

Protein determinants of chromosome domains

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MIT PRIMES Presentation

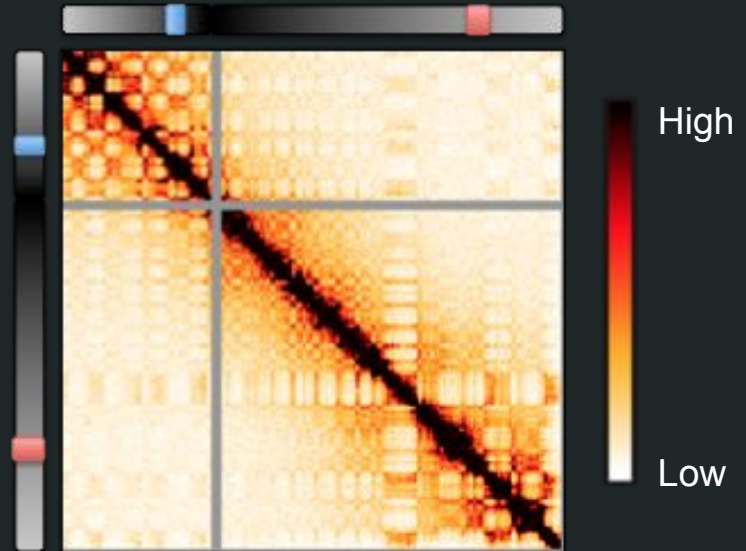
May 22, 2016

Background

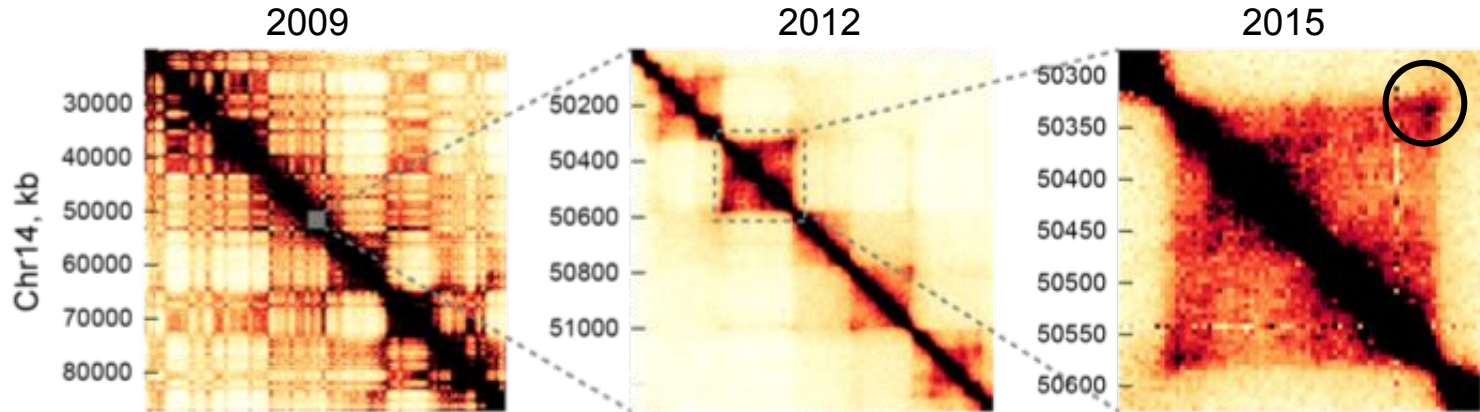
Hi-C

Loops and domains

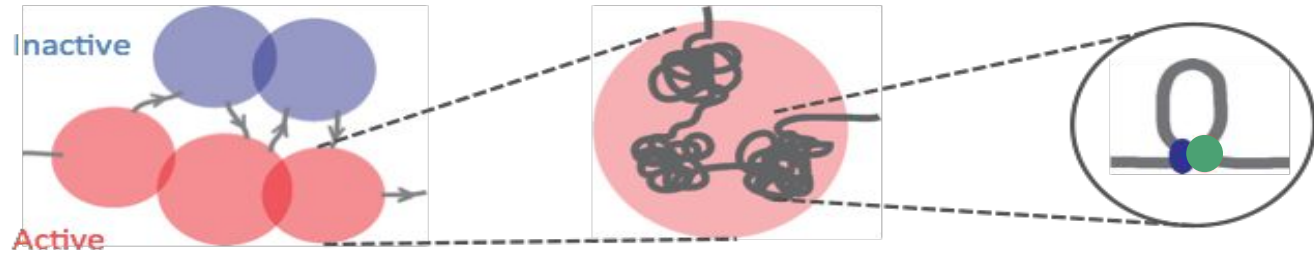
Chromosome contact maps



Loops and domains



A/B Compartments

