

Table S2. NMR and refinement statistics for protein structures

<i>A. ventricosus</i> MiSp CT	
NMR distance and dihedral constraints	
Distance constraints	
Total NOE	6060
Intra-residue	1024
Inter-residue	5036
Sequential ($ i-j = 1$)	1548
Medium-range ($ i-j < 4$)	1815
Long-range ($ i-j > 5$)	971
Intermolecular	702
Structure statistics	
Violations (mean and s.d.)	
Distance constraints (Å)	0.0109 ± 0.0004
Max. distance constraint violation (Å)	0.38 ± 0.05
Deviations from idealized geometry	
Bond lengths (Å)	0.0035 ± 0.0001
Bond angles (°)	0.440 ± 0.007
Improper (°)	1.241 ± 0.043
Average pairwise r.m.s.d.** (Å)	
Heavy	0.46 ± 0.07
Backbone	0.78 ± 0.07

**Pairwise r.m.s.d. was calculated for residues 20-120 of both chains among 20 refined structures.