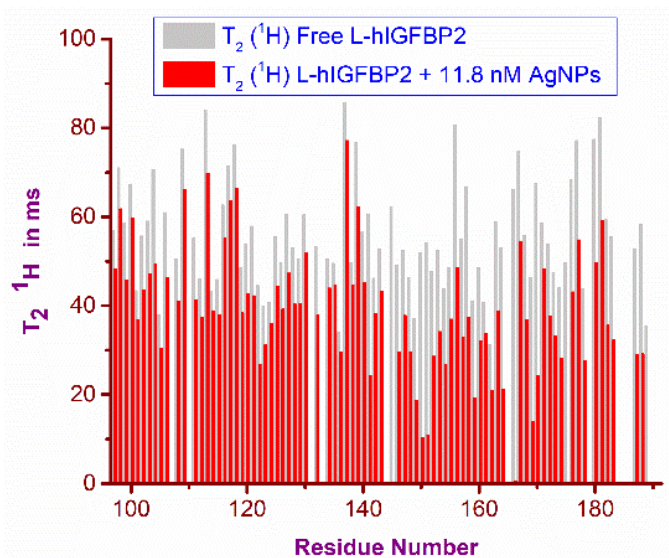


Figure S1: The schematic representation of the full length hIGFBP2 with three domains in different colors. The orange region represents the N-terminal domain (residues from E1 to E96), region in red represents the intrinsically disordered middle domain (K97-C191) and the blue region represents the C-terminal domain (Q192-Q287) of the protein. The N- and the C- termini have some structure while as middle region remains disordered.

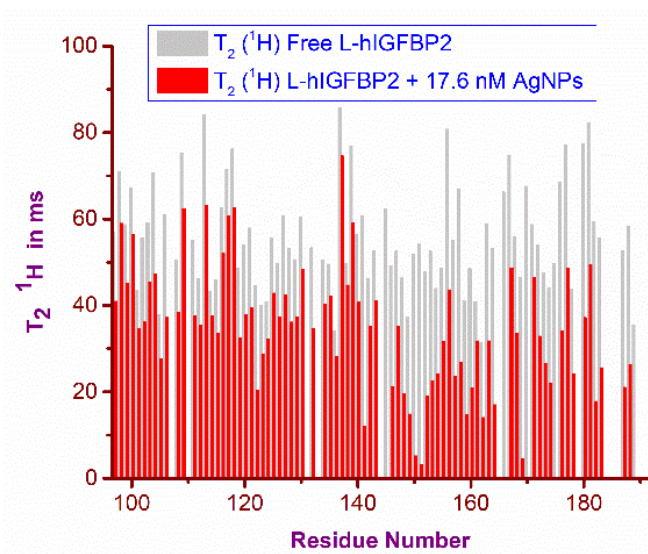
(a)



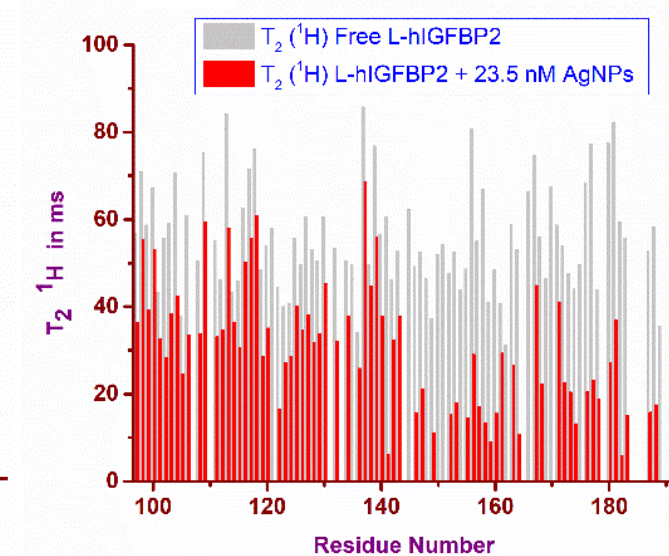
(b)

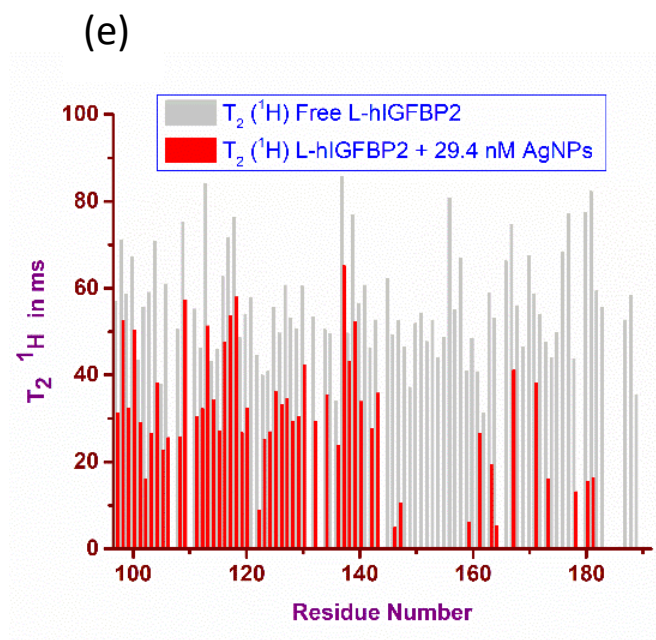


(c)



(d)





Figures S2 (a-e): The overlay of the $T_2 \text{ } ^1\text{H}_N$ (in ms) of free protein with that in presence of the indicated concentrations of the AgNPs.

