

Summary of integrative structure determination of Integrative structure of the non-canonical human COP9 Signalosome (PDB ID: 9A02, PDB-Dev ID: PDBDEV_00000038)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - CSN3: Chain C (423 residues) - CSN8: Chain H (209 residues) - CSN6: Chain F (327 residues) - CSN9: Chain I (57 residues) - CSN2: Chain B (443 residues) - CSN1: Chain A (491 residues) - CSN4: Chain D (406 residues) - CSN5: Chain E (334 residues) - CSN7: Chain G (264 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, 86 cross-links - Crosslinking-MS data, Linker name and number of cross-links: DSSO, 186 cross-links - Crosslinking-MS data, Linker name and number of cross-links: BMSO, 75 cross-links - Crosslinking-MS data, Linker name and number of cross-links: BMSO, 34 cross-links - Crosslinking-MS data, Linker name and number of cross-links: DHSO, 107 cross-links - Crosslinking-MS data, Linker name and number of cross-links: DHSO, 131 cross-links
2. Representation	
Resolution	Coarse-grained: 1, 2, 3, 5, 6, 29 residue(s) per bead
Number of <i>rigid bodies</i>, <i>flexible units</i>	23, 29
Rigid bodies	<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: -

<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: 1-57
<i>Structural coverage (rigid bodies)</i>	83%
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, 86 cross-links - 1 unique CrossLinkRestraint: DSSO, 186 cross-links - 1 unique CrossLinkRestraint: BMSO, 75 cross-links - 1 unique CrossLinkRestraint: BMSO, 34 cross-links - 1 unique CrossLinkRestraint: DHSO, 107 cross-links - 1 unique CrossLinkRestraint: DHSO, 131 cross-links
4. Validation	
<i>Number of ensembles</i>	1
<i>Number of models in ensembles</i>	125750
<i>Number of deposited models</i>	1
<i>Model precision (uncertainty of models)</i>	22.0, Å
<i>Data quality</i>	Data quality has not been assessed
<i>Model quality: assessment of excluded volume</i>	Satisfaction: 99.79-99.79%
<i>Fit to data used for modeling</i>	Fit of model to information used to compute it has not been determined
<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. Method</i>	Sampling
<i>Name</i>	Replica exchange monte carlo
<i>Number of computed models</i>	7500000

Software

- [IMP PMI module](#) (version 20200514.develop.17be5981c6)
- [Integrative Modeling Platform \(IMP\)](#) (version 20200514.develop.17be5981c6)
- [MODELLER](#) (version SVN)