Supplementary Table II. Input for the calculation and characterization of the energy-minimized NMR structures of Prp24-12 (residues 39-197).

Quantity		**Value**[a]
NOE upper distance limits		1670
Dihedral angle constraints		212
Hydrogen bond constraints		64
Residual target function value ($Å^2$)		2.85 ± 0.25
Residual distance constraint violations		
Number ≥ 0.1 Å		24 ± 5
Maximum Å		0.24 ± 0.2
Residual dihedral angle constraint violations		
Number ≥ 2.5°		1.0 ± 1.0
Maximum Å		2.8 ± 1.5
RMSD to the mean coordinates[b]		
N,Cα, C' (39-161)		1.53 ± 0.15
N,Cα, C' of regular secondary structure		0.97 ± 0.09
All heavy atoms of regular secondary structure		1.45 ± 0.17
	RRM1	**RRM2**
N,Cα, C' of regular secondary structure	0.42 ± 0.06	0.58 ± 0.08
All heavy atoms	1.14 ± 0.15	1.11 ± 0.13
Ramachandran plot statistics[c]		
Most favored region (%)		78.4
Additional allowed region (%)		17.8
Generously allowed region (%)		2.1

[a] Except for the top three entries, data characterize the bundle of 10 conformers used to represent the NMR structure; the mean value and standard deviation are given. RMSDs were determined by CYANA (Guntert et al. 1997) and MOLMOL (Koradi et al. 1996).
[b] Regular secondary structure elements are the α-helices (54-64,91-97,130-139,168-178) and β-strands (43-47,70-73,81-85,110-113,118-122,146-149,160-164,189-193).
[c] As determined by PROCHECK (Morris el al. 1992).

References:
-Morris, A.L., MacArthur, M.W., Hutchinson, E.G. and Thornton, J.M. (1992). Stereochemical quality of protein structure coordinates. *Proteins*, **12**, 345-364.
-Guntert, P., Mumenthaler, C. and Wuthrich, K. (1997). Torsion angle dynamics for NMR structure calculation with the new program DYANA. *J Mol Biol*, **273**, 283-298.
-Koradi, R., Billeter, M. and Wuthrich, K. (1996). MOLMOL: a program for display and analysis of macromolecular structures. *J Mol Graph*, **14**, 51-55, 29-32.