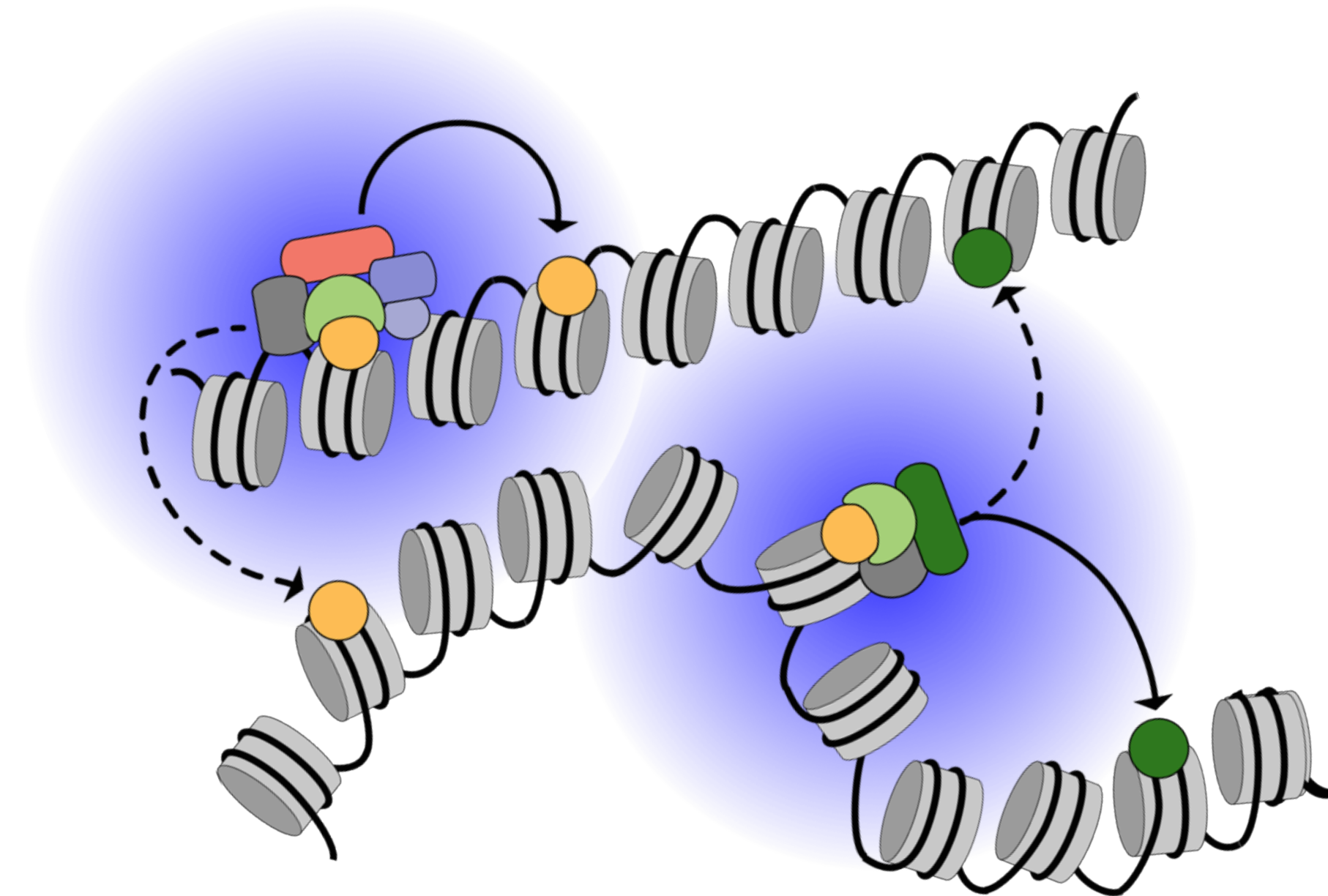


WS 24/25: Interactions of Proteins and Nucleic Acids: Biophysical Concepts and Theoretical Descriptions

Thursday 14.15-15.45, Bioquant SR 41 (unless noted otherwise)



Karsten Rippe

Division of Chromatin Networks
DKFZ & Bioquant

Coordinates for the seminar

Karsten Rippe

Division of Chromatin Networks

Bioquant, Room 645, 6th floor

Telefon: 54-51376

e-mail: Karsten.Rippe@bioquant.uni-heidelberg.de or Karsten.Rippe@dkfz.de

Overview on my Biophysics/Systems Biology teaching:

http://malone.bioquant.uni-heidelberg.de/teaching/index_teaching.html

Material for the lecture: Biophysical concepts and theoretical descriptions

http://malone.bioquant.uni-heidelberg.de/teaching/BPC_lectures/BPC_1+2.html

Username: teaching

Password: nonukes

Winter term 2024/25

Interactions of Proteins and Nucleic Acids: Biophysical Concepts and Theoretical Descriptions

Summer term 2025

Physico-chemical methods in systems biology within the Major Systems Biology (contact me for registration if you want to attend)

Literature

C. Cantor und P. Schimmel, Biophysical Chemistry, Vol I, II und III, Freeman Press, 1980

P. Nelson, Biological Physics, Freeman, 2004.

K. E. van Holde, W. C. Johnson, & S. P. Ho, Principles of Physical Biochemistry, Prentice-Hall, 1998; 2nd edition 2005

R. Philipps & R. Milo, Cell Biology by the Numbers, Garland Science, 2016

Research articles, book chapters and web links: see lecture web site:

http://malone.bioquant.uni-heidelberg.de/teaching/BPC_lectures/BPC_1+2.html

Computer programs

Viewing 3D protein and DNA structures: VMD (Visual Molecular Dynamics)

<http://www.ks.uiuc.edu/Research/vmd>

Kinetic simulations: Copasi (is being developed by the group of Ursula Kummer in the BioQuant)

<http://www.copasi.org>

Calculations and plotting: e. g. Maple, Mathematica, Excel, Origin, Kaleidagraph, R etc.

AI (LLM, large language models): perplexity.ai, chatgpt.com, claude.ai

Grades for “benotete Scheine”: 6 problem sets (biweekly)

Problem sets

- There will be problem sets every 2 weeks (6 in total)
- To be returned the following Thursday by mail to me before 14:15 hour (Karsten.Rippe@bioquant.uni-heidelberg.de, include BPC2024 in subject line)
- We will discuss the answers to the problem sets, as well as any issues you encountered. The corrected problem sets will be returned the next Thursday, ideally.
- To receive credit, you must obtain at least 50% of the possible points. Only the 5 highest-graded problem sets will be considered for your final grade, so you can still achieve 100% even if one problem set is missing.
- You are welcome to work in groups to complete the problem sets; however, each student must submit their own individual answers.
- Problem set #1, handed out today (October 17), is due on October 31.

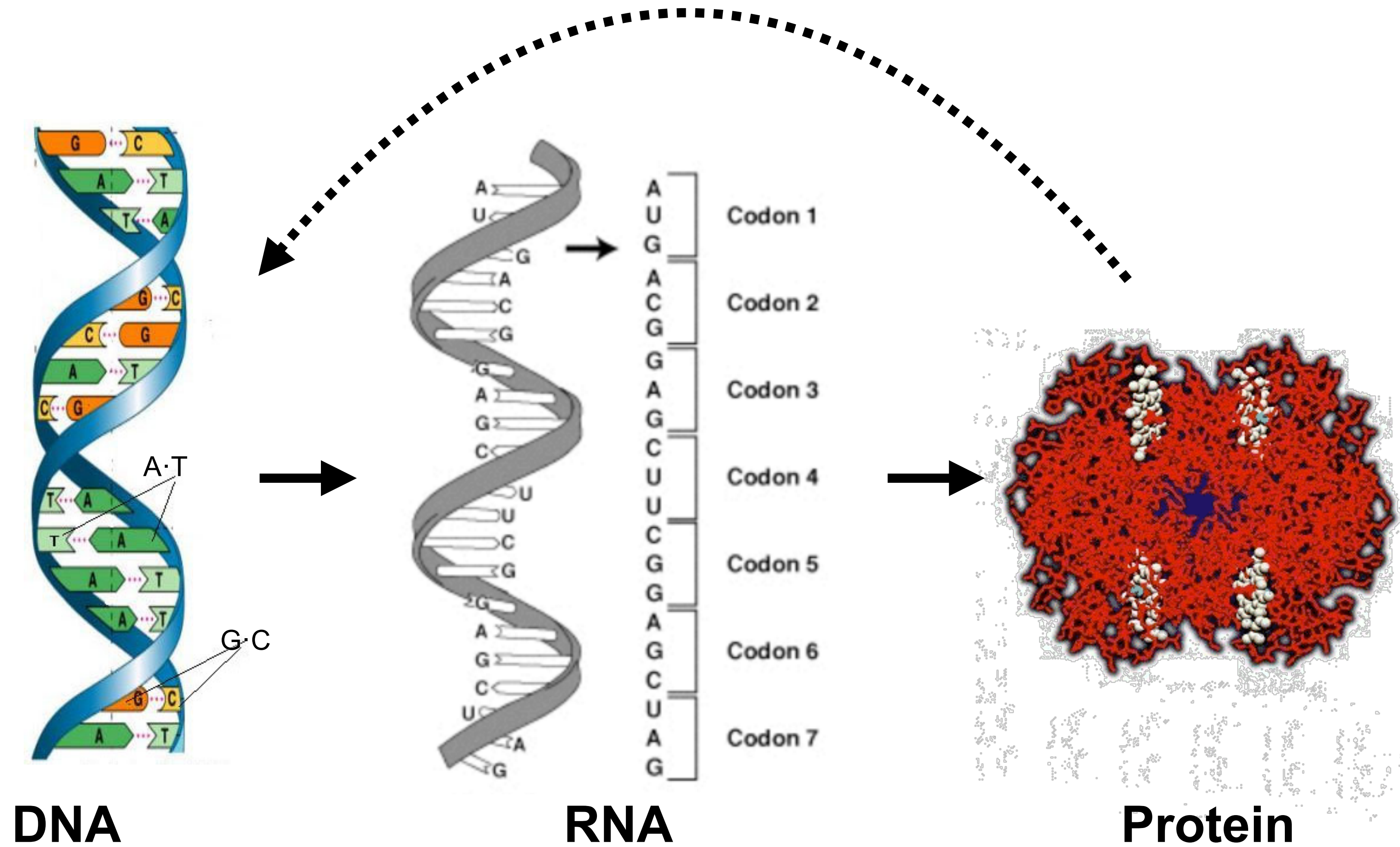
Lead questions of the seminar

- What drives binding of proteins to DNA and chromatin and target them to certain sites?
- How does the environment of the cell shape these interactions?
- How can we measure protein binding to DNA/chromatin in vitro and in living cells?
- What mechanisms partition the genome into active or silenced subcompartments?
- How is transcription regulated in bacteria vs. eukaryotes via macromolecular interactions?