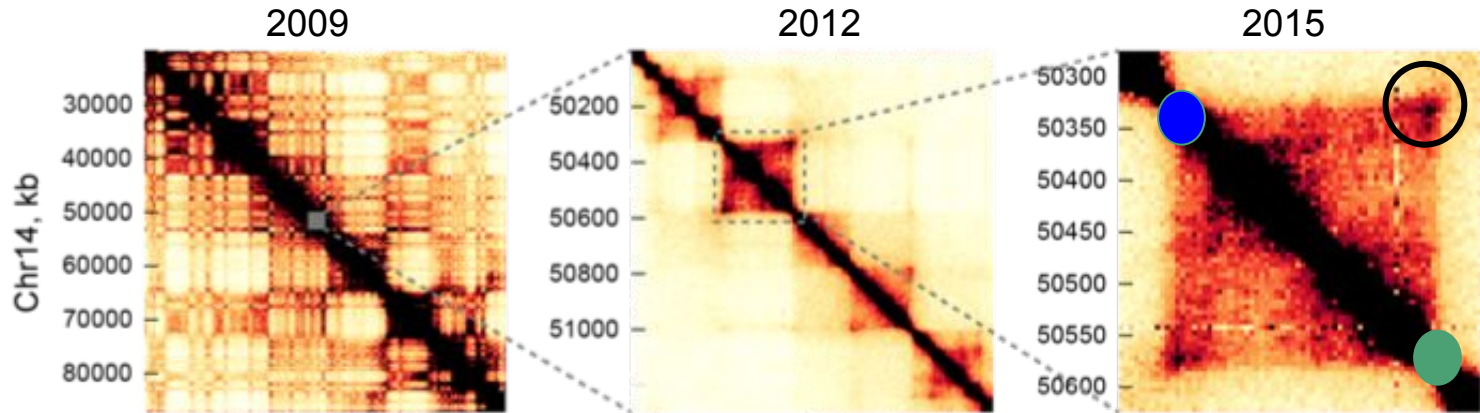


Lieberman Aiden, et al. Science 2009

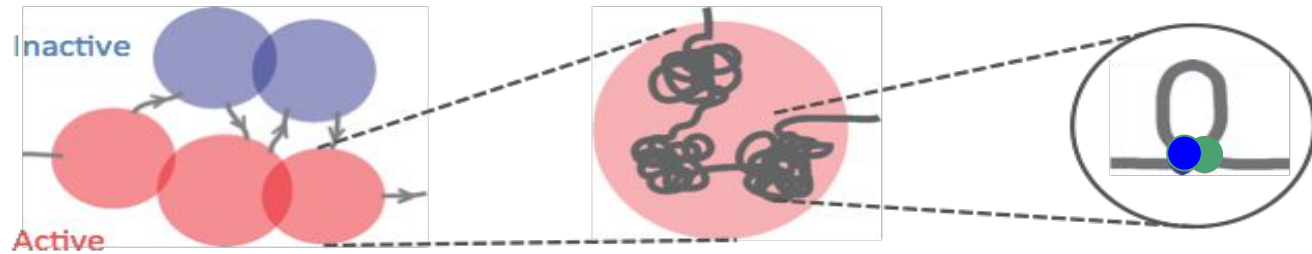
Nora et al. Nature 2012

Rao et al. Cell 2014

Loops and domains



A/B Compartments



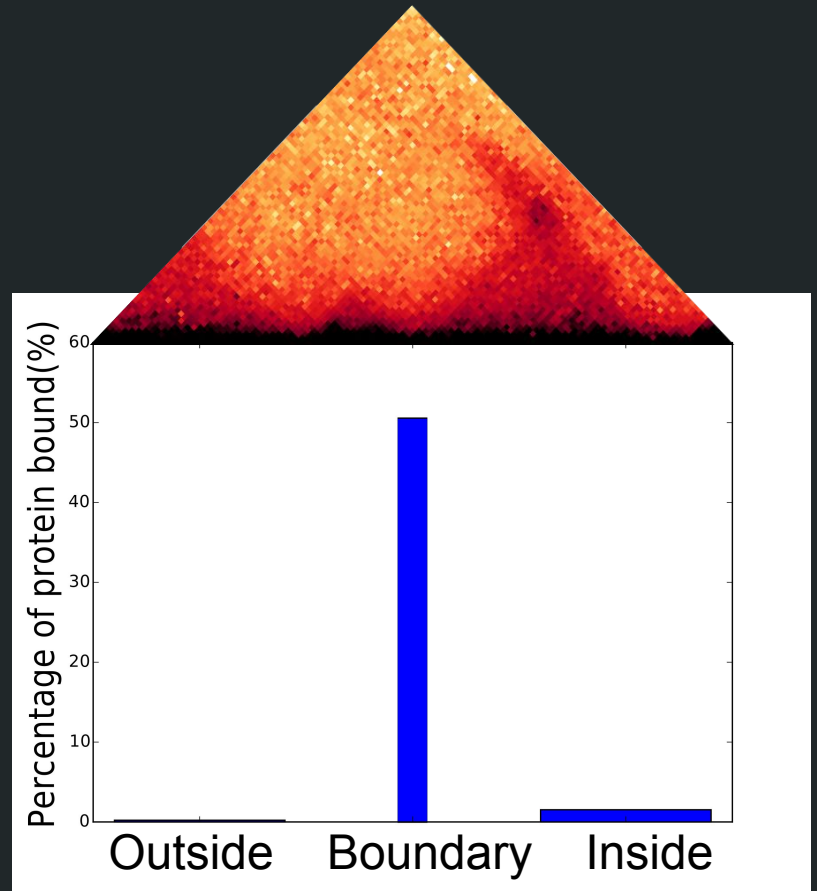
Lieberman Aiden, et al. Science 2009

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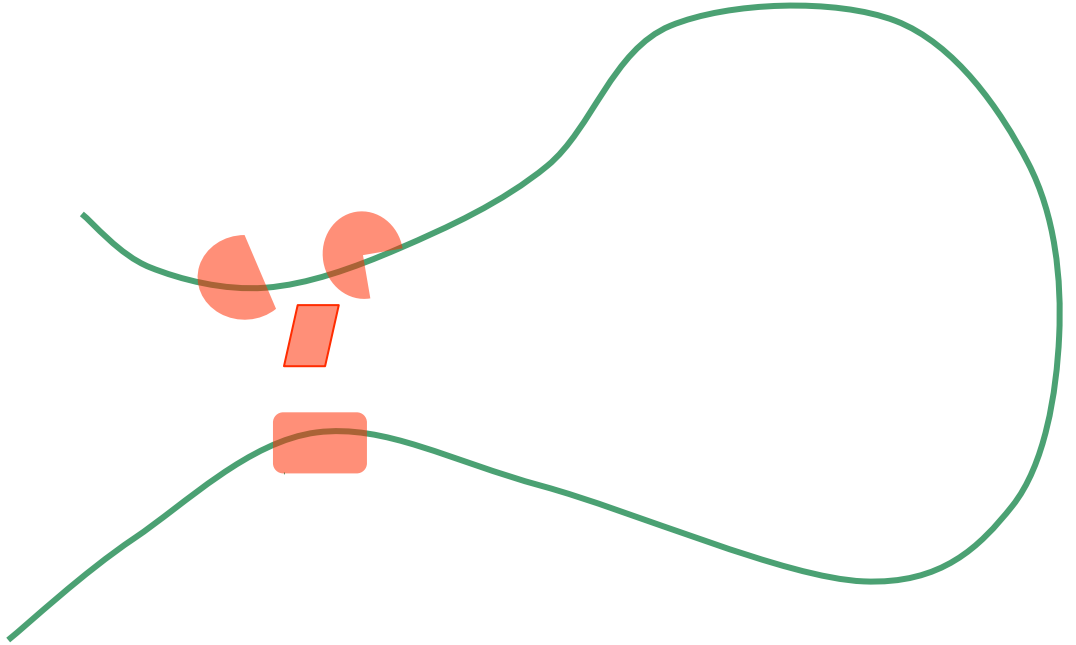
DNA - Binding Proteins

