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Supporting Material

A Self-Consistent Description of the Conformational Behaviour of Chemically-Denatured Proteins from NMR and Small Angle Scattering

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SUPPLEMENTARY INFORMATION

A Self-Consistent Description of the Conformational Behaviour of Chemically-Denatured Proteins from NMR and Small Angle Scattering

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TABLE S1. R_g s of Intrinsically Disordered Proteins.

Protein	#Residues	R_g	R_g^{RC} ^a	Ref.
Tau ht40	441	65±3	61.0	(1)
Tau K32	202	42±3	40.6	(1)
Tau K16	174	39±3	37.5	(1)
Tau K18	130	38±3	32.2	(1)
Tau ht23	352	53±3	54.2	(1)
Tau K27	171	37±2	37.2	(1)
Tau K17	143	36±2	33.9	(1)
Tau K19	99	35±1	28.0	(1)
Tau K44	283	52±2	48.4	(1)
Tau K10	167	40±1	36.7	(1)
Tau K25	185	41±2	38.7	(1)
Tau K23	254	49±2	45.7	(1)
Tau K32 AT8 AT100	202	41±3	40.6	(1)
Tau ht23 S214E	352	54±3	54.2	(1)
Tau ht23 AT8 AT100	352	52±3	54.2	(1)
Tau K18 P301L	130	35±2	32.2	(1)
Prothymosin α , pH 7.5	109	37.8±0.9	29.4	(2)
Prothymosin α , pH 2.5	109	27.6±0.9	29.4	(2)
α -Synuclein, pH 7.5	140	40±1	33.5	(3)
α -Synuclein, pH 3.0	140	30±1	33.5	(3)
PIR domain	75	26.5±0.5	24.2	(4)
N-tail nucleoprotein MV	139	27.2±0.5	33.4	(5)
p53 (1-93)	93	28.7±0.3	27.1	(6)
Neuroigin 3	118	31.5±1.0	30.6	(7)
Ki-1/57	292	47.5±1.0	49.2	(8)
Msh6 N-term	304	56±2	50.2	(9)
Pig Calpastatin domain I	148	35.4	34.5	(10)
HrpO	147	35.0	34.4	(11)

a- Threshold R_g value obtained from the parametrization of Flory's relationship with the coil database.

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