

Summary of integrative structure determination of Integrative structure of the yeast gammaTuSC-Spc110 tetramer complex (PDB ID: 9A17, PDB-Dev ID: PDBDEV_00000079)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - Spc97: chain(s) A, B (823 residues) - Spc98: chain(s) C, D (846 residues) - Tub4: chain(s) E, F, G, H (473 residues) - Spc110: chain(s) I, J, K, L (222 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - Experimental model, Zenodo: 10.5281/zenodo.4584457 - Crosslinking-MS data, Zenodo: 10.5281/zenodo.4584457 - Crosslinking-MS data, Zenodo: 10.5281/zenodo.4584457
2. Representation	
Number of representations	1
Scale	Multiscale: Coarse-grained: 1 - 20 residue(s) per bead
Number of rigid and flexible segments	0, 74
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	<ul style="list-style-type: none"> - 1 unique CrossLinkRestrict: EDC, 44 crosslinks - 1 unique CrossLinkRestrict: DSS, 42 crosslinks
4. Validation	
Number of ensembles	1
Number of models in ensembles	2069
Number of deposited models	1
Model precision (uncertainty of models)	28.30, Å
Data quality	Data quality has not been assessed
Model quality: assessment of excluded volume	Satisfaction: 99.88%
Fit to data used for modeling	Satisfaction of crosslinks: 26.74%
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. Name	Sampling
Method	Replica exchange monte carlo
Number of computed models	1000000
Software	<ul style="list-style-type: none">- IMP PMI module (version 2.14.0)- Integrative Modeling Platform (IMP) (version 2.14.0)