Functional aspect



Binding factors at boundaries

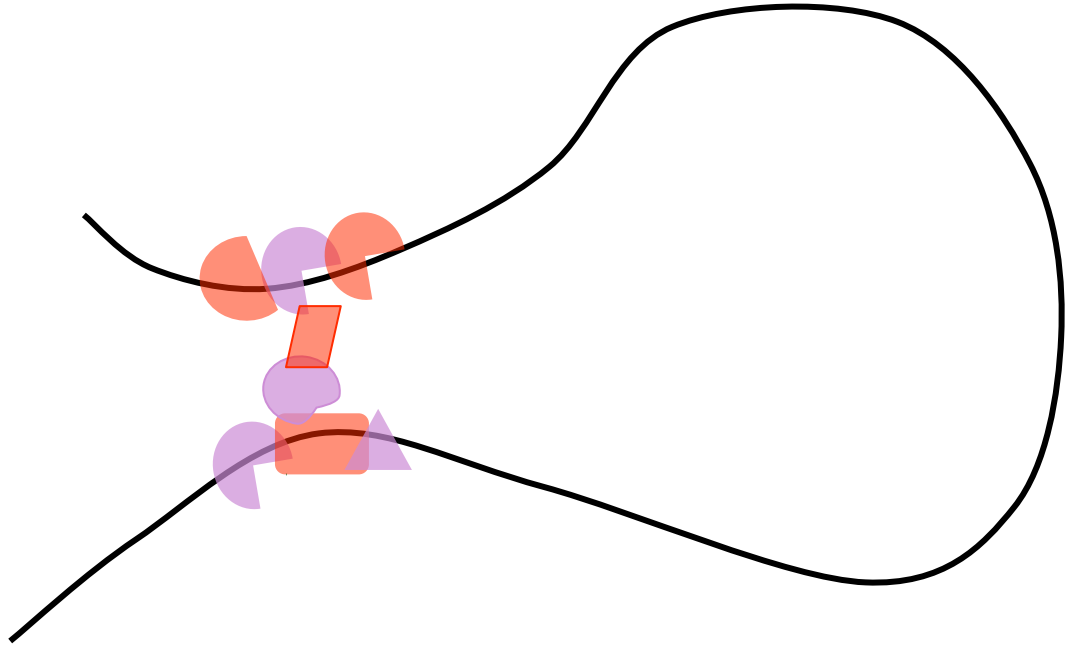
- Architectural Proteins



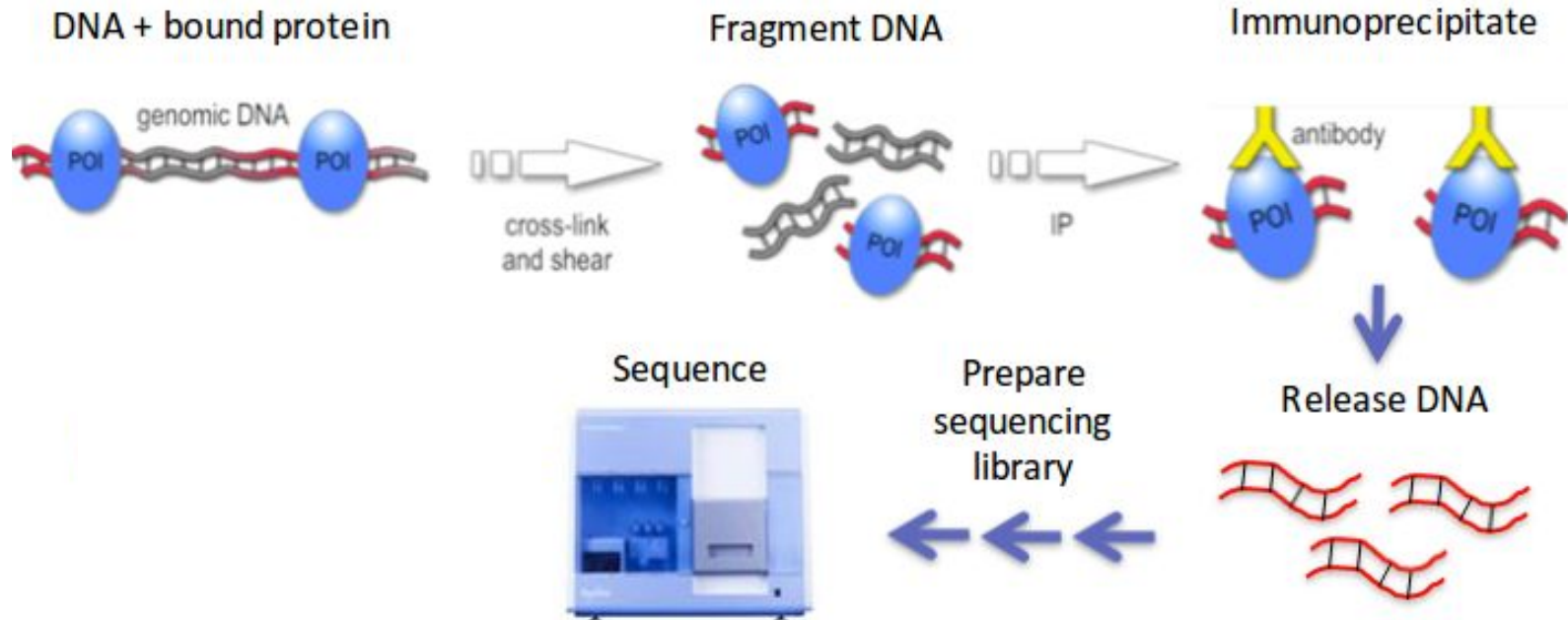
Binding factors at boundaries

● Architectural Proteins

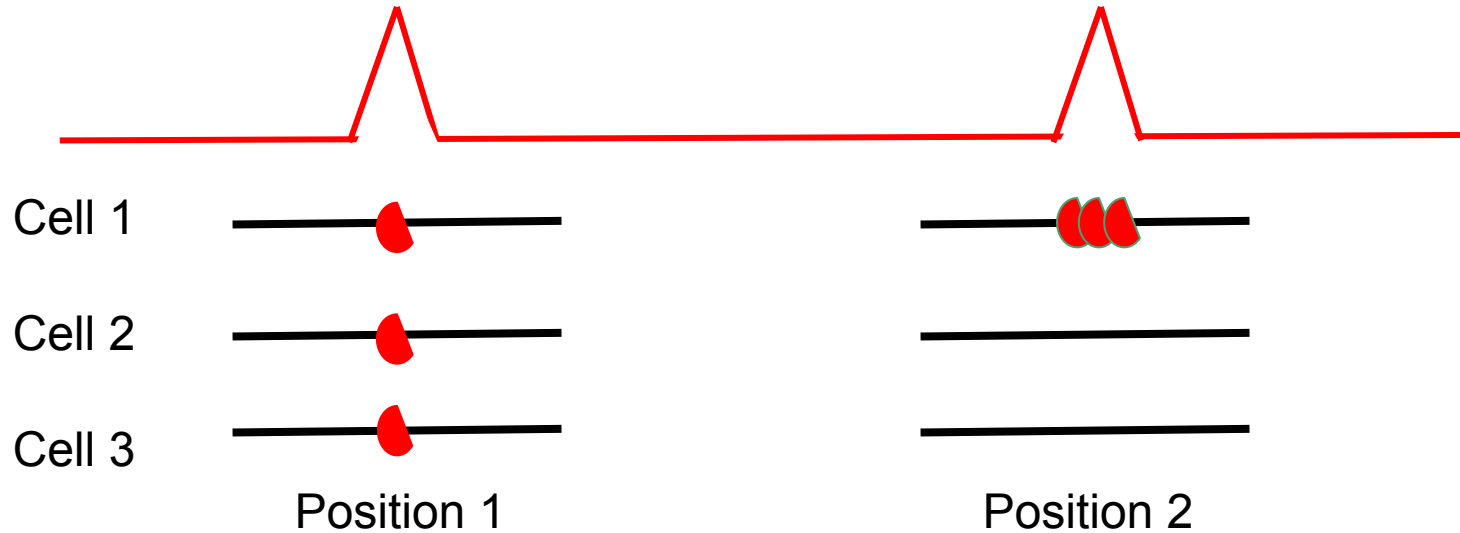
● Transcription Factors



Chromatin Immunoprecipitation Seq (ChIP-seq)



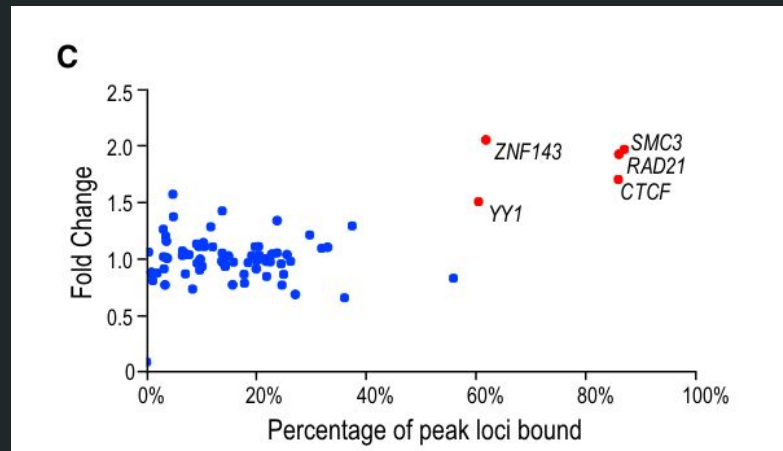
Chromatin Immunoprecipitation Seq (ChIP-seq)



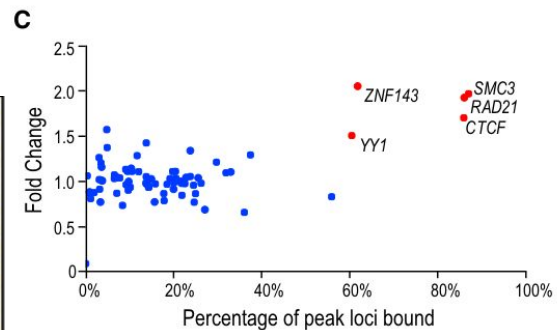
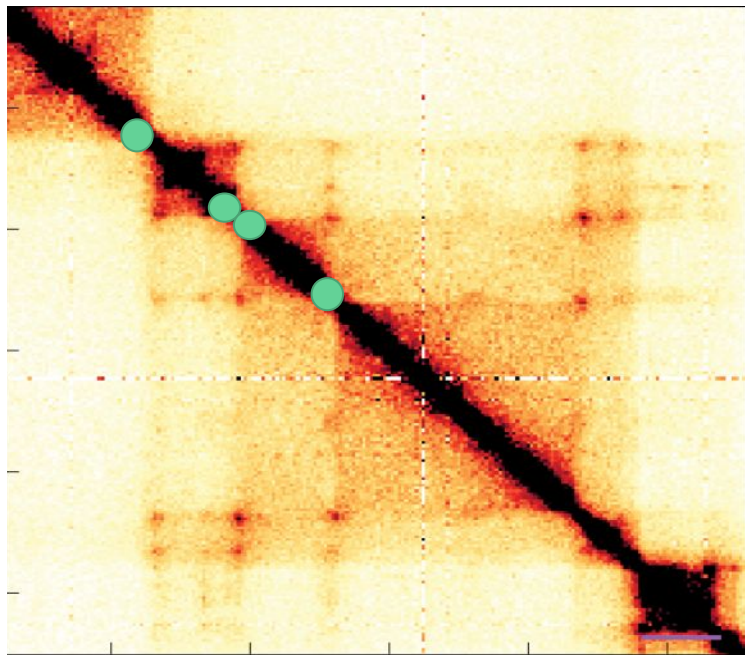
Methods and Results

