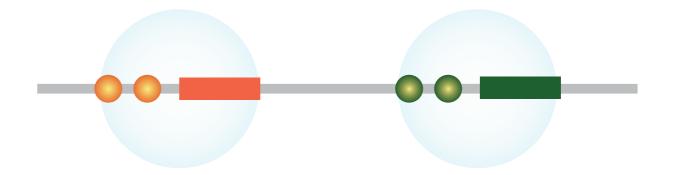
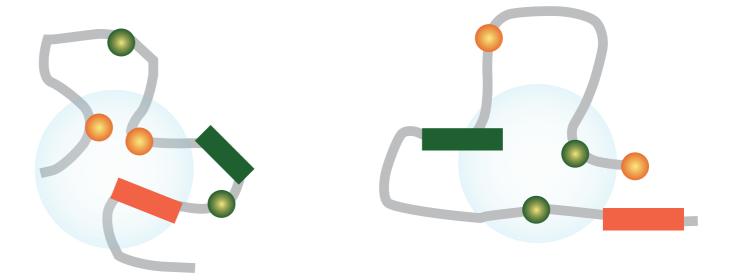


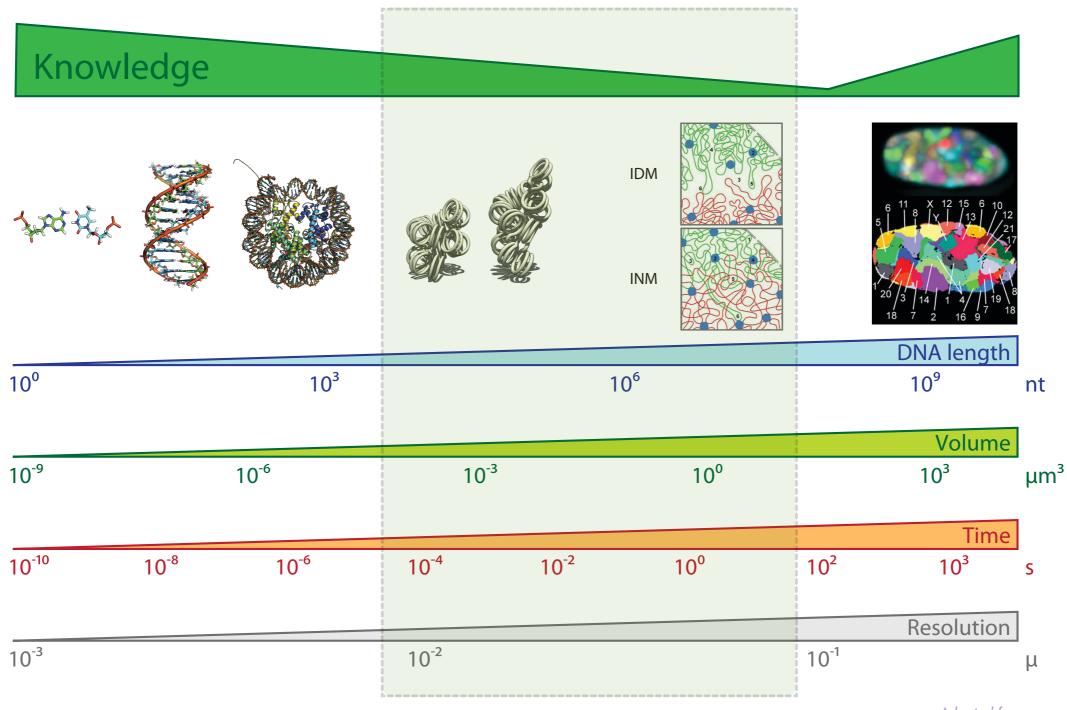
Simple genomes





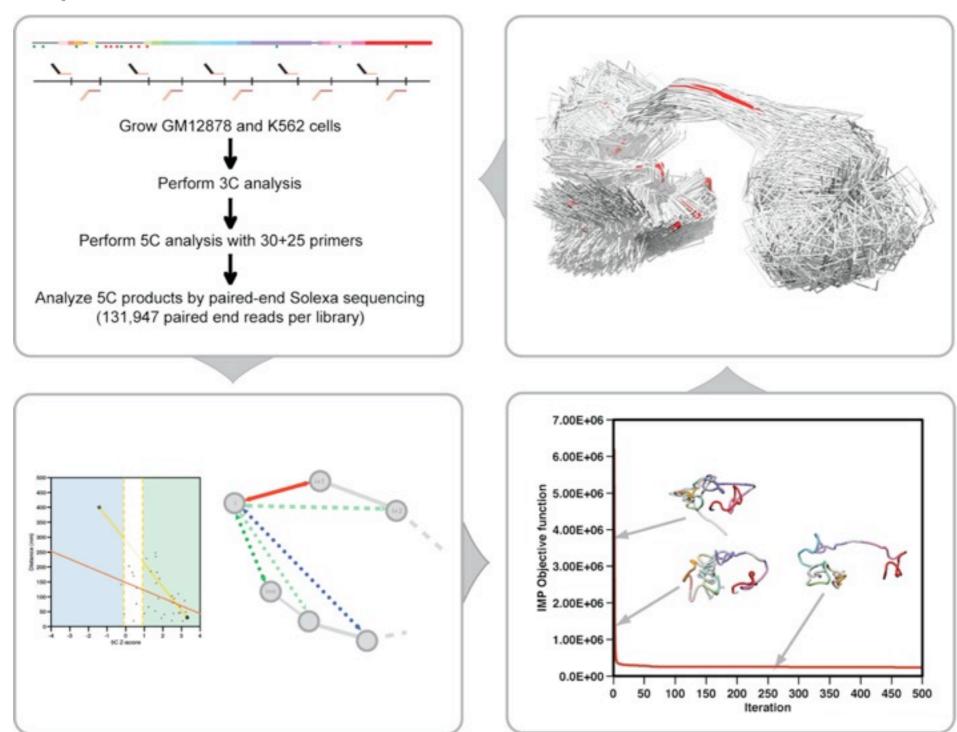
Complex genomes



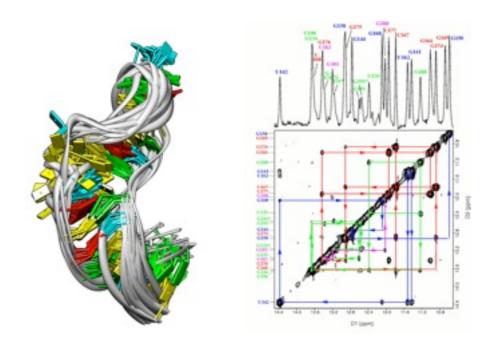


Adapted from: Langowski and Heermann. Semin Cell Dev Biol (2007) vol. 18 (5) pp. 659-67

