Summary of integrative structure determination of Structure of Saccharomyces cerevisiae exosome determined with CX-MS (PDB ID: 8ZZ2, PDB-Dev ID: PDBDEV_00000002)

1. Model Composition	
Entry composition	- Dis3: chain(s) A (1001 residues) - Rrp45: chain(s) B (305 residues) - Rrp4: chain(s) C (359 residues) - Csl4: chain(s) D (292 residues) - Mtr3: chain(s) E (250 residues) - Rrp40: chain(s) F (240 residues) - Rrp42: chain(s) G (265 residues) - Ski6: chain(s) H (265 residues) - Rrp46_gfp: chain(s) I (475 residues) - Rrp43: chain(s) J (394 residues) - Lrp1: chain(s) K (184 residues) - Rrp6: chain(s) L (733 residues) - MPP6: chain(s) M (186 residues) - Ski7: chain(s) N (747 residues)
Datasets used for modeling	- Experimental model, PDB: 4IFD - Experimental model, PDB: 1GFL - Experimental model, PDB: 2HBJ - Comparative model, Zenodo: 10.5281/zenodo.583313 - Crosslinking-MS data, Zenodo: 10.5281/zenodo.583313
2. Representation	
Number of representations	1
Scale	Multiscale: Coarse-grained: 1 - 5 residue(s) per bead
Number of rigid and flexible segments	30, 31
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique CrossLinkRestraint: DSS, 218 crosslinks
4. Validation	
Number of ensembles	4
Number of models in ensembles	69, 131, 159, 41
Number of deposited models	4

Model precision (uncertainty of models)	- 24.37, Å - 19.26, Å - 9.80, Å - 11.52, Å
Data quality	Data quality has not been assessed
Model quality: assessment of excluded volume	Satisfaction: 99.89-99.89%
Fit to data used for modeling	Satisfaction of crosslinks: 75.17-81.66%
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	50000
2. Name	Sampling
Method	Replica exchange monte carlo
Number of computed models	50000
Software	- Integrative Modeling Platform (IMP) (version develop-0a5706e202) - IMP PMI module (version 67456c0) - Phyre2 (version 2.0)