Protein Enrichment

Peak enrichment vs
percentage states occupied



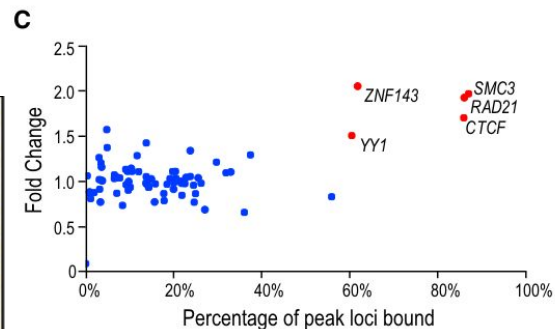
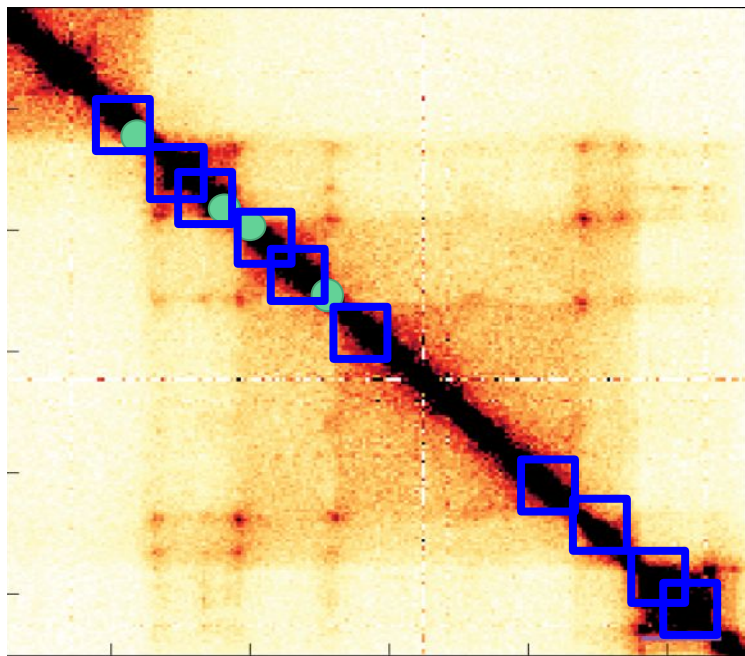
Percentage of loop or domain boundaries with protein



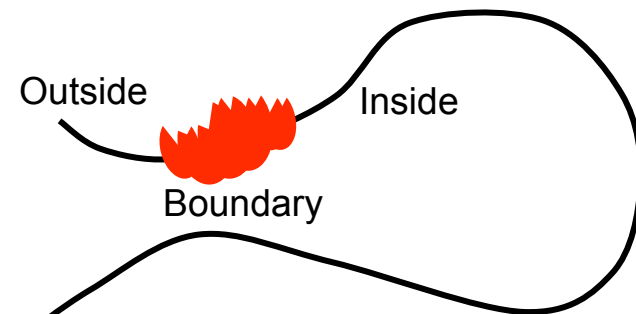
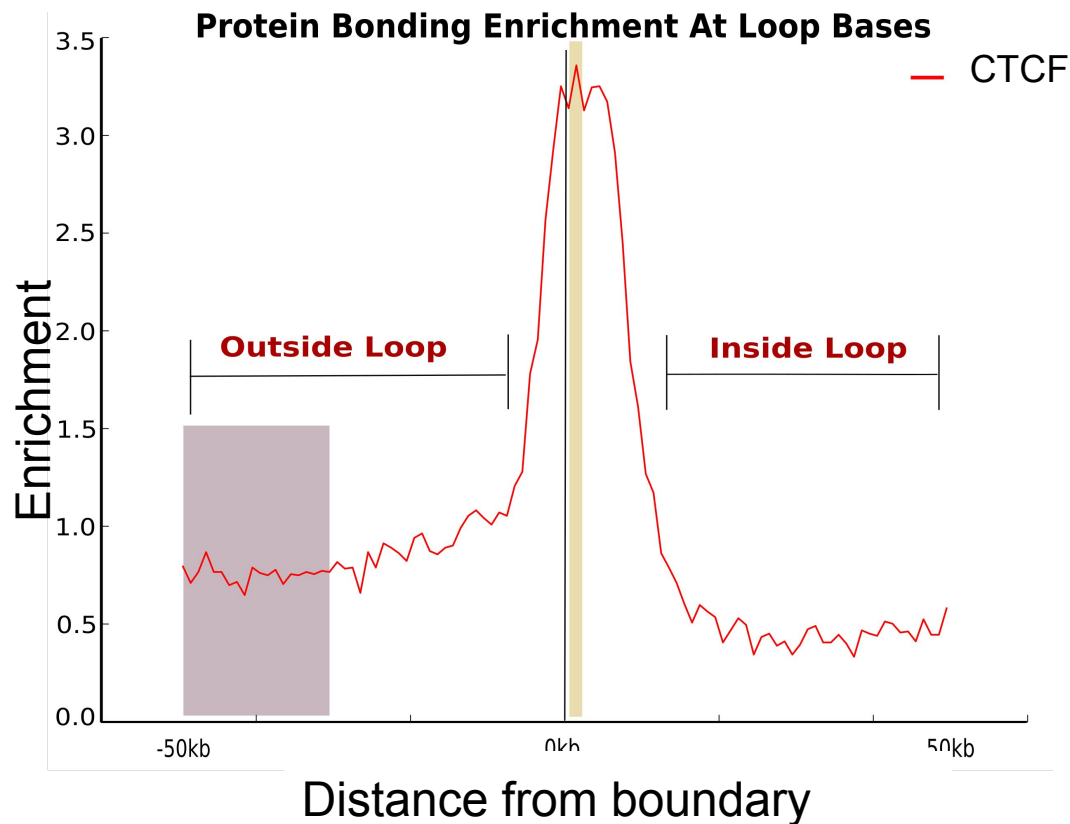
Percentage of loop or domain boundaries with protein

Example:

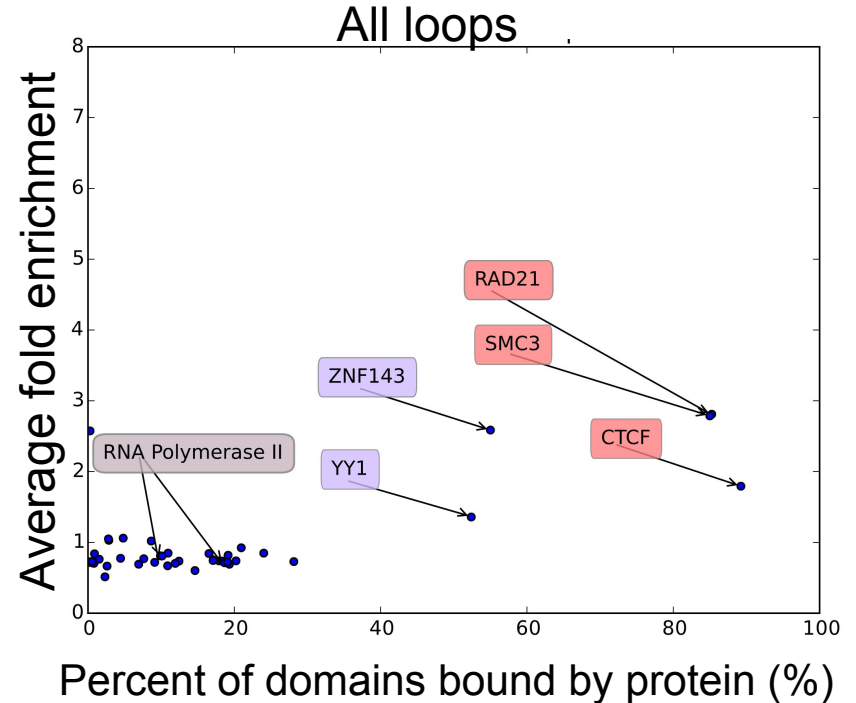
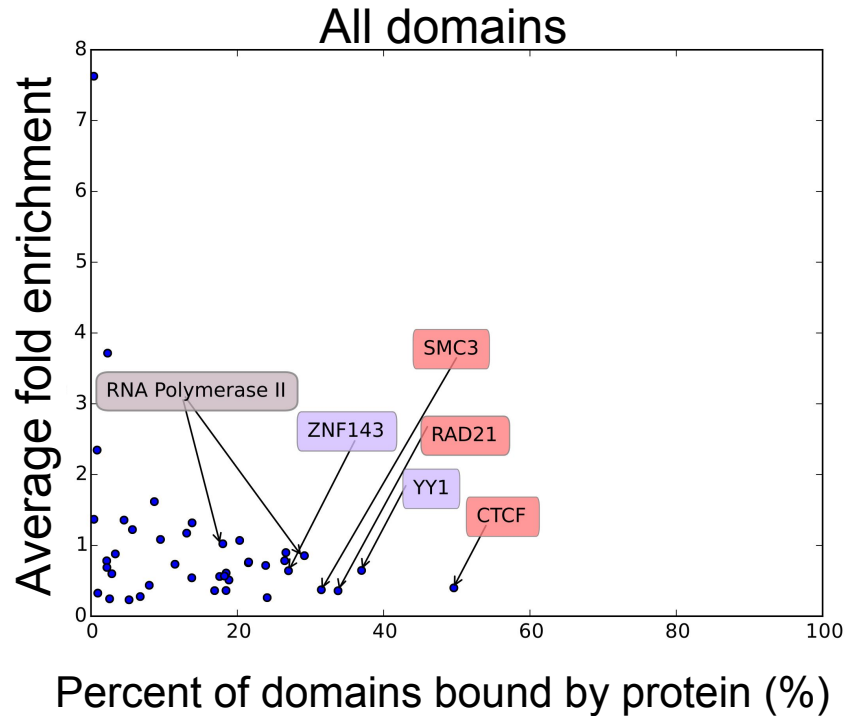
- 10 total boundaries
- 4 with green protein
- $4/10 = 40\%$ green protein



