Supplementary data

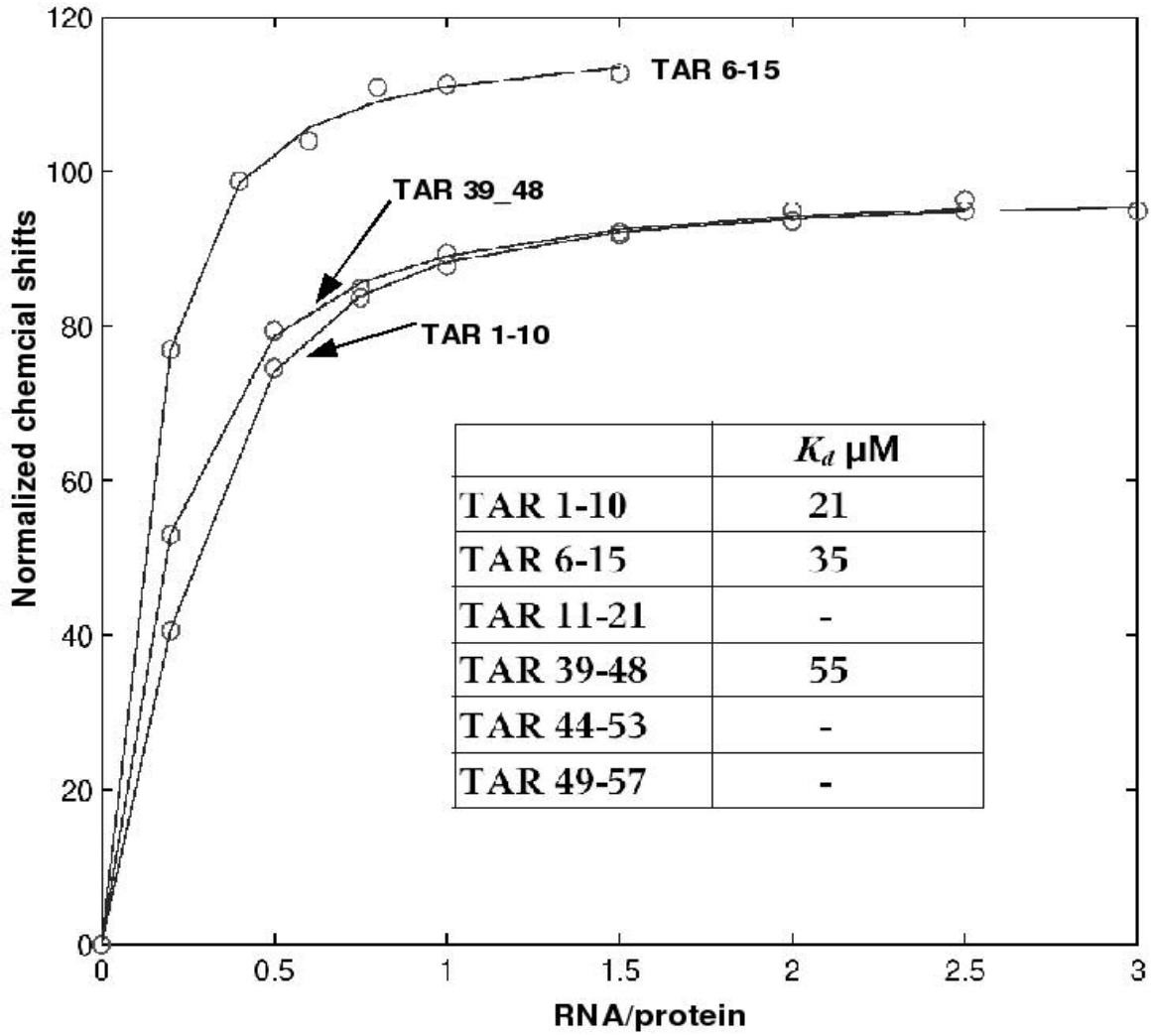
Table 1 Structural statistics. E_{pot}, overall potential energy; E_{impr}, potential energy of improper angle; E_{cdih}, potential energy for dihedral restraints; E_{sani}, potential energy for RDC restraints.

experimental restraints		
distance restraints	total	1929
	intraresidual sequential medium-range long-range	468 423 289 638
dihedral angles		32
dipolar couplings		55
hydrogen bonds (two restraints each)		24
molecular dynamics statistics		
energies (kcal/mol)		
	E_{pot}	12.9 ± 1.4
	E_{bond}	0.73 ± 0.06
	E_{angle}	7.9 ± 0.6

experimental restraints		
	E_{impr}	2.1 ± 0.2
	E_{repel}	0.79 ± 0.3
	E_{NOE}	1.3 ± 0.5
	E_{cdih}	0.03 ± 0.03
	E_{sani}	0.7 ± 0.2
RMSDs from ideal distances (Å)	bond lengths distance restraints	0.00074 ± 0.00004 0.0035 ± 0.0007
RMSDs from ideal angles (deg)	bond angles dihedral angle restraints	0.14 ± 0.06 0.15 ± 0.15
RMSDs from dipolar couplings (Hz)		0.11 ± 0.02
atomic coordinate precision (RMSD) (Å)		
backbone heavy atoms		0.69 (Gly39-Thr118)
heavy atoms		1.19 (Gly39-Thr118)
Ramachandran plot statistics		
residues in		
	most favored regions	88.0%

experimental restraints		
	allowed regions	12.0%

Fig. Dissociation constants for NELF-E RRM:TAR complexes. Fitting of the curves yielded the calculated Kd values shown in the inset. Normalized chemical shift changes of G39 were used.



	K_d μM
TAR 1-10	21
TAR 6-15	35
TAR 11-21	-
TAR 39-48	55
TAR 44-53	-
TAR 49-57	-