

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

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

<i>Flexible units</i>	<ul style="list-style-type: none"> - A: 1-43, 108-127, 228-245, 427-430, 463-491. - B: 1-29, 180-191, 290-307, 398-416. - C: 1-2, 164-176, 362-367, 402-423. - D: 1-2, 132-138, 362-364. - E: 1-24, 284-295, 334-334. - F: 1-28, 208-214, 268-270, 317-327. - G: 1-7, 159-162, 213-264. - H: 1-10, 165-193.
<i>Resolution</i>	<ul style="list-style-type: none"> - Rigid bodies: 1 residue per bead. - Flexible regions: N/A
3. Restraints	
<i>Physical principles</i>	Information about physical principles was not provided
<i>Experimental data</i>	<ul style="list-style-type: none"> - 1 unique CrossLinkRestraint: DSSO, 74 cross-links - 1 unique CrossLinkRestraint: DSSO, 141 cross-links - 1 unique CrossLinkRestraint: BMSO, 40 cross-links - 1 unique CrossLinkRestraint: BMSO, 31 cross-links - 1 unique CrossLinkRestraint: DHSO, 91 cross-links - 1 unique CrossLinkRestraint: DHSO, 79 cross-links
4. Validation	
<i>Sampling validation</i>	- Information related to sampling validation has not been provided
<i>Clustering algorithm ,clustering feature</i>	Distance threshold-based clustering used if ensembles are deposited, dRMSD
<i>Number of ensembles</i>	7
<i>Number of models in ensembles</i>	54702, 132407, 98186, 87368, 243067, 312515, 357350
<i>Model precision (uncertainty of models)</i>	16.0Å, 22.0Å, 24.0Å, 27.0Å, 27.0Å, 29.0Å, 37.0Å
<i>Quality of data</i>	- Quality of input data has not be assessed
<i>Model quality: assessment of atomic segments</i>	Not applicable
<i>Model quality: assessment of excluded volume</i>	<ul style="list-style-type: none"> - Model-1: Number of violations-6767.0 - Model-2: Number of violations-6862.0 - Model-3: Number of violations-6769.0 - Model-4: Number of violations-6810.0 - Model-5: Number of violations-6831.0 - Model-6: Number of violations-6840.0 - Model-7: Number of violations-6830.0

<i>Fit of the model to information used to compute it</i>	<ul style="list-style-type: none"> - CX-MS Fit of mediod: model # 1, percentage satisfied 71.05% - CX-MS Fit of mediod: model # 2, percentage satisfied 71.93% - CX-MS Fit of mediod: model # 3, percentage satisfied 72.37% - CX-MS Fit of mediod: model # 4, percentage satisfied 67.76% - CX-MS Fit of mediod: model # 5, percentage satisfied 63.16% - CX-MS Fit of mediod: model # 6, percentage satisfied 65.79% - CX-MS Fit of mediod: model # 7, percentage satisfied 51.54%
<i>Fit of the model to information not used to compute it</i>	- Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
<i>Method</i>	Sampling
<i>Name</i>	Replica exchange Monte Carlo
<i>Details</i>	- Method details unspecified
<i>Software</i>	<ul style="list-style-type: none"> - IMP PMI module (version 20191117.develop.2de7fdb984) - Integrative Modeling Platform (IMP) (version 20191117.develop.2de7fdb984) - MODELLER (version SVN) - No location specified