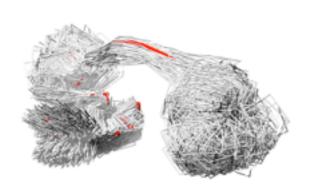
Experiments

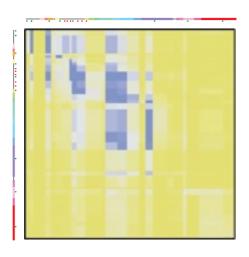


Computation



Biomolecular structure determination 2D-NOESY data



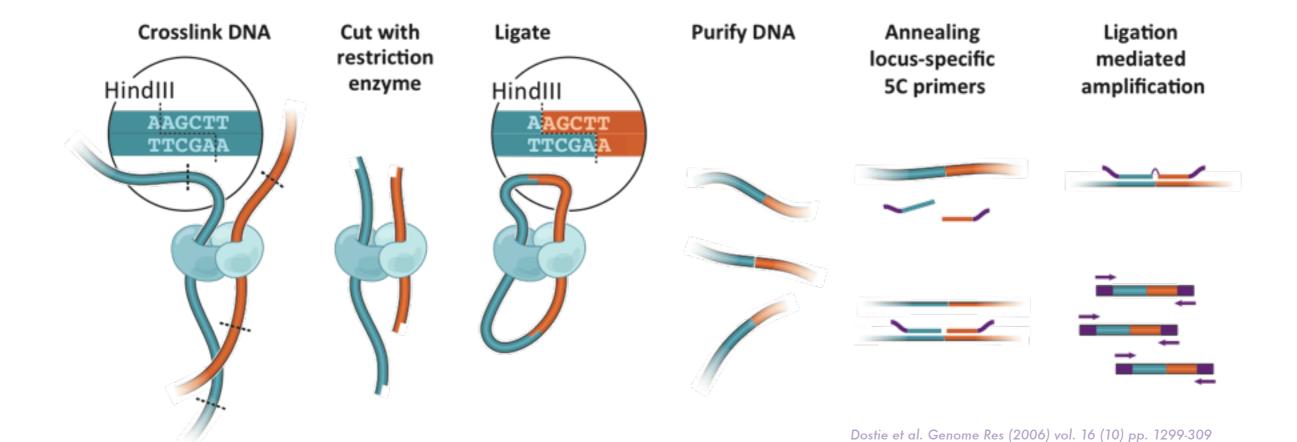


Chromosome structure determination 5C data



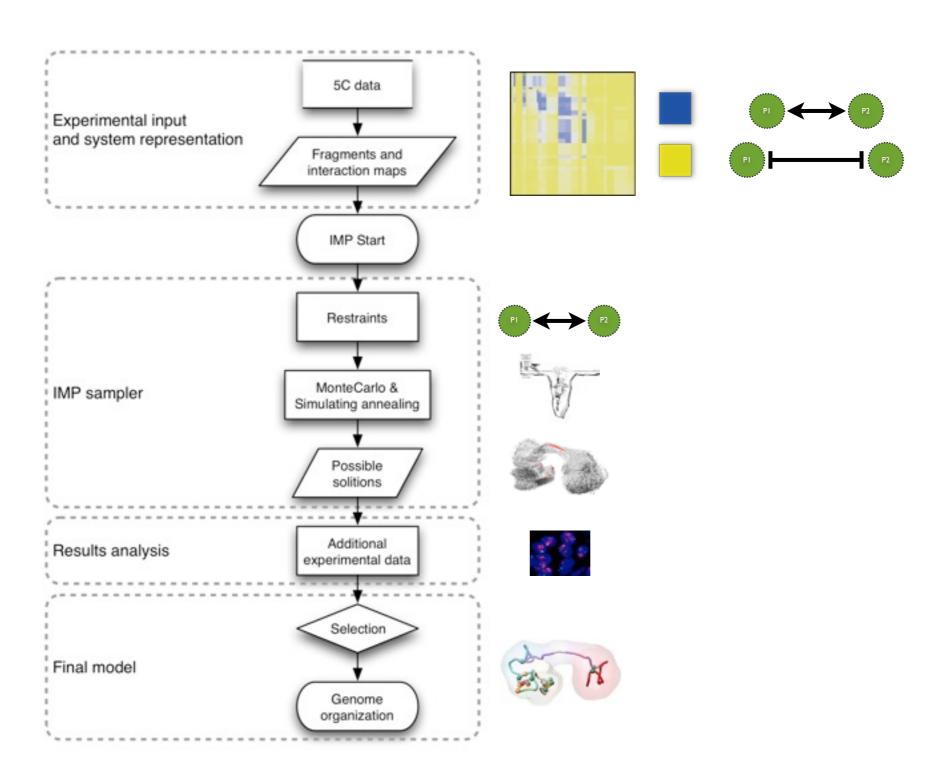
5C technology

http://my5C.umassmed.edu

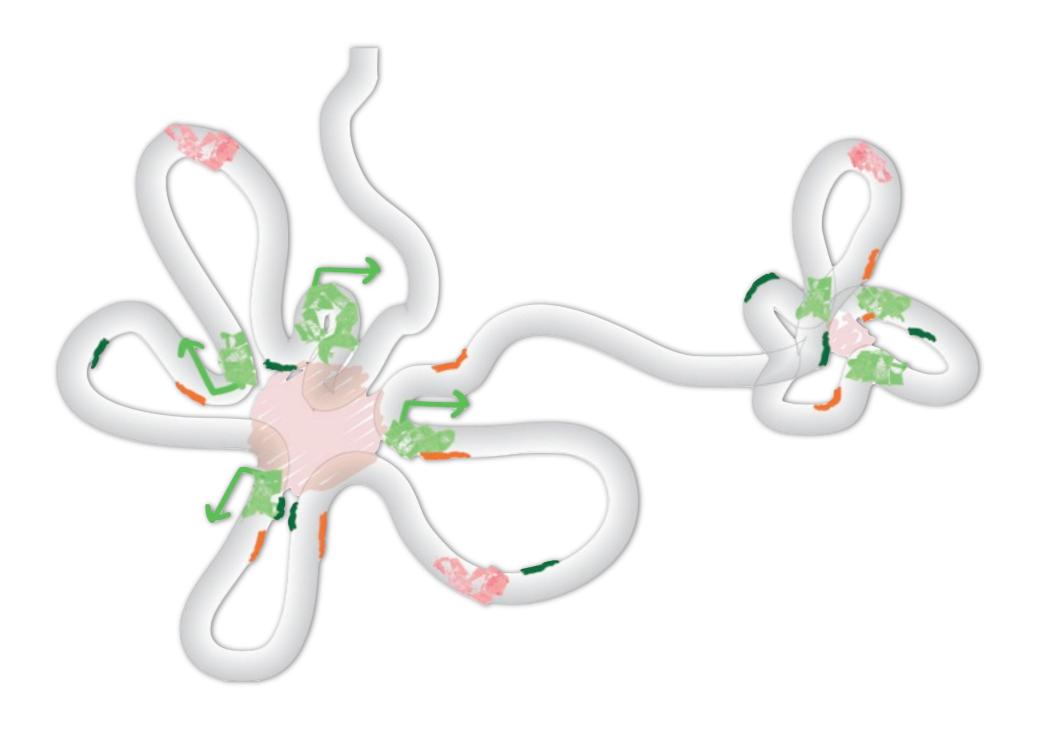


Integrative Modeling

http://www.integrativemodeling.org

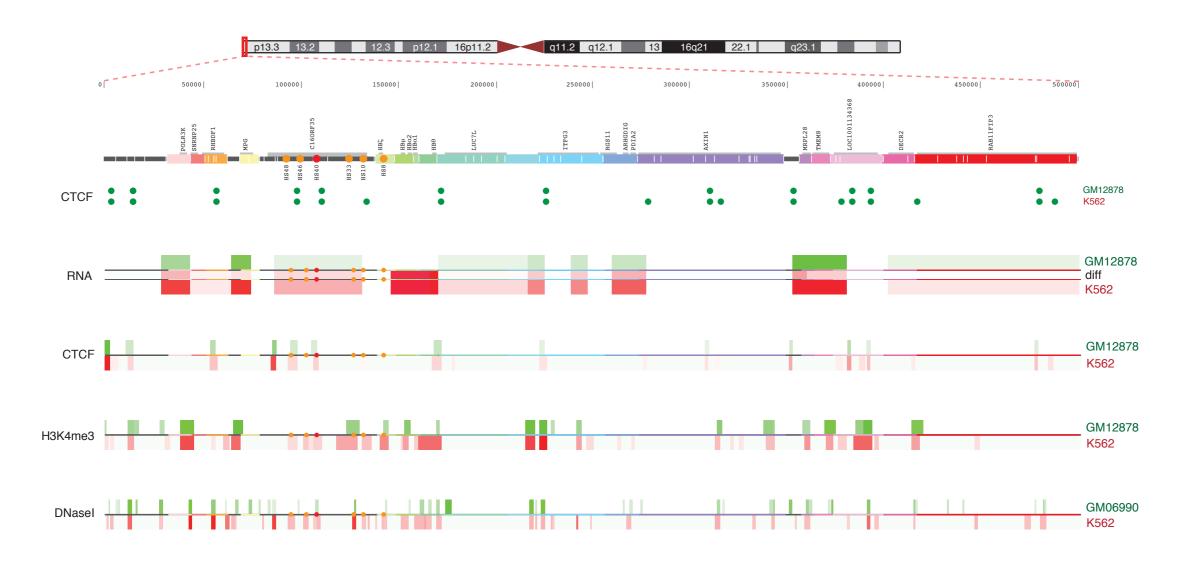


Human α -globin domain



Human α -globin domain

ENm008 genomic structure and environment



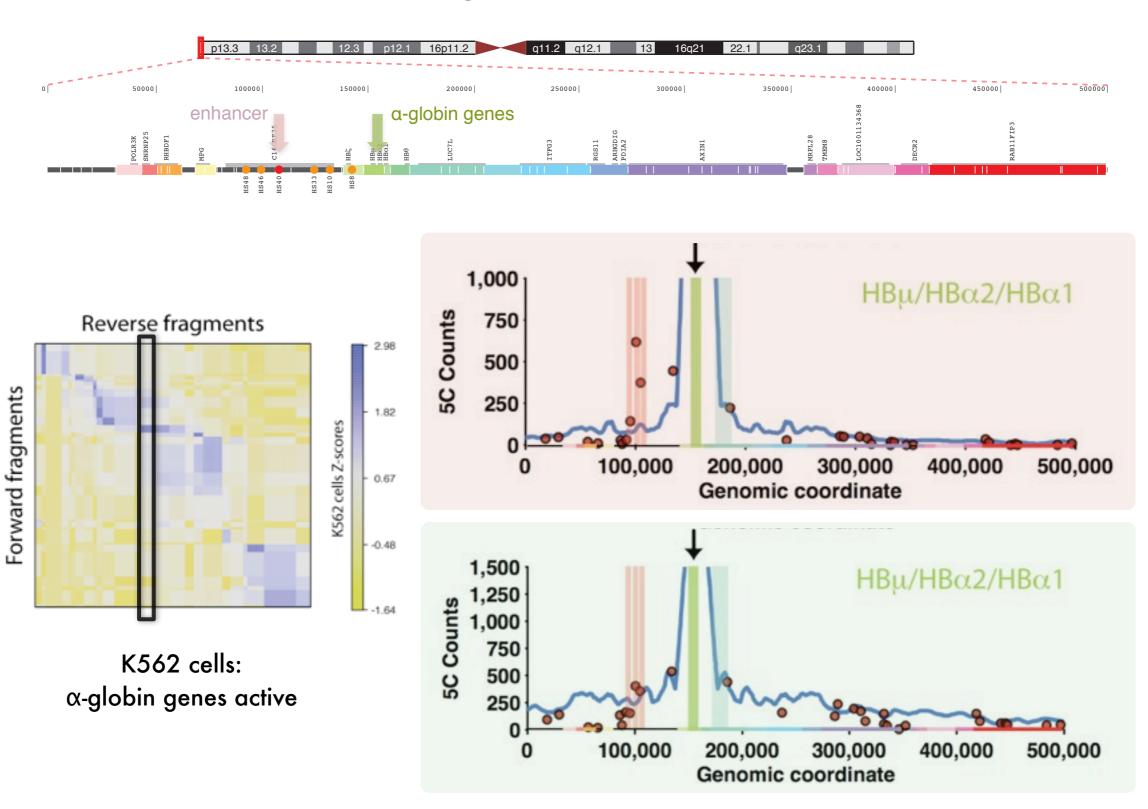
The ENCODE data for ENm008 region was obtained from the UCSC Genome Browser tracks for: RefSeq annotated genes, Affymetrix/CSHL expression data (Gingeras Group at Cold Spring Harbor), Duke/NHGRI DNasel Hypersensitivity data (Crawford Group at Duke University), and Histone Modifications by Broad Institute ChIP-seq (Bernstein Group at Broad Institute of Harvard and MIT).

