

Summary of integrative structure determination of Integrative structure of the canonical human COP9 Signalosome (PDB ID: 9A01, PDB-Dev ID: PDBDEV_0000037)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - CSN8: Chain H (209 residues) - CSN5: Chain E (334 residues) - CSN7: Chain G (264 residues) - CSN2: Chain B (443 residues) - CSN3: Chain C (423 residues) - CSN4: Chain D (406 residues) - CSN1: Chain A (491 residues) - CSN6: Chain F (327 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - Experimental model, PDB ID: Not available - Comparative model, template PDB ID: Not available - Experimental model, PDB ID: 4D10 - Experimental model, PDB ID: Not available - Comparative model, template PDB ID: Not available - Crosslinking-MS data, Linker name and number of cross-links: DSSO, 74 cross-links - Crosslinking-MS data, Linker name and number of cross-links: DSSO, 141 cross-links - Crosslinking-MS data, Linker name and number of cross-links: BMSO, 40 cross-links - Crosslinking-MS data, Linker name and number of cross-links: BMSO, 31 cross-links - Crosslinking-MS data, Linker name and number of cross-links: DHSO, 91 cross-links - Crosslinking-MS data, Linker name and number of cross-links: DHSO, 79 cross-links
2. Representation	
Resolution	Coarse-grained: 1, 2, 3, 5, 6 residue(s) per bead
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, 128-227, 246-426, 431-462 - B: 30-179, 192-289, 308-397, 417-443 - C: 3-163, 177-361, 368-401 - D: 3-131, 139-361, 365-406 - E: 25-283, 296-333 - F: 29-207, 215-267, 271-316 - G: 8-158, 163-212 - H: 11-164, 194-209
<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

Structural coverage (rigid bodies)	85%
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	<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	
Number of ensembles	7
Number of models in ensembles	54702, 132407, 98186, 87368, 243067, 312515, 357350
Number of deposited models	7
Model precision (uncertainty of models)	16.0, Å, 22.0, Å, 24.0, Å, 27.0, Å, 27.0, Å, 29.0, Å, 37.0, Å
Data quality	Data quality has not been assessed
Model quality: assessment of excluded volume	Satisfaction: 99.78-99.79%
Fit to data used for modeling	Fit of model to information used to compute it has not been determined
Fit to data used for validation	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
1. Method	Sampling
Name	Replica exchange monte carlo
Number of computed models	5250000
Software	<ul style="list-style-type: none"> - IMP PMI module (version 20200514.develop.17be5981c6) - Integrative Modeling Platform (IMP) (version 20200514.develop.17be5981c6) - MODELLER (version SVN)