Biophysical Concepts and Theoretical Descriptions

- Intro lecture and length and time coordinate system
- Interactions between molecules and associated energies
- Thermodynamics of protein-DNA interactions
- Equilibrium binding of proteins and nucleic acids
- Diffusion and protein transport
- Measuring protein-DNA/chromatin interactions in living cells
- Nuclear subcompartments - assembly mechanisms & functions
- Gene expression analysis in living cells
- Chromatin organization and remodeling
- Protein interactions mediated by DNA and chromatin looping (enhancers)
- Applying sequencing-based methods to study protein-DNA interactions
- Integrating sequencing and microscopy in spatially resolved “omics”

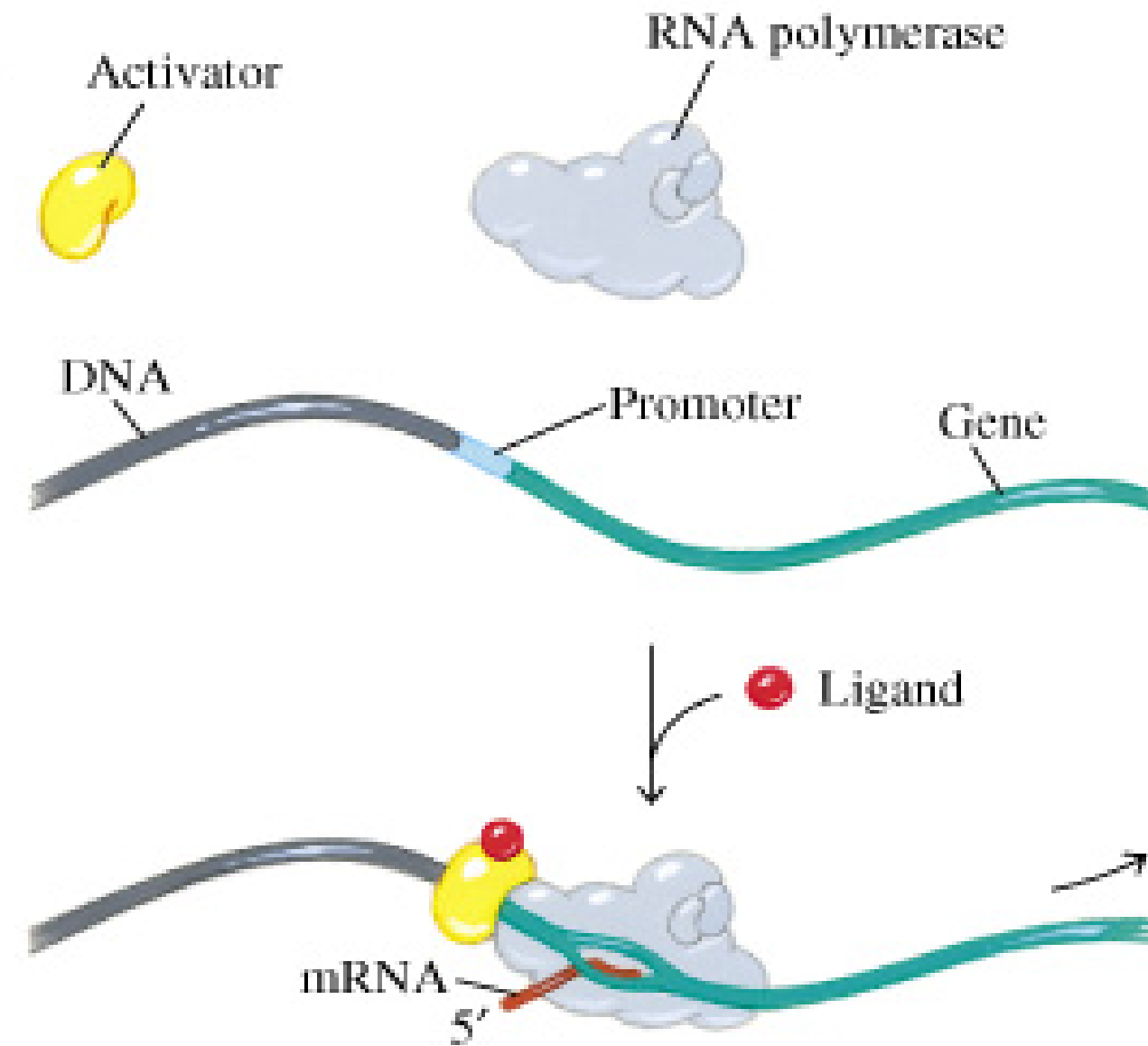
The central dogma in molecular biology



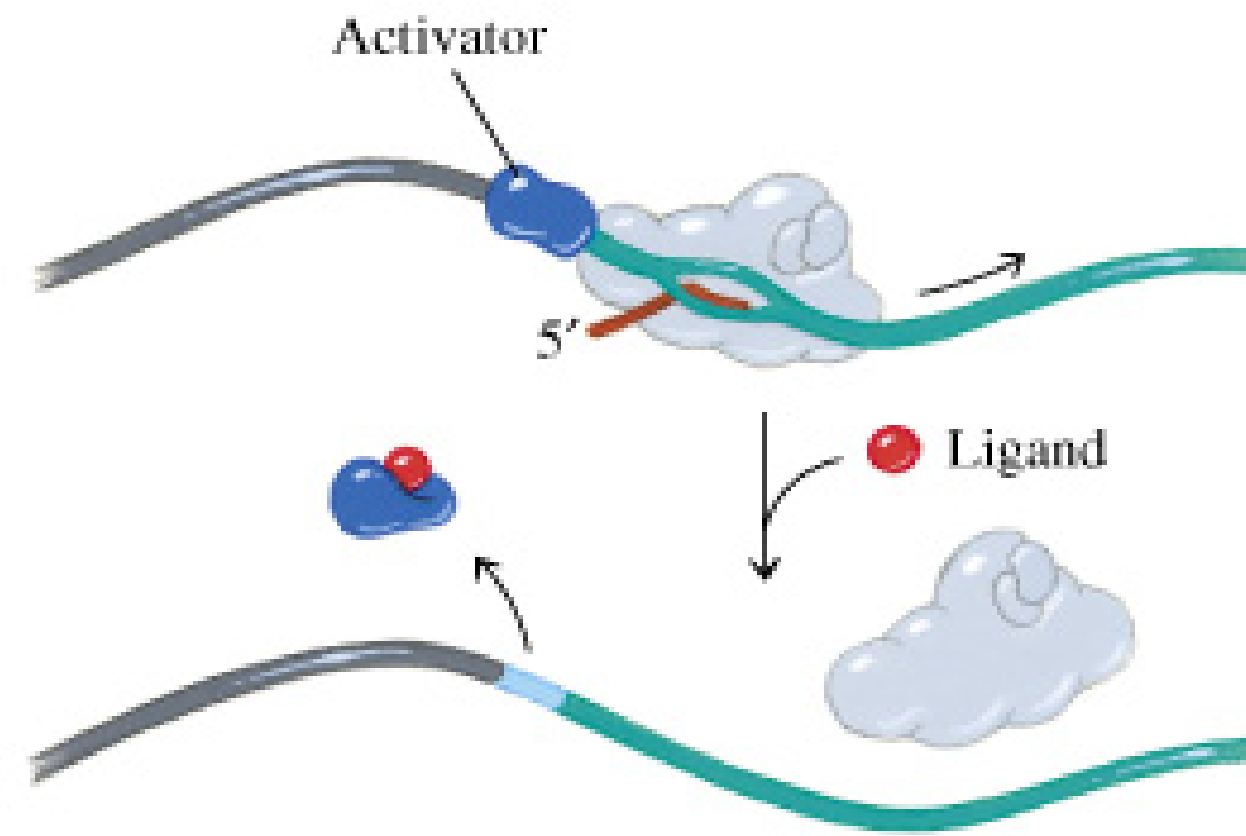
... with some feedback loops

Strategies for transcription regulation in bacteria

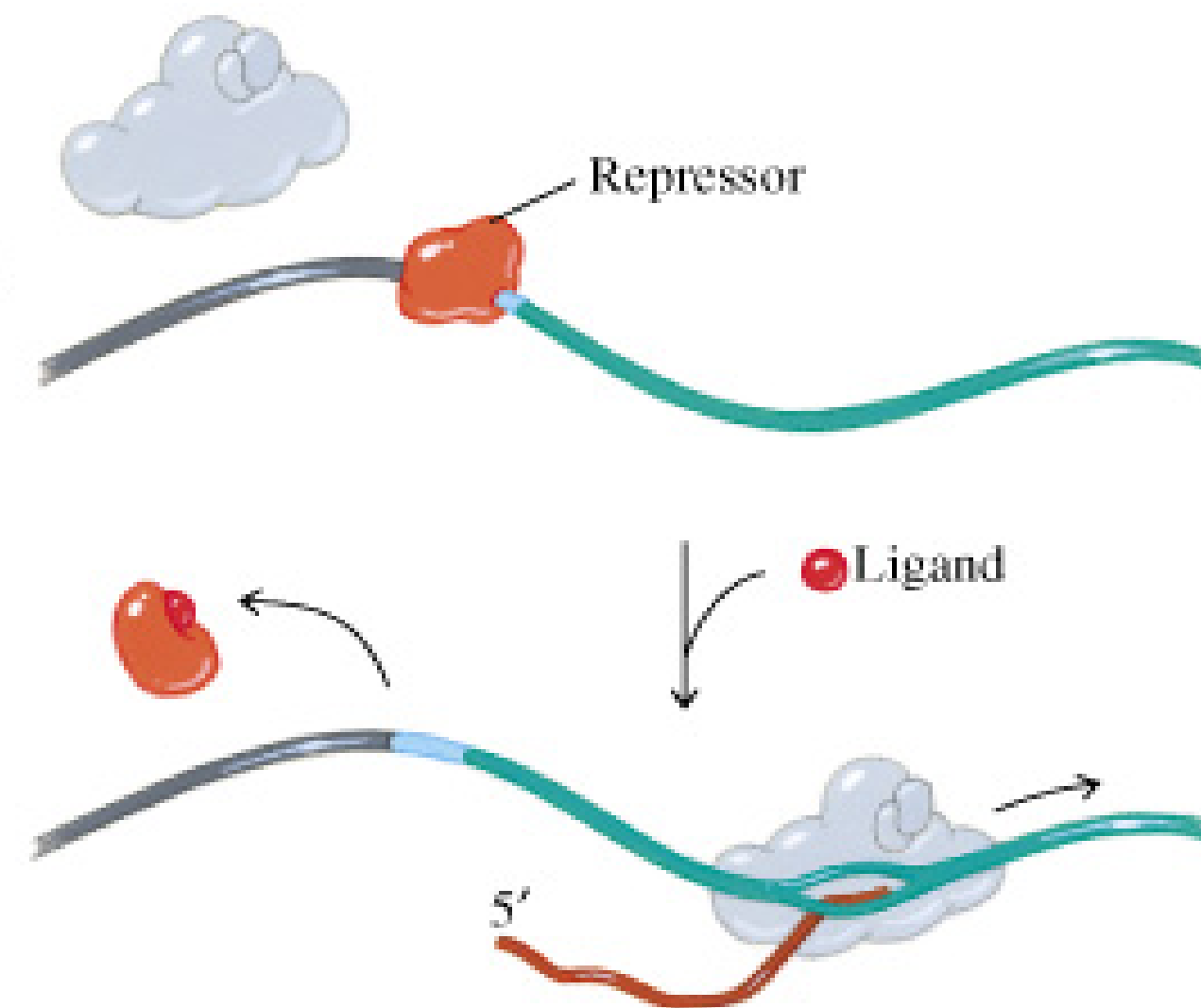
(a) An activator with bound ligand stimulates transcription.



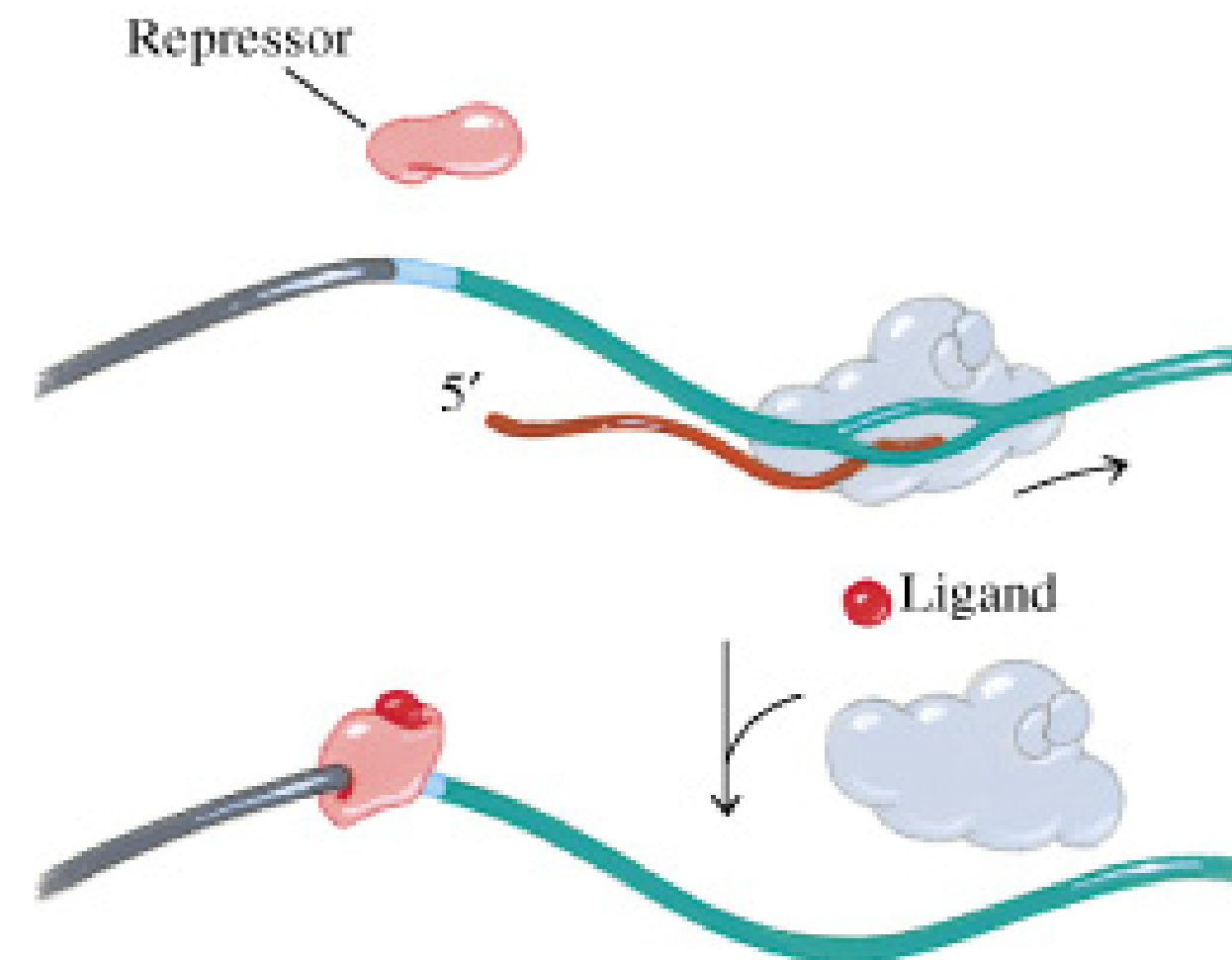
(b) An activator stimulates transcription. In the presence of ligand, the activator is inhibited.



(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.



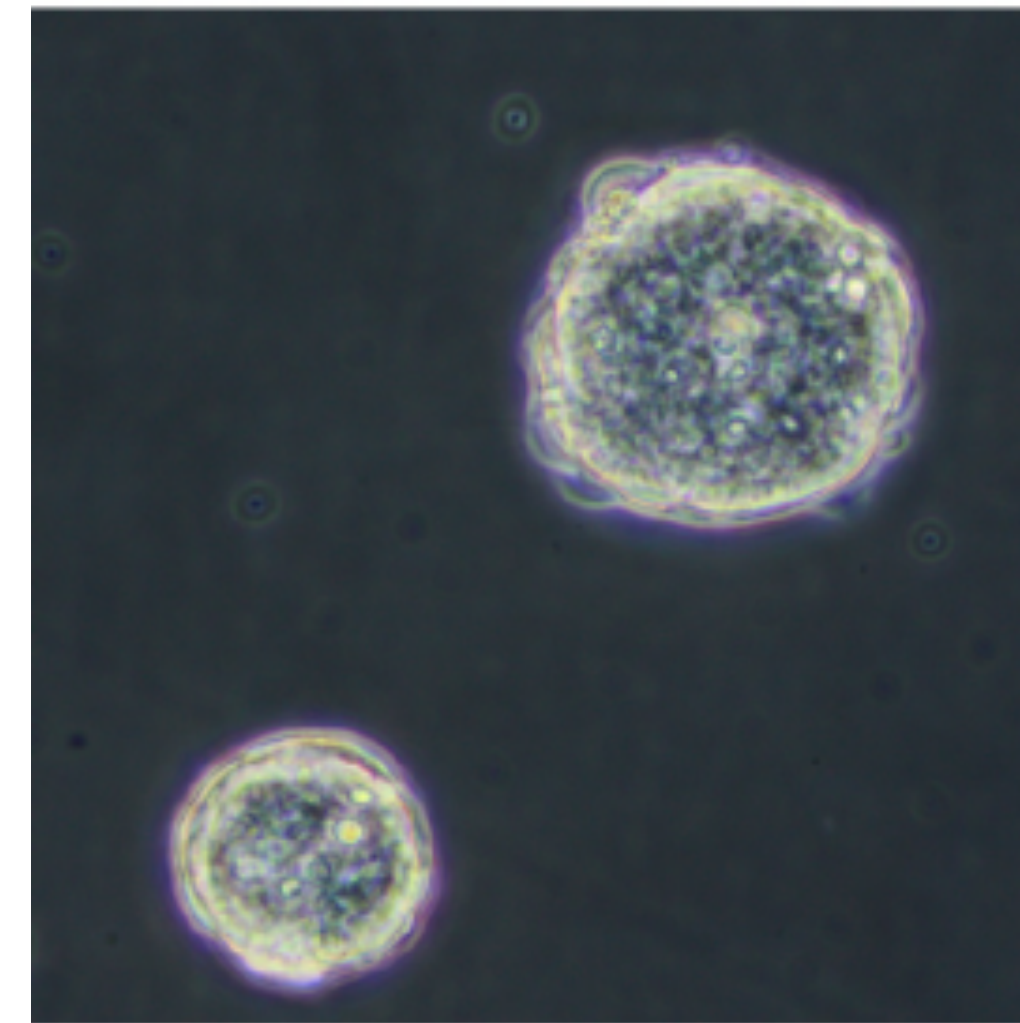
Epigenetic differences determine gene expression programs in higher eukaryotes