ENCODE Consortium. Nature (2007) vol. 447 (7146) pp. 799-816



Human α -globin domain

ENm008 genomic structure and environment

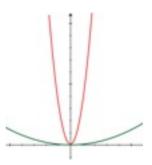


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Representation

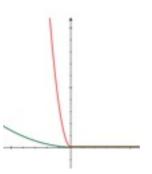
Harmonic

$$H_{i,j} = k \left(d_{i,j} - d_{i,j}^0 \right)^2$$



Harmonic Lower Bound

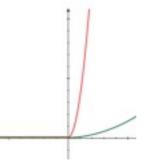
$$\begin{cases} if \ d_{i,j} \le d_{i,j}^0; & lbH_{i,j} = k(d_{i,j} - d_{i,j}^0)^2 \\ if \ d_{i,j} > d_{i,j}^0; & lbH_{i,j} = 0 \end{cases}$$



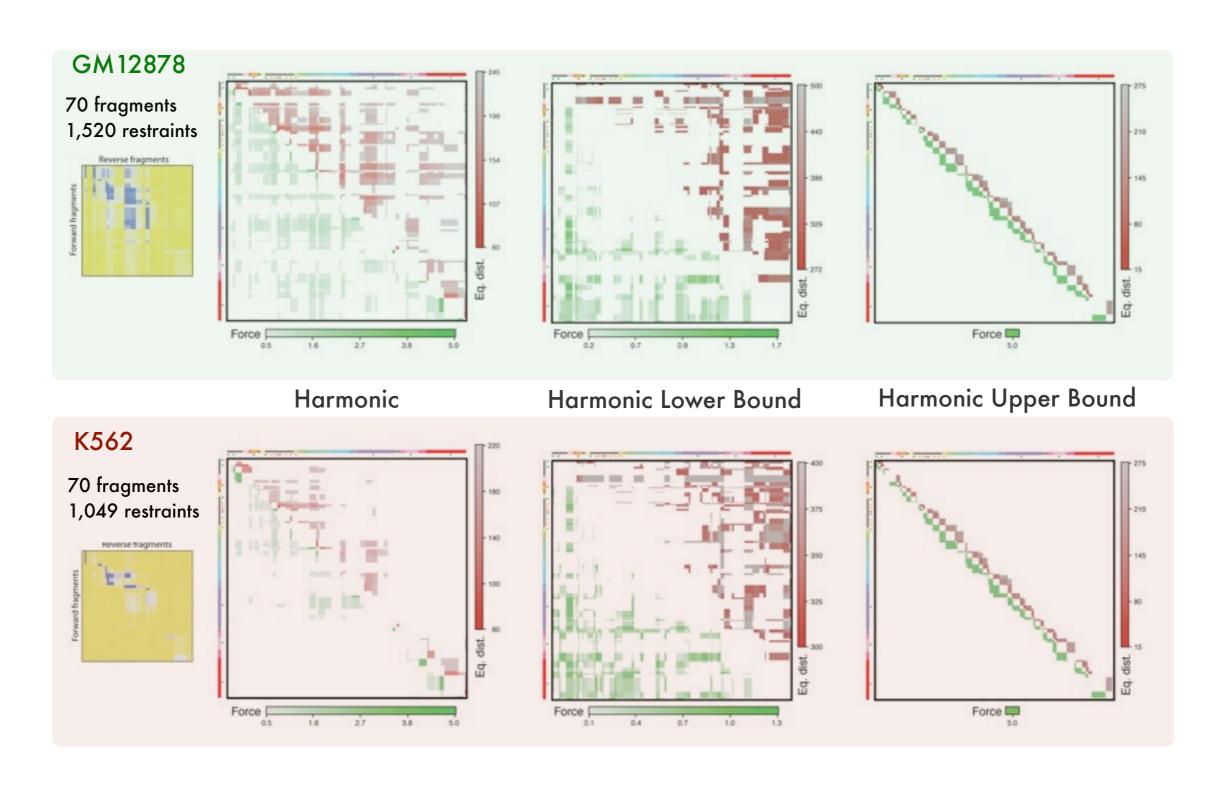
i i+2

Harmonic Upper Bound

$$\begin{cases} if \ d_{i,j} \ge d_{i,j}^0; & ubH_{i,j} = k \left(d_{i,j} - d_{i,j}^0 \right)^2 \\ if \ d_{i,j} < d_{i,j}^0; & ubH_{i,j} = 0 \end{cases}$$

