Table S1: Summary of Integrative Structure Determination of Architecture of Pol II(G) and molecular mechanism of transcription regulation by Gdown1 (PDBDEV00000025)

1. Model Composition	
Entry composition	- RPB1: Chain A (1970 residues) - RPB2: Chain B (1174 residues) - RPB3: Chain C (275 residues) - RPB4: Chain D (142 residues) - RPB5: Chain E (210 residues) - RPB6: Chain F (127 residues) - RPB7: Chain G (172 residues) - RPB8: Chain H (150 residues) - RPB9: Chain I (125 residues) - RPB10: Chain J (67 residues) - RPB11: Chain K (117 residues) - RPB12: Chain L (58 residues) - GDOWN1: Chain M (368 residues)
Datasets used for modeling	- Experimental model, PDB ID: 5FLM - Experimental model, PDB ID: Not listed - CX-MS data, Linker name: DSS, Number of cross-links: 40 cross-links
2. Representation	
Atomic structural coverage	0%
Number of rigid bodies, flexible units	0, 71
Rigid bodies	- A: - - B: - - C: - - D: - - E: - - F: - - G: - - H: - - I: - - J: - - K: - - L: - - M: -
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.
Resolution	Rigid bodies: 1 residue per bead. Flexible regions: 10 residues per bead.
3. Restraints	
Physical principles	Excluded volume and Sequence connectivity.
Experimental data	- CrossLinkRestraint: 40 cross-links, DSS
4. Validation	
Sampling validation	
Clustering algorithm ,*clustering feature*	None, dRMSD
Number of ensembles	1
Number of models in ensembles	1640
Model precision (uncertainty of models)	12.2Å
Quality of data	-
Assessment of atomic segments	-
Fit of the model to information used to compute it	
Fit of the model to information not used to compute it	
5. Methodology and Software	
Method	Sampling
Name	Replica exchange Monte Carlo
Details	
Software	- IMP PMI module (version develop-7c7c0f4348) - Integrative Modeling Platform (IMP) (version develop-0a5706e202)