

## Summary of integrative structure determination of integrative structure of the non-canonical human cop9 signalosome (PDBDEV00000038)

<b>1. Model Composition</b>	
<a href="#">Entry composition</a>	<ul style="list-style-type: none"> <li>- CSN8: Chain H (209 residues)</li> <li>- CSN4: Chain D (406 residues)</li> <li>- CSN2: Chain B (443 residues)</li> <li>- CSN3: Chain C (423 residues)</li> <li>- CSN5: Chain E (334 residues)</li> <li>- CSN7: Chain G (264 residues)</li> <li>- CSN1: Chain A (491 residues)</li> <li>- CSN6: Chain F (327 residues)</li> <li>- CSN9: Chain I (57 residues)</li> </ul>
<a href="#">Datasets used for modeling</a>	<ul style="list-style-type: none"> <li>- Experimental model, PDB ID: Not listed</li> <li>- Comparative model, template PDB ID: Not listed</li> <li>- Experimental model, PDB ID: 4D10</li> <li>- Experimental model, PDB ID: Not listed</li> <li>- Comparative model, template PDB ID: Not listed</li> <li>- CX-MS data, Linker name and number of cross-links: DSSO, 86 cross-links</li> <li>- CX-MS data, Linker name and number of cross-links: DSSO, 186 cross-links</li> <li>- CX-MS data, Linker name and number of cross-links: BMSO, 75 cross-links</li> <li>- CX-MS data, Linker name and number of cross-links: BMSO, 34 cross-links</li> <li>- CX-MS data, Linker name and number of cross-links: DHSO, 107 cross-links</li> <li>- CX-MS data, Linker name and number of cross-links: DHSO, 131 cross-links</li> </ul>
<b>2. Representation</b>	
<a href="#">Atomic structural coverage</a>	83%
<a href="#">Number of <i>rigid bodies</i>, <i>flexible units</i></a>	23, 29
<i>Rigid bodies</i>	<ul style="list-style-type: none"> <li>- A: 44-107:Comparative model/None, 128-227:Comparative model/None, 246-426:Comparative model/None, 431-462:Comparative model/None.</li> <li>- B: 30-179:Experimental model/4D10, 192-289:Experimental model/4D10, 308-397:Experimental model/4D10, 417-443:Experimental model/4D10.</li> <li>- C: 3-163:Experimental model/4D10, 177-361:Experimental model/4D10, 368-401:Experimental model/4D10.</li> <li>- D: 3-131:Experimental model/4D10, 139-361:Experimental model/4D10, 365-406:Experimental model/4D10.</li> <li>- E: 25-283:Experimental model/4D10, 296-333:Experimental model/4D10.</li> <li>- F: 29-207:Experimental model/4D10, 215-267:Experimental model/4D10, 271-316:Experimental model/4D10.</li> <li>- G: 8-158:Comparative model/None, 163-212:Comparative model/None.</li> <li>- H: 11-164:Experimental model/4D10, 194-209:Experimental model/4D10.</li> <li>- I: -</li> </ul>

<i>Flexible units</i>	<ul style="list-style-type: none"> <li>- A: 1-43, 108-127, 228-245, 427-430, 463-491.</li> <li>- B: 1-29, 180-191, 290-307, 398-416.</li> <li>- C: 1-2, 164-176, 362-367, 402-423.</li> <li>- D: 1-2, 132-138, 362-364.</li> <li>- E: 1-24, 284-295, 334-334.</li> <li>- F: 1-28, 208-214, 268-270, 317-327.</li> <li>- G: 1-7, 159-162, 213-264.</li> <li>- H: 1-10, 165-193.</li> <li>- I: 1-57.</li> </ul>
<a href="#"><i>Resolution</i></a>	<ul style="list-style-type: none"> <li>- Rigid bodies: 1 residue per bead.</li> <li>- Flexible regions: N/A</li> </ul>
<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>	<ul style="list-style-type: none"> <li>- 1 unique CrossLinkRestraint: DSSO, 86 cross-links</li> <li>- 1 unique CrossLinkRestraint: DSSO, 186 cross-links</li> <li>- 1 unique CrossLinkRestraint: BMSO, 75 cross-links</li> <li>- 1 unique CrossLinkRestraint: BMSO, 34 cross-links</li> <li>- 1 unique CrossLinkRestraint: DHSO, 107 cross-links</li> <li>- 1 unique CrossLinkRestraint: DHSO, 131 cross-links</li> </ul>
<b>4. Validation</b>	
<a href="#"><i>Sampling validation</i></a>	- Information related to sampling validation has not been provided
<a href="#"><i>Clustering algorithm ,clustering feature</i></a>	Distance threshold-based clustering used if ensembles are deposited, dRMSD
<a href="#"><i>Number of ensembles</i></a>	1
<a href="#"><i>Number of models in ensembles</i></a>	125750
<a href="#"><i>Model precision (uncertainty of models)</i></a>	22.0Å
<a href="#"><i>Quality of data</i></a>	- Quality of input data has not be assessed
<a href="#"><i>Model quality: assessment of atomic segments</i></a>	Not applicable
<a href="#"><i>Model quality: assessment of excluded volume</i></a>	- Model-1: Number of violations-6806.0
<a href="#"><i>Fit of the model to information used to compute it</i></a>	- Fit of model to information used to compute it has not been determined
<a href="#"><i>Fit of the model to information not used to compute it</i></a>	- Fit of model to information not used to compute it has not been determined
<b>5. Methodology and Software</b>	
<a href="#"><i>Method</i></a>	Sampling
<a href="#"><i>Name</i></a>	Replica exchange Monte Carlo
<a href="#"><i>Details</i></a>	- Method details unspecified

Software

- IMP PMI module (version 20200514.develop.17be5981c6)
- Integrative Modeling Platform (IMP) (version 20200514.develop.17be5981c6)
- MODELLER (version SVN)
- No location specified