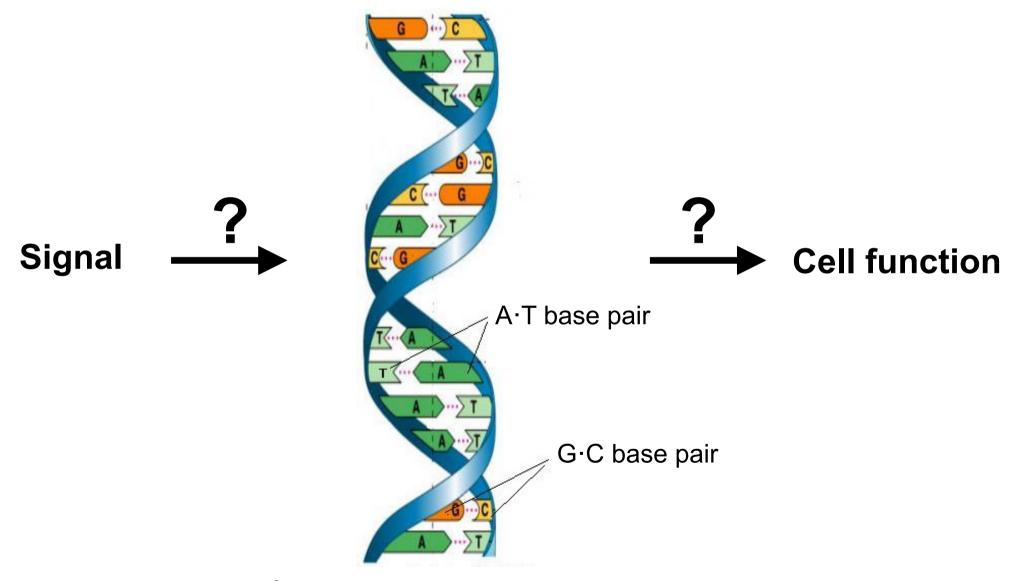
Translating genome information into cellular function

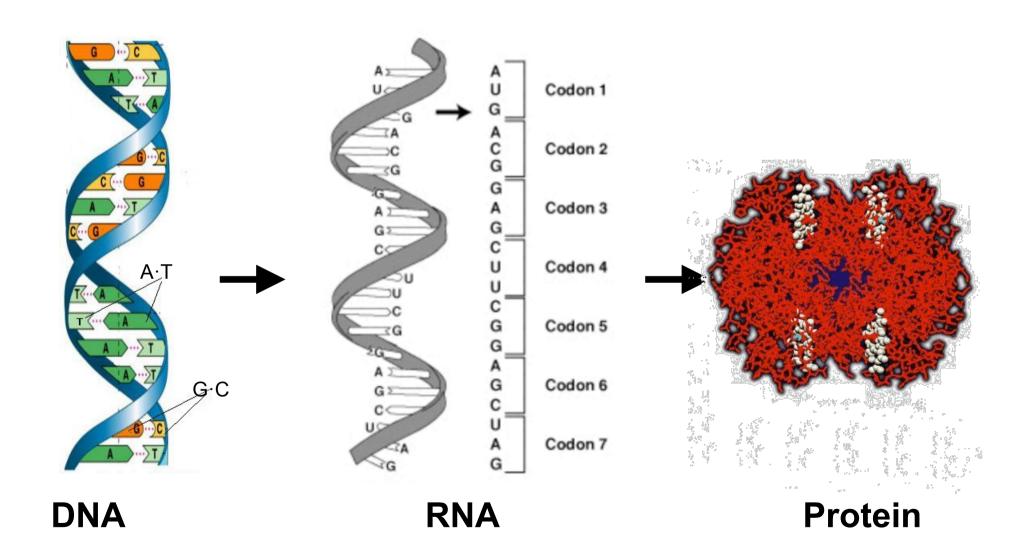


Human genome: 3·10⁹ base pairs (**A**denine, **C**ytosine, **G**uanine or **T**hymine)

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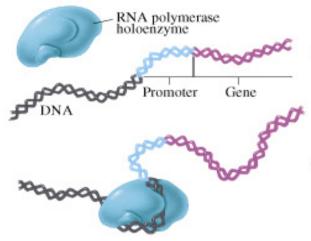


If you know the DNA sequence it is all very simple...