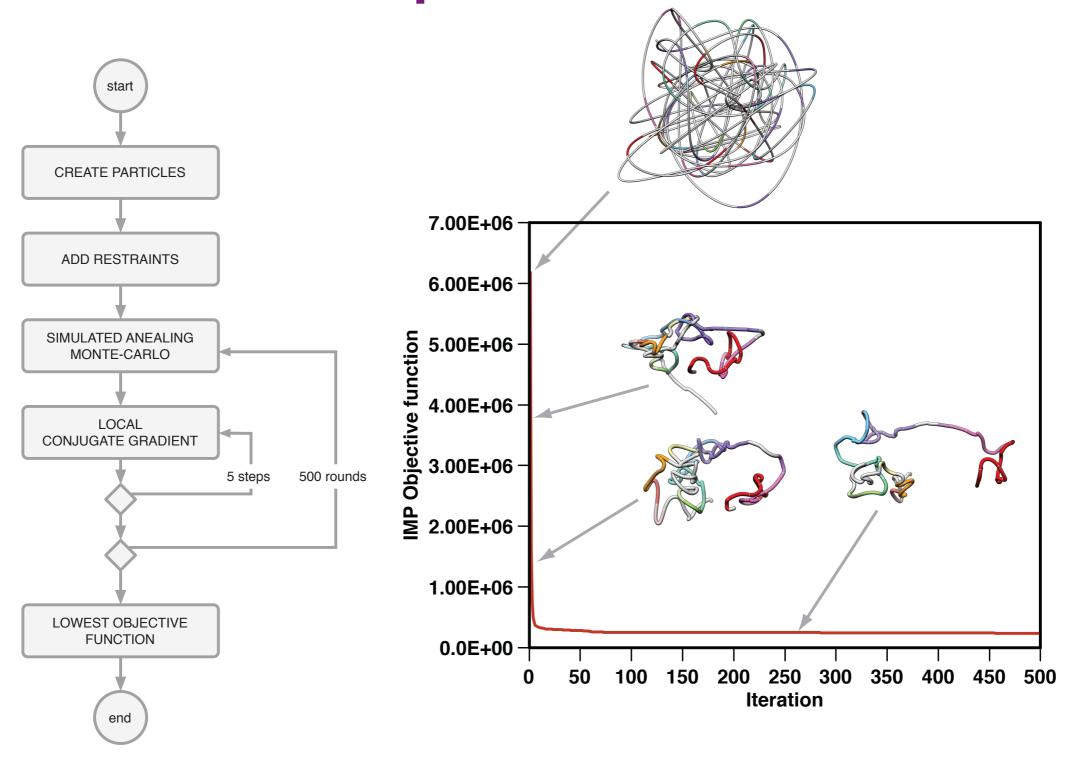


Scoring

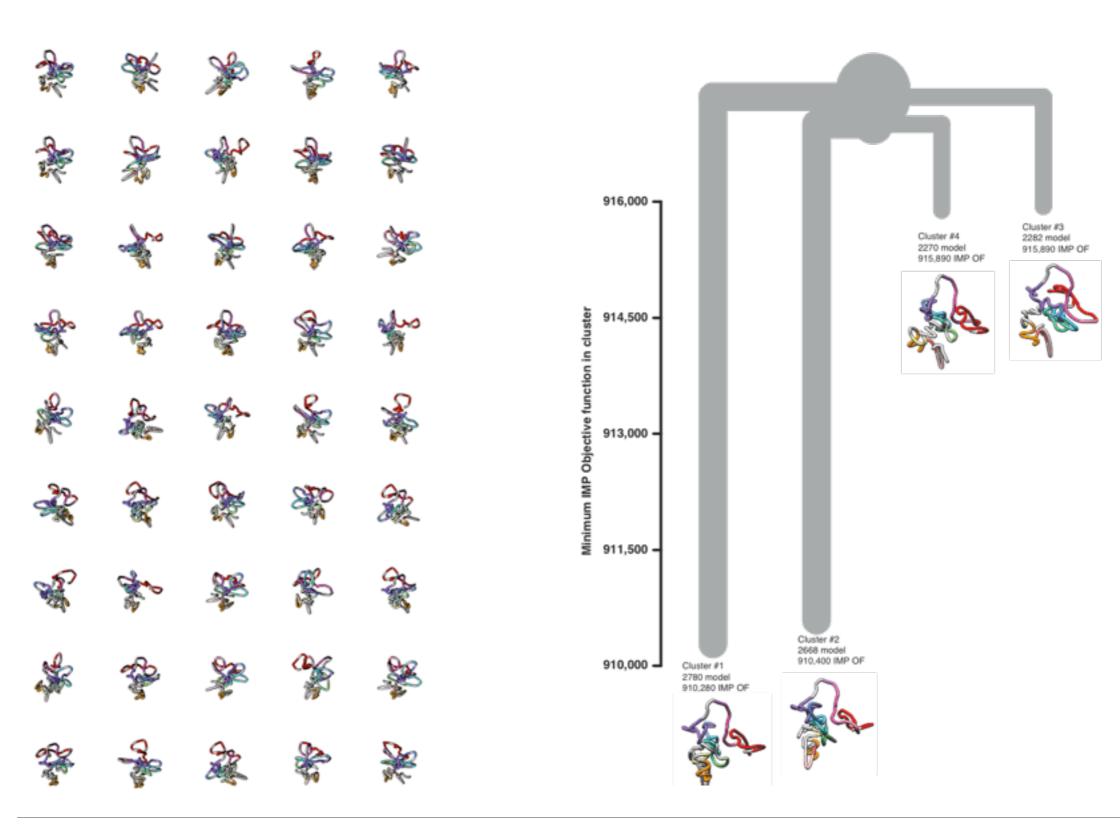




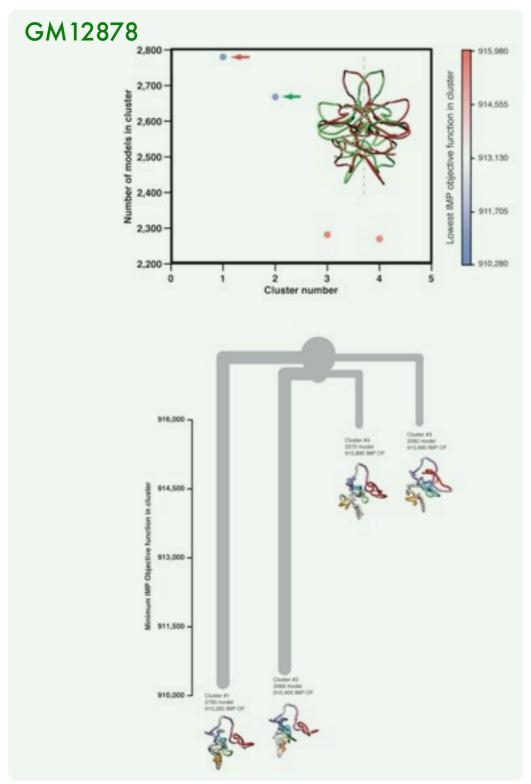
Optimization

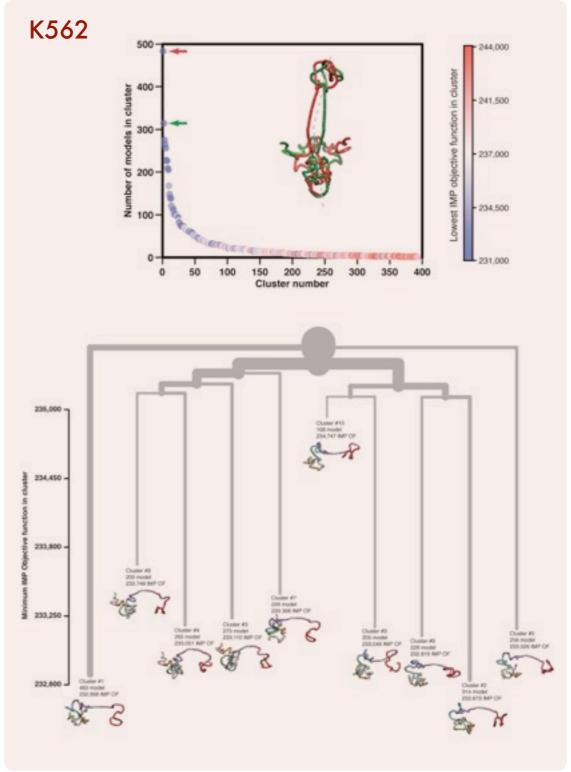


Clustering



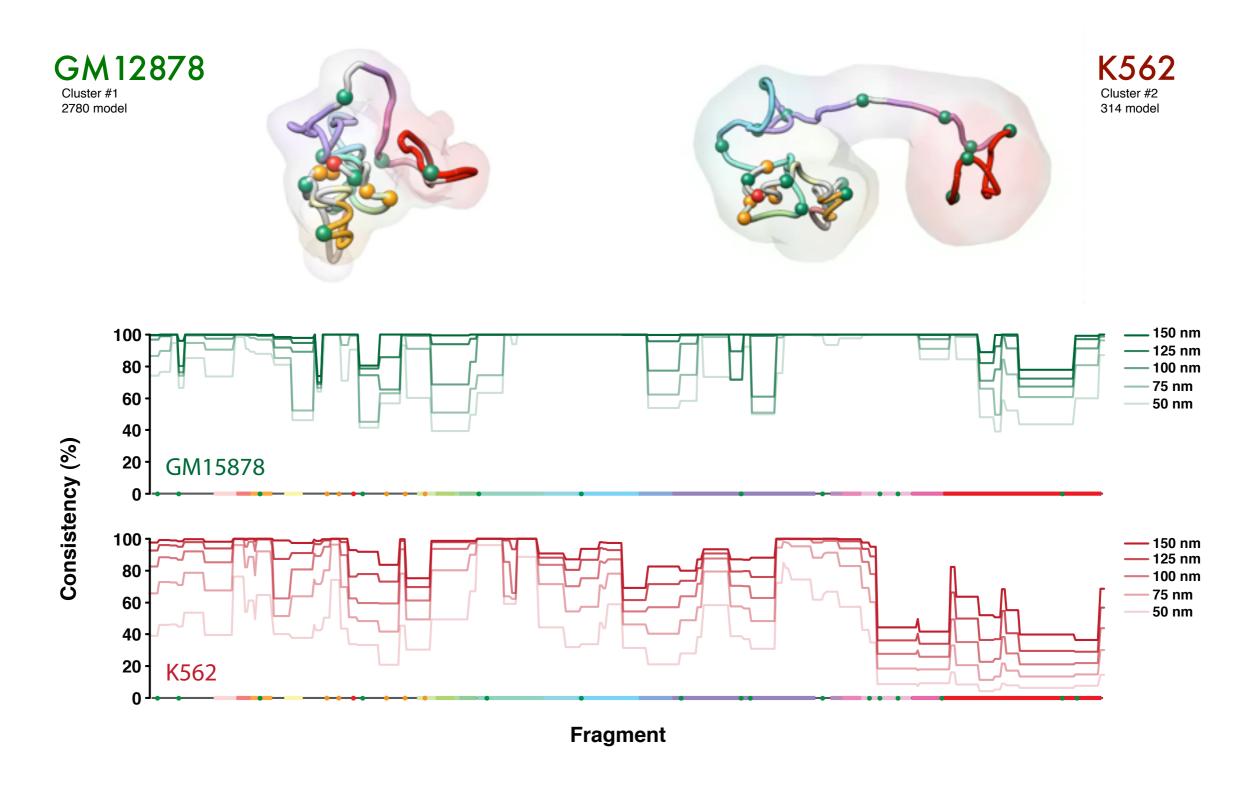
Not just one solution



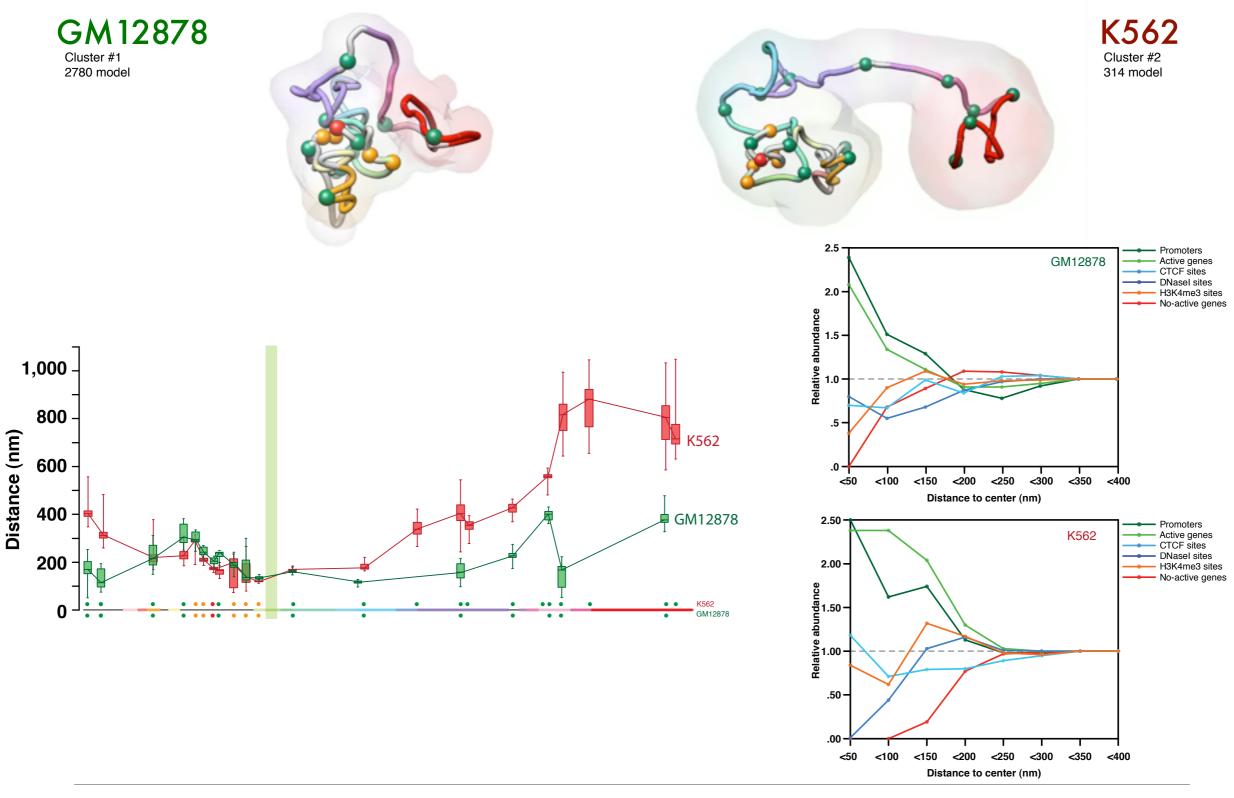




Consistency

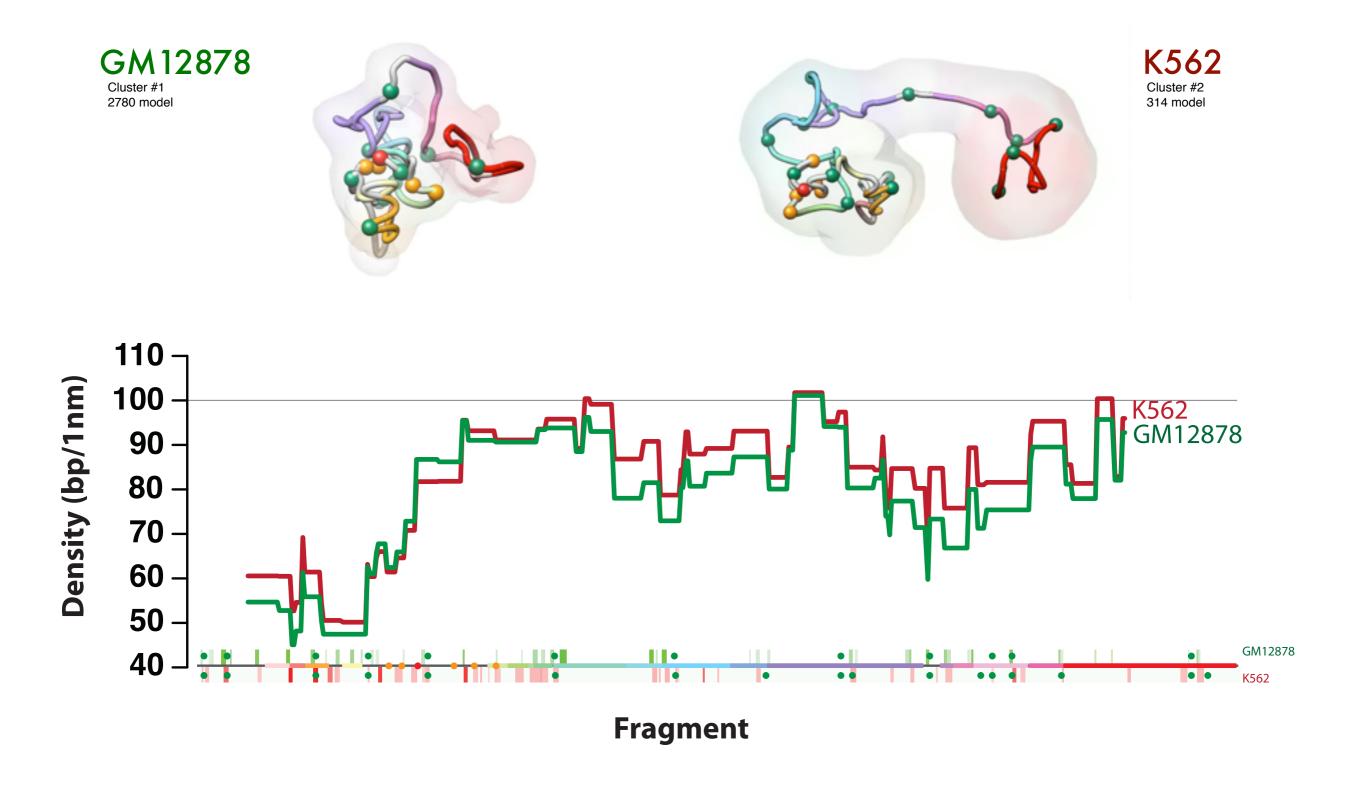


Regulatory elements



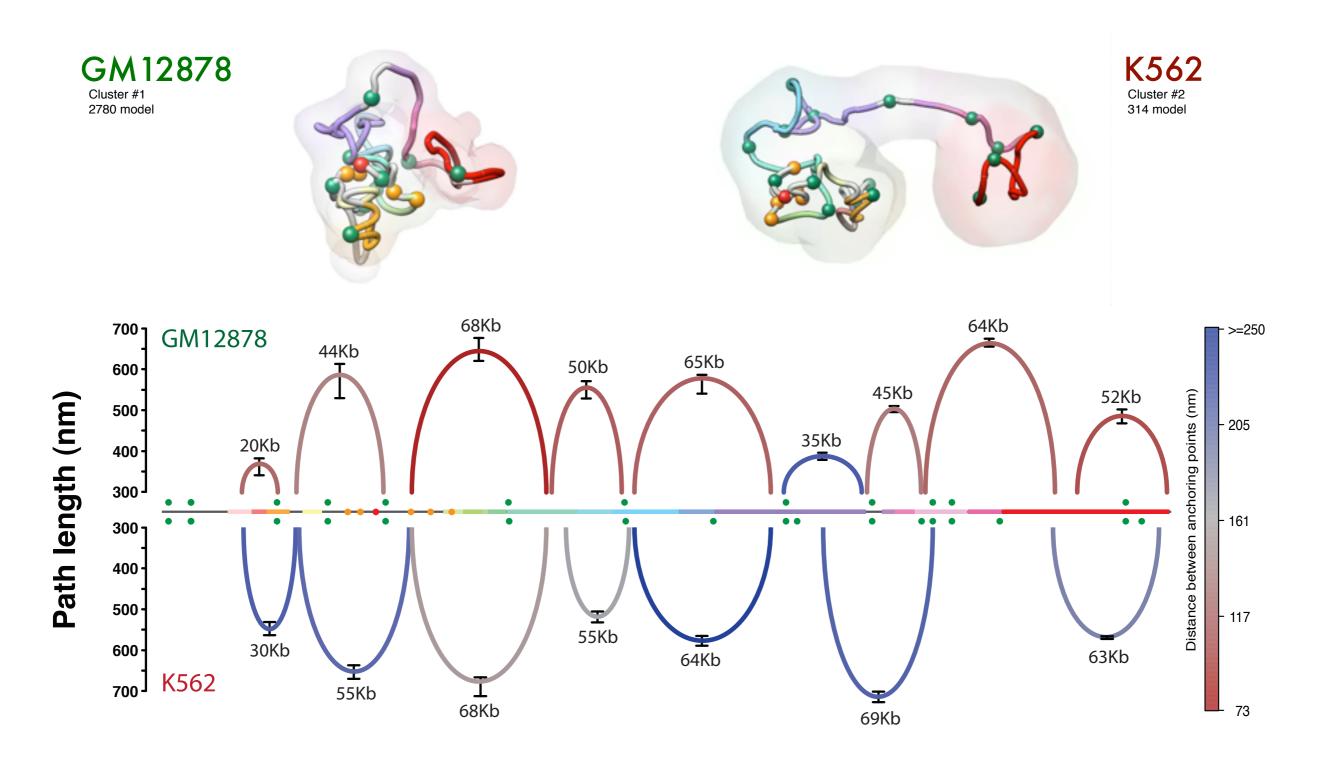
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Compactness



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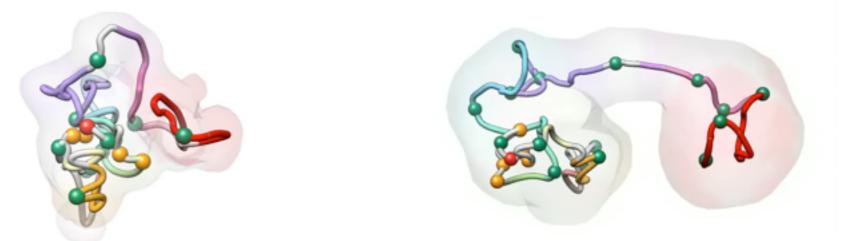
