

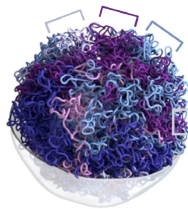
Hi-C and the 3D genome

What is the 3D genome?

Eukaryotic DNA doesn't float freely – it's folded into a dynamic 3D architecture that dictates which genes are active, how enhancers find promoters, and how the cell interprets its sequence. Understanding this spatial organization is critical for understanding gene regulation.

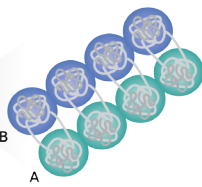
3D genome architecture

Chromosome Territories



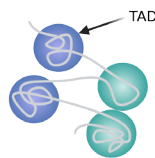
In the nucleus chromosomes are organized into chromosome territories

Compartments



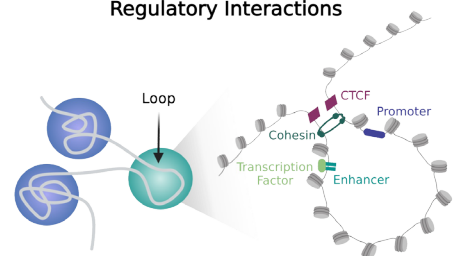
Chromosomes are divided into cell-specific A/B compartments

Domains



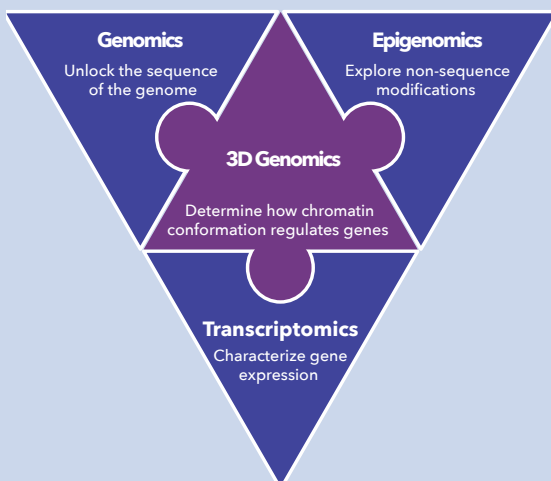
Compartments are organized into topologically associated domains (TADs)

Regulatory Interactions



Within TADs, DNA is looped together with the assistance of architectural proteins and histones

How does 3D genome fit into the multi-omics landscape?



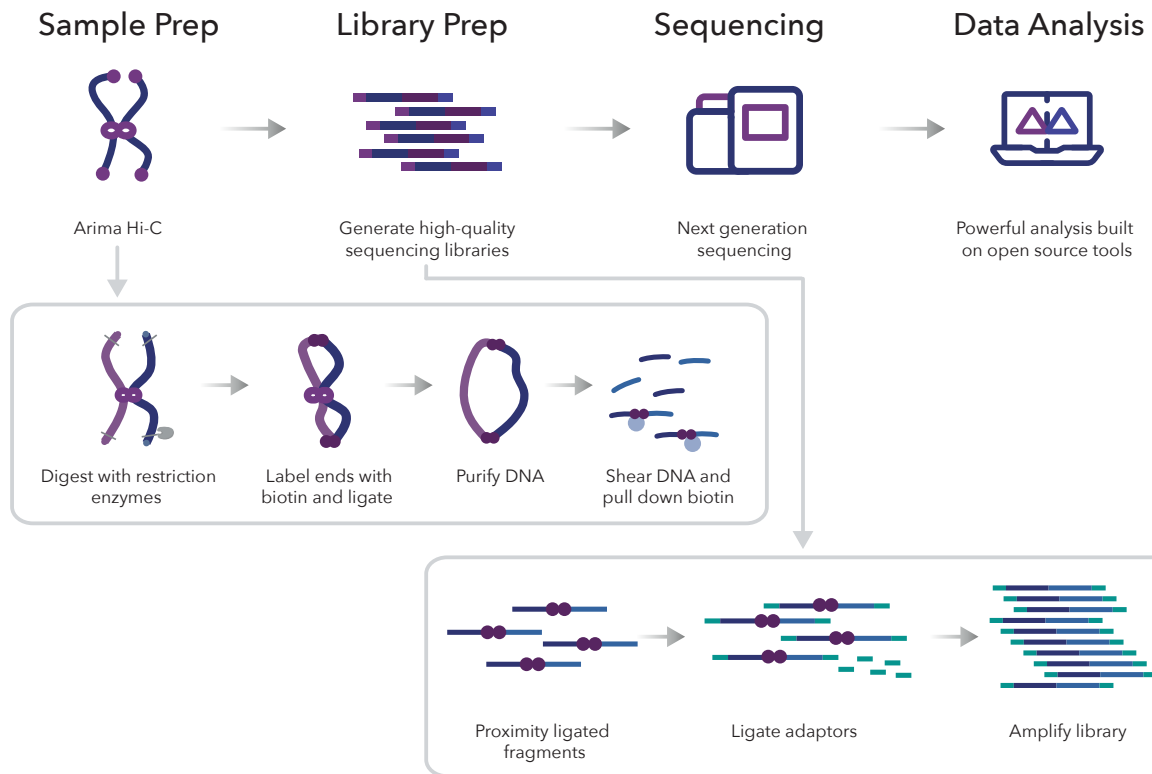
What is Hi-C?

Hi-C is a genome-wide chromatin conformation capture method that captures all pairwise foundation of 3D genomics: it connects sequence identity to 3D spatial proximity across the entire genome in a single assay.

What Hi-C enables

- Chromatin conformation and gene regulation
- Structural variant detection
- Chromosome-scale genome assembly
- Disease mechanism discovery
- Therapeutic target identification
- Conservation and agrigenomics

How does Hi-C work?



What does the data look like?

Hi-C contact matrix (example below) visualizes all pairwise chromatin interactions across the genome – brighter dots indicate higher contact frequency between two genomic loci. The off-diagonal dots highlight specific long-range loops, revealing how distant regions of the linear genome fold together in 3D space.