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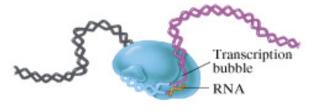
(a) RNA polymerase holoenzyme binds nonspecifically to DNA.

(b) The holoenzyme conducts a one-dimensional search for a promoter.

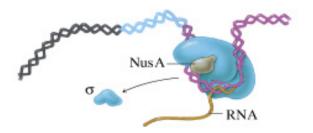
Initiation of transcription in the bacterium E. coli



(c) When a promoter is found, the holoenzyme and the promoter form a closed complex.



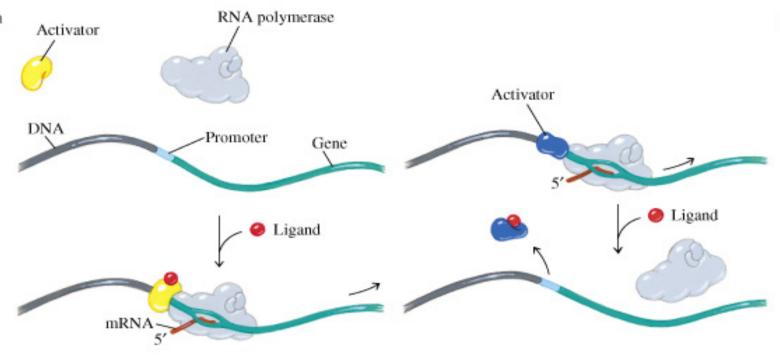
(d) A conformational change from the closed complex to an open complex produces a transcription bubble at the initiation site. A short stretch of RNA is then synthesized.



(e) The σ subunit dissociates from the core enzyme, and RNA polymerase clears the promoter. Accessory proteins, including NusA, bind to the polymerase.

Strategies for transcription regulation in bacteria

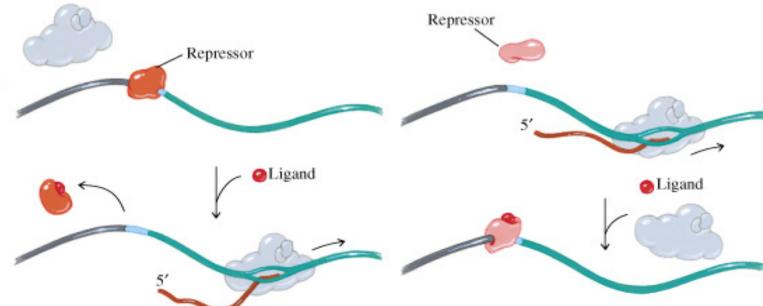
(a) An activator with bound ligand stimulates transcription.



(b) An activator stimulates transcription. In the presence of ligand, the activator is inhibited.

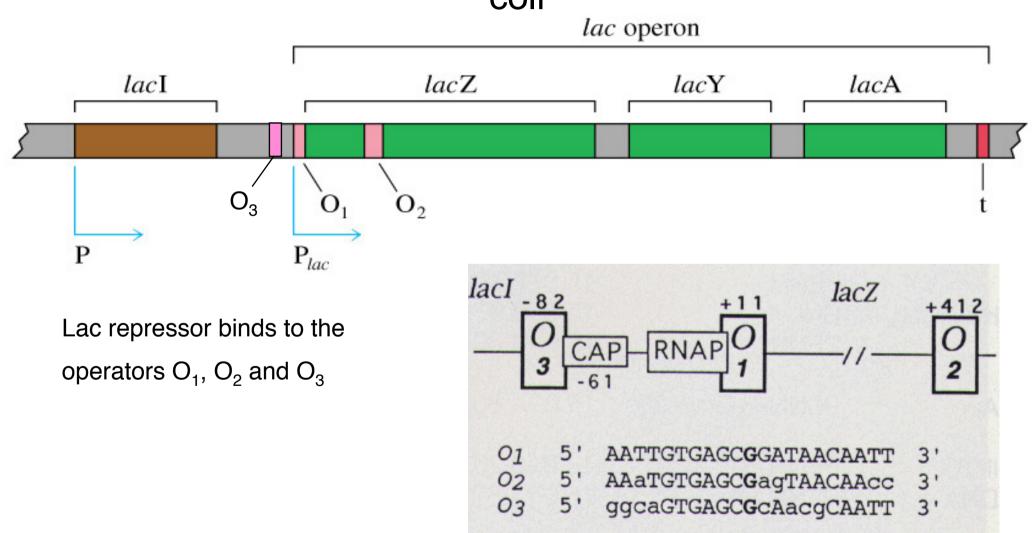
(c) A repressor prevents transcription.

