Table 1. NMR and refinement statistics for the structure of the ATP7B N-domain in a complex with ATP

NMR distance and dihedral constraints	**Value**
Distance constraints	
Total NOEs	1896
Intraresidue	983
Sequential (|i-j| = 1)	560
Medium-range (|i-j| ≤ 4)	172
Long-range (|i-j| > 4)	183
Hydrogen bonds	34
Total dihedral angle constraints	198
phi	99
psi	99
Structure Statistics	
Consistent violations in three or more structures	
Distance constraints (>0.2 Å)	6
Dihedral angle constraints (>5^{o})	0
Max. dihedral angle violation	0
Max. distance constraint violation (Å)	0.48
Ramachandran plot distribution (res. 1038-1113;1143-1196)	
Most favored regions	90
Additionally allowed regions	7
Disallowed region	3
Average rms deviation to mean structure, Å (res. 1038-1113,1143-1196)	
Heavy	1.3 ± 0.3
Backbone	0.9 ± 0.2

NOE, nuclear Overhauser effect.