

# **Full wwPDB Integrative Structure Validation Report**

### September 06, 2019 -- 02:06 PM

PDB ID	PDBDEV00000025
Molecule Name	Architecture of Pol II(G) and molecular mechanism of transcription regulation by Gdown1
Title	Architecture of Pol II(G) and molecular mechanism of transcription regulation by Gdown1.
Authors	Jishage M;Yu X;Shi Y;Ganesan SJ;Chen WY;Sali A;Chait BT;Asturias FJ;Roeder RG

#### The following softwares were used in the production of this report:

Integrative Modeling Package: Version XX
Molprobity: Version XX
Phenix: Version XX
Integrative Modeling Validation Package: Version XX

#### 1. Overall quality at a glance

#### 2. Entry composition

There is 1 unique type of model in this entry. Model has 13 chains respectively.

Molecule ID	Molecule Name	Chain ID	Total Residues
1	RPB1	Α	1970
1	RPB2	В	1174
1	RPB3	С	275
1	RPB4	D	142
1	RPB5	E	210
1	RPB6	F	127
1	RPB7	G	172
1	RPB8	Н	150
1	RPB9	Ī	125
1	RPB10	J	67
1	RPB11	К	117
1	RPR12	ı	58

	111 012	_	
1	GDOWN1	M	368

There are 2 software packages reported in this entry.

ID	Software Name	Software Version	Software Classification
1	IMP PMI module	develop-7c7c0f4348	integrative model building
2	Integrative Modeling Platform (IMP)	develop-0a5706e202	integrative model building

There are 3 unique datasets used to build the model in this entry.

ID	Dataset Type	Database Name	Data Access Code
1	Experimental model	PDB	5FLM
2	Experimental model	Not Listed	None
3	CX-MS data	Not Listed	None

### 3. Data quality

### 4. Model quality

- 4.1 Too-close contacts
- 4.2 Torsion angles
- 4.2.1 Protein backbone
- 4.2.2 Protein sidechains

#### 5. Fit of model and data

# 6. Uncertaintiy of model