Binding of ligand (inducer) to the repressor inactivates the repressor and allows transcription.

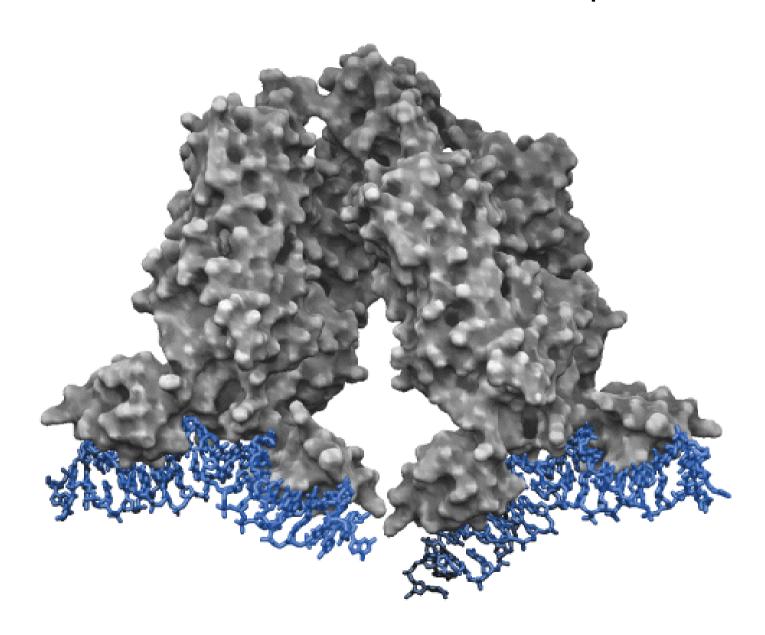


(d) In the absence of ligand, the repressor does not bind to DNA. Repression occurs only when ligand (corepressor) is present.

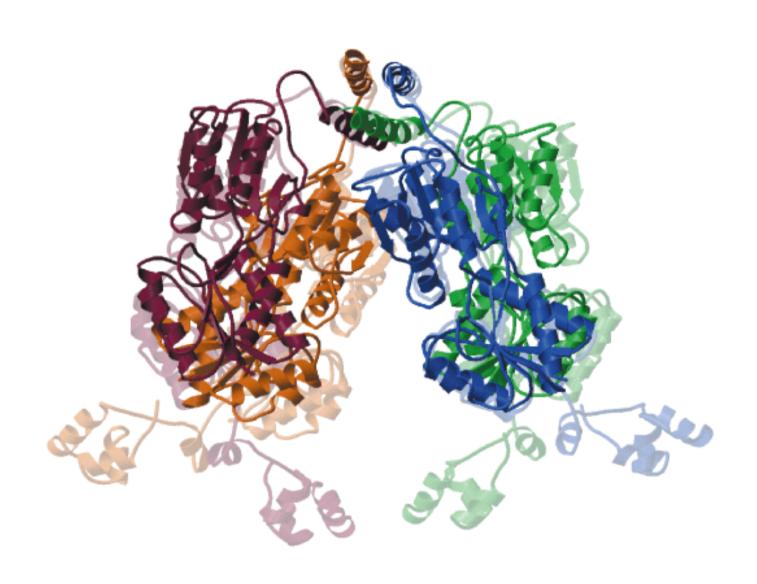
Organization of the genes regulated by Lac repressor, a transcription repressor protein in the bacterium E. coli



