

**Summary of integrative structure determination of Structure of the human Rev7 dimer
(PDB ID: 8ZZ9, PDB-Dev ID: PDBDEV_00000009)**

1. Model Composition	
<u>Entry composition</u>	<ul style="list-style-type: none"> - Rev3-RBM2: Chain D (28 residues) - Rev3-RBM2: Chain B (28 residues) - Rev7-monomer: Chain A (212 residues) - Rev7-monomer: Chain C (212 residues)
<u>Datasets used for modeling</u>	<ul style="list-style-type: none"> - SAS data, SASBDB: SASDC29 - Experimental model, PDB ID: 6BC8 - Mutagenesis data, File: 10.5281/zenodo.1323686
2. Representation	
<u>Resolution</u>	Atomic
<u>Number of rigid bodies, flexible units</u>	0, 4
<u>Flexible units</u>	<ul style="list-style-type: none"> - A: 1-212 - B: 1-28 - C: 1-212 - D: 1-28
<u>Structural coverage (rigid bodies)</u>	100%
3. Restraints	
<u>Physical principles</u>	Information about physical principles was not provided
<u>Experimental data</u>	<ul style="list-style-type: none"> - 64 unique DerivedDistanceRestraint: Upper Bound Distance: 2.0 - 1 unique SASRestraint: Assembly name: Complete assembly Fitting method: FoXS Multi-state: False
4. Validation	
<u>Number of ensembles</u>	0
<u>Number of models in ensembles</u>	Not applicable
<u>Number of deposited models</u>	1
<u>Model precision (uncertainty of models)</u>	Model precision can not be calculated with one structure
<u>Data quality</u>	SASDC29: Rg from Gunier is 2.93nm and Rg from p(r) is 3.01nm
<u>Model quality: assessment of atomic segments</u>	Model-1: Clashscore = 8.73, Number of Ramachandran outliers = 2, Number of sidechain outliers = 16

<u>Model quality: assessment of excluded volume</u>	Not applicable
<u>Fit to data used for modeling</u>	Fit of model to information used to compute it has not been determined
<u>Fit to data used for validation</u>	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
<u>1. Method</u>	None
<u>Name</u>	None
<u>Software</u>	HADDOCK (version Not available)