

**Table S1: Summary of Integrative Structure Determination of Structure of the human Rev7 dimer (PDBDEV00000009)**

<b>1. Model Composition</b>	
<a href="#">Entry composition</a>	<ul style="list-style-type: none"> <li>- Rev3-RBM2: Chain B (28 residues)</li> <li>- Rev3-RBM2: Chain D (28 residues)</li> <li>- Rev7-monomer: Chain C (212 residues)</li> <li>- Rev7-monomer: Chain A (212 residues)</li> </ul>
<a href="#">Datasets used for modeling</a>	<ul style="list-style-type: none"> <li>- SAS data, SASDC29</li> <li>- Experimental model, PDB ID: 6BC8</li> <li>- Mutagenesis data, Not listed</li> </ul>
<b>2. Representation</b>	
<a href="#">Atomic structural coverage</a>	100%
<a href="#">Number of rigid bodies, flexible units</a>	,
<i>Rigid bodies</i>	<ul style="list-style-type: none"> <li>- A: -</li> <li>- B: -</li> <li>- C: -</li> <li>- D: -</li> </ul>
<i>Flexible units</i>	<ul style="list-style-type: none"> <li>- A: 1-212.</li> <li>- B: 1-28.</li> <li>- C: 1-212.</li> <li>- D: 1-28.</li> </ul>
<a href="#">Resolution</a>	Rigid bodies: 1 residue per bead. Flexible regions: N/A
<b>3. Restraints</b>	
<a href="#">Physical principles</a>	Physical principles were not used for modeling
<a href="#">Experimental data</a>	<ul style="list-style-type: none"> <li>- 64 unique DerivedDistanceRestraint: Upper Bound Distance: 2.0</li> <li>- 1 unique SASRestraint: Assembly name: Complete assembly Fitting method: FoXS Multi-state: False</li> </ul>
<b>4. Validation</b>	
<a href="#">Sampling validation</a>	1. Information related to sampling validation has not been provided
<a href="#">Clustering algorithm, clustering feature</a>	Distance threshold-based clustering used if ensembles are deposited, Not applicable
<a href="#">Number of ensembles</a>	
<a href="#">Number of models in ensembles</a>	Not applicable
<a href="#">Model precision (uncertainty of models)</a>	Model precision can not be calculated with one structure
<a href="#">Quality of data</a>	-

<a href="#"><i>Assessment of atomic segments</i></a>	-
<a href="#"><i>Fit of the model to information used to compute it</i></a>	1. SASDC29: Fit 1 with X <sup>2</sup> value 25.13
<a href="#"><i>Fit of the model to information not used to compute it</i></a>	1. Fit of model to information not used to compute it has not been determined
<b>5. Methodology and Software</b>	
<a href="#"><i>Method</i></a>	None
<a href="#"><i>Name</i></a>	None
<a href="#"><i>Details</i></a>	- Method details unspecified
<a href="#"><i>Software</i></a>	- Software details not provided - No location specified