Multi-loops



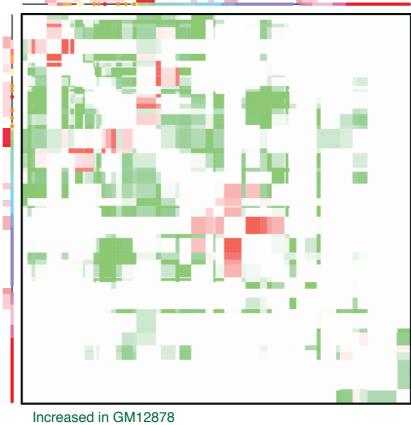
Expression

GM12878

Cluster #1 2780 model



K562 Cluster #2 314 model

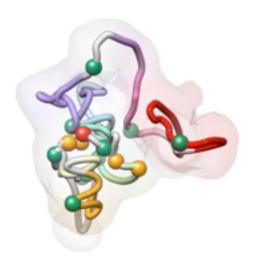


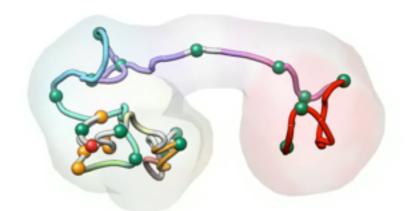
Increased in K562



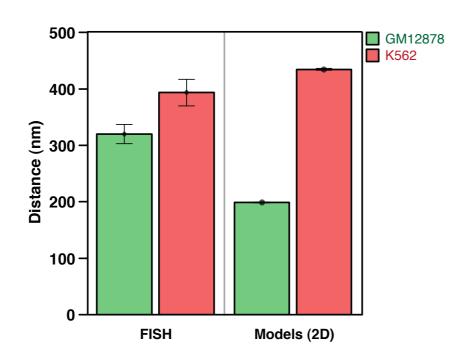
FISH validation

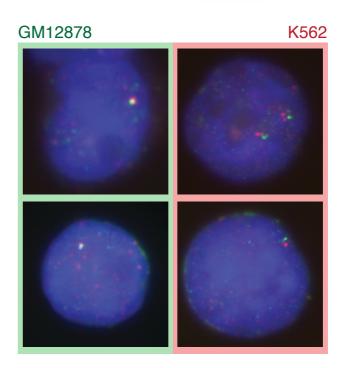






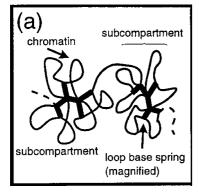
K562 Cluster #2 314 model



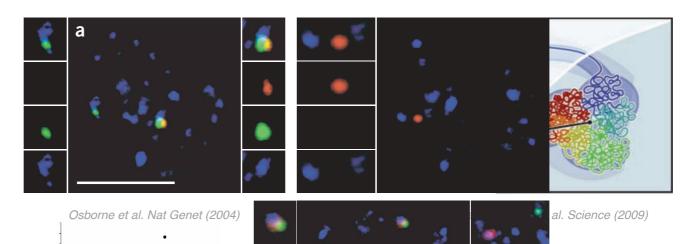


The "Chromatin Globule" model





Münkel et al. JMB (1999)

