

**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\_0000026)**

<b>1. Model Composition</b>	
<a href="#">Entry composition</a>	<ul style="list-style-type: none"> <li>- Rpn11: Chain I (310 residues)</li> <li>- ecm29: Chain S (1845 residues)</li> <li>- Rpn8: Chain Q (324 residues)</li> <li>- Rpn12: Chain G (350 residues)</li> <li>- Rpt4: Chain B (389 residues)</li> <li>- Rpt2: Chain D (440 residues)</li> <li>- Rpn10: Chain H (377 residues)</li> <li>- Rpn5: Chain N (456 residues)</li> <li>- Rpn7: Chain P (389 residues)</li> <li>- Rpn6: Chain O (422 residues)</li> <li>- Rpn2: Chain L (953 residues)</li> <li>- Rpt1: Chain F (433 residues)</li> <li>- Rpn15: Chain J (70 residues)</li> <li>- Rpn9: Chain R (376 residues)</li> <li>- Rpn1: Chain K (908 residues)</li> <li>- Rpt3: Chain E (418 residues)</li> <li>- Rpt6: Chain A (406 residues)</li> <li>- Rpn3: Chain M (534 residues)</li> <li>- Rpt5: Chain C (439 residues)</li> </ul>
<a href="#">Datasets used for modeling</a>	<ul style="list-style-type: none"> <li>- Experimental model, PDB ID: 5GJR</li> <li>- Experimental model, PDB ID: Not available</li> <li>- Experimental model, PDB ID: 1U6G</li> <li>- Comparative model, template PDB ID: Not available</li> <li>- Experimental model, PDB ID: 3W3W</li> <li>- Comparative model, template PDB ID: Not available</li> <li>- Crosslinking-MS data, Linker name and number of cross-links: DSSO, 63 cross-links</li> </ul>
<b>2. Representation</b>	
<a href="#">Resolution</a>	Coarse-grained: 1, 2, 3, 4, 5, 6, 7, 9, 11, 19, 36 residue(s) per bead
<a href="#">Number of rigid bodies, flexible units</a>	7, 101

<i>Rigid bodies</i>	<ul style="list-style-type: none"> <li>- A: -</li> <li>- B: -</li> <li>- C: -</li> <li>- D: -</li> <li>- E: -</li> <li>- F: -</li> <li>- G: -</li> <li>- H: -</li> <li>- I: -</li> <li>- J: -</li> <li>- K: -</li> <li>- L: -</li> <li>- M: -</li> <li>- N: -</li> <li>- O: -</li> <li>- P: -</li> <li>- Q: -</li> <li>- R: -</li> <li>- S: 352-504, 686-760, 788-911, 934-1035, 1062-1306, 1331-1666, 1689-1738</li> </ul>
<i>Flexible units</i>	<ul style="list-style-type: none"> <li>- A: 1-23, 24-250, 251-266, 267-397, 398-406</li> <li>- B: 1-14, 15-389</li> <li>- C: 1-43, 44-99, 100-119, 120-439</li> <li>- D: 1-64, 65-84, 85-90, 91-429, 430-440</li> <li>- E: 1-38, 39-418</li> <li>- F: 1-46, 47-72, 73-79, 80-433</li> <li>- G: 1-88, 89-130, 131-134, 135-350</li> <li>- H: 1-193, 194-377</li> <li>- I: 1-27, 28-163, 164-189, 190-310</li> <li>- J: 1-2, 3-27, 28-34, 35-68, 69-70</li> <li>- K: 1-105, 106-170, 171-178, 179-301, 302-308, 309-618, 619-652, 653-848, 849-870, 871-908</li> <li>- L: 1-2, 3-272, 273-320, 321-750, 751-752, 753-816, 817-877, 878-917, 918-922, 923-939, 940-953</li> <li>- M: 1-56, 57-101, 102-103, 104-116, 117-159, 160-496, 497-499, 500-525, 526-534</li> <li>- N: 1-4, 5-24, 25-39, 40-94, 95-98, 99-112, 113-116, 117-132, 133-138, 139-332, 333-340, 341-454, 455-456</li> <li>- O: 1-1, 2-422</li> <li>- P: 1-13, 14-389</li> <li>- Q: 1-3, 4-142, 143-151, 152-295, 296-324</li> <li>- R: 1-2, 3-54, 55-56, 57-376</li> <li>- S: 1-351, 505-685, 761-787, 912-933, 1036-1061, 1307-1330, 1667-1688, 1739-1845</li> </ul>
<a href="#"><i>Structural coverage (rigid bodies)</i></a>	11%
<b>3. Restraints</b>	
<a href="#"><i>Physical principles</i></a>	Information about physical principles was not provided
<a href="#"><i>Experimental data</i></a>	- 1 unique CrossLinkRestraint: DSSO, 63 cross-links
<b>4. Validation</b>	
<a href="#"><i>Number of ensembles</i></a>	2

<a href="#"><i>Number of models in ensembles</i></a>	11980, 6261
<a href="#"><i>Number of deposited models</i></a>	2
<a href="#"><i>Model precision (uncertainty of models)</i></a>	60.0, Å, 60.0, Å
<a href="#"><i>Data quality</i></a>	Data quality has not been assessed
<a href="#"><i>Model quality: assessment of excluded volume</i></a>	Satisfaction: 99.93-99.93%
<a href="#"><i>Fit to data used for modeling</i></a>	Fit of model to information used to compute it has not been determined
<a href="#"><i>Fit to data used for validation</i></a>	Fit of model to information not used to compute it has not been determined
<b>5. Methodology and Software</b>	
<b>1. Method</b>	Sampling
<a href="#"><i>Name</i></a>	Replica exchange monte carlo
<a href="#"><i>Number of computed models</i></a>	3750000
<a href="#"><i>Software</i></a>	<ul style="list-style-type: none"> <li>- <a href="#">IMP PMI module</a> (version develop-7c7c0f4348)</li> <li>- <a href="#">Integrative Modeling Platform (IMP)</a> (version develop-0a5706e202)</li> <li>- <a href="#">MODELLER</a> (version 9.17)</li> </ul>