

Summary of integrative structure determination of The proteasome-interacting Ecm29 protein disassembles the 26S proteasome in response to oxidative stress (PDB ID: 8ZZQ, PDB-Dev ID: PDBDEV_00000026)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - Rpt6: chain(s) A (406 residues) - Rpt4: chain(s) B (389 residues) - Rpt5: chain(s) C (439 residues) - Rpt2: chain(s) D (440 residues) - Rpt3: chain(s) E (418 residues) - Rpt1: chain(s) F (433 residues) - Rpn12: chain(s) G (350 residues) - Rpn10: chain(s) H (377 residues) - Rpn11: chain(s) I (310 residues) - Rpn15: chain(s) J (70 residues) - Rpn1: chain(s) K (908 residues) - Rpn2: chain(s) L (953 residues) - Rpn3: chain(s) M (534 residues) - Rpn5: chain(s) N (456 residues) - Rpn6: chain(s) O (422 residues) - Rpn7: chain(s) P (389 residues) - Rpn8: chain(s) Q (324 residues) - Rpn9: chain(s) R (376 residues) - ecm29: chain(s) S (1845 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - Experimental model, PDB: 5GJR - Experimental model, Zenodo: 10.5281/zenodo.1445841 - Experimental model, PDB: 1U6G - Comparative model, Zenodo: 10.5281/zenodo.1445841 - Experimental model, PDB: 3W3W - Comparative model, Zenodo: 10.5281/zenodo.1445841 - Crosslinking-MS data, Zenodo: 10.5281/zenodo.1445841
2. Representation	
Number of representations	1
Scale	Multiscale: Coarse-grained: 1 - 10 residue(s) per bead
Number of rigid and flexible segments	7, 101
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique CrossLinkRestraint: DSSO, 63 crosslinks
4. Validation	

<i>Number of ensembles</i>	2
<i>Number of models in ensembles</i>	11980, 6261
<i>Number of deposited models</i>	2
<i>Model precision (uncertainty of models)</i>	- 60.00, Å - 60.00, Å
<i>Data quality</i>	Data quality has not been assessed
<i>Model quality: assessment of excluded volume</i>	Satisfaction: 99.93-99.93%
<i>Fit to data used for modeling</i>	Satisfaction of crosslinks: 52.38-53.97%
<i>Fit to data used for validation</i>	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
1. <i>Name</i>	Sampling
<i>Method</i>	Replica exchange monte carlo
<i>Number of computed models</i>	3750000
<i>Software</i>	<ul style="list-style-type: none"> - IMP PMI module (version develop-7c7c0f4348) - Integrative Modeling Platform (IMP) (version develop-0a5706e202) - MODELLER (version 9.17)