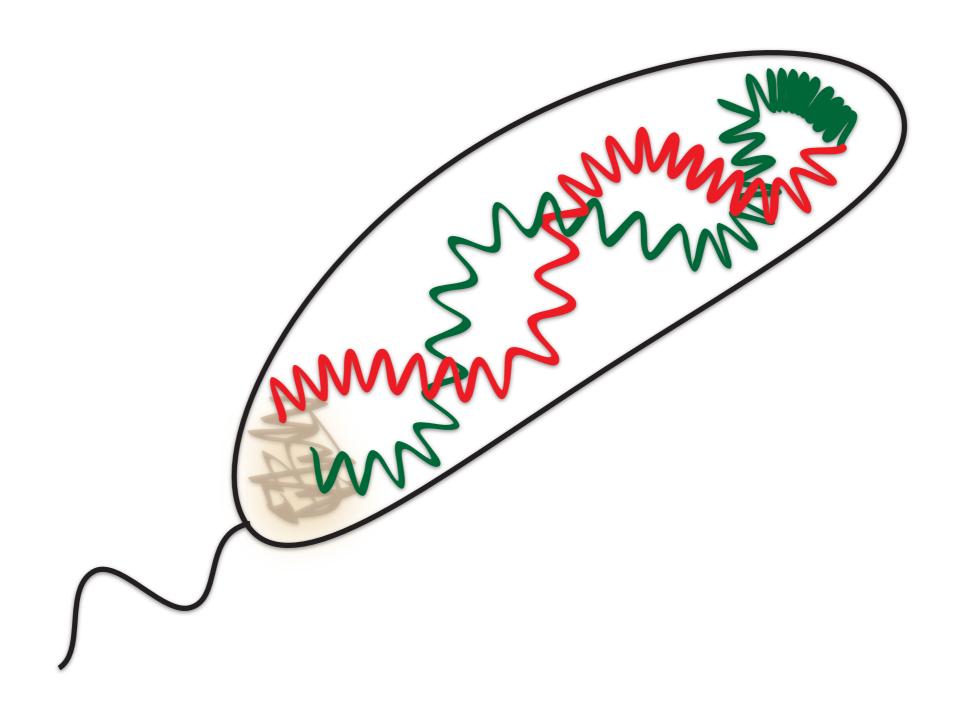


D. Baù et al. Nat Struct Mol Biol (2011) 18:107-14

A. Sanyal et al. Current Opinion in Cell Biology (2011) 23:325-33.

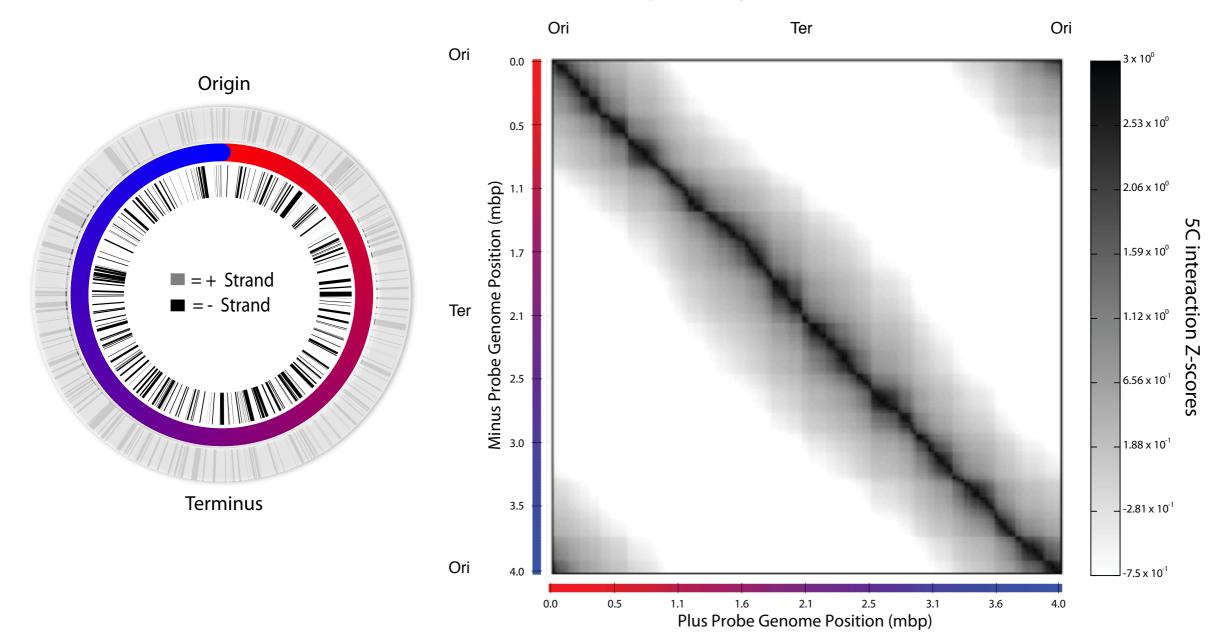


Caulobacter crescentus genome



The 3D architecture of Caulobacter Crescentus

4,016,942 bp & 3,767 genes

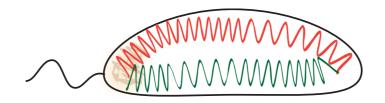


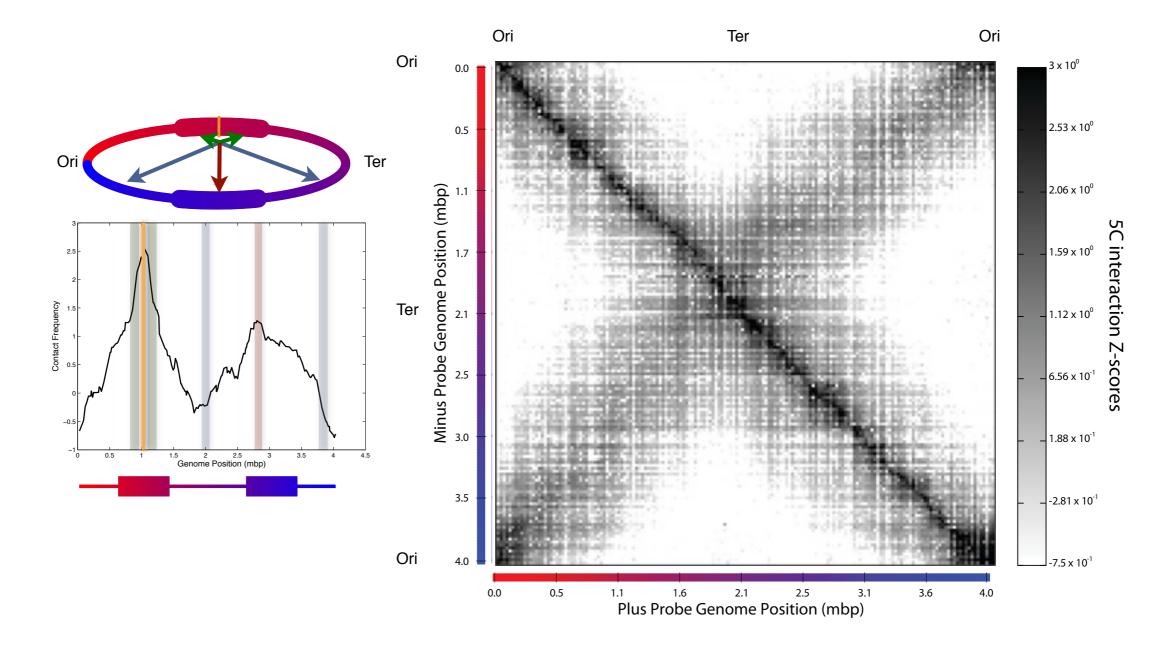
169 5C primers on + strand 170 5C primers on - strand 28,730 chromatin interactions



