# A Pseudo-Atomic Model of the COPII Cage Obtained from Cryoemand Mass Spectrometry Analyses

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## Results and Discussion

COPII vesicles transport proteins from the endoplasmic retibulum to the Golgi apparatus in a cell. Prior cryo-eelectron microscopy structures of the COPII cage lacked the resolution necessary to determine the residues of the Sec13 and Sec31 subunits that mediate assembly and flexibility of the COPII cage. Here, we present a 12Å-resolution structure of the COPII cage, in which the tertiary structure of Sec13 and Sec31 is clearly identifiable. We employ that structure and a homology model of the Sec13-Sec31 complex to create a reliable pseudo-atomic model of the COPII cage. We combine the model with hydrogen/deuterium exchange mass spectrometry analysis to characterize four distinct contact regions at the vertices of the COPII cage. Furthermore, we find that the 2-fold symmetry of the Sec31 dimeric region of Sec13-31 is broken upon cage formation, and that the resulting hinge is essential to form the proper edge geometry in COPII cages.

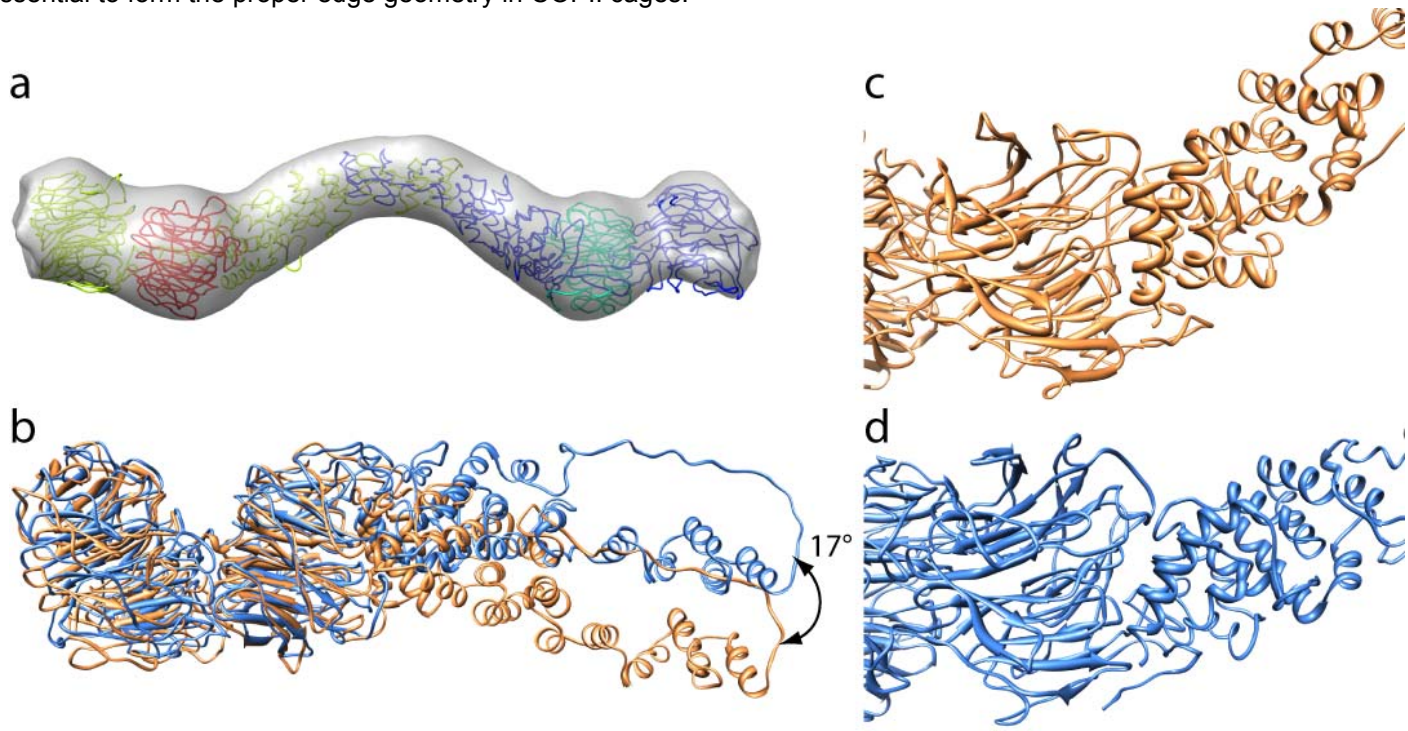


**Figure 1. Pseudo-atomic model of human Sec13-31.** a) Human homology model flexibly-fitted into a single edge of the cryoEM reconstruction of the Sec13-31 cage. The Sec13 chains are colored red and cyan and the Sec31 chains are colored yellow and blue. The α-solenoid domains of Sec31 are highlighted with a bracket. b) Superposition of the plus and minus end of an individual Sec13-31 heterotetramer. The chains were superimposed based on Sec13 (dark orange/blue) to highlight the conformational change in Sec31 (light orange/blue). c) Plus end of the fitted heterotetramer. d) Minus end of the fitted heterotetramer. The plus end α-solenoid domain is more tightly packed against Sec13 at the plus end in c) than it is at the minus end in d).

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## References

[1] Noble, A. J.; et al., Nature Struc. Mol. Biol., **20**, 167-174 (2013).