Enrichment of proteins at loop and domain boundaries



Architectural and transcription proteins are enriched at loop boundaries



Architectural proteins enriched at loop boundaries

CTCF

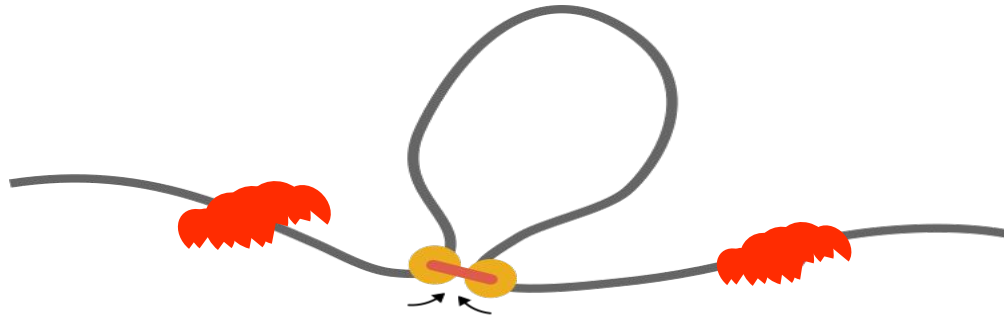


- Known to be related to 3D genome structure and loop formation

Cohesin

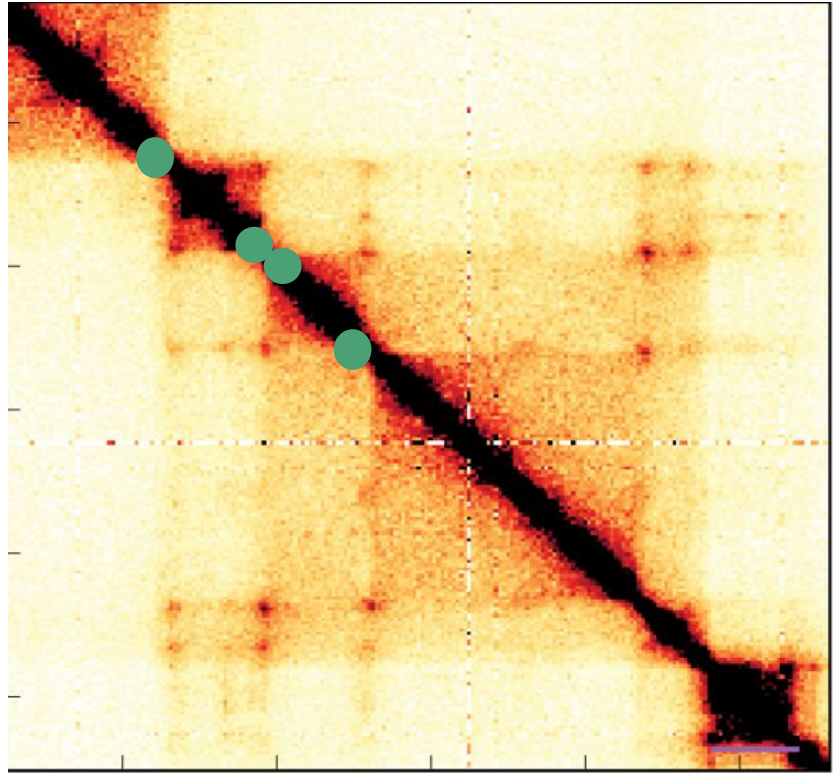


- RAD21 and SMC3 subunits
- Forms chromatin loops in Interphase



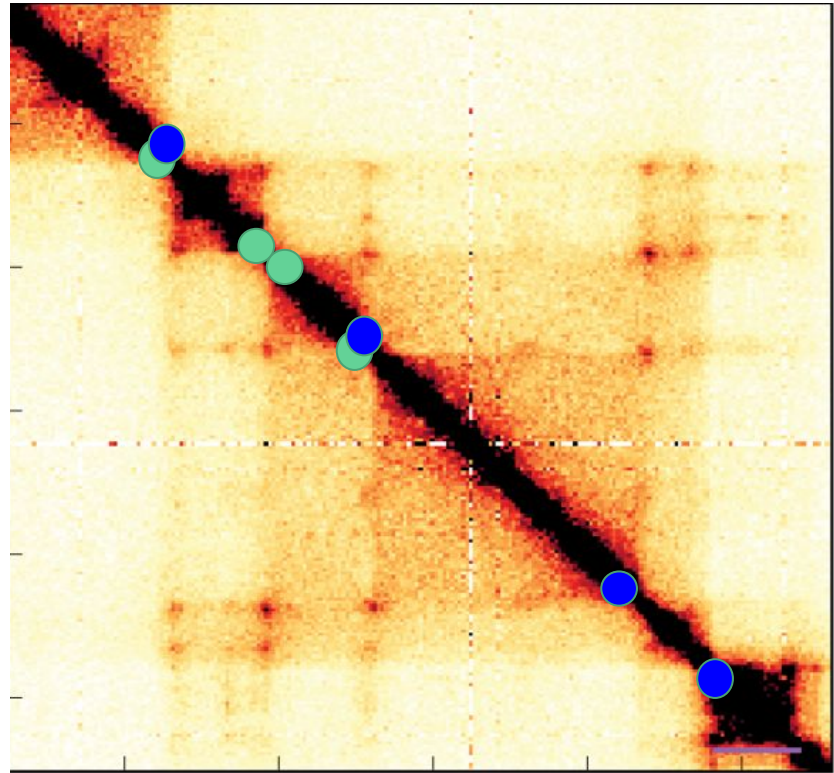
Considering boundaries with a particular protein

- Only interested in boundaries with a particular protein (green)

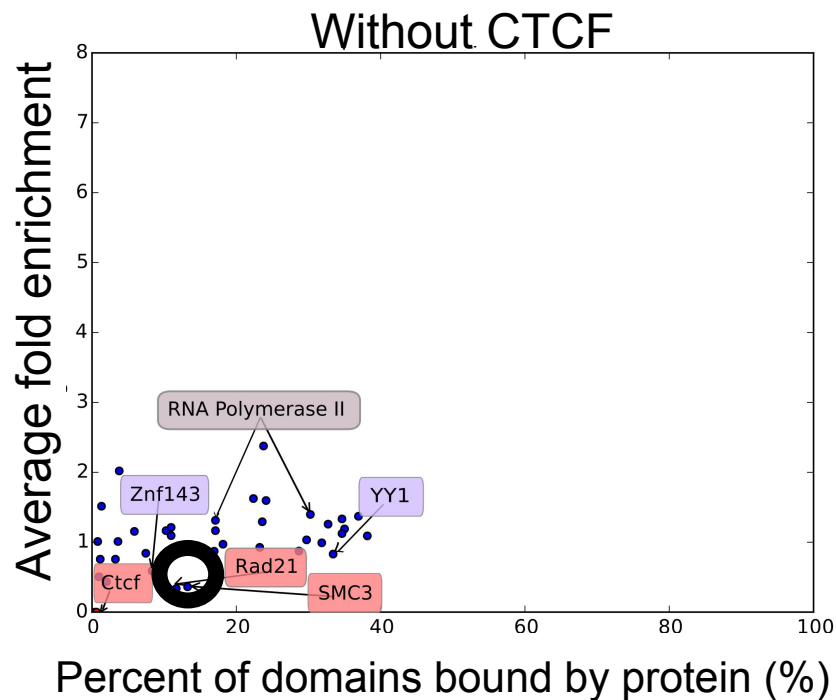
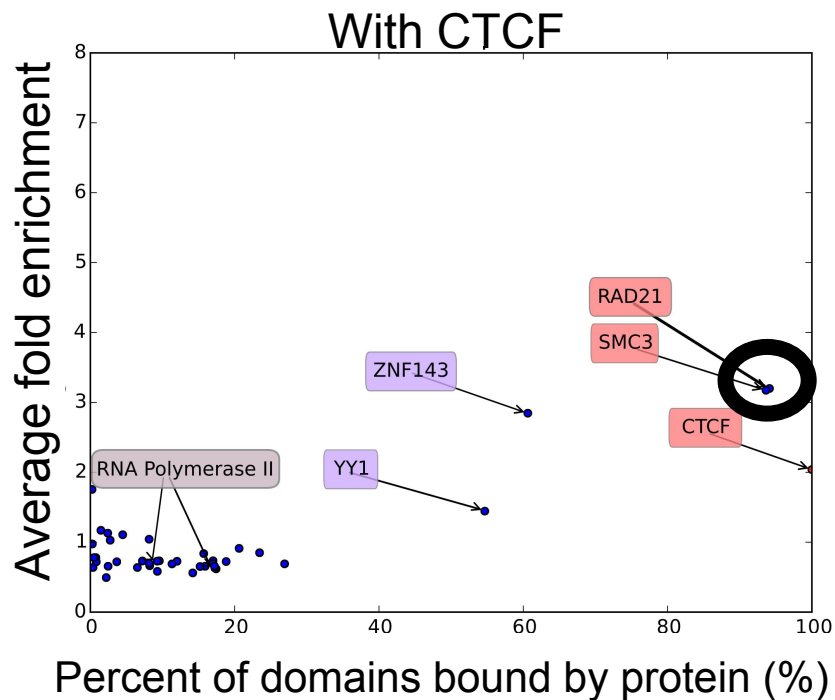


