Summary of integrative structure determination of structure of the human rev7 dimer (PDBDEV00000009)

1. Model Composition	
Entry composition	- Rev7-monomer: Chain A (212 residues) - Rev3-RBM2: Chain B (28 residues) - Rev7-monomer: Chain C (212 residues) - Rev3-RBM2: Chain D (28 residues)
Datasets used for modeling	- SAS data, SASDC29 - Experimental model, PDB ID: 6BC8 - Mutagenesis data, Not listed
2. Representation	
Atomic structural coverage	100%
Number of *rigid bodies*, *flexible units*	0, 4
Rigid bodies	- A: - - B: - - C: - - D: -
Flexible units	- A: 1-212. - B: 1-28. - C: 1-212. - D: 1-28.
Resolution	- Rigid bodies: 1 residue per bead. - Flexible regions: N/A
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 64 unique DerivedDistanceRestraint: Upper Bound Distance: 2.0 - 1 unique SASRestraint: Assembly name: Complete assembly Fitting method: FoXS Multi-state: False
4. Validation	
Sampling validation	- 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	- SASDC29: Rg from Gunier is 3.01nm and Rg from p(r) is 2.93nm
Model quality: assessment of atomic segments	Clashscore: 8.73, Ramachandran outliers: 0.42% , Sidechain outliers: 3.52%
Model quality: assessment of excluded volume	- Not applicable
Fit of the model to information used to compute it	- SASDC29: Fit 1 with X^2 value 25.13
Fit of the model to information not used to compute it	- Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
Method	None
Name	None
Details	- Method details unspecified
Software	- Software details not provided - No location specified