## 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	- RPB7: Chain G (172 residues) - RPB10: Chain J (67 residues) - RPB12: Chain L (58 residues) - RPB9: Chain I (125 residues) - RPB2: Chain B (1174 residues) - RPB1: Chain A (1970 residues) - RPB6: Chain F (127 residues) - RPB11: Chain K (117 residues) - RPB3: Chain C (275 residues) - RPB8: Chain H (150 residues) - RPB4: Chain D (142 residues) - RPB4: Chain D (142 residues) - GDOWN1: Chain M (368 residues) - RPB5: Chain E (210 residues)
Datasets used for modeling	- Experimental model, PDB ID: 5FLM - Experimental model, PDB ID: Not listed - CX-MS data, Linker name and number of cross-links: DSS, 40 cross-links
2. Representation	
Atomic structural coverage	0%
Number of <u>rigid bodies</u> , <u>flexible units</u>	0, 71
Rigid bodies	- A: B: C: D: E: F: G: H: I: -

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: N/A
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique CrossLinkRestraint: DSS, 40 cross-links
4. Validation	
Sampling validation	- Information related to sampling validation has not been provided
Clustering algorithm ,clustering feature	Distance threshold-based clustering used if ensembles are deposited, dRMSD
Number of ensembles	1
Number of models in ensembles	1640
Model precision (uncertainty of models)	12.2Å
Quality of data	- Quality of input data has not be assessed
Model quality: assessment of atomic segments	Not applicable
Model quality: assessment of excluded volume	- Model-1: Number of violations-8765.0
Fit of the model to information used to compute it	- CX-MS Fit of medioid: model # 1, percentage satisfied 100.0%
Fit of the model to information not used to compute it	- Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
<u>Method</u>	Sampling

<u>Name</u>	Replica exchange Monte Carlo
<u>Details</u>	- Method details unspecified
<u>Software</u>	- IMP PMI module (version develop-7c7c0f4348) - Integrative Modeling Platform (IMP) (version develop-0a5706e202) - No location specified