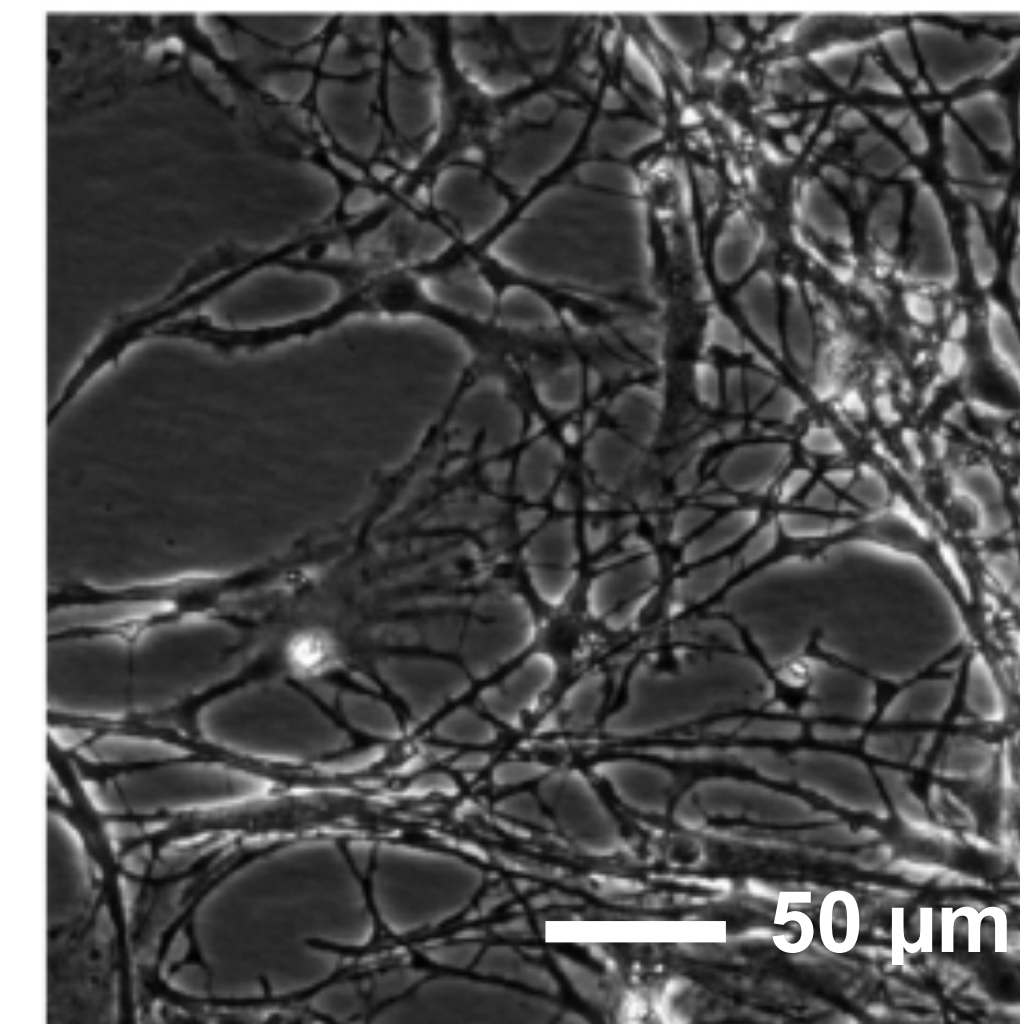
1% genomic differences

Image: James Balog Getty Images

Embryonic stem cells



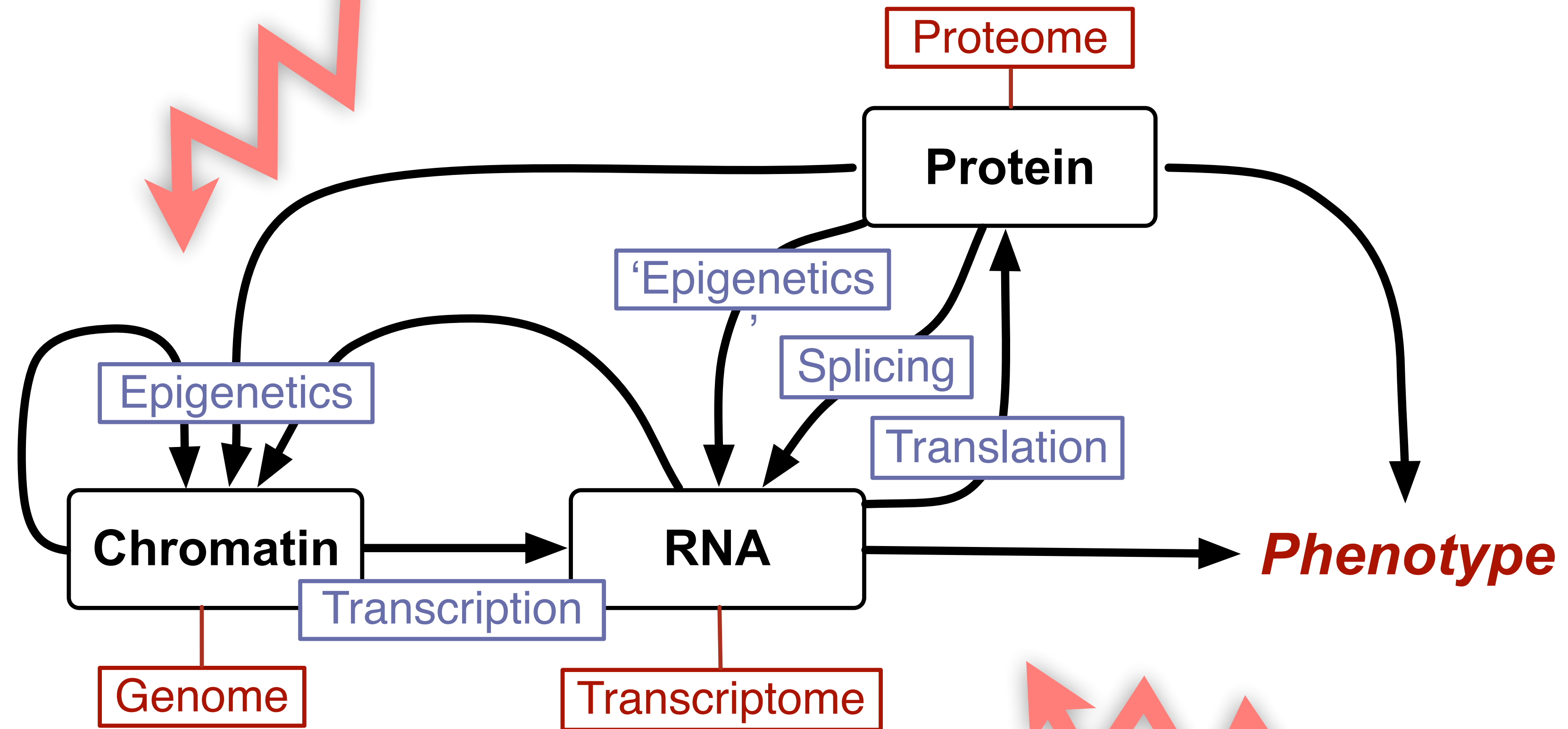
Neural cells



No genomic differences

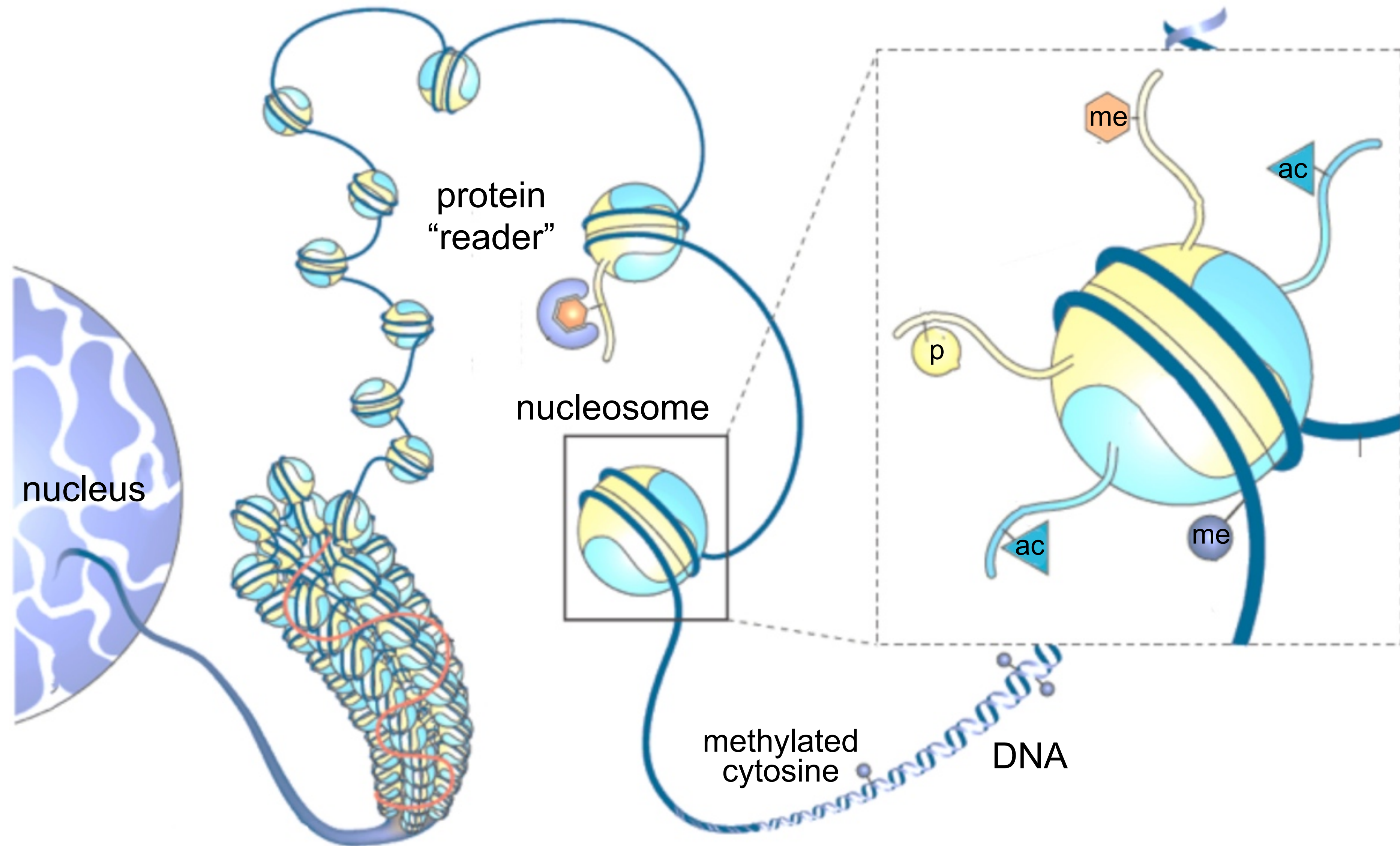
A complex network links DNA to phenotype in eukaryotes

