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

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| ***1. Model Composition*** | |
| *Entry composition* | - Estrogen receptor: Chain A (184 residues)<br>- Estrogen receptor: Chain A (184 residues)<br>- Estrogen receptor: Chain A (184 residues)<br>- Estrogen receptor: Chain A (184 residues)<br>- Estrogen receptor: Chain A (184 residues)<br>- Estrogen receptor: Chain A (184 residues)<br>- Estrogen receptor: Chain A (184 residues)<br>- Estrogen receptor: Chain A (184 residues)<br>- Estrogen receptor: Chain A (184 residues)<br>- Estrogen receptor: Chain A (184 residues) |
| *Datasets used for modeling* | - SAS data, SASDEE2<br>- 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.<br>Flexible regions: 50 residues per bead. |
| ***3. Restraints*** | |
| *Physical principles* | Excluded volume and Sequence connectivity. |
| *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, 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. Quality of input data has not be assessed |
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| *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. Fit of model to information used to compute it has not been determined |
| *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)<br>- No location specified |