

Summary of integrative structure determination of Integrative structure of human SNAPc-DNA (PDB ID: 9A8W)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - snRNA-activating protein complex subunit 2: chain(s) A (334 residues) - snRNA-activating protein complex subunit 3: chain(s) B (411 residues) - snRNA-activating protein complex subunit 5: chain(s) C (98 residues) - snRNA-activating protein complex subunit 1: chain(s) D (368 residues) - snRNA-activating protein complex subunit 4: chain(s) E (1519 residues) - T strand: chain(s) F (20 residues) - NT strand: chain(s) G (20 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - Crosslinking-MS data, PRIDE: PXD053341 - 3DEM volume, Zenodo: 10.5281/zenodo.14746890 - 3DEM volume, Zenodo: 10.5281/zenodo.14746890 - De Novo model, MODEL ARCHIVE: ma-pgtjz - Experimental model, PDB: 9FSO - Experimental model, PDB: 7ZX8 - Experimental model, PDB: 7XUR - 3DEM volume, EMDB: EMD-50730
2. Representation	
Number of representations	1
Scale	Multiscale: Coarse-grained: 1 - 20 residue(s) per bead
Number of rigid and flexible segments	16, 16
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	<ul style="list-style-type: none"> - 1 unique CrossLinkRestraint: SDA, 268 crosslinks - 1 unique EM3DRestraint: Gaussian mixture models
4. Validation	
Number of ensembles	1
Number of models in ensembles	5766
Number of deposited models	1
Model precision (uncertainty of models)	Not available
Data quality	Data quality has not been assessed

<i>Model quality: assessment of excluded volume</i>	Satisfaction: 99.71%
<i>Fit to data used for modeling</i>	Satisfaction of crosslinks: 80.88%
<i>Fit to data used for validation</i>	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
1. <i>Name</i>	Sampling
<i>Method</i>	Replica exchange monte carlo
<i>Number of computed models</i>	320000
<i>Software</i>	<ul style="list-style-type: none"> - IMP PMI module (version 2.20.0) - Integrative Modeling Platform (IMP) (version 2.20.0) - AlphaPulldown (version 0.30.7) - AlphaFold2 (version 2.3.2)