Microenvironment

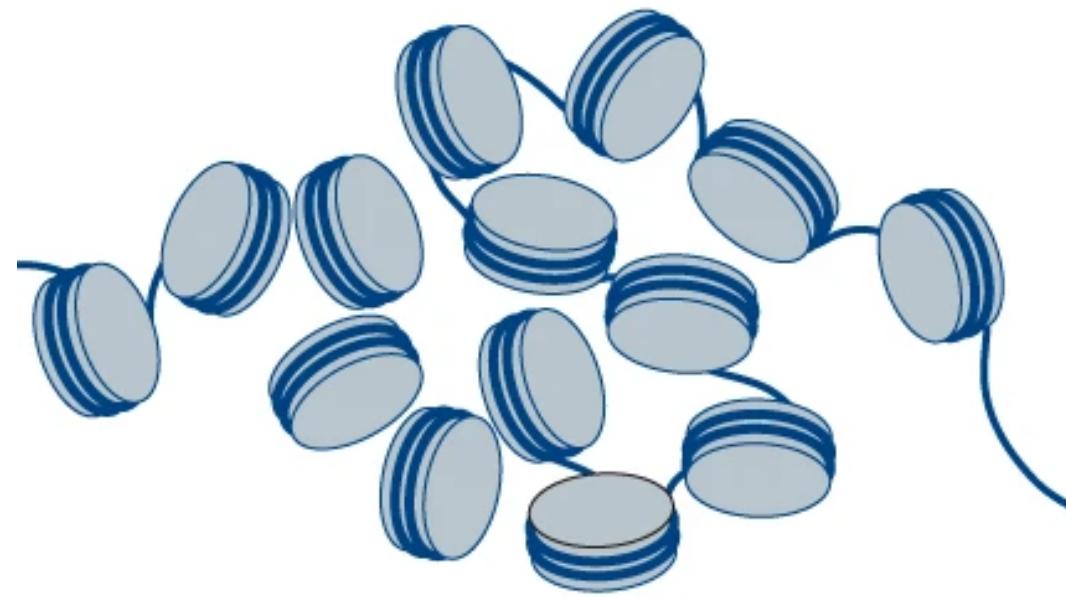


Drug treatment

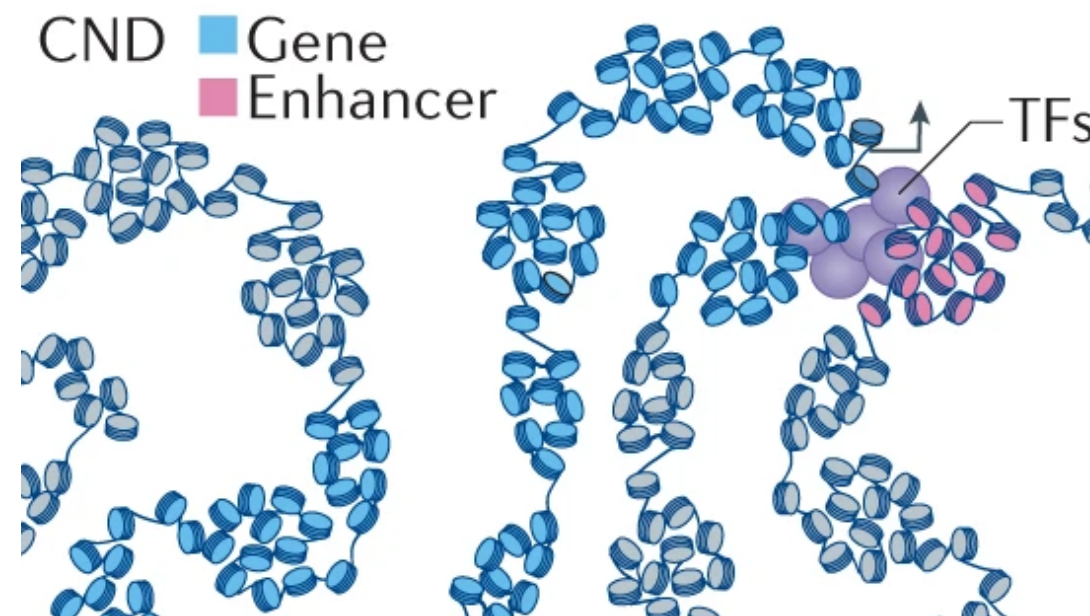
Epigenetic signals define access to the DNA genome and cell type specific chromatin state patterns



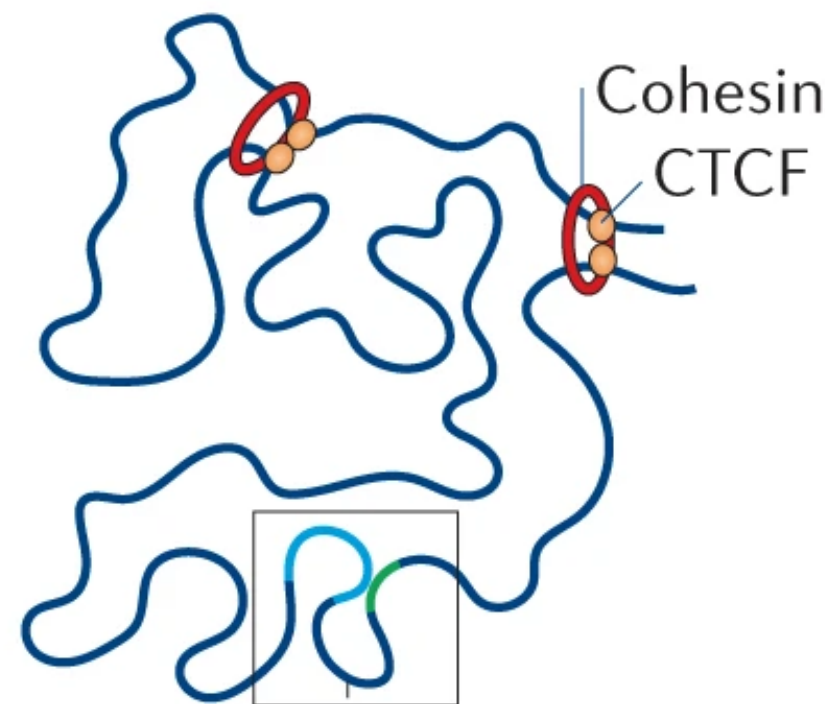
Chromatin organization on different length scales



