

Summary of integrative structure determination of Integrative structure of the canonical human COP9 Signalosome (PDB ID: 9A01, PDB-Dev ID: PDBDEV_00000037)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - CSN1: chain(s) A (491 residues) - CSN2: chain(s) B (443 residues) - CSN3: chain(s) C (423 residues) - CSN4: chain(s) D (406 residues) - CSN5: chain(s) E (334 residues) - CSN6: chain(s) F (327 residues) - CSN7: chain(s) G (264 residues) - CSN8: chain(s) H (209 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - Experimental model, Zenodo: 10.5281/zenodo.3827934 - Comparative model, Zenodo: 10.5281/zenodo.3827934 - Experimental model, PDB: 4D10 - Experimental model, Zenodo: 10.5281/zenodo.3827934 - Comparative model, Zenodo: 10.5281/zenodo.3827934 - Crosslinking-MS data, Zenodo: 10.5281/zenodo.3827934 - Crosslinking-MS data, Zenodo: 10.5281/zenodo.3827934 - Crosslinking-MS data, Zenodo: 10.5281/zenodo.3827934 - Crosslinking-MS data, Zenodo: 10.5281/zenodo.3827934 - Crosslinking-MS data, Zenodo: 10.5281/zenodo.3827934 - Crosslinking-MS data, Zenodo: 10.5281/zenodo.3827934
2. Representation	
Number of representations	1
Scale	Multiscale: Coarse-grained: 1 - 10 residue(s) per bead
Number of <i>rigid</i> and <i>flexible</i> segments	23, 28
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	<ul style="list-style-type: none"> - 1 unique CrossLinkRestraint: DSSO, 74 crosslinks - 1 unique CrossLinkRestraint: DSSO, 141 crosslinks - 1 unique CrossLinkRestraint: BMSO, 40 crosslinks - 1 unique CrossLinkRestraint: BMSO, 31 crosslinks - 1 unique CrossLinkRestraint: DHSO, 91 crosslinks - 1 unique CrossLinkRestraint: DHSO, 79 crosslinks

4. Validation	
<i>Number of ensembles</i>	7
<i>Number of models in ensembles</i>	54702, 132407, 98186, 87368, 243067, 312515, 357350
<i>Number of deposited models</i>	7
<i>Model precision (uncertainty of models)</i>	<ul style="list-style-type: none"> - 16.00, Å - 22.00, Å - 24.00, Å - 27.00, Å - 27.00, Å - 29.00, Å - 37.00, Å
<i>Data quality</i>	Data quality has not been assessed
<i>Model quality: assessment of excluded volume</i>	Satisfaction: 99.78-99.79%
<i>Fit to data used for modeling</i>	Satisfaction of crosslinks: 43.02-60.98%
<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	
<i>1. Name</i>	Sampling
<i>Method</i>	Replica exchange monte carlo
<i>Number of computed models</i>	5250000
<i>Software</i>	<ul style="list-style-type: none"> - IMP PMI module (version 20200514.develop.17be5981c6) - Integrative Modeling Platform (IMP) (version 20200514.develop.17be5981c6) - MODELLER (version SVN)