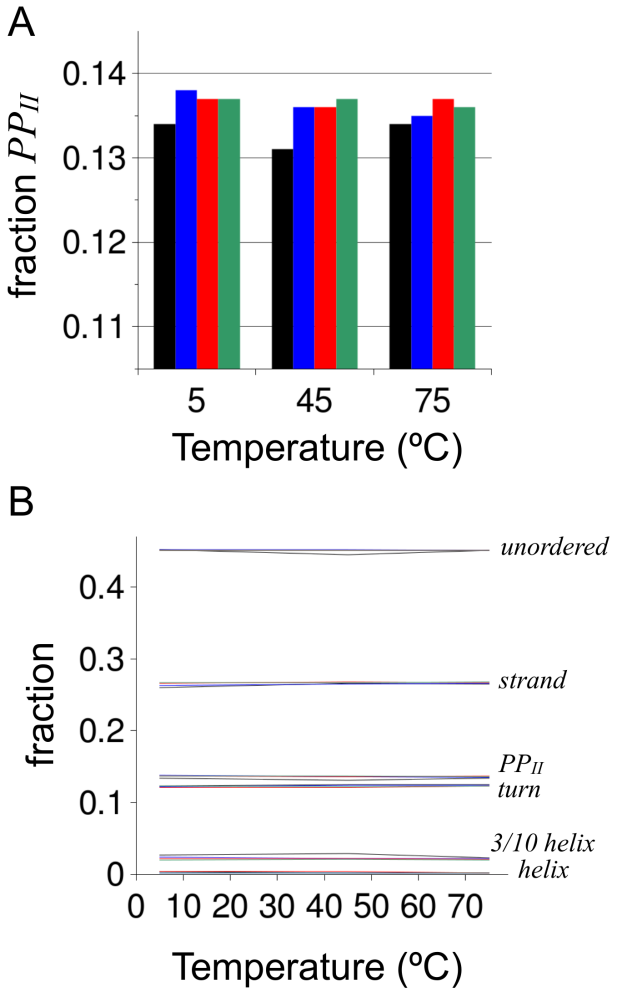

Figure S1. Fraction of residues with *PP_{II}* structure predicted from the CD spectrum of p53(1-93) using the CONTIN/LL algorithm and SP22X basis set. In both panels, values for wild type were shown with black, ALA$^-$ with blue, PRO$^-$ with red, and ALA$^-$PRO$^-$ with green. In panel **A**, the *PP_{II}* propensities returned by the CD fitting routine for spectra measured at 5°C, 45°C, and 75°C were given by the columns. In panel **B**, lines provide a comparison of the *PP_{II}* propensities to the other secondary structure elements (as indicated in the figure) returned by the CD fitting routine.

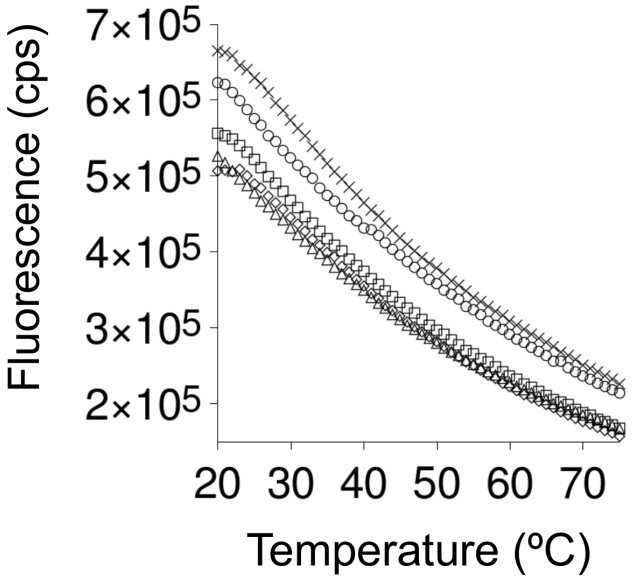

Figure S2. Temperature effects on acrylamide induced fluorescence quenching. The temperature dependence in the fluorescence of p53(1-93) in the presence of 50 mM aqueous acrylamide is shown for wild type (circles), ALA^- (squares), PRO^- (triangles), and ALA^-PRO^- (diamonds). Temperature dependence in the fluorescence of NATA in the presence of 37.5 mM aqueous acrylamide is shown by X symbols. The observations of increased quenching with added heat and similarity to the acrylamide induced quenching of NATA fluorescence suggested a dynamic rather than static quenching mechanism for the p53(1-93) variants. Fluorescence emission was monitored at 359 nm from excitation at 295 nm. Temperature was incremented using a rate of 2°C min^{-1}.