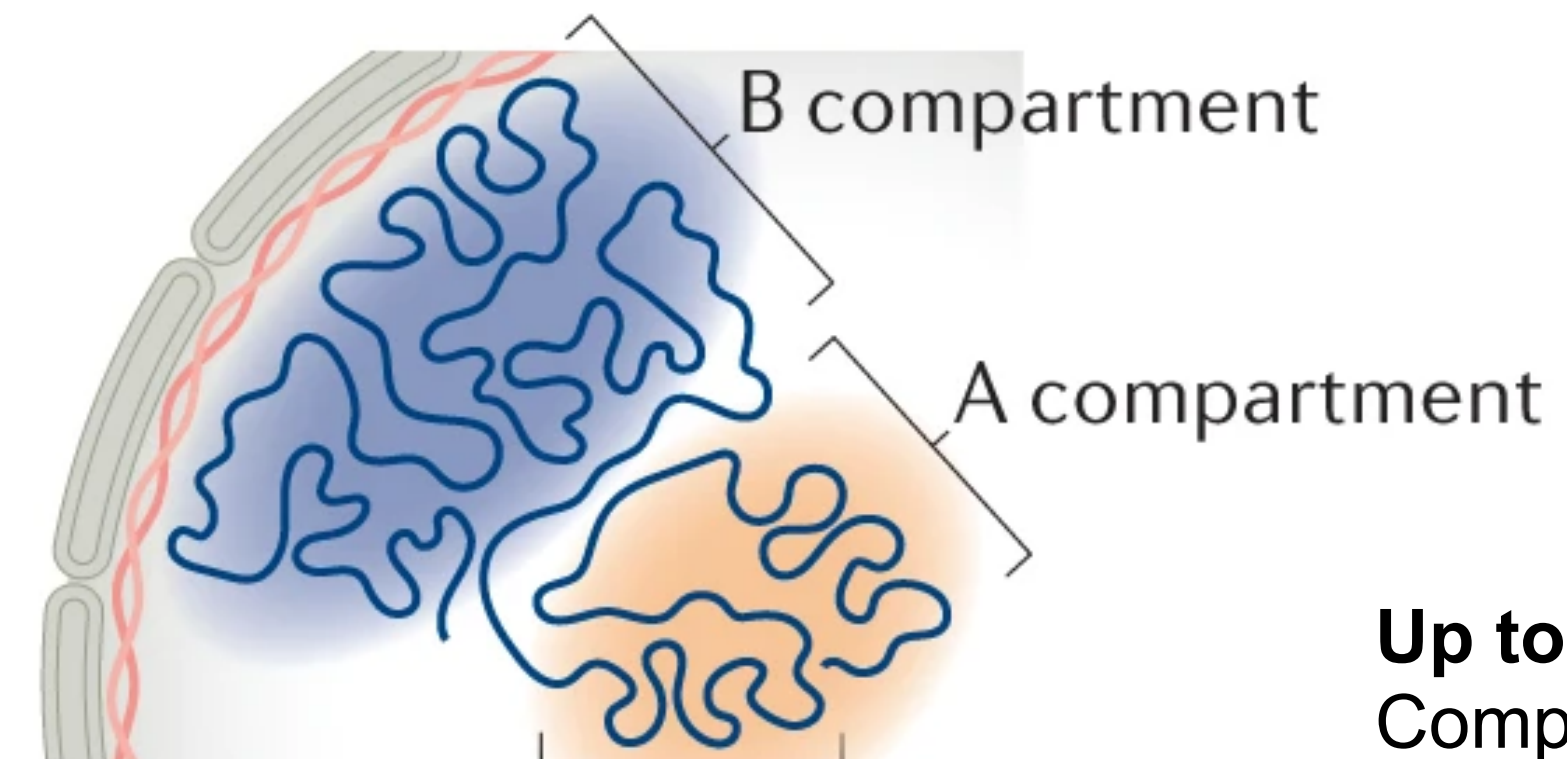
1-2 kb: Nucleosome clutches



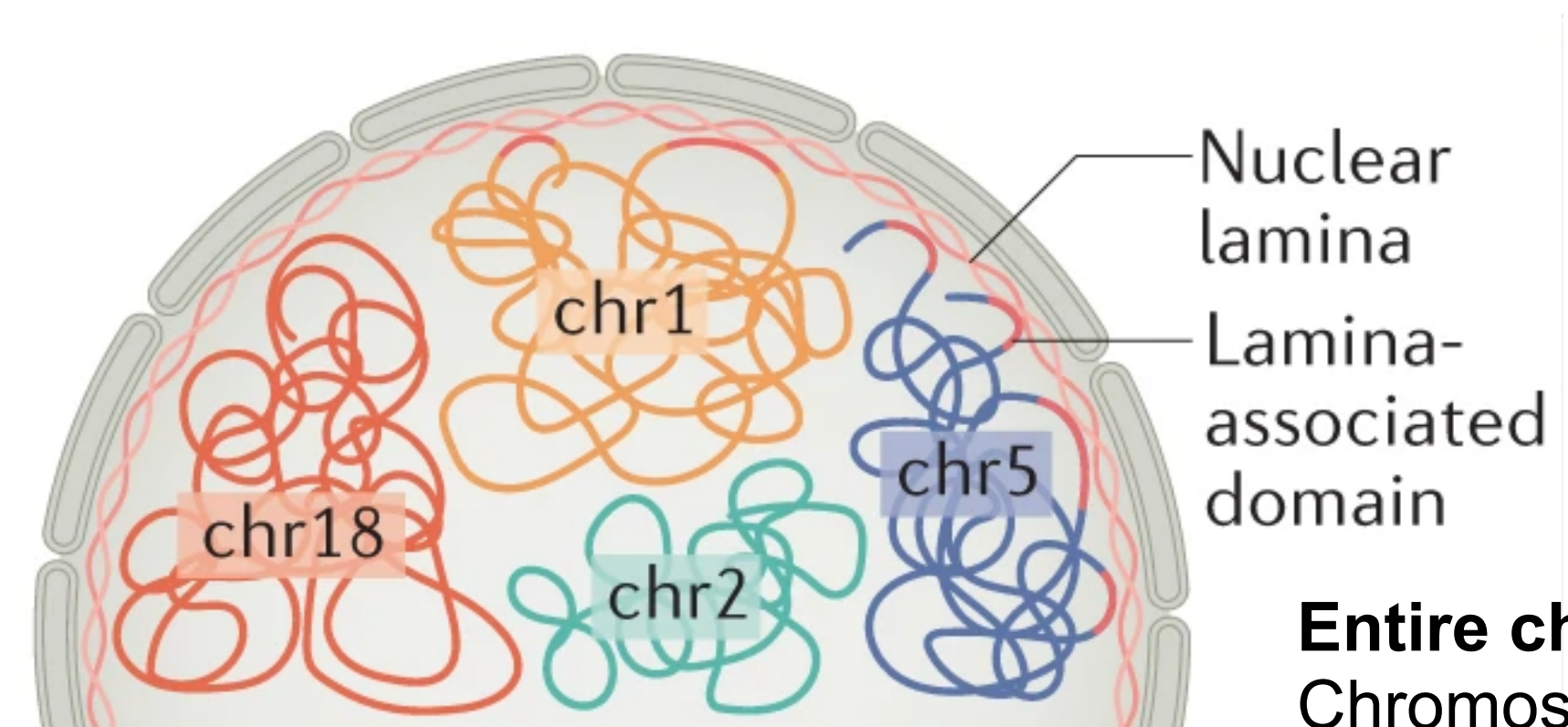
10-100 kb: Chromatin domains and functional loops (enhancer-promoter contacts)



100 kb to a few Mb: Chromatin loops and topologically associating domains (TADs)



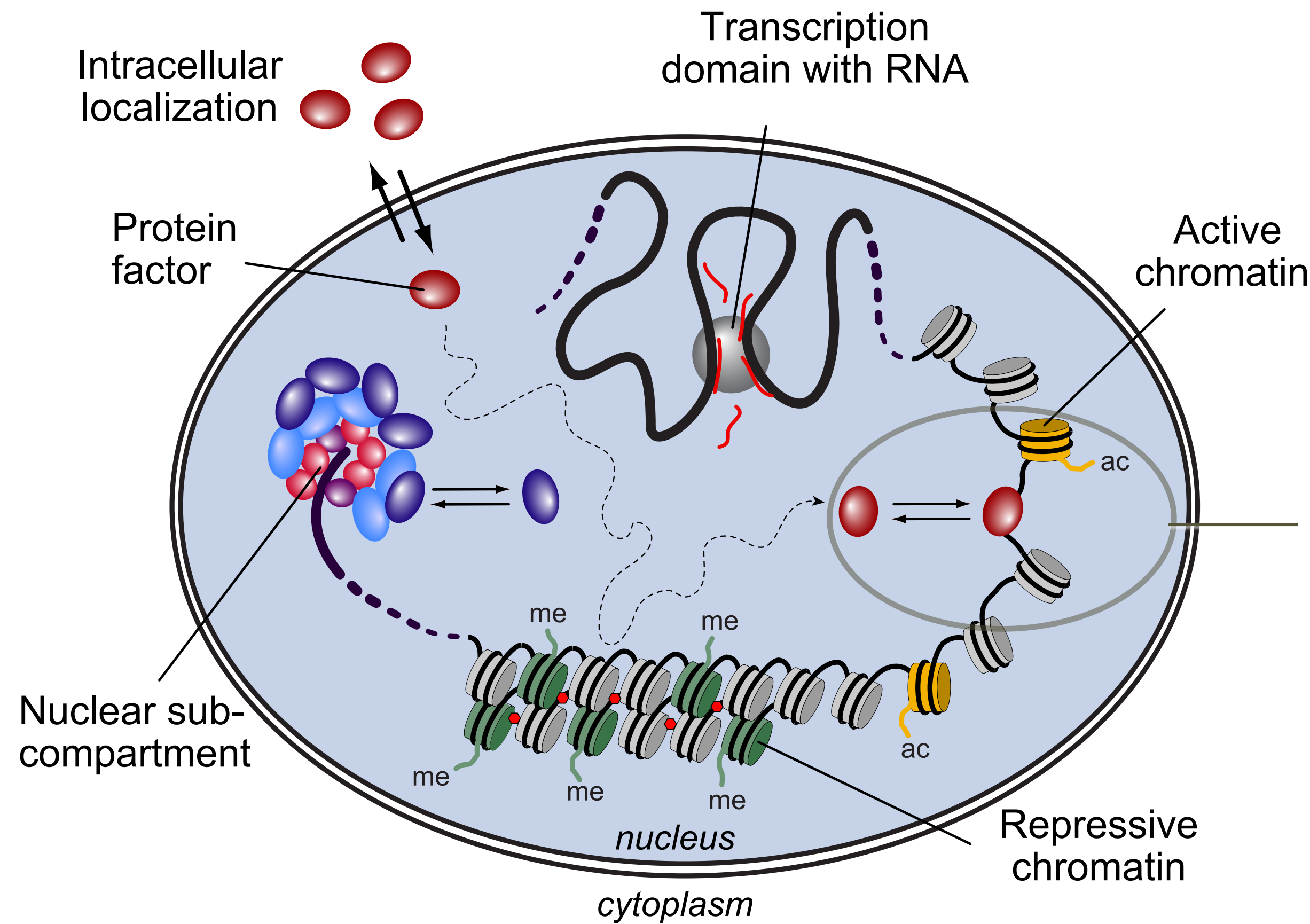
Up to 100s of Mb: Compartments and hubs



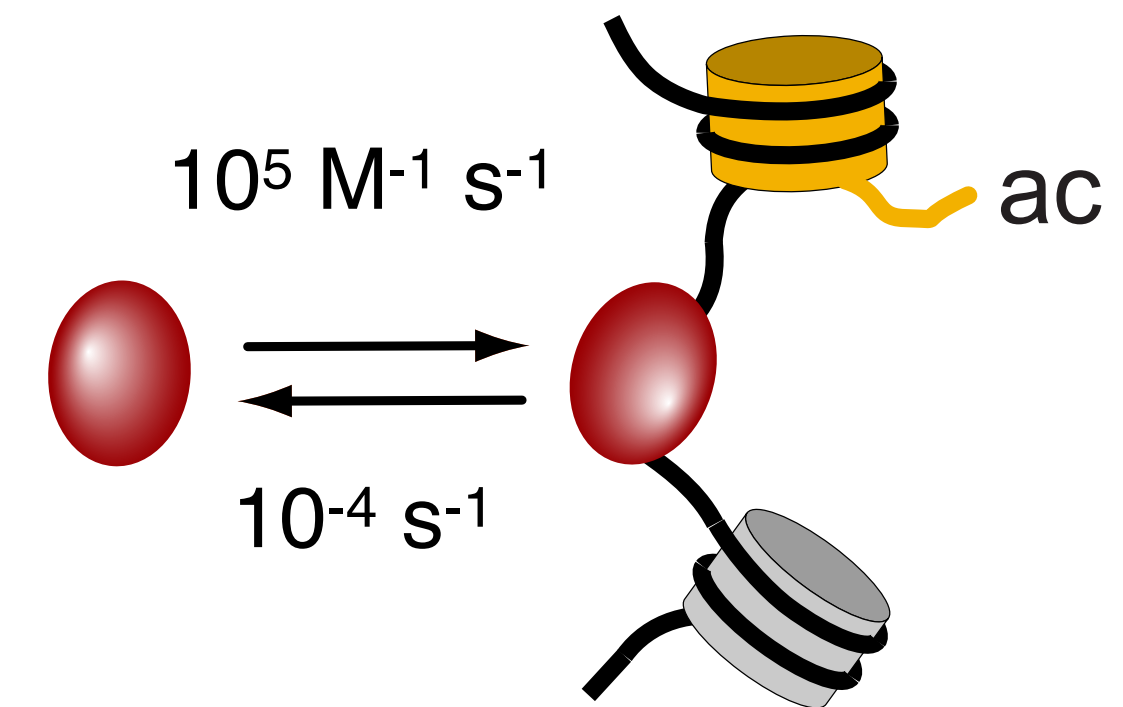
Entire chromosomes: Chromosome territories

