Supplementary Data

Structural resemblance of the DNAJA-family protein, Tid1, to the DNAJB-family Hsp40

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Table 1. Structural statistics for the 20 energy-minimized conformers of Tid1-JD

Experimental constraints	
NOE constraint total	1365
Intra-residue	431
Sequential	331
Medium-range	381
Long-range	222
Dihedral constraints	
ϕ	62
ψ	62
RMSD to the mean structure (Å) for residues 94-99, 105-118, 131-145, 149-157	
Backbone atoms (N, C, CO)	0.39 +/- 0.08
All heavy atoms	0.97 +/- 0.10
Violations (mean and s.d.)	
Distance constraints (Å)	0.079 +/- 0.003
Dihedral angle constraints (º)	3.240 +/- 0.762
Max. dihedral angle violation (º)	156.941
Max. distance constraint violation (Å)	0.08
Deviations from idealized geometry (RMS Z-score)	
Bond lengths (Å)	0.820
Bond angles (º)	0.939
Impropers (º)	0.621
Ramachandran statistics	
MolProbity	
Favored	97.46

Allowed	2.54
outlier	0
Scores[a]	
DOPE	−6730.983
nDOPE	−1.814
dDFIRE	−151.937

[a]The optimal energy properties (DOPE, nomalized DOPE (nDOPE), and dDFIRE) were calculated by CHARMM program