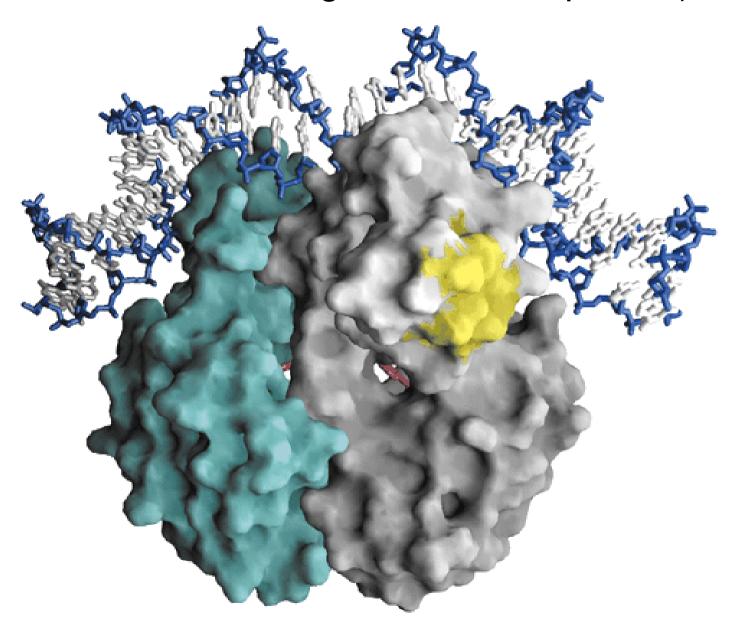
Molecular structure of E. coli lac repressor

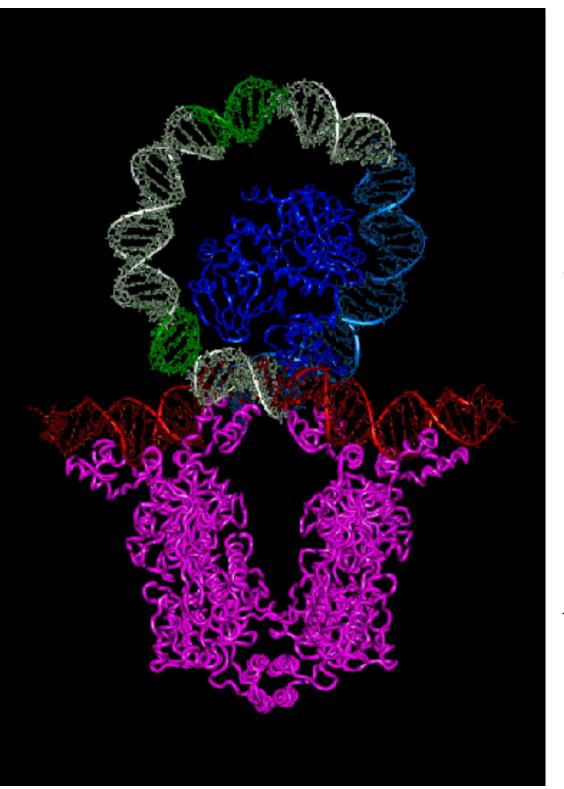


E. coli lac repressor + ligand allolactose that signals the presence of lactose in the medium and reduces DNA binding



Molecular structure of E. coli CRP (also called CAP for catabolite gene activator protein)





