

# Full wwPDB Integrative Structure Validation Report

September 06, 2019 -- 02:06 PM

PDB ID	PDBDEV00000003
Molecule Name	Molecular architecture of the yeast Mediator complex
Title	Molecular architecture of the yeast Mediator complex.
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**The following softwares were used in the production of this report:**

*Integrative Modeling Package : Version XX*  
*Molprobit : Version XX*  
*Phenix : Version XX*  
*Integrative Modeling Validation Package : Version XX*

## 1. Overall quality at a glance

## 2. Entry composition

There are 3 unique types of models in this entry. Models have 21,10,6 chains respectively.

Molecule ID	Molecule Name	Chain ID	Total Residues
1	med6	A	295
1	med8	B	223
1	med11	C	115
1	med17	D	687
1	med18	E	307
1	med20	F	210
1	med22	G	121
1	med4	H	284
1	med7	I	222
1	med9	J	149
1	med31	K	127
1	med21	I	140

ID	Model ID	Label	Count
1	med10	M	157
1	med1	N	566
1	med14	O	1082
1	med19	P	220
1	med2	Q	436
1	med3	R	401
1	med5	S	1146
1	med15	T	1094
1	med16	U	986

There are 5 software packages reported in this entry.

ID	Software Name	Software Version	Software Classification
1	Integrative Modeling Platform (IMP)	develop-0a5706e202	integrative model building
2	IMP PMI module	67456c0	integrative model building
3	Protein Prospector	5.13.1	mass spectrometry
4	Situs	2.7	density map fitting
5	Phyre2	2.0	protein homology modeling

There are 16 unique datasets used to build the model in this entry.

ID	Dataset Type	Database Name	Data Access Code
1	Experimental model	PDB	4GWP
2	Comparative model	Not Listed	None
3	Comparative model	Not Listed	None
4	Experimental model	PDB	3FBI
5	Experimental model	Not Listed	None
6	Experimental model	PDB	1YKH
7	Experimental model	Not Listed	None
8	Experimental model	PDB	4BZK
9	Comparative model	Not Listed	None
10	Mass Spectrometry data	MASSIVE	MSV000079237

11	CX-MS data	Not Listed	None
12	3DEM volume	EMDB	EMD-2634
13	3DEM volume	Not Listed	None
14	3DEM volume	Not Listed	None
15	3DEM volume	Not Listed	None
16	3DEM volume	Not Listed	None

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### 3. Data quality

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### 4. Model quality

#### 4.1 Too-close contacts

#### 4.2 Torsion angles

##### 4.2.1 Protein backbone

##### 4.2.2 Protein sidechains

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### 5. Fit of model and data

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### 6. Uncertainty of model

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