Protein interactions with DNA and RNA

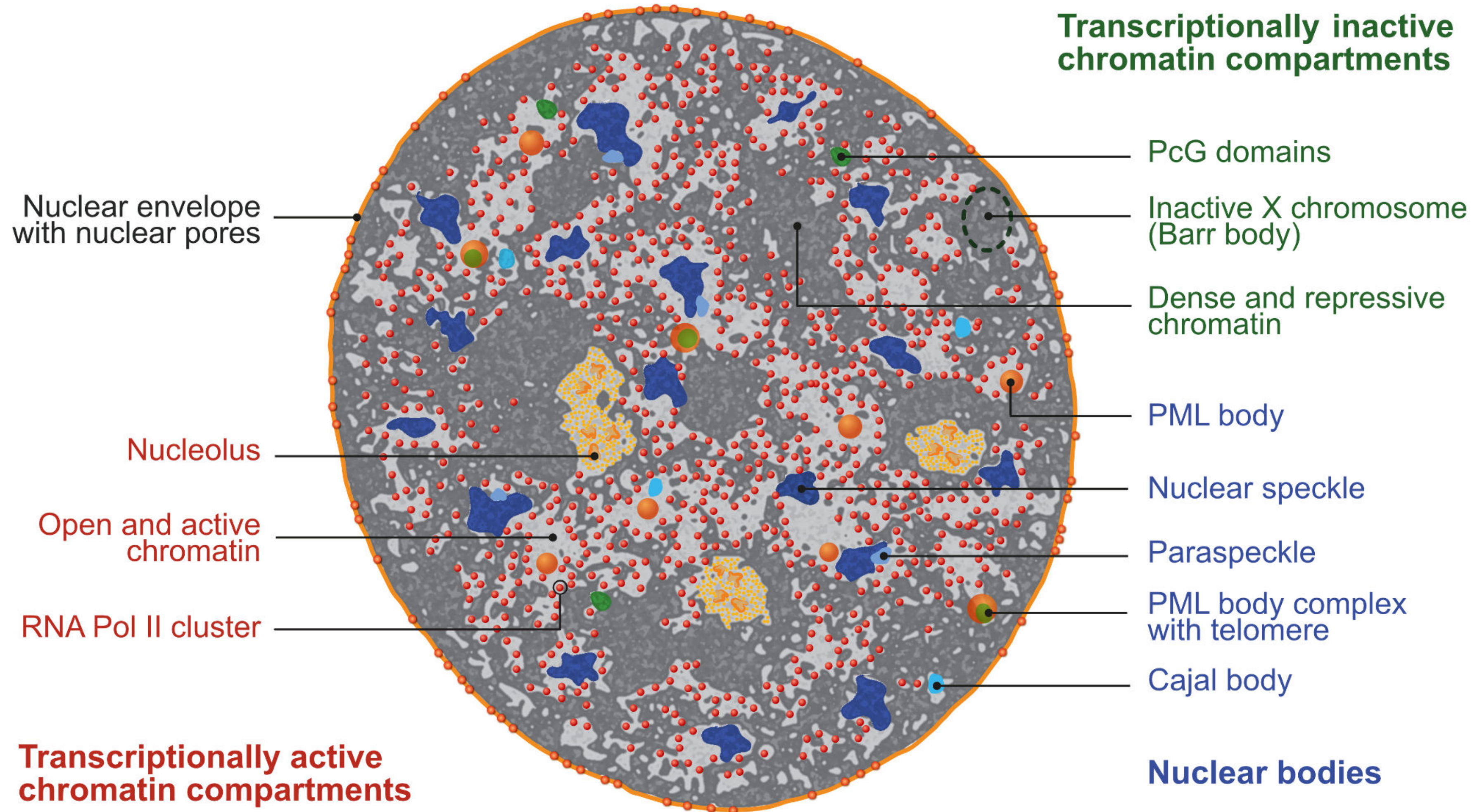
in living cells



in vitro



The mammalian nucleus organizes genome functions in subcompartments



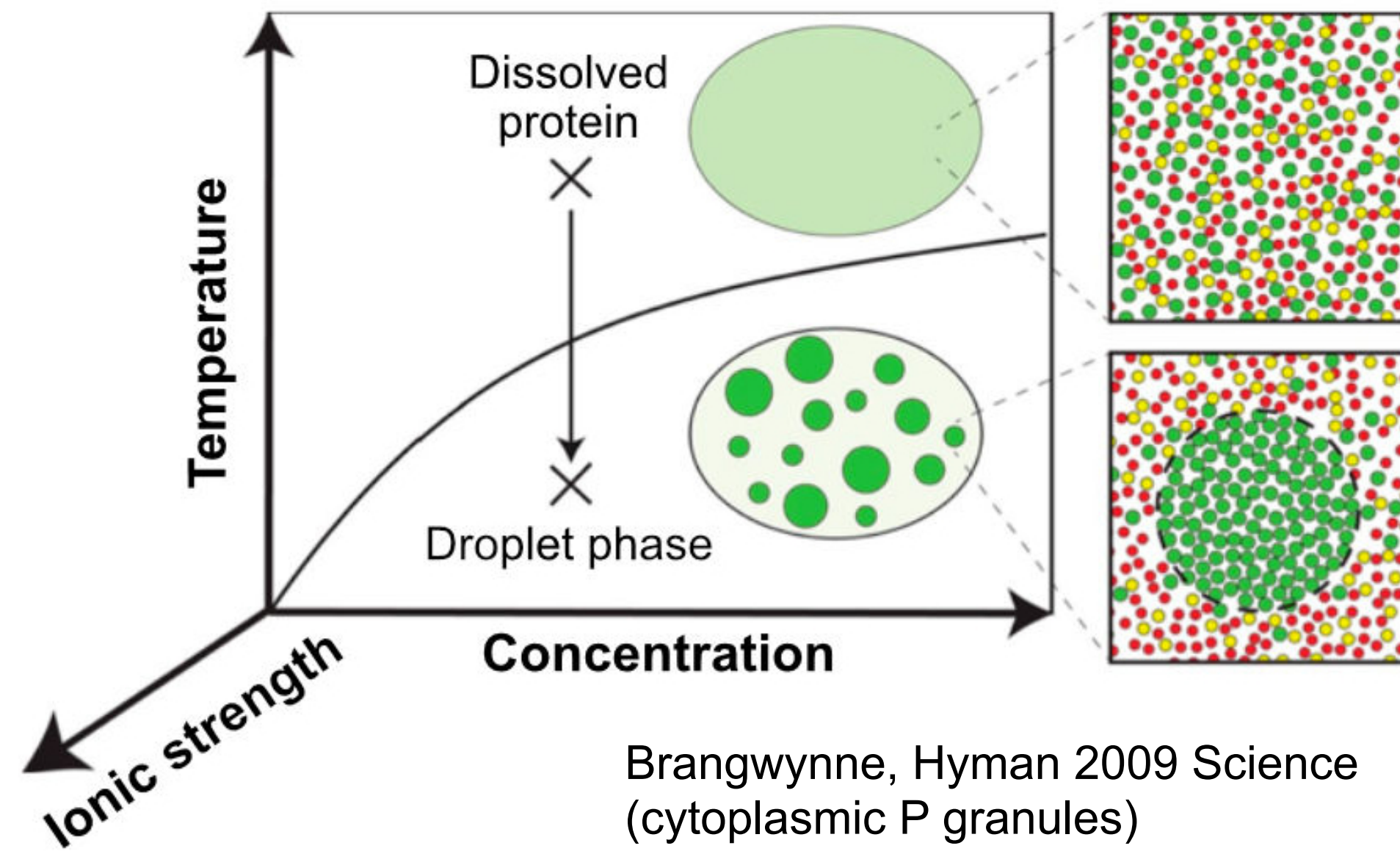
On the $10\ \mu\text{m}$ length scale of the nucleus proteins mix fast by diffusion



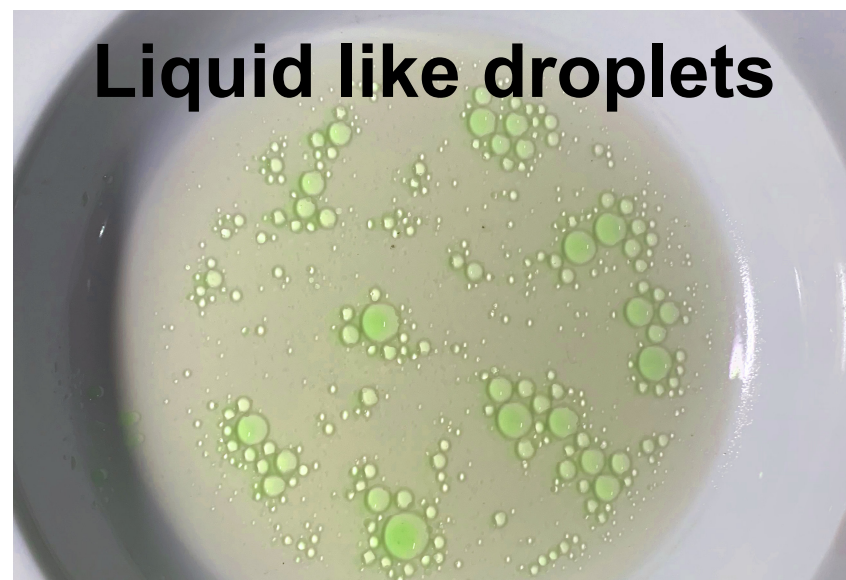
- Thermal energy at $25\ ^\circ\text{C}$:
 $k \cdot T = 4 \cdot 10^{-21}\ \text{J}$
- GFP translocation in 1 sec
($D = 30\ \mu\text{m}^2\ \text{s}^{-1}$): $13\ \mu\text{m}$
- Gravitational energy *PEG*
GFP (27 kDa, $10\ \mu\text{m}$):
 $4 \cdot 10^{-27}\ \text{J}$ or $0.000001\ \text{kT}$

