Summary of integrative structure determination of Molecular architecture of the endocytic TPLATE/TSET complex (PDB ID: 9A0T, PDB-Dev ID: PDBDEV_00000065)

1. Model Composition	
Entry composition	- tash3: Chain B (1198 residues) - tplate: Chain C (1176 residues) - lol: Chain A (147 residues) - wd2: Chain F (1376 residues) - eh1: Chain G (1019 residues) - eh2: Chain H (1218 residues) - tml: Chain D (646 residues) - wd1: Chain E (1592 residues)
Datasets used for modeling	- Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Crosslinking-MS data, Linker name and number of cross-links: BS3, 119 cross-links - Experimental model, PDB ID: 5NZR - Experimental model, PDB ID: 5MU7 - Experimental model, PDB ID: 6OWT - Experimental model, PDB ID: 2KYM - Experimental model, PDB ID: 2JKR - Experimental model, PDB ID: 5JP2 - Experimental model, PDB ID: 5AWS - Experimental model, PDB ID: 3G9H - Experimental model, PDB ID: 3MKQ - Experimental model, PDB ID: 3MKR - Experimental model, PDB ID: 2YNP - Experimental model, PDB ID: 6YEU - Experimental model, PDB ID: 6YET
2. Representation	

Resolution	Coarse-grained: 1, 2, 3, 5, 6, 7, 12, 15 residue(s) per bead
Number of rigid bodies, flexible units	26, 24
Rigid bodies	- A: 1-147 - B: 104-171, 205-258, 281-419, 464-499, 551-686, 716-734, 766-812, 1131-1198 - C: 1-467, 771-1045 - D: 1-40, 96-191, 407-646 - E: 18-349, 450-1002, 1303-1592 - F: 1-52, 125-534, 676-752, 771-974, 1012-1167 - G: 1-110, 346-449 - H: 1-112, 400-512
Flexible units	- A: - - B: 1-103, 172-204, 259-280, 420-463, 500-550, 687-715, 735-765, 813-1130 - C: 468-770, 1046-1176 - D: 41-95, 192-406 - E: 1-17, 350-449, 1003-1302 - F: 53-124, 535-675, 753-770, 975-1011, 1168-1376 - G: 111-345, 450-1019 - H: 113-399, 513-1218
Structural coverage (rigid bodies)	52%
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique CrossLinkRestraint: BS3, 119 cross-links
4. Validation	
Number of ensembles	1
Number of models in ensembles	3981
Number of deposited models	1
Model precision (uncertainty of models)	39.4, 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	Fit of model to information used to compute it has not been determined
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. Method	Sampling
Name	Replica exchange monte carlo
Number of computed models	1000000
Software	- IMP PMI module (version 2.12.0) - Integrative Modeling Platform (IMP) (version 2.12.0)

1. Method	Sampling
Name	Replica exchange monte carlo