

## Histones

5 primary types of histones in eukaryotes

- H1
- H2A
- H2B
- H3 (highly conserved)
- H4 (highly conserved)
- histone tails are targets for many modifications that alter histone structure

## Chromatin folding

1. string of nucleosomes (nucleosome filament)
2. filament is further folded into 30-nm fiber
3. fiber forms loops, centered to the central matrix of chromosomes

## Effects of histones on transcription

- core histones repress transcription
- H1 causes further repression
- repression counteracted by transcription factors
- TFs can recruit transferases to modify histones
- nucleosome positioning is important for gene expression

## Chromatin modification

We will focus on specific modifications to the tails of H3/H4 histones

- acK (lysine acetylation)
- meR (arginine methylation)
- meK (lysine methylation)
- PS (serine phosphorylation)
- UK (lysine ubiquitination)

## Histone code

- one histone modification can influence other
- histone code: a combination of histone modifications that determine gene activities by helping to form euchromatin (active) or heterochromatin (inactive) states
- can be translated by bromodomain
  - interacts with acetylated lysine
  - BRG1 (SWI/SNF):H4 K8
  - TAF250 (TFIID): H3 K9K14
  - bromo-HATs (GCN5, PCAF, TAF250)
- can be translated by chromodomain
  - targets methylation marks
  - HP1 (methylated K9), repression
  - SUV39 HMT (interacts with HP1)
  - chromo-HATs (ESA1), activation
- Other domain
  - PHD (TAF3 or TAF110),
  - Recognizes H3K4me3 activation

## Chromatin remodeling

- disrupt the core histones in nucleosomes (ATP-dependent)
- may also move nucleosomes
- create nucleosome-free enhancers with histone acetylases and other proteins

## Need to memorize

