Table S1: Summary of Integrative Structure Determination of A metastable contact and structural disorder in the estrogen receptor transactivation domain (PDBDEV00000027)

1. Model Composition	
Entry composition	- Estrogen receptor: Chain A (184 residues)
Datasets used for modeling	- SAS data, SASDEE2 - Hydroxyl radical protein footprinting, Not listed
2. Representation	
Atomic structural coverage	100%
Number of rigid bodies, flexible units	1, 0
Rigid regions	- A: 1-184:None.
Flexible units	- A: -
Resolution	Rigid bodies: 1 residue per bead. Flexible regions: N/A
3. Restraints	
Physical principles	Physical principles were not used for modeling
Experimental data	- 1 unique SASRestraint: Assembly name: Complete assembly Fitting method: ? Multi-state: False
4. Validation	
Sampling validation	1. Information related to sampling validation has not been provided
Clustering algorithm ,clustering feature	Distance threshold-based clustering used if ensembles are deposited, Not applicable
Number of ensembles	0
Number of models in ensembles	Not applicable
Model precision (uncertainty of models)	Model precision can not be calculated with one structure
Quality of data	1. SASDEE2: Rg from Gunier is 3.11nm and Rg from p(r) is 3.0nm
Assessment of atomic regions	Clashscore: 0.0, Ramachandran outliers: 2.56% , Sidechain outliers: 5.51%
Assessment of excluded volume	1. Not applicable
Fit of the model to information used to compute it	1. SASDEE2: Fit 1 with X^2 value 0.14 2. SASDEE2: Fit 2 with X^2 value 0.34 3. SASDEE2: Fit 3 with X^2 value 0.51

Fit of the model to information not used to compute it	1. Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
Method	Modeling estrogen receptor N-terminal domain
Name	?
Details	- Method details unspecified
Software	- iSPOT (version None) - No location specified