Summary of integrative structure determination of Integrative structure of the yeast gammaTuSC-Spc110 monomer complex (PDB ID: 9A15, PDB-Dev ID: PDBDEV_00000077)

1. Model Composition	
Entry composition	- Tub4: Chain D (473 residues) - Spc98: Chain B (846 residues) - Tub4: Chain C (473 residues) - Spc110: Chain E (222 residues) - Spc97: Chain A (823 residues)
Datasets used for modeling	- Experimental model, PDB ID: 5FLZ - Crosslinking-MS data, Linker name and number of cross-links: EDC, 44 cross-links - Crosslinking-MS data, Linker name and number of cross-links: DSS, 42 cross-links
2. Representation	
Resolution	Coarse-grained: 1, 2, 3, 4, 9, 33 residue(s) per bead
Number of rigid bodies, flexible units	0, 34
Flexible units	- A: 1-54, 55-80, 81-89, 90-205, 206-242, 243-304, 305-319, 320-490, 491-553, 554-614, 615-622, 623-714, 715-753, 754-800, 801-823 - B: 1-179, 180-367, 368-378, 379-612, 613-627, 628-671, 672-718, 719-743, 744-755, 756-780, 781-797, 798-846 - C: 1-445, 446-473 - D: 1-445, 446-473 - E: 1-165, 166-205, 206-222
Structural coverage (rigid bodies)	0%
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique CrossLinkRestraint: EDC, 44 cross-links - 1 unique CrossLinkRestraint: DSS, 42 cross-links
4. Validation	
Number of ensembles	1
Number of models in ensembles	1621
Number of deposited models	1
Model precision (uncertainty of models)	12.0, Å
Data quality	Data quality has not been assessed

Model quality: assessment of excluded volume	Satisfaction: 99.75-99.75%
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	500000
Software	- IMP PMI module (version 2.14.0) - Integrative Modeling Platform (IMP) (version 2.14.0)