

Summary of integrative structure determination of Integrative structure of the yeast gammaTuSC-Spc110 dimer complex (PDB ID: 9A16, PDB-Dev ID: PDBDEV_0000078)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - Spc110: Chain E (222 residues) - Spc97: Chain A (823 residues) - Spc98: Chain B (846 residues) - Spc110: Chain F (222 residues) - Tub4: Chain D (473 residues) - Tub4: Chain C (473 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - 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, 37
Flexible units	<ul style="list-style-type: none"> - 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 - F: 1-165, 166-205, 206-222
Structural coverage (rigid bodies)	0%
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	<ul style="list-style-type: none"> - 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	2840
Number of deposited models	1
Model precision (uncertainty of models)	18.6, Å
Data quality	Data quality has not been assessed

<i>Model quality: assessment of excluded volume</i>	Satisfaction: 99.76-99.76%
<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	
1. Method	Sampling
<i>Name</i>	Replica exchange monte carlo
<i>Number of computed models</i>	500000
<i>Software</i>	- IMP PMI module (version 2.14.0) - Integrative Modeling Platform (IMP) (version 2.14.0)