5C interaction matrix

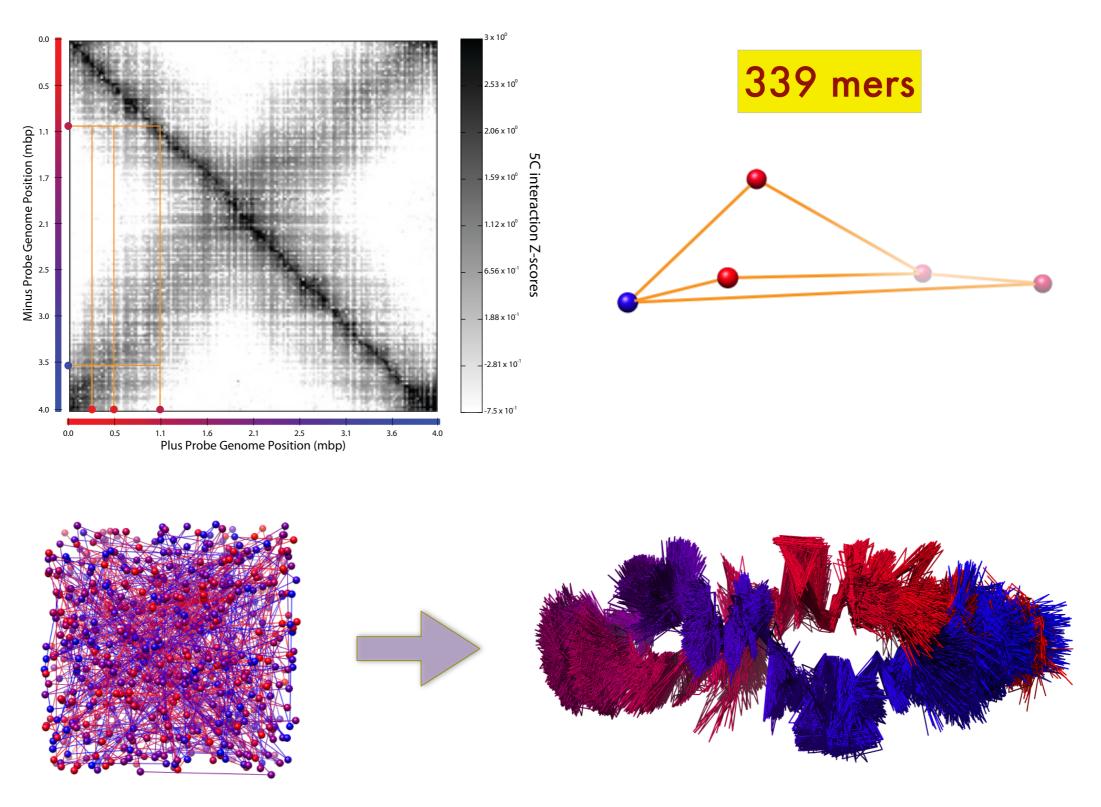
ELLIPSOID for Caulobacter cresentus



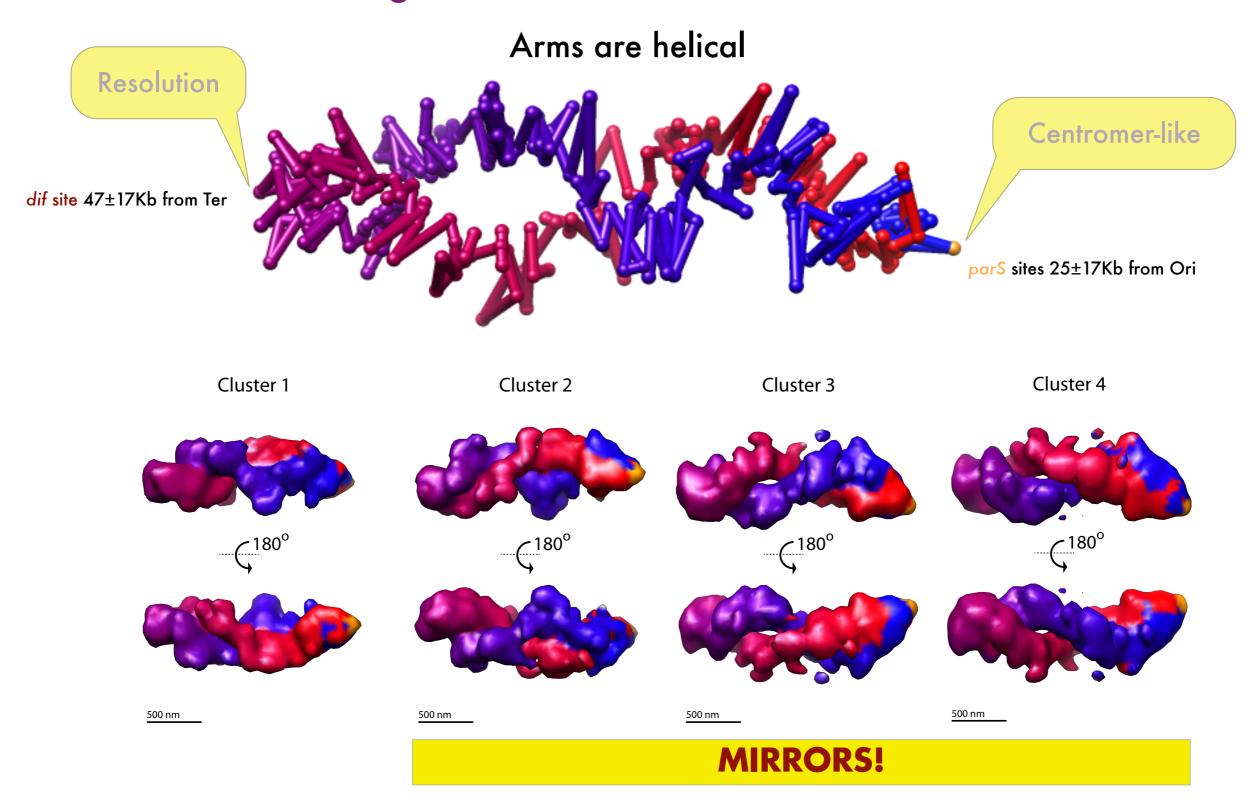




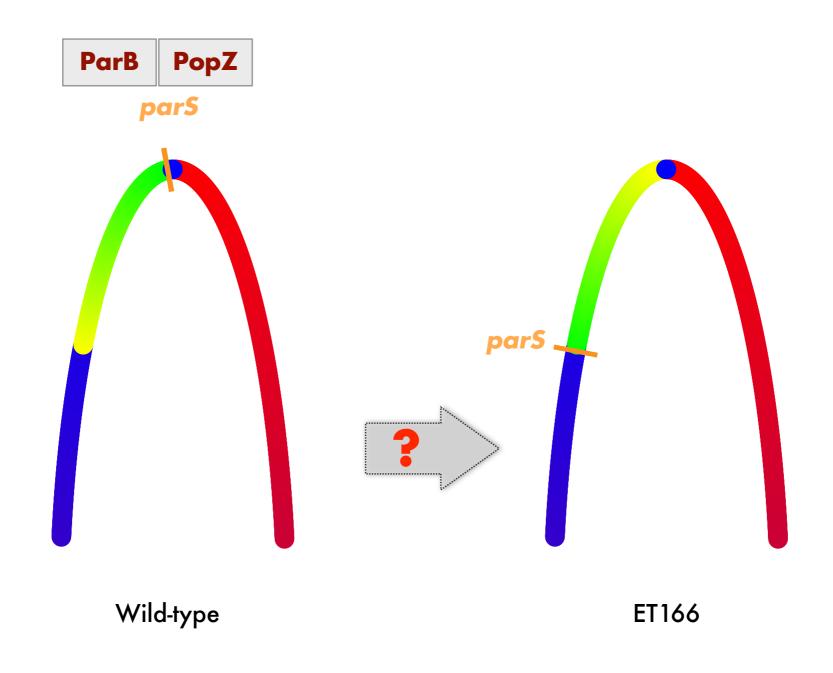
3D model building with the 5C + IMP approach



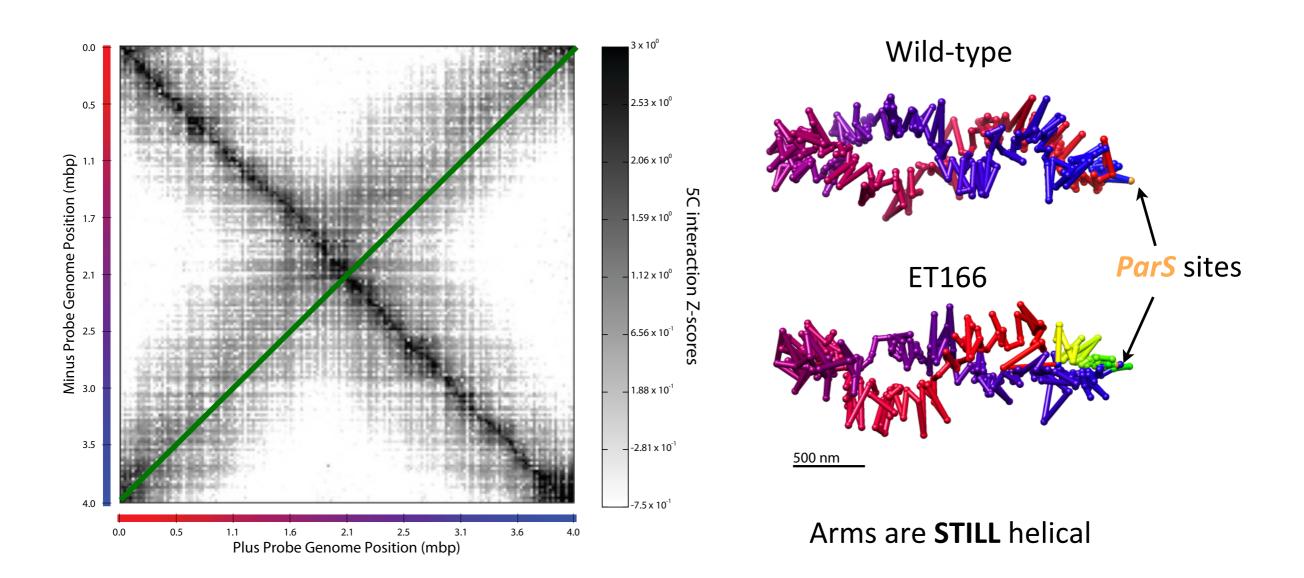
Genome organization in Caulobacter crescentus



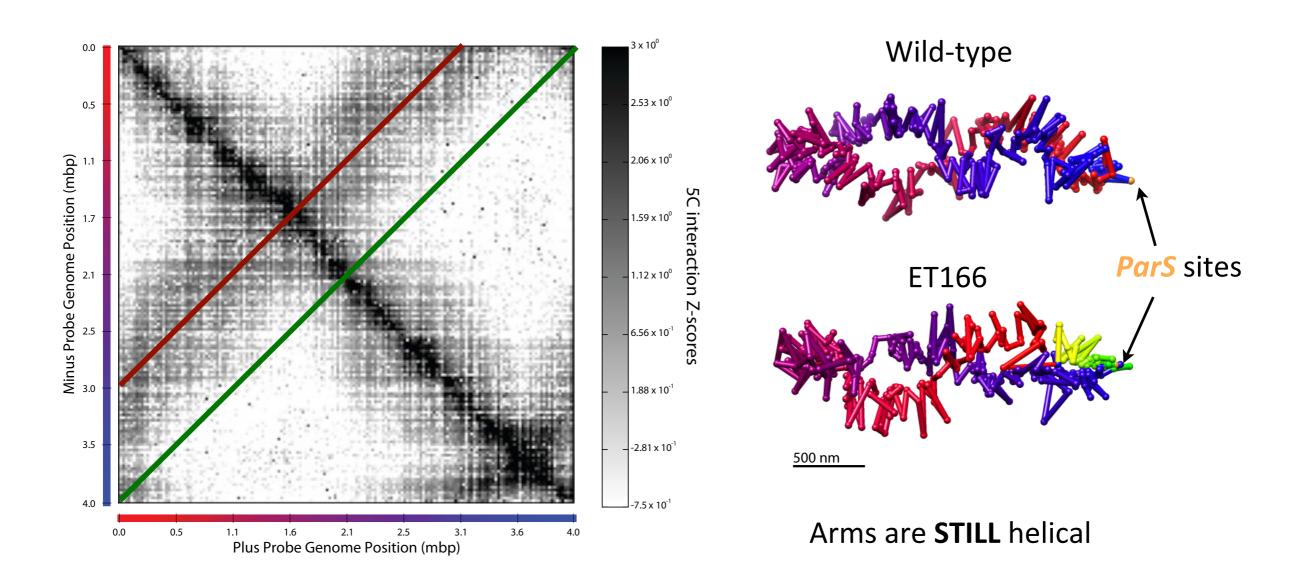
Moving the parS sites 400 Kb away from Ori



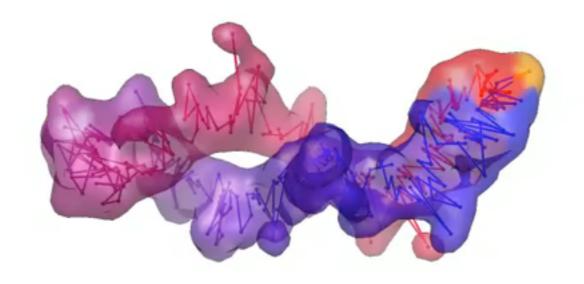
Moving the parS sites results in whole genome rotation!