Model for the complex of CAP and Lacl at the lac operator

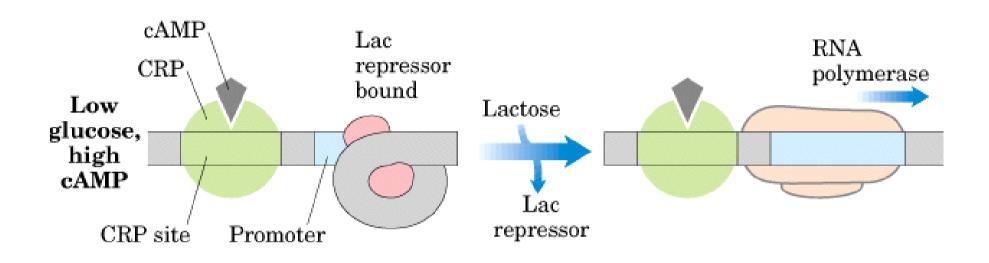
← CAP

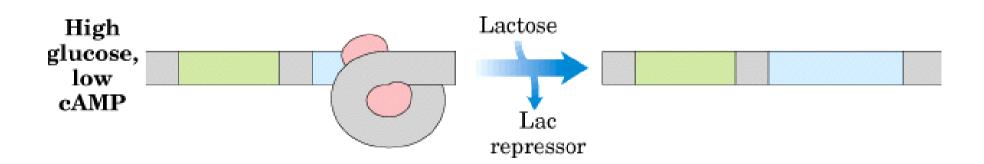
low glucose and low lactose

- => both CAP and LacI bound
- => repression

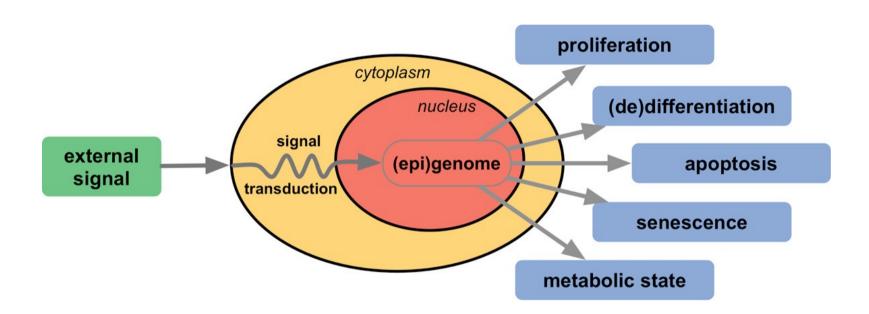
Lac repressor bound to operator sites O1 and O3

"On" and "off" states of the E. coli lac repressor





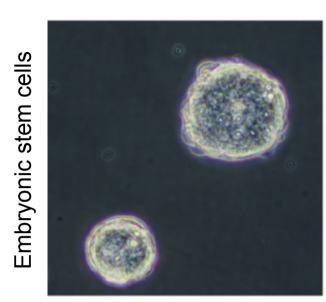
Eukaryotes: Decisions on the cell's fate made in the nucleus



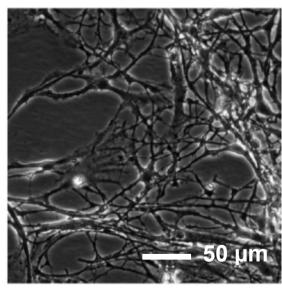
About genomic and epigenomic differences