Considering boundaries with a particular protein

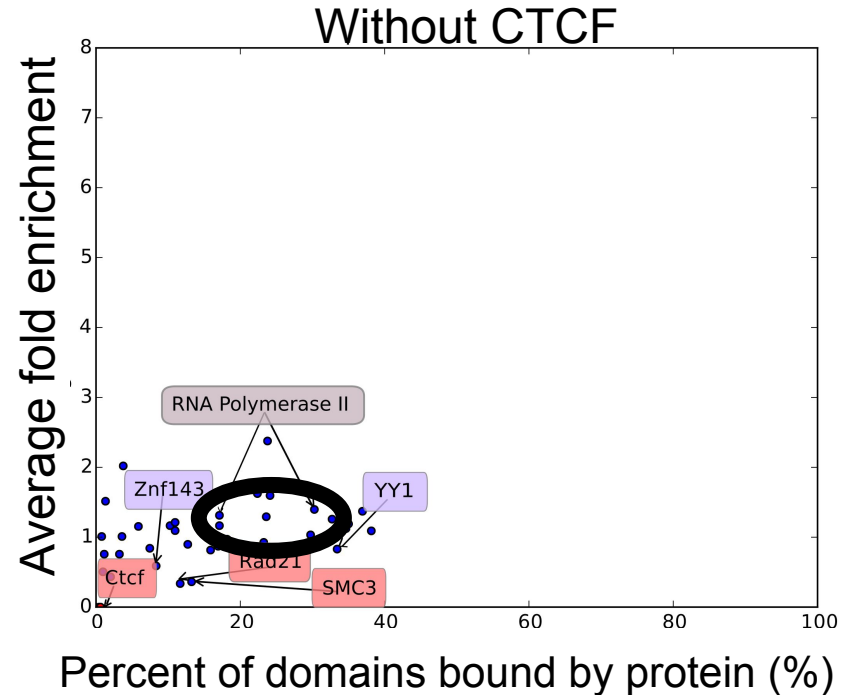
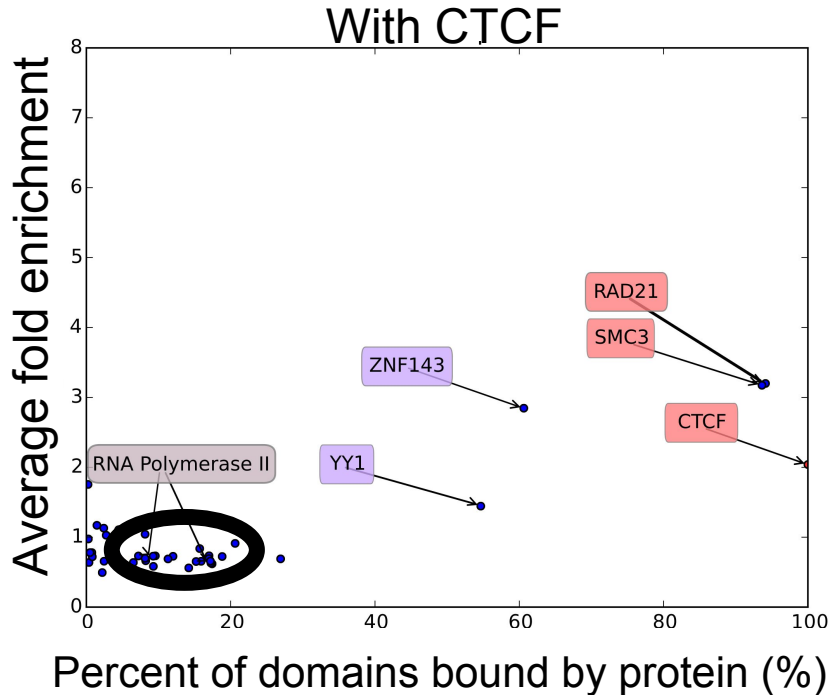
- Only interested in boundaries with a particular protein (green)
- 2 boundaries with both CTCF and the blue protein/ 4 boundaries with CTCF



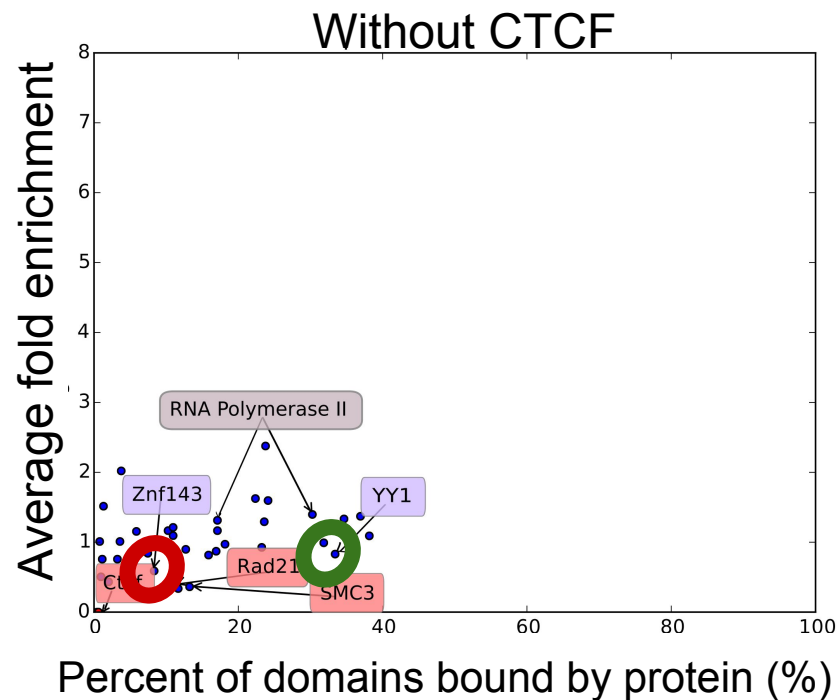
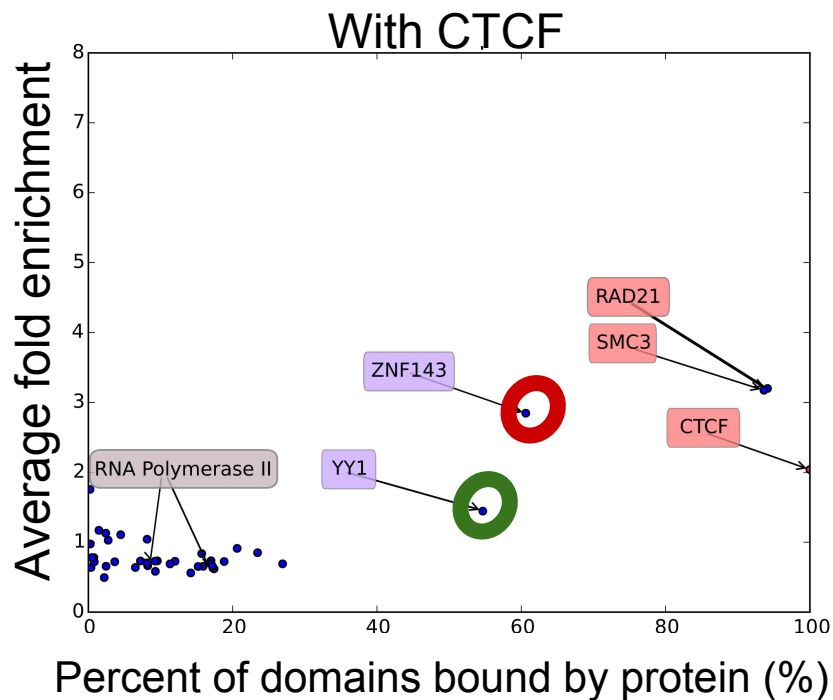
Architectural proteins CTCF, SMC3, RAD21 are co-enriched at loop boundaries