Table 1: The measured T_2 (1H_N) values for the free and the AgNP-bound protein at different indicated concentrations of the added AgNPs

Residue name	Residue number	T_2 1H_N (ms)					
		Free L-hIGFBP2	with 5.9 nM AgNPs	with 11.8 nM AgNPs	with 17.6 nM AgNPs	with 23.5 nM AgNPs	with 29.4 nM AgNPs
K	97	56.8±6.6	52.3±5.5	48.3±4.5	40.9±3.1	36.4±2.3	31.3±1.6
R	98	71±10.9	63.9±8.6	61.8±8	58.9±7.2	55.4±6.2	52.5±5.5
R	99	58.7±7.1	51.6±5.3	45.8±4	45.2±3.9	39.3±2.8	32.3±1.7
D	100	67.2±9.7	61.8±8	59.8±7.4	56.4±6.5	53.1±5.7	50.4±5
A	101	43.4±3.5	38.2±2.6	36.9±2.4	34.7±2.1	32.5±1.8	29.1±1.3
E	102	55.7±6.3	48.4±4.6	43.4±3.5	36.2±2.3	28.4±1.2	16.2±0.3
Y	103	59±7.2	53.7±5.8	47.2±4.3	45.5±3.9	38.4±2.6	26.6±1
G	104	70.7±10.8	56.6±6.5	49.5±4.8	47.4±4.3	42.4±3.3	38.2±2.6
A	105	37.9±2.6	34.2±1.9	30.4±1.5	27.7±1.2	24.7±0.9	22.8±0.7
S	106	60.9±7.7	53±5.6	46.3±4.1	37.2±2.4	33.5±1.9	25.6±1
P	107	-	-	-	-	-	-
E	108	50.5±5.0	45.5±3.9	40.9±3.07	38.4±2.6	33.8±1.9	25.8±1
Q	109	75.2±12.4	68.5±10.1	66.2±9.3	62.4±8.2	59.4±7.3	57.2±6.7
V	110	-	-	-	-	-	-
A	111	55.1±6.2	44.1±3.7	41.3±3.2	37.5±2.5	33.1±1.8	30.3±1.5
D	112	46.1±4.1	41.5±3.2	37.3±2.5	35.5±2.2	34.6±2	32.3±1.7
N	113	84.1±15.8	76.5±12.9	69.8±10.5	63.1±8.4	58±6.9	51.3±5.2
G	114	43.2±3.5	39.3±2.8	38.9±2.7	37.6±2.5	36.3±2.3	34.1±2
D	115	45.9±4	41.3±3.1	38.1±2.6	33.5±1.9	30.7±1.5	27.1±1.1
D	116	62.7±8.3	57.6±6.8	55.1±6.2	52±5.4	50.1±5	47.6±4.4
H	117	71.5±11.1	66.5±9.4	63.62±8.5	60.8±7.7	55.8±6.3	53.6±5.8
S	118	76.2±12.8	68.6±10.1	66.3±9.4	62.5±8.2	60.95±7.8	57.9±6.9
E	119	48.6±4.6	42.24±3.3	38.4±2.6	32.5±1.8	28.6±1.3	26.7±1.1
G	120	54±5.9	47.5±3.3	42.6±3.4	37.8±2.5	35.1±2.1	32.4±1.7
G	121	57.9±6.9	46.3±4.1	42.2±3.3	39.3±2.8	-	-
L	122	44.5±3.8	31.2±1.6	26.7±1.1	20.5±0.5	16.5±0.3	8.9±0
V	123	40±2.9	32.8±1.8	31.2±1.6	28.8±1.3	27.2±1.1	25.2±1
E	124	40.8±3.1	37.6±2.5	35.9±2.3	32.3±1.7	28.6±1.3	26.9±1.1
N	125	55.6±6.3	47.3±4.3	44.5±3.8	42.8±3.4	40±2.9	36.1±2.3
H	126	49.6±4.8	40.7±3	39.2±2.8	37.2±2.5	34.7±2.1	33.3±1.9
V	127	60.6±7.7	51.5±5.3	47.3±4.3	42.5±3.4	38.2±2.6	34.6±2
D	128	53.1±5.7	42.5±3.4	40.4±3	36.1±2.3	31.9±1.7	29.2±1.3
S	129	50.6±5.1	44±3.7	40.5±3	37.4±2.5	33.9±1.9	30.3±1.5
T	130	60.4±7.6	53.8±5.8	52±5.4	48.4±4.6	45.3±3.9	42.3±3.3
M	131	-	-	-	-	-	-
N	132	53.3±5.7	43.7±3.6	37.9±2.6	34.7±2.1	32±1.7	29.3±1.4

