

Summary of integrative structure determination of Architecture of Pol II(G) and molecular mechanism of transcription regulation by Gdown1 (PDB ID: 8ZZP, PDB-Dev ID: PDBDEV_00000025)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - RPB1: chain(s) A (1970 residues) - RPB2: chain(s) B (1174 residues) - RPB3: chain(s) C (275 residues) - RPB4: chain(s) D (142 residues) - RPB5: chain(s) E (210 residues) - RPB6: chain(s) F (127 residues) - RPB7: chain(s) G (172 residues) - RPB8: chain(s) H (150 residues) - RPB9: chain(s) I (125 residues) - RPB10: chain(s) J (67 residues) - RPB11: chain(s) K (117 residues) - RPB12: chain(s) L (58 residues) - GDOWN1: chain(s) M (368 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - Experimental model, PDB: 5FLM - Experimental model, Zenodo: 10.5281/zenodo.1438479 - Crosslinking-MS data, Zenodo: 10.5281/zenodo.1438479
2. Representation	
Number of representations	1
Scale	Multiscale: Coarse-grained: 1 - 10 residue(s) per bead
Number of <i>rigid</i> and <i>flexible</i> segments	0, 71
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique CrossLinkRestraint: DSS, 40 crosslinks
4. Validation	
Number of ensembles	1
Number of models in ensembles	1640
Number of deposited models	1
Model precision (uncertainty of models)	12.20, Å
Data quality	Data quality has not been assessed
Model quality: assessment of excluded volume	Satisfaction: 99.87%

<i>Fit to data used for modeling</i>	Satisfaction of crosslinks: 100.00%
<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>	5000000
<i>Software</i>	<ul style="list-style-type: none"> - IMP PMI module (version develop-7c7c0f4348) - Integrative Modeling Platform (IMP) (version develop-0a5706e202)