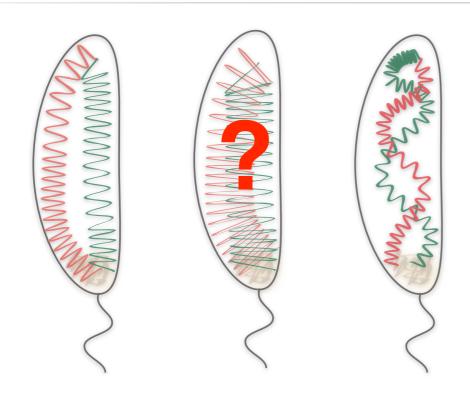


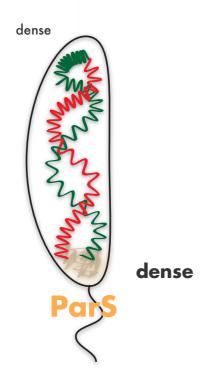
Moving the parS sites results in whole genome rotation!



Genome architecture in Caulobacter







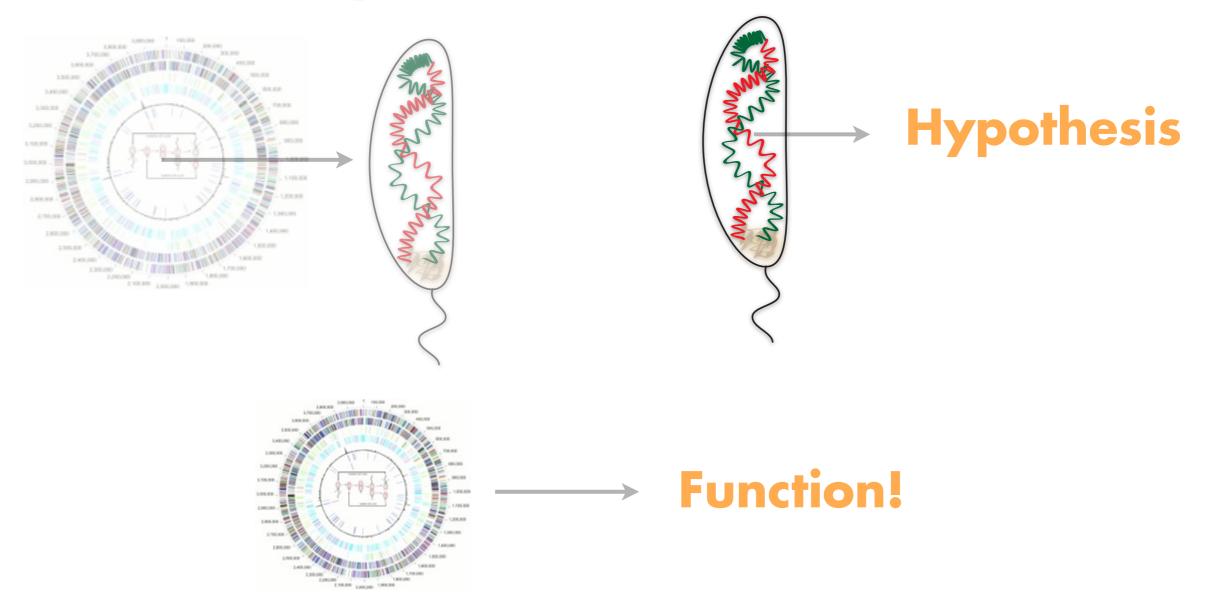
M.A. Umbarger, et al. Molecular Cell (2011) 44:252-264

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From Sequence to Function

5C + IMP

Technology



D. Baù and M.A. Marti-Renom Chromosome Res (2011) 19:25-35.

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PLoS CB Outlook

Marti-Renom MA, Mirny LA (2011) PLoS Comput Biol 7(7): e1002125.

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PLOS COMPUTATIONAL BIOLOGY

Review

Bridging the Resolution Gap in Structural Modeling of 3D Genome Organization

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1 Structural Genomics Laboratory, Bioinformatics and Genomics Department, Centro de Investigación Príncipe Felipe, Valencia, Spain, 2 Harvard-MIT Division of Health Sciences and Technology, and Department of Physics, Massachusetts Institute of Technology, Cambridge, Massachusetts, United States of America

Abstract: Over the last decade, and especially after the advent of fluorescent in situ hybridization imaging and chromosome conformation capture methods, the availability of experimental data on genome three-dimensional organization has dramatically increased. We now have access to unprecedented details of how genomes organize within the interphase nucleus. Development of new computational approaches to leverage this data has already resulted in the first three-dimensional structures of genomic domains and genomes. Such approaches expand our knowledge of the chromatin folding principles, which has been classically studied using polymer physics and molecular simulations. Our outlook describes computational approaches for integrating experimental data with polymer physics, thereby bridging the resolution gap for structural determination of genomes and qenomic domains.

This is an "Editors' Outlook" article for PLoS Computational Biology

Recent experimental and computational advances are resulting in an increasingly accurate and detailed characterization of how genomes are organized in the three-dimensional (3D) space of the nucleus (Figure 1) [1]. At the lowest level of chromatin organization, naked DNA is packed into nucleosomes, which forms the so-called chromatin fiber composed of DNA and proteins. However, this initial packing, which reduces the length of the DNA by about seven times, is not sufficient to explain the higher-order folding of chromosomes during interphase and metaphase. It is now accepted that chromosomes and genes are non-randomly and dynamically positioned in the cell nucleus during the interphase, which challenges the classical representation of genomes as linear static sequences. Moreover, compartmentalization, chromatin organization, and spatial location of genes are associated with gene expression and the functional status of the cell. Despite the importance of 3D genomic architecture, we have a limited understanding of the molecular mechanisms that determine the higher-order organization of genomes and its relation to function. Computational biology plays an important role in the plethora of new technologies aimed at addressing this knowledge gap [2]. Indeed, Thomas Cremer, a pioneer in studying nuclear organization using light microscopy, recently highlighted the importance of computational science in complementing and leveraging experimental observations of genome organization [2]. Therefore, computational approaches to integrate experimental observations with chromatin physics are needed to determine the architecture (3D) and dynamics (4D) of genomes.

We present two complementary approaches to address this challenge: (i) the first approach aims at developing simple polymer models of chromatin and determining relevant interactions (both

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the second approach aims at integrating diverse experimental observations into a system of spatial restraints to be satisfied, thereby constraining possible structural models of the chromatin. The goal of both approaches is dual: to obtain most accurate 3D and 4D representation of chromatin architecture and to understand physical constraints and biological phenomena that determine is organization. These approaches are reminiscent of the protein-folding field where the first strategy was used for characterizing protein "foldability" and the second was implemented for modeling the structure of proteins using nuclear magnetic resonance and other experimental constraints. In fact, our outlook consistently returns to the many connections between the two fields.

hysical and biological) that explain experimental observations; (ii)

What Does Technology Show Us?

Today, it is possible to quantitatively study structural features of genomes at diverse scales that range from a few specific loci, through chromosomes, to entire genomes (Table 1) [3]. Broadly, there are two main approaches for studying genomic organization: light microscopy and cell/molecular biology (Figure 2). Light microcopy [4], both with fixed and living cells, can provide images of a few loci within individual cells [5,6], as well as their dynamics as a function of time [7] and cell state [8]. On a larger scale, light microscopy combined with whole-chromosome staining reveals chromosomal territories during interphase and their reorganization upon cell division. Immunofluorescence with fluorescent antibodies in combination with RNA, and DNA fluorescence in situ hybridization (FISH) has been used to determine the colocalization of loci and nuclear substructures.

Using cellular and molecular biology, novel chromosome conformation capture (3C)-based methods such 3C [9], 3C-onchip or circular 3C (the so-called 4C) [10,11], 3C carbon copy (5C) [12], and Hi-C [13] quantitatively measure frequencies of spatial contacts between genomic loci averaged over a large

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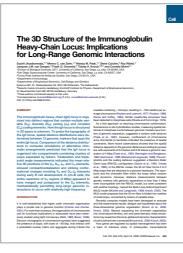
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MURRE Cell (2008) **133**:265-79



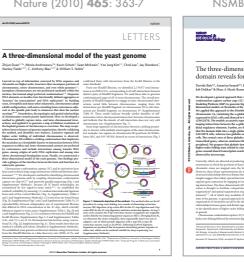
DOSTIE/BLANCHETTE Genome Biol (2009) 10: R37



DEKKER/LANDER/MIRNY Science (2009) **326**:289-93



NOBLE Nature (2010) **465**: 363-7



DEKKER/MARTI-RENOM NSMB (2011) 18:107-14



OPEN POSITIONS! Starting spring 2012

Acknowledgments



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