Summary of integrative structure determination of structure of the human rev7 dimer (PDBDEV_00000009)

1. Model Composition	
Entry composition	- Rev7-monomer: Chain C (212 residues) - Rev7-monomer: Chain A (212 residues) - Rev3-RBM2: Chain B (28 residues) - Rev3-RBM2: Chain D (28 residues)
Datasets used for modeling	- SAS data, SASDC29 - Experimental model, PDB ID: 6BC8 - Mutagenesis data, Not available
2. Representation	
Atomic structural coverage	100%
Number of <u>rigid bodies</u> , <u>flexible units</u>	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

Data quality	- SASDC29: Rg from Gunier is 3.01nm and Rg from p(r) is 2.93nm
Model quality: assessment of atomic segments	- Model-1: Clashscore = 8.73, Number of Ramachandran outliers = 2, Number of sidechain outliers = 16
Model quality: assessment of excluded volume	- Not applicable
Fit to data used for modeling	- SASDC29: Fit 1 with X ² value 25.13
Fit to data used for validation	- Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
<u>Method</u>	None
<u>Name</u>	None
<u>Details</u>	- Method details not available
<u>Software</u>	- <u>HADDOCK</u> (version Not available)