Summary of integrative structure determination of Modeling of the interaction between doublecortin and microtubule, NDCs fixed at longitudinal orientation (PDB ID: 9A11, PDB-Dev ID: PDBDEV_00000073)

1. Model Composition	
Entry composition	- Alpha-Tubulin: Chain L (451 residues) - Beta-Tubulin: Chain Y (445 residues) - Alpha-Tubulin: Chain J (451 residues) - Alpha-Tubulin: Chain C (451 residues) - Beta-Tubulin: Chain R (445 residues) - Beta-Tubulin: Chain Q (445 residues) - Beta-Tubulin: Chain Z (445 residues) - Beta-Tubulin: Chain T (445 residues) - Beta-Tubulin: Chain U (445 residues) - Beta-Tubulin: Chain P (445 residues) - Alpha-Tubulin: Chain M (451 residues) - Doublecortin: Chain B (365 residues) - Alpha-Tubulin: Chain F (451 residues) - Alpha-Tubulin: Chain O (451 residues) - Alpha-Tubulin: Chain G (451 residues) - Alpha-Tubulin: Chain H (451 residues) - Beta-Tubulin: Chain AA (445 residues) - Alpha-Tubulin: Chain N (451 residues) - Beta-Tubulin: Chain V (445 residues) - Alpha-Tubulin: Chain K (451 residues) - Beta-Tubulin: Chain W (445 residues) - Beta-Tubulin: Chain S (445 residues) - Beta-Tubulin: Chain X (445 residues) - Doublecortin: Chain A (365 residues) - Alpha-Tubulin: Chain I (451 residues) - Alpha-Tubulin: Chain D (451 residues) - Alpha-Tubulin: Chain E (451 residues)
Datasets used for modeling	- Experimental model, PDB ID: 4ATU - Experimental model, PDB ID: 6FNZ - Experimental model, PDB ID: 6EVZ - Crosslinking-MS data, Linker name and number of cross-links: LCSDA, 445 cross-links
2. Representation	
Resolution	Coarse-grained: 1, 4, 8 residue(s) per bead
Number of rigid bodies, flexible units	52, 4

Rigid bodies	- A: 51-140, 177-251 - B: 51-140, 177-251 - C: 1-37, 47-435 - D: 1-37, 47-435 - E: 47-435 - F: 1-37 - G: 1-37, 47-435 - H: 1-37, 47-435 - I: 1-37, 47-435 - J: 1-37, 47-435 - K: 1-37, 47-435 - L: 1-37, 47-435 - M: 1-37, 47-435 - N: 1-37, 47-435 - O: 1-37, 47-435 - P: 1-37, 38-429 - Q: 1-37, 38-429 - R: 1-37, 38-429 - S: 1-37, 38-429 - T: 1-37, 38-429 - U: 1-37, 38-429 - V: 1-37, 38-429 - W: 1-37, 38-429 - X: 1-37, 38-429 - Y: 1-37, 38-429 - Z: 1-37, 38-429 - AA: 1-37, 38-429
Flexible units	- A: 141-176, 252-330 - B: 141-176, 252-330 - C: - - D: - - E: - - F: - - G: - - H: - - I: - - J: - - K: - - L: - - M: - - N: - - O: - - P: - - Q: - - R: - - S: - - T: - - U: - - V: - - W: - - X: - - Y: - - Z: - - AA: -
Structural coverage (rigid bodies)	98%
3. Restraints	

Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique CrossLinkRestraint: LCSDA, 445 cross-links
4. Validation	
Number of ensembles	1
Number of models in ensembles	30000
Number of deposited models	1
Model precision (uncertainty of models)	None, Å
Data quality	Data quality has not been assessed
Model quality: assessment of excluded volume	Satisfaction: 99.96-99.96%
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	240000
Software	- IMP PMI module (version 2.14.0) - Integrative Modeling Platform (IMP) (version 2.14.0)