Determining cellular CTCF and cohesin abundances to constrain 3D genome models.

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Authors: Claudia Cattoglio, Iryna Pustova, Nike Walther, Jaclyn J Ho, Merle Hantsche-Grininger, Carla J Inouye, M Julius Hossain, Gina M Dailey, Jan Ellenberg, Xavier Darzacq, Robert Tjian, Anders S Hansen

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Public Summary:
Achieving a quantitative and predictive understanding of 3D genome architecture remains a major challenge, as it requires quantitative measurements of the key proteins involved. Here, we report the quantification of CTCF and cohesin, two causal regulators of topologically associating domains (TADs) in mammalian cells. Extending our previous imaging studies (Hansen et al., 2017), we estimate bounds on the density of putatively DNA loop-extruding cohesin complexes and CTCF binding site occupancy. Furthermore, co-immunoprecipitation studies of an endogenously tagged subunit (Rad21) suggest the presence of cohesin dimers and/or oligomers. Finally, based on our cell lines with accurately measured protein abundances, we report a method to conveniently determine the number of molecules of any Halo-tagged protein in the cell. We anticipate that our results and the established tool for measuring cellular protein abundances will advance a more quantitative understanding of 3D genome organization, and facilitate protein quantification, key to comprehend diverse biological processes.

Scientific Abstract:
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