Summary of integrative structure determination of Integrative structure and function of the yeast exocyst complex (PDB ID: 9A05, PDB-Dev ID: PDBDEV_00000041)

1. Model Composition	
Entry composition	- Sec03: chain(s) A (1336 residues) - Sec05: chain(s) B (971 residues) - Sec06: chain(s) C (805 residues) - Sec08: chain(s) D (1065 residues) - Sec10: chain(s) E (871 residues) - Sec15: chain(s) F (910 residues) - Exo70: chain(s) G (623 residues) - Exo84: chain(s) H (753 residues)
Datasets used for modeling	- Experimental model, PDB: 2PFT - Comparative model, Zenodo: 10.5281/zenodo.3951752 - Experimental model, PDB: 2D2S - Comparative model, Zenodo: 10.5281/zenodo.3951752 - Experimental model, PDB: 2A2F - Comparative model, Zenodo: 10.5281/zenodo.3951752 - Experimental model, PDB: 2FJI - Comparative model, Zenodo: 10.5281/zenodo.3951752 - Experimental model, PDB: 3FHN - Comparative model, Zenodo: 10.5281/zenodo.3951752 - Experimental model, PDB: 5H11 - Comparative model, Zenodo: 10.5281/zenodo.3951752 - Comparative model, Zenodo: 10.5281/zenodo.3951752 - Experimental model, PDB: 2B1E - Experimental model, PDB: 1ZC3 - Comparative model, Zenodo: 10.5281/zenodo.3951752 - Experimental model, PDB: 2D2S - Crosslinking-MS data, Zenodo: 10.5281/zenodo.3951752 - Crosslinking-MS data, Zenodo: 10.5281/zenodo.3951752 - 3DEM volume, EMDB: EMD-21226 - 3DEM volume, Zenodo: 10.5281/zenodo.3951752
2. Representation	
Number of representations	1
Scale	Multiscale: Coarse-grained: 1 - 50 residue(s) per bead
Number of rigid and flexible segments	43, 48
3. Restraints	

Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique CrossLinkRestraint: DSS, 256 crosslinks - 1 unique CrossLinkRestraint: EDC, 178 crosslinks - 1 unique EM3DRestraint: Gaussian mixture models
4. Validation	
Number of ensembles	1
Number of models in ensembles	9669
Number of deposited models	1
Model precision (uncertainty of models)	38.00, Å
Data quality	Data quality has not been assessed
Model quality: assessment of excluded volume	Satisfaction: 99.84%
Fit to data used for modeling	Satisfaction of crosslinks: 71.89%
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	200000
Software	- IMP PMI module (version 2.13.0) - Integrative Modeling Platform (IMP) (version 2.13.0) - MODELLER (version SVN)