Supporting information Table 1 Comparison of target values of R_{gyr} with the calculated values of R_{gyr} for the NMR structures obtained with and without the R_{gyr} restraint, and for the X-ray structures.

Structure	R_{gyr} (Å)			
	Target value[a]	NMR structure without R_{gyr}	NMR structure with R_{gyr}	X-ray structure
GB1 (residues 1-56)	10.16	10.94	10.73	10.59
BAF dimer (residues 1-89)	15.76	17.36	16.47	16.54
gp41 trimer[b]				
residues 3-26 and 97-122	14.76	15.27	14.96	-
residues 10-33 and 90-114	14.54	15.49	14.95	15.02
residues 20-43 and 78-104	14.88	16.33	15.54	-
residues 30-53 and 72-92	14.18	15.89	15.10	-
p53 tetramer (residues 325-355)	13.57	14.95	14.38	14.61

[a] The target values are calculated using the formula $2.2N^{0.38}$ where N is the number of residues. GB1, the BAF dimer and the p53 tetramer are approximately globular. gp41 is highly anisotropic and has been divided up into four overlapping globular segments.

[b] The X-ray structure of SIV gp41 only comprises residues 8-43 and 86-119.