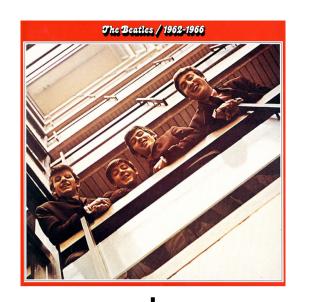
1% genomic differences



Neural cells



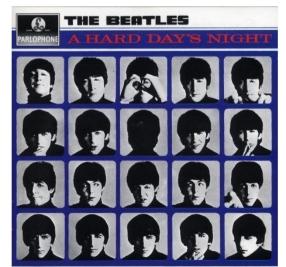
no genomic differences







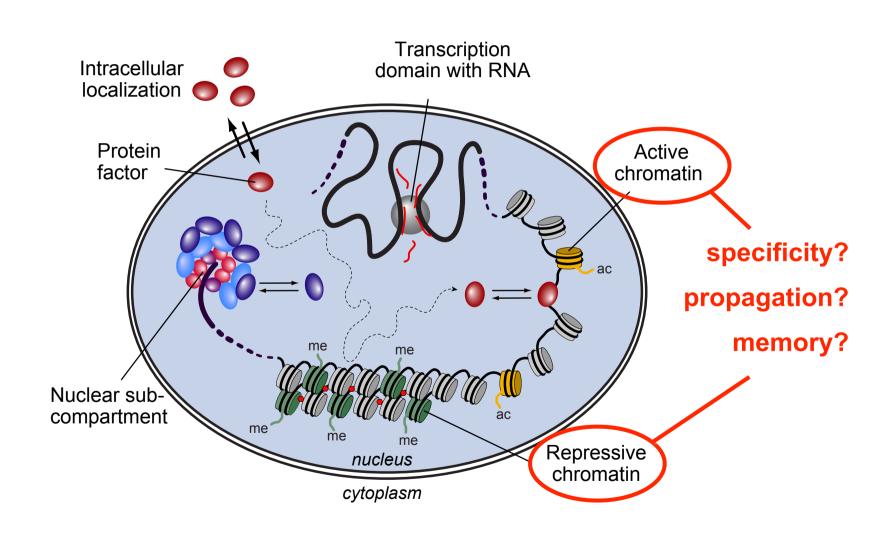




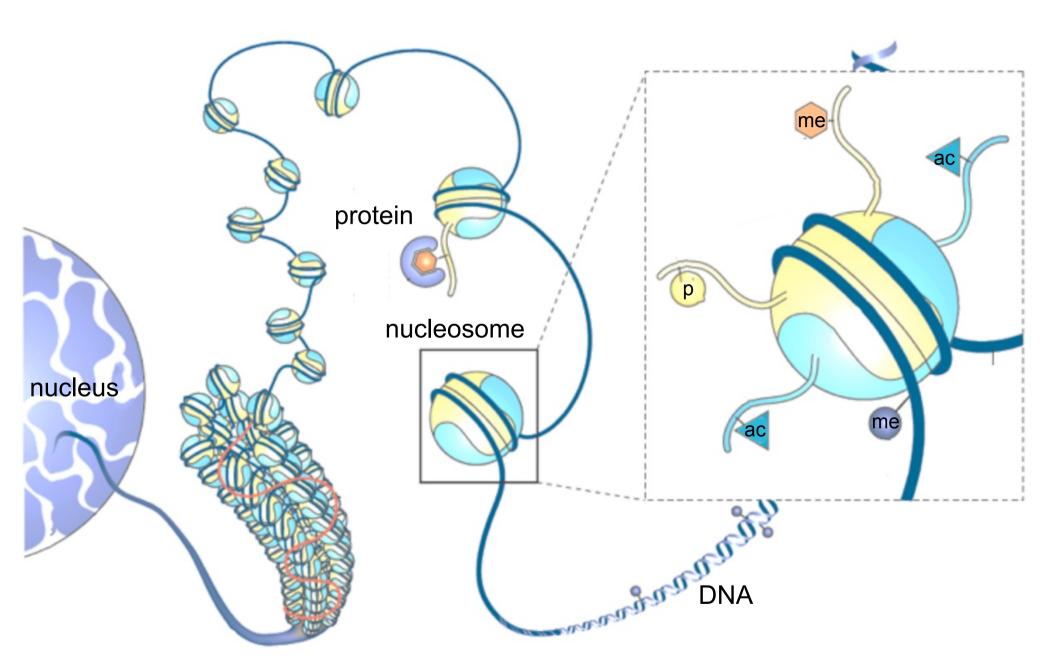




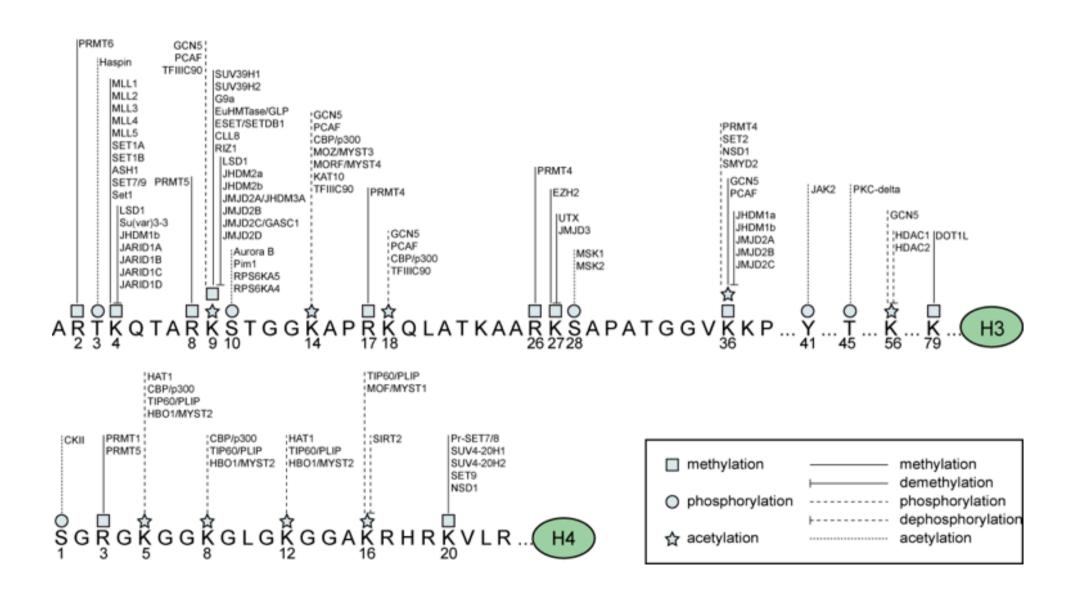
