Table S1: Summary of Integrative Structure Determination of Structure of Saccharomyces cerevisiae exosome determined with CX-MS (PDBDEV00000002)

1. Model Composition	
Entry composition	- Dis3: Chain A (1001 residues) - Csl4: Chain D (292 residues) - Rrp42: Chain G (265 residues) - Lrp1: Chain K (184 residues) - Rrp45: Chain B (305 residues) - MPP6: Chain M (186 residues) - Ski7: Chain N (747 residues) - Mtr3: Chain E (250 residues) - Rrp6: Chain L (733 residues) - Ski6: Chain H (265 residues) - Rrp46_gfp: Chain I (475 residues) - Rrp4: Chain C (359 residues) - Rrp40: Chain F (240 residues) - Rrp43: Chain J (394 residues)
Datasets used for modeling	- Experimental model, PDB ID: 4IFD - Experimental model, PDB ID: 1GFL - Experimental model, PDB ID: 2HBJ - Comparative model, template PDB ID: Not listed - CX-MS data, Linker name and number of cross-links: DSS, 218 cross-links
2. Representation	
Atomic structural coverage	79%
Number of rigid bodies, flexible units	,
Rigid bodies	- A: 9-237:Experimental model/4IFD, 249-329:Experimental model/4IFD, 364-471:Experimental model/4IFD, 472-1001:Experimental model/4IFD. - B: 2-301:Experimental model/4IFD. - C: 2-17:Experimental model/4IFD, 50-102:Experimental model/4IFD, 103-245:Experimental model/4IFD, 275-357:Experimental model/4IFD. - D: 1-71:Experimental model/4IFD, 99-113:Experimental model/4IFD, 126-162:Experimental model/4IFD, 185-291:Experimental model/4IFD. - E: 4-22:Experimental model/4IFD, 42-149:Experimental model/4IFD, 163-248:Experimental model/4IFD. - F: 1-60:Experimental model/4IFD, 61-236:Experimental model/4IFD. - G: 1-265:Experimental model/4IFD. - H: 1-242:Experimental model/4IFD. - I: 1-223:Experimental model/4IFD, 247-475:Experimental model/1GFL. - J: 7-99:Experimental model/4IFD, 121-193:Experimental model/4IFD, 206-309:Experimental model/4IFD, 327-394:Experimental model/4IFD. - K: - - L: 127-516:Experimental model/2HBJ, 532-557:Experimental model/4IFD, 565-619:Experimental model/4IFD. - M: - - N: 259-747:Comparative model/None.

Flexible units	- A: 1-8, 238-248, 330-363. - B: 1-1, 302-305. - C: 1-1, 18-49, 246-274, 358-359. - D: 72-98, 114-125, 163-184, 292-292. - E: 1-3, 23-41, 150-162, 249-250. - F: 237-240. - G: - - H: 243-265. - I: 224-246. - J: 1-6, 100-120, 194-205, 310-326. - K: 1-184. - L: 1-126, 517-531, 558-564, 620-733. - M: 1-186. - N: 1-258.
Resolution	Rigid bodies: 1 residue per bead. Flexible regions: N/A
3. Restraints	
Physical principles	Excluded volume and Sequence connectivity.
Experimental data	- 1 unique CrossLinkRestraint: DSS, 218 cross-links
4. Validation	
Sampling validation	1. Information related to sampling validation has not been provided
Clustering algorithm ,*clustering feature*	Distance threshold-based clustering used if ensembles are deposited, RMSD
Number of ensembles	
Number of models in ensembles	69, 131, 159, 41
Model precision (uncertainty of models)	24.374Å, 19.258Å, 9.798Å, 11.517Å
Quality of data	-
Assessment of atomic segments	-
Fit of the model to information used to compute it	1. Fit of model to information used to compute it has not been determined
Fit of the model to information not used to compute it	1. Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
Method	Sampling
Name	Replica exchange Monte Carlo
Details	- Method details unspecified

Software	- Integrative Modeling Platform (IMP) (version develop-0a5706e202) - IMP PMI module (version 67456c0) - Phyre2 (version 2.0) - No location specified