

Table S1: Summary of Integrative Structure Determination of Integrative structure of the human CSN complex (PDBDEV000000X)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - CSN1: Chain A (491 residues) - CSN2: Chain B (443 residues) - CSN3: Chain C (423 residues) - CSN4: Chain D (406 residues) - CSN5: Chain E (334 residues) - CSN6: Chain F (327 residues) - CSN7: Chain G (264 residues) - CSN8: Chain H (209 residues) - CSN1: Chain A (491 residues) - CSN2: Chain B (443 residues) - CSN3: Chain C (423 residues) - CSN4: Chain D (406 residues) - CSN5: Chain E (334 residues) - CSN6: Chain F (327 residues) - CSN7: Chain G (264 residues) - CSN8: Chain H (209 residues) - CSN1: Chain A (491 residues) - CSN2: Chain B (443 residues) - CSN3: Chain C (423 residues) - CSN4: Chain D (406 residues) - CSN5: Chain E (334 residues) - CSN6: Chain F (327 residues) - CSN7: Chain G (264 residues) - CSN8: Chain H (209 residues) - CSN1: Chain A (491 residues) - CSN2: Chain B (443 residues) - CSN3: Chain C (423 residues) - CSN4: Chain D (406 residues) - CSN5: Chain E (334 residues) - CSN6: Chain F (327 residues) - CSN7: Chain G (264 residues) - CSN8: Chain H (209 residues) - CSN1: Chain A (491 residues) - CSN2: Chain B (443 residues) - CSN3: Chain C (423 residues) - CSN4: Chain D (406 residues) - CSN5: Chain E (334 residues) - CSN6: Chain F (327 residues) - CSN7: Chain G (264 residues) - CSN8: Chain H (209 residues) - CSN1: Chain A (491 residues) - CSN2: Chain B (443 residues) - CSN3: Chain C (423 residues) - CSN4: Chain D (406 residues) - CSN5: Chain E (334 residues) - CSN6: Chain F (327 residues) - CSN7: Chain G (264 residues) - CSN8: Chain H (209 residues) - CSN1: Chain A (491 residues) - CSN2: Chain B (443 residues) - CSN3: Chain C (423 residues) - CSN4: Chain D (406 residues) - CSN5: Chain E (334 residues) - CSN6: Chain F (327 residues) - CSN7: Chain G (264 residues) - CSN8: Chain H (209 residues)

Datasets used for modeling	<ul style="list-style-type: none"> - 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: DSS_Inter, Number of cross-links: 74 cross-links - CX-MS data, Linker name: DSS_Intra, Number of cross-links: 141 cross-links - CX-MS data, Linker name: BMS_Inter, Number of cross-links: 40 cross-links - CX-MS data, Linker name: BMS_Intra, Number of cross-links: 31 cross-links - CX-MS data, Linker name: DHS_Inter, Number of cross-links: 91 cross-links - CX-MS data, Linker name: DHS_Intra, Number of cross-links: 79 cross-links
2. Representation	
Atomic structural coverage	85%
Number of rigid bodies , flexible units	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.
Resolution	
3. Restraints	

Physical principles	Excluded volume and Sequence connectivity.
Experimental data	<ul style="list-style-type: none"> - CrossLinkRestraint: ('DSS_Inter', '74 cross-links') - CrossLinkRestraint: ('DSS_Intra', '141 cross-links') - CrossLinkRestraint: ('BMS_Inter', '40 cross-links') - CrossLinkRestraint: ('BMS_Intra', '31 cross-links') - CrossLinkRestraint: ('DHS_Inter', '91 cross-links') - CrossLinkRestraint: ('DHS_Intra', '79 cross-links')
4. Validation	
Sampling validation	1. Information related to sampling validation has not been provided
Clustering algorithm ,clustering feature	distance threshold-based clustering, 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	1. Quality of input data has not be assessed
Assessment of atomic regions	Not applicable
Assessment of excluded volume	<ol style="list-style-type: none"> 1. Model-1: Number of violations-6767.0 2. Model-2: Number of violations-6862.0 3. Model-3: Number of violations-6769.0 4. Model-4: Number of violations-6810.0 5. Model-5: Number of violations-6831.0 6. Model-6: Number of violations-6840.0 7. Model-7: Number of violations-6830.0
Fit of the model to information used to compute it	1. Fit of model to information used to compute it has not been determined
Fit of the model to information not used to compute it	1. 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	<ul style="list-style-type: none"> - IMP PMI module (version 20191107.develop.2640aeee5c) - Integrative Modeling Platform (IMP) (version 20191107.develop.2640aeee5c) - MODELLER (version SVN) - No location specified