

**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\\_00009a1v](#), PDB-Dev ID: PDBDEV\_00000124 )**

<b>1. Model Composition</b>	
<a href="#">1.1. Entry composition</a>	<ul style="list-style-type: none"> <li>- RPA70: chain(s) A (434 residues)</li> <li>- RPA32: chain(s) B (226 residues)</li> <li>- RPA14: chain(s) C (115 residues)</li> <li>- XPA: chain(s) D (239 residues)</li> <li>- DNA (5'-D(P*GP*GP*CP*CP*CP*GP*CP*GP*GP*CP*TP*TP*TP*TP*TP*3'): chain(s) E (18 residues)</li> <li>- DNA (40-MER): chain(s) F (40 residues)</li> <li>- ZINC ION: chain(s) G, H</li> </ul>
<a href="#">1.2. Datasets used for modeling</a>	<ul style="list-style-type: none"> <li>- SAS data, SASBDB: <a href="#">SASDP24</a></li> <li>- Experimental model, PDB: <a href="#">pdb_00001jmc</a></li> <li>- Integrative model, PDB: <a href="#">pdb_00009a03</a></li> <li>- Experimental model, PDB: <a href="#">pdb_0000111o</a></li> <li>- Experimental model, PDB: <a href="#">pdb_00001dpu</a></li> <li>- Comparative model, Not available</li> <li>- De Novo model, Not available</li> </ul>
<b>2. Representation</b>	
<a href="#">2.1. Number of representations</a>	1
<a href="#">2.2. Scale</a>	Atomic
<a href="#">2.3. Number of rigid and flexible segments</a>	0, 12
<b>3. Restraints</b>	
<a href="#">3.1. Physical principles</a>	Information about physical principles was not provided
<a href="#">3.2. Experimental data</a>	<ul style="list-style-type: none"> <li>- 1 unique SASRestraint: Assembly name: Nucleotide excision repair complex of XPA and RPA Fitting method: FoXS Multi-state: False</li> </ul>
<b>4. Validation</b>	
<a href="#">4.2. Number of ensembles</a>	0
<a href="#">4.3. Number of models in ensembles</a>	Not applicable
<a href="#">4.4. Number of deposited models</a>	1
<a href="#">4.5. Model precision</a>	Not available
<a href="#">4.6. Data quality</a>	Data quality has not been assessed
<a href="#">4.7. Model quality: assessment of atomic segments</a>	<ul style="list-style-type: none"> <li>- Clashscore: 166.70</li> <li>- Ramachandran outliers: 53</li> <li>- Sidechain outliers: 82</li> </ul>
<a href="#">4.8. Fit to data used for modeling</a>	Fit of model to information used to compute it has not been determined
<a href="#">4.9. Fit to data used for validation</a>	Fit of model to information not used to compute it has not been determined
<b>5. Methodology and Software</b>	
<a href="#">1. 5.1. Method name</a>	Not available

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<a href="#">5.4. Number of computed models</a>	1
<a href="#">5.5. Software</a>	<ul style="list-style-type: none"><li>- <a href="#">Modeller</a> (version 9v4)</li><li>- <a href="#">FoXSDock</a> (version main.c2a7893)</li></ul>