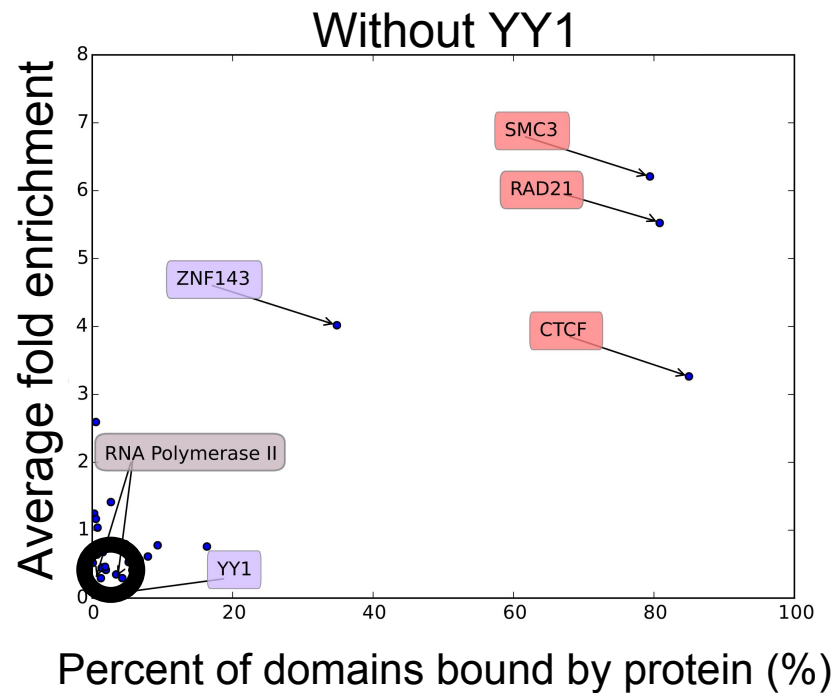
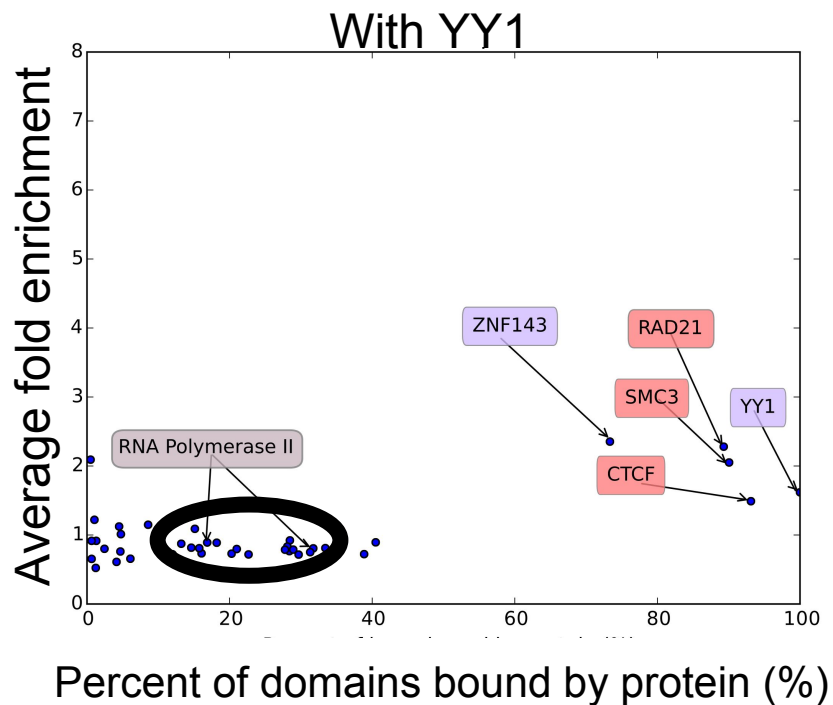
RNA Polymerase II is more common on boundaries without CTCF than with CTCF



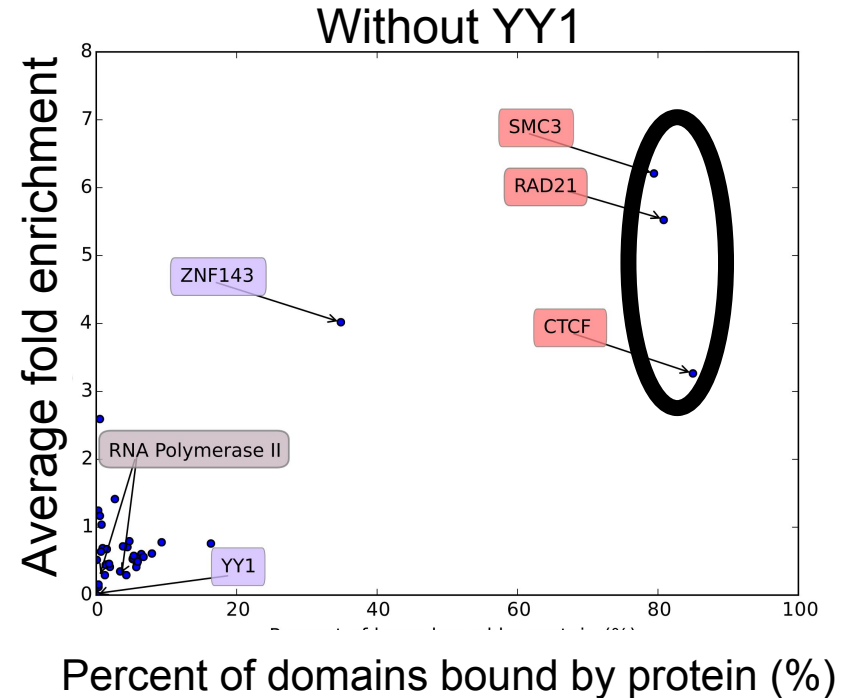
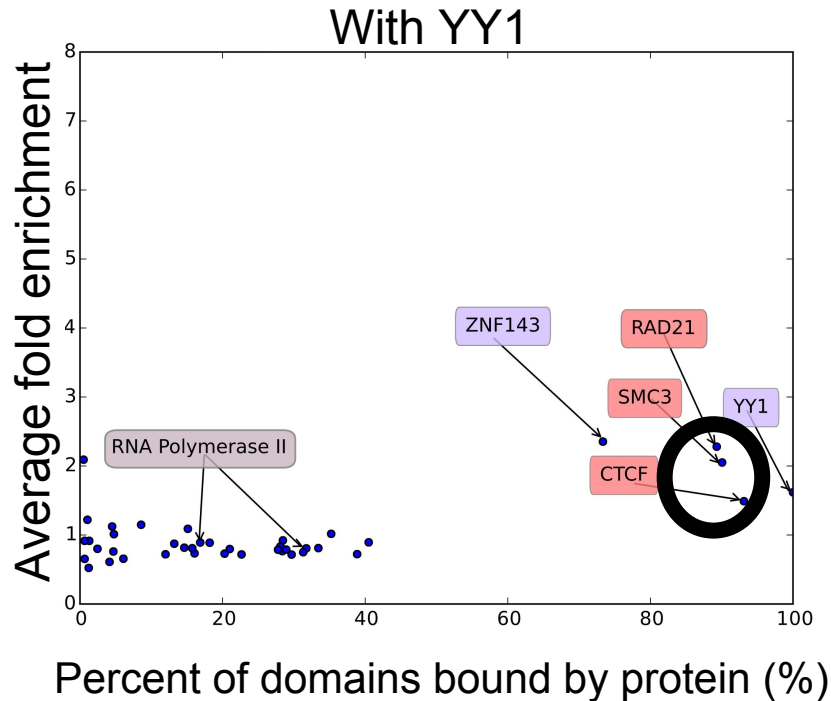
ZNF143 is more co-enriched with CTCF than YY1



