Full wwPDB Integrative Structure Validation Report

August 20, 2019 -- 05:25 PM

PDB ID	PDBDEV00000026
Molecule Name	The proteasome-interacting Ecm29 protein disassembles the 26S proteasome in response to oxidative s
Title	The proteasome-interacting Ecm29 protein disassembles the 26S proteasome in response to oxidative s
Authors	Wang X;Chemmama IE;Yu C;Huszagh A;Xu Y;Viner R;Block SA;Cimermancic P;Rychnovsky SD;Ye Y;S A;Huang L

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

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1. Overall quality at a glance

2. Entry composition

There are 1 unique types of models in this entry. The entry contains 19 chains.

Molecule ID	Molecule Name	Chain ID	Total Residues
1	Rpt6	A	406
1	Rpt4	B	389
1	Rpt5	C	439
1	Rpt2	D	440
1	Rpt3	E	418
1	Rpt1	F	433
1	Rpn12	G	350
1	Rpn10	H	377
1	Rpn11	I	310
1	Rpn15	J	70
1	Rpn1	K	908

1	Rpn2	L	953
1	Rpn3	M	534
1	Rpn5	N	456
1	Rpn6	O	422
1	Rpn7	P	389
1	Rpn8	Q	324
1	Rpn9	R	376
1	ecm29	S	1845

There are 3 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
3	MODELLER	9.17	comparative modeling

There are 7 unique datasets used to build the model(s) in this entry.

ID	Dataset Type	Database Name	Data Access Code
1	Experimental model	PDB	5GJR
2	Experimental model	Not Listed	None
3	Experimental model	PDB	1U6G
4	Comparative model	Not Listed	None
5	Experimental model	PDB	3W3W
6	Comparative model	Not Listed	None
7	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