

**Summary of integrative structure determination of Integrative model of Nucleotide excision repair complex of XPA and RPA on 5' junction substrate (PDB ID: 9A1V, PDB-Dev ID: PDBDEV\_00000124)**

<b>1. Model Composition</b>	
<a href="#"><u>Entry composition</u></a>	<ul style="list-style-type: none"> <li>- DNA (5'-D(P*GP*GP*CP*CP*CP*GP*CP*GP*GP*CP*TP*TP*TP*TP*TP*TP*3'): Chain E (18 residues)</li> <li>- XPA: Chain D (239 residues)</li> <li>- RPA70: Chain A (434 residues)</li> <li>- DNA (40-MER): Chain F (40 residues)</li> <li>- RPA32: Chain B (226 residues)</li> <li>- ZINC ION: Chain G (Not available residues)</li> <li>- RPA14: Chain C (115 residues)</li> <li>- ZINC ION ON 3-FOLD CRYSTAL AXIS: Chain H (Not available residues)</li> </ul>
<a href="#"><u>Datasets used for modeling</u></a>	<ul style="list-style-type: none"> <li>- SAS data, SASBDB: SASDP24</li> <li>- Experimental model, PDB ID: 1JMC</li> <li>- Integrative model, PDB-Dev: PDBDEV_00000039</li> <li>- Experimental model, PDB ID: 1L1O</li> <li>- Experimental model, PDB ID: 1DPU</li> <li>- Comparative model, template PDB ID: Not available</li> <li>- De Novo model, Not available</li> </ul>
<b>2. Representation</b>	
<a href="#"><u>Resolution</u></a>	Atomic
<a href="#"><u>Number of rigid bodies, flexible units</u></a>	0, 14
<a href="#"><u>Flexible units</u></a>	<ul style="list-style-type: none"> <li>- A: 1-238, 239-253, 254-434</li> <li>- B: 1-128, 129-226</li> <li>- C: 1-115</li> <li>- D: 1-28, 29-48, 49-97, 98-239</li> <li>- E: 1-18</li> <li>- F: 1-40</li> <li>- G: None-None</li> <li>- H: None-None</li> </ul>
<a href="#"><u>Structural coverage (rigid bodies)</u></a>	100%
<b>3. Restraints</b>	
<a href="#"><u>Physical principles</u></a>	Information about physical principles was not provided
<a href="#"><u>Experimental data</u></a>	<ul style="list-style-type: none"> <li>- 1 unique SASRestraint: Assembly name: Nucleotide excision repair complex of XPA and RPA</li> <li>Fitting method: FoXS Multi-state: False</li> </ul>
<b>4. Validation</b>	
<a href="#"><u>Number of ensembles</u></a>	0
<a href="#"><u>Number of models in ensembles</u></a>	Not applicable
<a href="#"><u>Number of deposited models</u></a>	1
<a href="#"><u>Model precision (uncertainty of models)</u></a>	Model precision can not be calculated with one structure
<a href="#"><u>Data quality</u></a>	

<u>Model quality: assessment of atomic segments</u>	Model-1: Clashscore = 166.7, Number of Ramachandran outliers = 53, Number of sidechain outliers = 82
<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
<b>5. Methodology and Software</b>	
<u>1. Method</u>	None
<u>Name</u>	None
<u>Number of computed models</u>	1
<u>Software</u>	<ul style="list-style-type: none"> <li>- <a href="#">Modeller</a> (version 9v4)</li> <li>- <a href="#">FoXSdock</a> (version main.c2a7893)</li> </ul>