The dynamic organization of the nucleus and of chromatin control genome function



Epigenetic signals



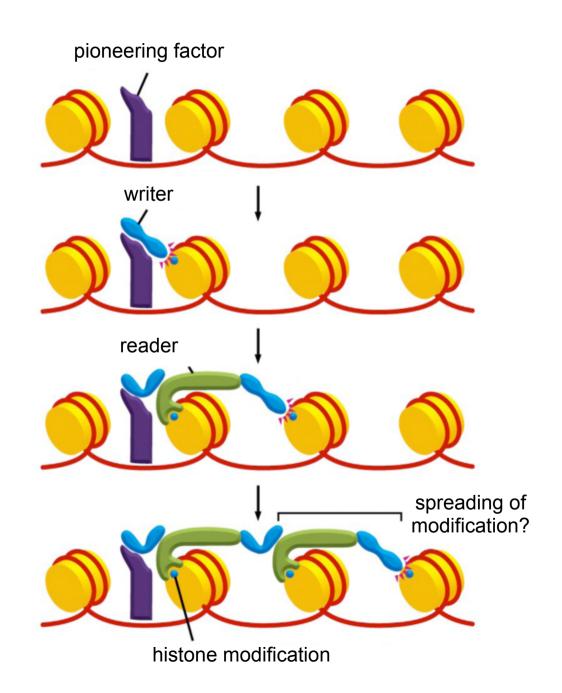
A complex network of proteins sets and removes a variety of histone modifications at multiple sites



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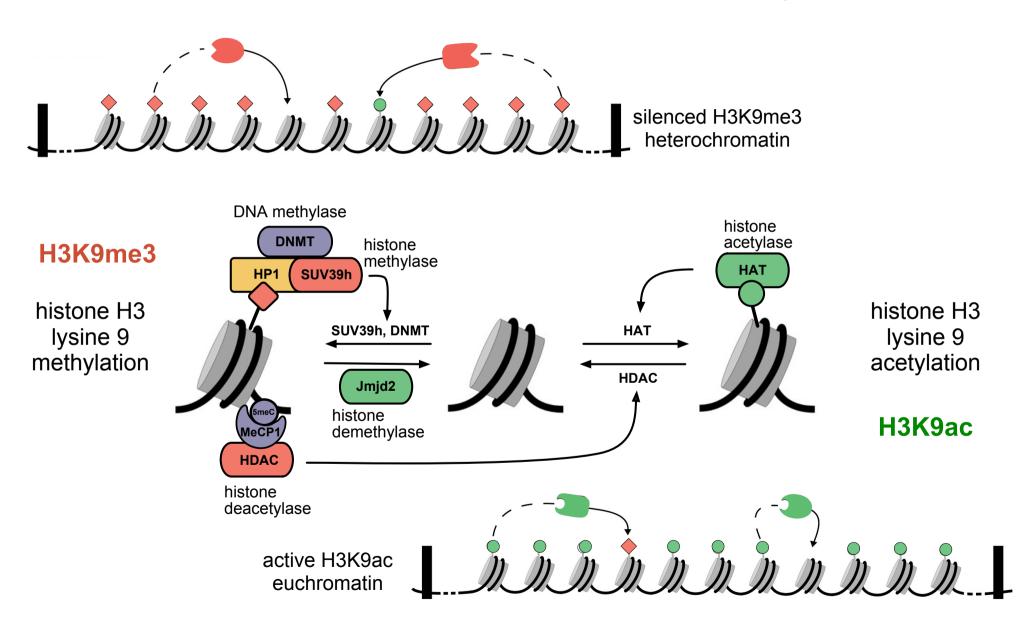


