

Full wwPDB Integrative Structure Validation Report

September 06, 2019 -- 02:06 PM

PDB ID	PDBDEV00000002
Molecule Name	Structure of Saccharomyces cerevisiae exosome determined with CX-MS
Title	A strategy for dissecting the architectures of native macromolecular assemblies.
Authors	Shi Y;Pellarin R;Fridy PC;Fernandez-Martinez J;Thompson MK;Li Y;Wang QJ;Sali A;Rout MP;Chait B

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

Integrative Modeling Package : Version XX
Molprobrity : 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 14,13,11 chains respectively.

Molecule ID	Molecule Name	Chain ID	Total Residues
1	Dis3	A	1001
1	Rrp45	B	305
1	Rrp4	C	359
1	Csl4	D	292
1	Mtr3	E	250
1	Rrp40	F	240
1	Rrp42	G	265
1	Ski6	H	265
1	Rrp46_gfp	I	475
1	Rrp43	J	394
1	Lrp1	K	184
1	Rrn6	L	733

ID	Type	Length	Res
1	MPP6	M	186
1	RPL3	N	747

There are 3 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	Phyre2	2.0	protein homology modeling

There are 5 unique datasets used to build the model in this entry.

ID	Dataset Type	Database Name	Data Access Code
1	Experimental model	PDB	4IFD
2	Experimental model	PDB	1GFL
3	Experimental model	PDB	2HBJ
4	Comparative model	Not Listed	None
5	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. Uncertainty of model
