

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	<ul style="list-style-type: none"> - lol: chain(s) A (147 residues) - tash3: chain(s) B (1198 residues) - tplate: chain(s) C (1176 residues) - tml: chain(s) D (646 residues) - wd1: chain(s) E (1592 residues) - wd2: chain(s) F (1376 residues) - eh1: chain(s) G (1019 residues) - eh2: chain(s) H (1218 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - Comparative model, Zenodo: 10.5281/zenodo.3979550 - Comparative model, Zenodo: 10.5281/zenodo.3979550 - Comparative model, Zenodo: 10.5281/zenodo.3979550 - Comparative model, Zenodo: 10.5281/zenodo.3979550 - Comparative model, Zenodo: 10.5281/zenodo.3979550 - Comparative model, Zenodo: 10.5281/zenodo.3979550 - Comparative model, Zenodo: 10.5281/zenodo.3979550 - Comparative model, Zenodo: 10.5281/zenodo.3979550 - Comparative model, Zenodo: 10.5281/zenodo.3979550 - Comparative model, Zenodo: 10.5281/zenodo.3979550 - Comparative model, Zenodo: 10.5281/zenodo.3979550 - Comparative model, Zenodo: 10.5281/zenodo.3979550 - Comparative model, Zenodo: 10.5281/zenodo.3979550 - Comparative model, Zenodo: 10.5281/zenodo.3979550 - Crosslinking-MS data, Zenodo: 10.5281/zenodo.3979550 - Experimental model, PDB: 5NZR - Experimental model, PDB: 5MU7 - Experimental model, PDB: 6OWT - Experimental model, PDB: 2KYM - Experimental model, PDB: 2JKR - Experimental model, PDB: 5JP2 - Experimental model, PDB: 5AWS - Experimental model, PDB: 3G9H - Experimental model, PDB: 3MKQ - Experimental model, PDB: 3MKR - Experimental model, PDB: 2YNP - Experimental model, PDB: 6YEU - Experimental model, PDB: 6YET
2. Representation	

<i>Number of representations</i>	1
<i>Scale</i>	Multiscale: Coarse-grained: 1 - 50 residue(s) per bead
<i>Number of <i>rigid</i> and <i>flexible</i> segments</i>	26, 24
3. Restraints	
<i>Physical principles</i>	Information about physical principles was not provided
<i>Experimental data</i>	- 1 unique CrossLinkRestraint: BS3, 119 crosslinks
4. Validation	
<i>Number of ensembles</i>	1
<i>Number of models in ensembles</i>	3981
<i>Number of deposited models</i>	1
<i>Model precision (uncertainty of models)</i>	39.40, Å
<i>Data quality</i>	Data quality has not been assessed
<i>Model quality: assessment of excluded volume</i>	Satisfaction: 99.89%
<i>Fit to data used for modeling</i>	Satisfaction of crosslinks: 96.64%
<i>Fit to data used for validation</i>	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
<i>1. <i>Name</i></i>	Sampling
<i>Method</i>	Replica exchange monte carlo
<i>Number of computed models</i>	1000000
<i>Software</i>	- IMP PMI module (version 2.12.0) - Integrative Modeling Platform (IMP) (version 2.12.0)