**Summary of integrative structure determination of integrative structure of the canonical human cop9 signalosome (PDBDEV00000037)**

| 1. Model Composition | |
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| *Entry composition* | - CSN7: Chain G (264 residues)<br>- CSN8: Chain H (209 residues)<br>- CSN3: Chain C (423 residues)<br>- CSN5: Chain E (334 residues)<br>- CSN4: Chain D (406 residues)<br>- CSN6: Chain F (327 residues)<br>- CSN1: Chain A (491 residues)<br>- CSN2: Chain B (443 residues) |
| *Datasets used for modeling* | - Experimental model, PDB ID: Not listed<br>- Comparative model, template PDB ID: Not listed<br>- Experimental model, PDB ID: 4D10<br>- Experimental model, PDB ID: Not listed<br>- Comparative model, template PDB ID: Not listed<br>- CX-MS data, Linker name and number of cross-links: DSSO, 74 cross-links<br>- CX-MS data, Linker name and number of cross-links: DSSO, 141 cross-links<br>- CX-MS data, Linker name and number of cross-links: BMSO, 40 cross-links<br>- CX-MS data, Linker name and number of cross-links: BMSO, 31 cross-links<br>- CX-MS data, Linker name and number of cross-links: DHSO, 91 cross-links<br>- CX-MS data, Linker name and number of cross-links: DHSO, 79 cross-links |
| **2. Representation** | |
| *Atomic structural coverage* | 85% |
| Number of *rigid bodies*, *flexible units* | 23, 28 |
| *Rigid bodies* | - A: 44-107:Comparative model/None, 128-227:Comparative model/None, 246-426:Comparative model/None, 431-462:Comparative model/None.<br>- B: 30-179:Experimental model/4D10, 192-289:Experimental model/4D10, 308-397:Experimental model/4D10, 417-443:Experimental model/4D10.<br>- C: 3-163:Experimental model/4D10, 177-361:Experimental model/4D10, 368-401:Experimental model/4D10.<br>- D: 3-131:Experimental model/4D10, 139-361:Experimental model/4D10, 365-406:Experimental model/4D10.<br>- E: 25-283:Experimental model/4D10, 296-333:Experimental model/4D10.<br>- F: 29-207:Experimental model/4D10, 215-267:Experimental model/4D10, 271-316:Experimental model/4D10.<br>- G: 8-158:Comparative model/None, 163-212:Comparative model/None.<br>- H: 11-164:Experimental model/4D10, 194-209:Experimental model/4D10. |

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|---|---|
| *Flexible units* | - A: 1-43, 108-127, 228-245, 427-430, 463-491.<br>- B: 1-29, 180-191, 290-307, 398-416.<br>- C: 1-2, 164-176, 362-367, 402-423.<br>- D: 1-2, 132-138, 362-364.<br>- E: 1-24, 284-295, 334-334.<br>- F: 1-28, 208-214, 268-270, 317-327.<br>- G: 1-7, 159-162, 213-264.<br>- H: 1-10, 165-193. |
| *Resolution* | - Rigid bodies: 1 residue per bead.<br>- Flexible regions: N/A |
| **3. Restraints** | |
| *Physical principles* | Information about physical principles was not provided |
| *Experimental data* | - 1 unique CrossLinkRestraint: DSSO, 74 cross-links<br>- 1 unique CrossLinkRestraint: DSSO, 141 cross-links<br>- 1 unique CrossLinkRestraint: BMSO, 40 cross-links<br>- 1 unique CrossLinkRestraint: BMSO, 31 cross-links<br>- 1 unique CrossLinkRestraint: DHSO, 91 cross-links<br>- 1 unique CrossLinkRestraint: DHSO, 79 cross-links |
| **4. Validation** | |
| *Sampling validation* | - Information related to sampling validation has not been provided |
| *Clustering algorithm ,clustering feature* | Distance threshold-based clustering used if ensembles are deposited, dRMSD |
| *Number of ensembles* | 7 |
| *Number of models in ensembles* | 54702, 132407, 98186, 87368, 243067, 312515, 357350 |
| *Model precision (uncertainty of models)* | 16.0Å, 22.0Å, 24.0Å, 27.0Å, 27.0Å, 29.0Å, 37.0Å |
| *Quality of data* | - Quality of input data has not be assessed |
| *Model quality: assessment of atomic segments* | Not applicable |
| *Model quality: assessment of excluded volume* | - Model-1: Number of violations-6767.0<br>- Model-2: Number of violations-6862.0<br>- Model-3: Number of violations-6769.0<br>- Model-4: Number of violations-6810.0<br>- Model-5: Number of violations-6831.0<br>- Model-6: Number of violations-6840.0<br>- Model-7: Number of violations-6830.0 |
| *Fit of the model to information used to compute it* | - Fit of model to information used to compute it has not been determined |
| *Fit of the model to information not used to compute it* | - Fit of model to information not used to compute it has not been determined |
| **5. Methodology and Software** | |
| *Method* | Sampling |

| *Name* | Replica exchange Monte Carlo |
|---|---|
| *Details* | - Method details unspecified |
| *Software* | - IMP PMI module (version 20200514.develop.17be5981c6)<br>- Integrative Modeling Platform (IMP) (version 20200514.develop.17be5981c6)<br>- MODELLER (version SVN)<br>- No location specified |