Writing, reading and transmitting epigenetic signals

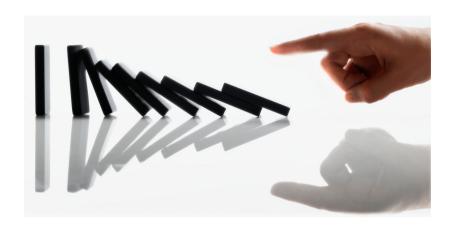


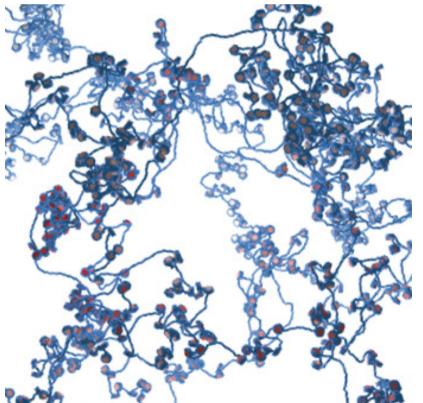
from Molecular Biology of the Cell

Distinct chromatin states can be established and maintained via interlinked feedback loops



The domino cascade model for spreading histone modifications along the DNA - what about 3D?





average distance between nucleosomes

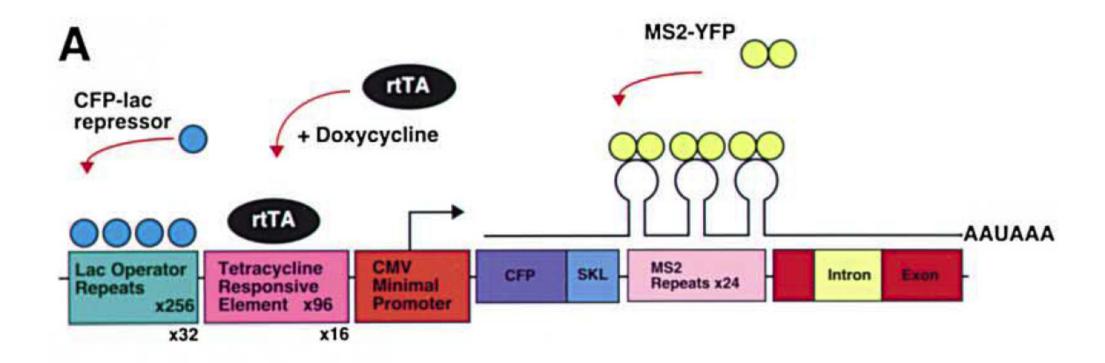
in 1D: ~25 nm (extended chain)

in 3D: ~28 nm ("sea of nucleosomes")

3D constructions with dominos are very fragile...



Following gene expression in living cells



Janicki, S. M., Tsukamoto, T., Salghetti, S. E., Tansey, W. P., Sachidanandam, R., Prasanth, K. V., Ried, T., Shav-Tal, Y., Bertrand, E., Singer, R. H., and Spector, D. L. (2004). From silencing to gene expression: real-time analysis in single cells. Cell 116, 683-698.