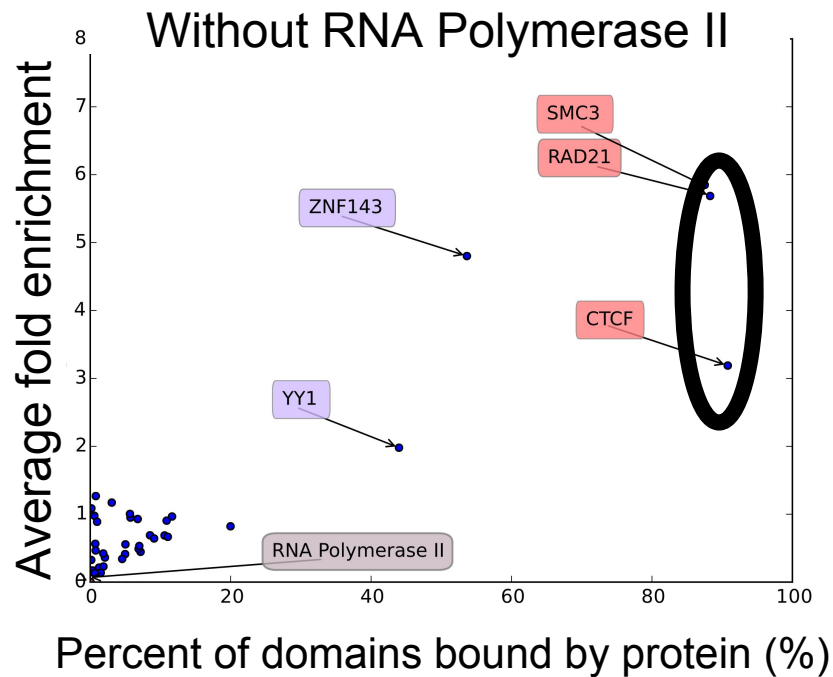
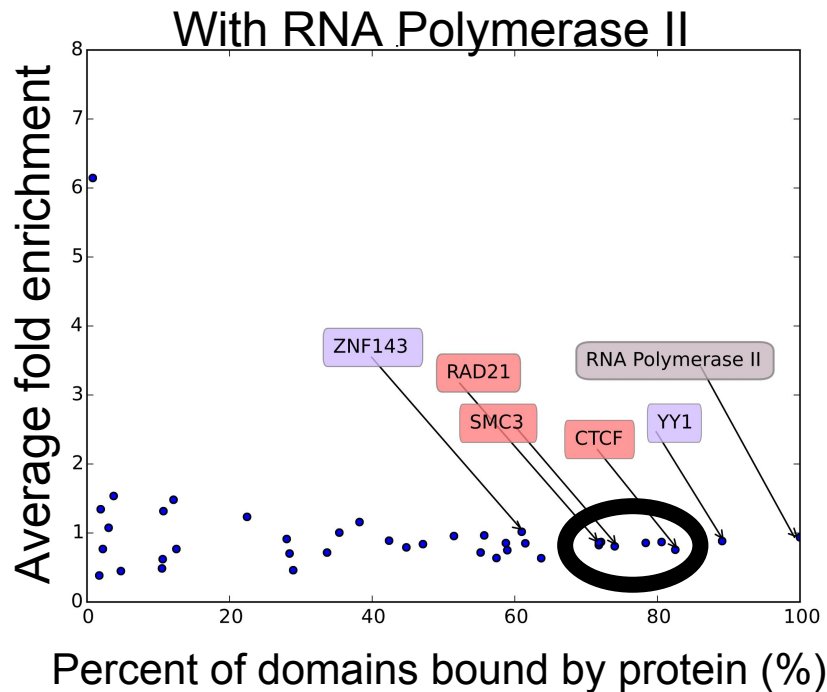
YY1 and RNA Polymerase II are correlated



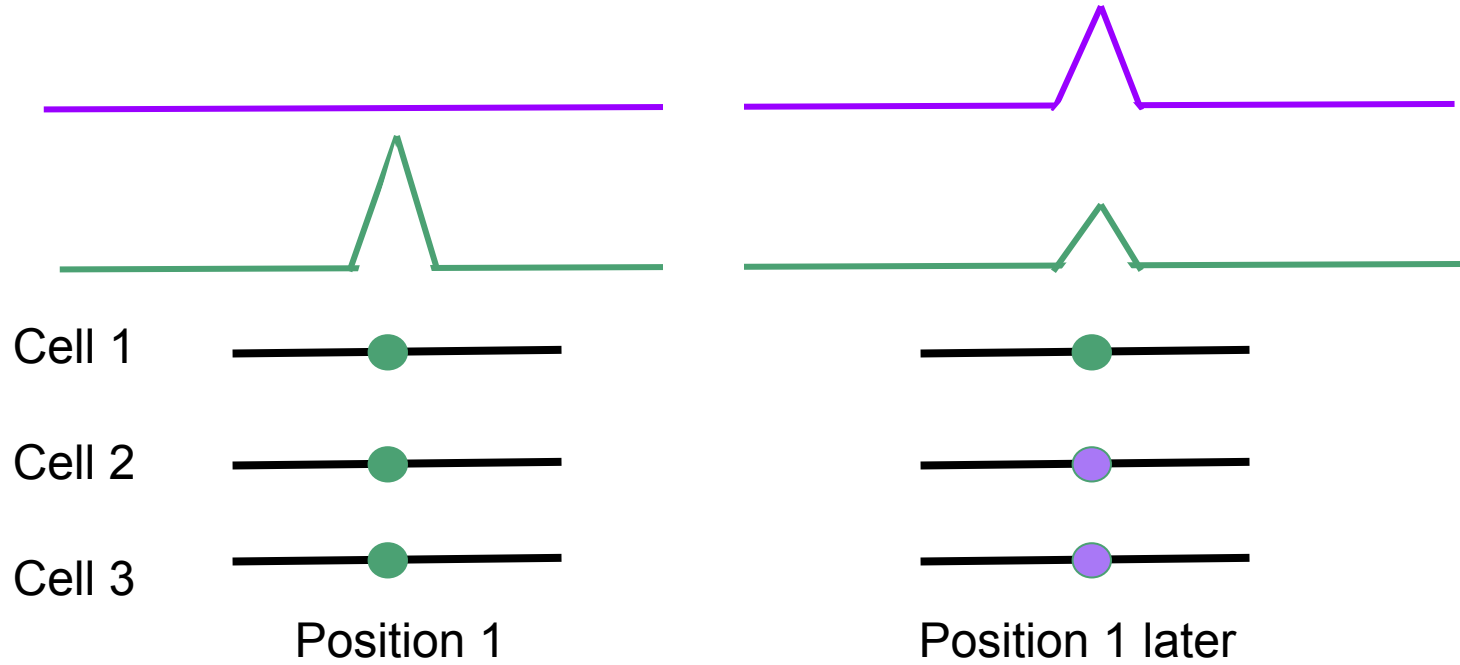
YY1 bound loci are bound by CTCF with a similar frequency but less enrichment



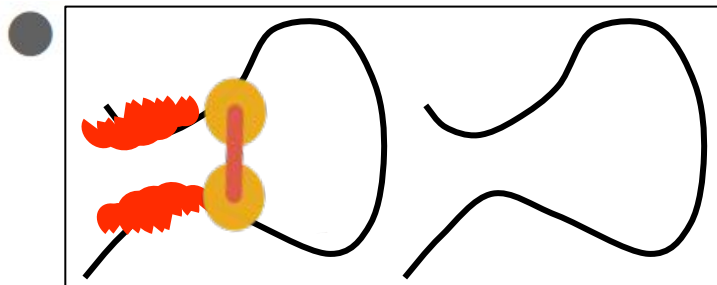
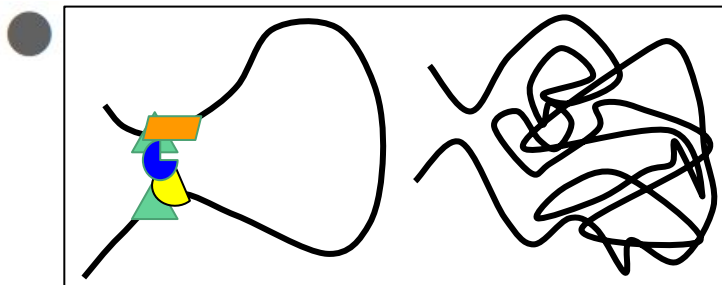
RNA Polymerase II bound loci are bound by CTCF with a similar frequency but less enrichment



Testable hypotheses: CTCF could be replaced with RNA Polymerase II after loops are created



Conclusion



- Hypothesized classifications:
 - ZNF143 = Architectural protein
 - YY1 = Transcription / RNA Polymerase II associated boundary factor
- Enrichment of RNA Polymerase II is anticorrelated with CTCF
- Testable hypothesis: RNA Polymerase II replaces CTCF at boundaries?

Acknowledgements

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adherence to deadlines

And my parents for

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