Table S1: Summary of Integrative Structure Determination of Structure of the human Rev7 dimer (PDBDEV0000009)

1. Model Composition	
Entry composition	- Rev7-monomer: Chain A (212 residues) - Rev7-monomer: Chain C (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 listed
2. Representation	
Atomic structural coverage	100%
Number of <u>rigid bodies</u> , <u>flexible units</u>	0, 4
Rigid regions	- A: - - B: - - C: - - D: -
Flexible units	- A: 1-212. - B: 1-28. - C: 1-212. - D: 1-28.
Resolution	
3. Restraints	
Physical principles	Physical principles were not used for modeling
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, 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

Assessment of atomic regions	Clashscore: 8.73, Ramachandran outliers: 0.42, Sidechain outliers: 3.52
Assessment of excluded volume	1. Not applicable
Fit of the model to information used to compute it	Fit of model to information used to compute it has not been determined
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	
5. Methodology and Software Method	None
	None None
<u>Method</u>	