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	- RPB10: Chain J (67 residues) - RPB3: Chain C (275 residues) - RPB6: Chain F (127 residues) - RPB8: Chain H (150 residues) - RPB9: Chain I (125 residues) - RPB5: Chain E (210 residues) - RPB4: Chain D (142 residues) - RPB2: Chain B (1174 residues) - RPB1: Chain A (1970 residues) - RPB12: Chain L (58 residues) - RPB11: Chain K (117 residues) - GDOWN1: Chain M (368 residues) - RPB7: Chain G (172 residues)
Datasets used for modeling	- Experimental model, PDB ID: 5FLM - Experimental model, PDB ID: Not available - Crosslinking-MS data, Linker name and number of cross-links: DSS, 40 cross-links
2. Representation	
Resolution	Coarse-grained: 1, 2, 3, 5, 7, 27, 37, 49 residue(s) per bead
Number of *rigid bodies*, *flexible units*	0, 71
Flexible units	- A: 1-265, 266-270, 271-320, 321-336, 337-354, 355-421, 422-437, 438-1108, 1109-1114, 1115-1267, 1268-1277, 1278-1424, 1425-1427, 1428-1428, 1429-1450, 1451-1458, 1459-1460, 1461-1487, 1488-1970 - B: 1-15, 16-68, 69-80, 81-833, 834-843, 844-874, 875-888, 889-1063, 1064-1076, 1077-1080, 1081-1082, 1083-1110, 1111-1174 - C: 1-1, 2-73, 74-74, 75-132, 133-145, 146-271, 272-275 - D: 1-13, 14-141, 142-142 - E: 1-1, 2-31, 32-32, 33-45, 46-46, 47-111, 112-113, 114-131, 132-132, 133-156, 157-157, 158-185, 186-186, 187-210 - F: 1-45, 46-127 - G: 1-171, 172-172 - H: 1-1, 2-149, 150-150 - I: 1-11, 12-125 - J: 1-67 - K: 1-115, 116-117 - L: 1-14, 15-58 - M: 1-368
Structural coverage (rigid bodies)	0%
3. Restraints	

Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique CrossLinkRestraint: DSS, 40 cross-links
4. Validation	
Number of ensembles	1
Number of models in ensembles	1640
Number of deposited models	1
Model precision (uncertainty of models)	12.2, Å
Data quality	Data quality has not been assessed
Model quality: assessment of excluded volume	Satisfaction: 99.87-99.87%
Fit to data used for modeling	Fit of model to information used to compute it has not been determined
Fit to data used for validation	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
1. Method	Sampling
Name	Replica exchange monte carlo
Number of computed models	5000000
Software	- IMP PMI module (version develop-7c7c0f4348) - Integrative Modeling Platform (IMP) (version develop-0a5706e202)