M	133	-	-	-	-	-	-
L	134	50.5±5	46.5±4.2	43.9±3.6	40.4±3	38±2.6	35.3±2.2
G	135	49.5±4.8	44.6±3.8	44.6±3.8	42.1±3.3	-	-
G	136	34.1±2	31.7±1.6	29.6±1.4	28.3±1.2	25.9±1	23.9±0.8
G	137	85.7±16.6	78±13.5	77.2±13.1	74.6±12.2	68.6±10.1	65.2±9
G	138	49.6±4.8	44.7±3.8	44.7±3.8	44.7±3.8	44.7±3.8	43.2±3.5
S	139	76.8±13	66.8±9.6	62.2±8.1	59.1±7.2	56.1±6.4	52.2±5.4
A	140	56.5±6.5	49.2±4.7	45.21±3.9	40.7±3	37.9±2.6	33.9±2
G	141	60.7±7.7	36.4±2.3	24.3±0.8	12.1±0.1	6.1±0	-
R	142	46.1±4.1	42±3.3	38.3±2.6	35.1±2.1	32.3±1.7	27.7±1.2
K	143	52.7±5.6	45.3±3.9	43.2±3.5	41.1±3.1	37.9±2.6	35.8±2.2
P	144	-	-	-	-	-	-
L	145	62.3±8.1	-	-	-	-	-
K	146	49.2±4.7	39.4±2.8	29.5±1.4	21.2±0.6	15.7±0.2	4.9±0
S	147	52.6±5.5	42.6±3.4	37.8±2.6	35.2±2.1	21±0.6	10.5±0
G	148	46.3±4.1	37.1±2.4	29.7±1.4	19.5±0.5	-	-
M	149	37.2±2.4	20.4±0.5	18.6±0.4	14.9±0.2	11.2±0.1	-
K	150	51.9±5.4	25.9±1	10.4±0.1	5.2±0	-	-
E	151	54.1±5.9	21.7±0.6	10.83±0.1	3.2±0	-	-
L	152	47.7±4.4	33.4±1.9	28.62±1.3	19.1±0.4	15.3±0.2	-
A	153	52.6±5.5	42.1±3.3	34.16±2	22.6±0.7	17.9±0.4	-
V	154	43.9±3.6	30.7±1.5	26.78±1.1	24.2±0.8	-	-
F	155	48.6±4.6	42.8±3.4	36.94±2.4	31.6±1.6	14.6±0.2	-
R	156	80.7±14.5	56.5±6.5	48.43±4.6	43.6±3.6	29.1±1.3	-
E	157	55±6.1	44±3.7	33±1.8	23.7±0.8	17.1±0.3	-
K	158	66.8±9.5	46.8±4.2	37.4±2.5	26.7±1.1	13.4±0.1	-
V	159	41±3.1	23.8±0.8	19.3±0.4	14.8±0.2	9±0	6.2±0
T	160	48.5±4.6	37.8±2.5	32±1.7	20.8±0.5	15.5±0.2	-
E	161	40.8±3	35.1±2.1	33.8±1.9	31.8±1.7	29.4±1.4	26.5±1.1
Q	162	31.3±1.6	25±0.9	21±0.6	14.1±0.2	-	-
H	163	58.9±7.2	45.3±3.9	38.9±2.7	31.8±1.7	26.5±1	19.4±0.4
R	164	53.1±5.7	31.8±1.7	21.2±0.6	17±0.3	10.6±0.1	5.3±0
Q	165	-	-	-	-	-	-
M	166	66.2±9.4	13.3±0.1	0.7±0.3	-	-	-
G	167	74.7±12.2	58.3±7	54.5±6	48.6±4.6	44.8±3.8	41.1±3.1
K	168	55.9±6.4	42.5±3.4	36.9±2.4	33.5±1.9	22.4±0.7	-
G	169	46.4±4.1	23.2±0.7	13.9±0.2	4.6±0	-	-
G	170	67.5±9.8	33.8±1.9	24.3±0.8	-	-	-
K	171	58.7±7.1	49.9±4.9	48.1±4.5	46.4±4.1	41.1±3.1	38.2±2.6
H	172	53.9±5.9	47.4±4.4	37.7±2.5	32.9±1.8	22.6±0.7	-
H	173	47.5±4.4	41.8±3.2	33.3±1.9	26.6±1.1	20.4±0.5	16.2±0.3
L	174	44±3.7	30.8±1.5	28.2±1.2	22±0.6	13.2±0.1	-
G	175	49.7±4.9	-	-	-	-	-
L	176	68.4±10	47.9±4.5	43.1±3.5	34.2±0.6	20.5±0.5	-
E	177	77.2±13.1	61.7±8	54.8±6.1	48.6±4.6	23.2±0.7	-
E	178	43.8±3.6	30.6±1.5	27.6±1.2	24.1±0.8	18.8±0.4	13.1±0.1