fitting parameter(s)	correlation with $R_{h,rel}$ (R^2)
f_{ALA}	0.0001
f_{PRO}	0.242
Q_{net}	0.194
f_{PRO}, Q_{net}	0.539
f_{PRO}, Q_{net}, f_{ALA}	0.542
f_{PRO}, Q_{net}, *random**	0.546 ± 0.008
f_{ALA} - *IDPs with* $f_{PRO} > 0.10$	0.472
f_{ALA} - *IDPs with* $Q_{net} > 10$	0.200
Q_{net} - *IDPs with* $f_{PRO} > 0.10$	0.028
Q_{net} - *IDPs with* $f_{PRO} < 0.10$	0.439

Table S1. $R_{h,rel}$ correlations with f_{ALA}, f_{PRO}, and Q_{net}. R^2 is the coefficient of determination calculated by multiple linear regression between the fitting parameter(s) and $R_{h,rel}$.

* Random numbers from 0 to 1 generated for each IDP, R^2 is the average of 10 trials.

protein	N	R_h	$R_{h,coil}$	$R_{h,rel}$	RCS_{PPII}	Q_{net}	$\#PRO$	$\#ALA$	f_{PRO}	f_{ALA}	DISPHOS score	# predicted phos sites
p53(1-93)	93	32.4	21.70	1.49	3.934	15	22	12	0.237	0.129	10.137	11
SBD	61	25.6	17.51	1.46	3.983	1	12	5	0.197	0.082	7.691	6
p53-TAD	73	23.8	19.18	1.24	2.405	14	13	4	0.178	0.055	8.303	9
p57-ID	73	24.0	19.18	1.25	2.468	7	4	5	0.055	0.068	3.836	2
PDE-gamma	87	24.8	20.97	1.18	2.014	4	10	4	0.115	0.046	4.443	5
Vmw65	89	28.0	21.22	1.32	2.818	19	6	10	0.067	0.112	7.482	10
LJIDP1	94	24.5	21.82	1.12	1.648	4	3	15	0.032	0.160	9.735	10
Hdm2-ABD	97	25.7	22.17	1.16	1.855	29	3	3	0.031	0.031	20.154	24
Mlph(147-240)	97	28.0	22.17	1.26	2.466	16	6	2	0.062	0.021	15.513	19
Sm1	105	23.4	23.08	1.01	1.059	5	5	7	0.048	0.067	11.513	11
prothymosin-alpha	110	33.7	23.63	1.43	3.386	43	1	11	0.009	0.100	8.684	10
Cad136	136	28.1	26.33	1.07	1.303	9	13	12	0.096	0.088	16.651	20
alpha-synuclein	140	28.2	26.72	1.06	1.243	9	5	19	0.036	0.136	8.839	7
ShB-C	146	32.9	27.30	1.21	2.052	4	5	11	0.034	0.075	16.141	18
Fos-AD	168	35.0	29.32	1.19	1.964	16	20	14	0.119	0.083	27.942	28
HIFq-alpha-503	170	38.3	29.50	1.30	2.531	10	13	13	0.076	0.076	27.394	34
CFTR-R-region	189	32.0	31.13	1.03	1.111	5	8	8	0.042	0.042	20.307	19
Tau-K45	198	45.0	31.88	1.41	3.097	19	19	6	0.096	0.030	26.731	27
HIF1-alpha-403	202	44.3	32.20	1.38	2.899	29	22	12	0.109	0.059	29.359	33
Securin	204	39.7	32.36	1.23	2.111	1	24	13	0.118	0.064	20.199	25
Mlph(147-403)	260	49.0	36.62	1.34	2.644	29	20	17	0.077	0.065	37.728	46
SNAP25	206	39.7	32.52	1.22	2.077	14	2	16	0.010	0.078	8.234	8

Table S2. R_h, RCS_{PPII}, Q_{net}, f_{PRO}, f_{ALA}, and DISPHOS score for intrinsically disordered proteins. N is the number of residues. R_h were from published reports (26,63-80). $R_{h,coil}$ was calculated as $2.16*N^{0.509}$ (i.e., from equations 1 and 2 with $S_{PPII} = 0$). $R_{h,rel}$ was calculated as $R_h/R_{h,coil}$. RCS_{PPII} was calculated as $\partial R_h/\partial f_{PPII}$ normalized to the statistical coil value. Q_{net} is the absolute value of the number of glutamic and aspartic residues minus the number of lysine and arginine residues. $\#PRO$ and $\#ALA$ are the number of proline and alanine residues, respectively. f_{PRO} is the number of proline residues divided by N. f_{ALA} is the number of alanine residues divided by N. DISPHOS score was calculated for an IDP sequence using the DISPHOS 1.3 website (www.dabi.temple.edu/disphos/pred.html) with "Default Predictor" selected. The number of phosphorylation sites predicted by DISPHOS 1.3 for each IDP sequence is given by the column labeled "# predicted phos sites."