

Summary of integrative structure determination of A metastable contact and structural disorder in the estrogen receptor transactivation domain (PDB ID: 8ZZR, PDB-Dev ID: PDBDEV_00000027)

1. Model Composition	
Entry composition	Estrogen receptor: chain(s) A (184 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - SAS data, SASBDB: SASDEE2 - Hydroxyl radical footprinting data, Not available: 10.1016/j.str.2018.10.026
2. Representation	
Number of representations	1
Scale	Atomic
Number of rigid and flexible segments	1, 0
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	<ul style="list-style-type: none"> - 1 unique SASRestraint: Assembly name: Complete assembly Fitting method: ? Multi-state: False
4. Validation	
Number of ensembles	0
Number of models in ensembles	Not applicable
Number of deposited models	10
Model precision (uncertainty of models)	Not available
Data quality	SASDEE2: Rg from Gunier is 3.0nm and Rg from p(r) is 3.11nm
Model quality: assessment of atomic segments	<ul style="list-style-type: none"> - Clashscore: 0.00-0.00 - Ramachandran outliers: 2-7 - Sidechain outliers: 2-14
Fit to data used for modeling	Fit of model to information used to compute it has not been determined
Fit to data used for validation	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	

1. Name	Modeling estrogen receptor N-terminal domain
Software	iSPOT (version Not available)