... and gravitation is irrelevant for proteins

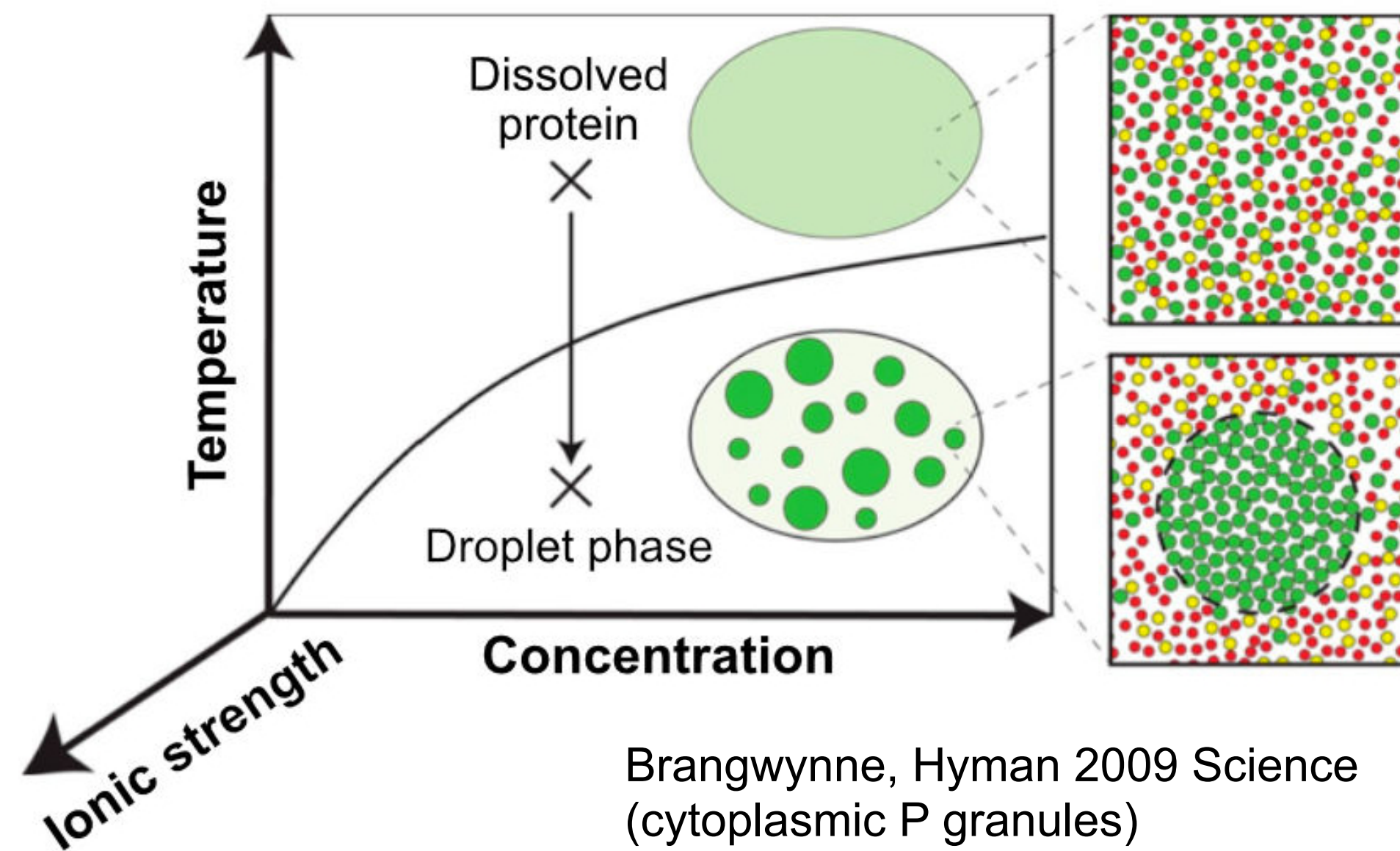
Liquid-liquid phase separation (LLPS) to form cellular subcompartments



or phase transitions to other states?



Liquid-liquid phase separation (LLPS) to form chromatin subcompartments



Nucleolus

Brangwynne 2011 *PNAS*
 Feric 2016 *Cell*
 Caragine 2019 *eLife*
 Frottin 2019 *Science*
 Riback 2020 *Nature*

(Peri)centromeres/ heterochromatin

Larson 2017 *Nature*
 Strom 2017 *Nature*
 Cerase 2019 *NSMB*
 Wang 2019 *Mol Cell*
 Trivedi 2019 *Nat Cell Biol*
 Huo 2020 *Mol Cell*

Telomeres

Shin 2018 *Cell*
 Min 2019 *Genes Dev*
 Jack 2022 *Dev Cell*

DNA repair sites

Kilic 2019 *EMBO J*
 Pessina 2019 *Nat Cell Biol*

“Transcriptional condensates”

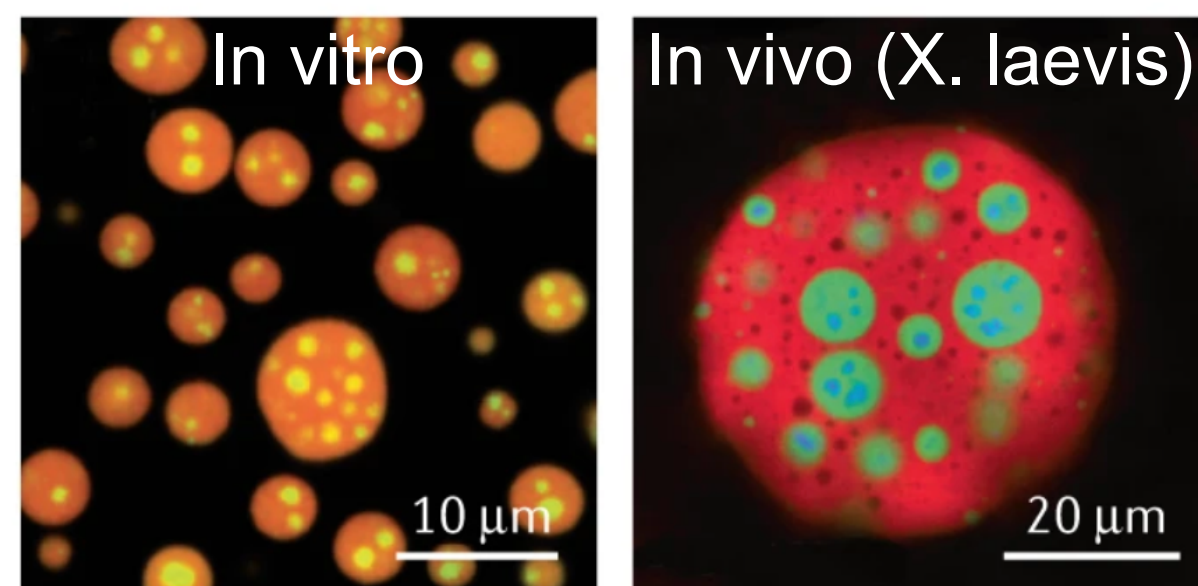
Hnisz 2017 *Cell*
 Sabari 2018 *Science*
 Boija 2018 *Cell*
 Boehning 2018 *NSMB*

Cho 2018 *Science*
 Lu 2018 *Nature*
 Chong 2018 *Science*
 Shrinivas 2019 *Mol Cell*
 Zamudio 2019 *Mol Cell*
 Klein 2020 *Science*
 Wei 2020 *Nat Cell Biol*
 Lu 2020 *Nat Cell Biol*
 Liu 2020 *Nat Cell Biol*
 Henninger 2020 *Cell*
 Ma 2021 *Mol Cell*

Chromatin

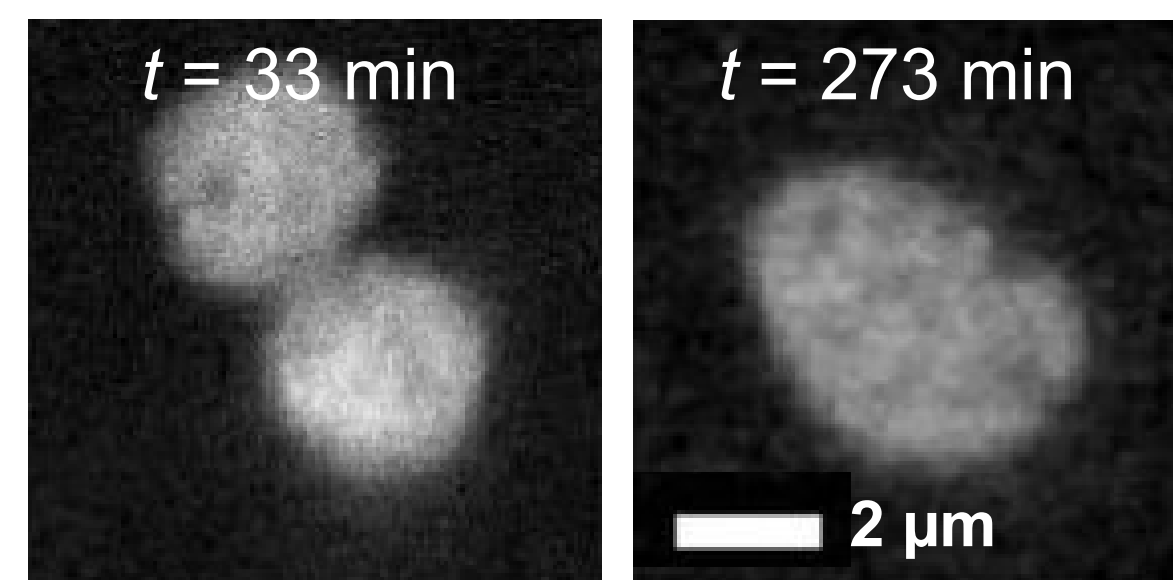
Gibson 2019 *Cell*
 Gallego 2020 *Nature*

Droplets of nucleolar proteins



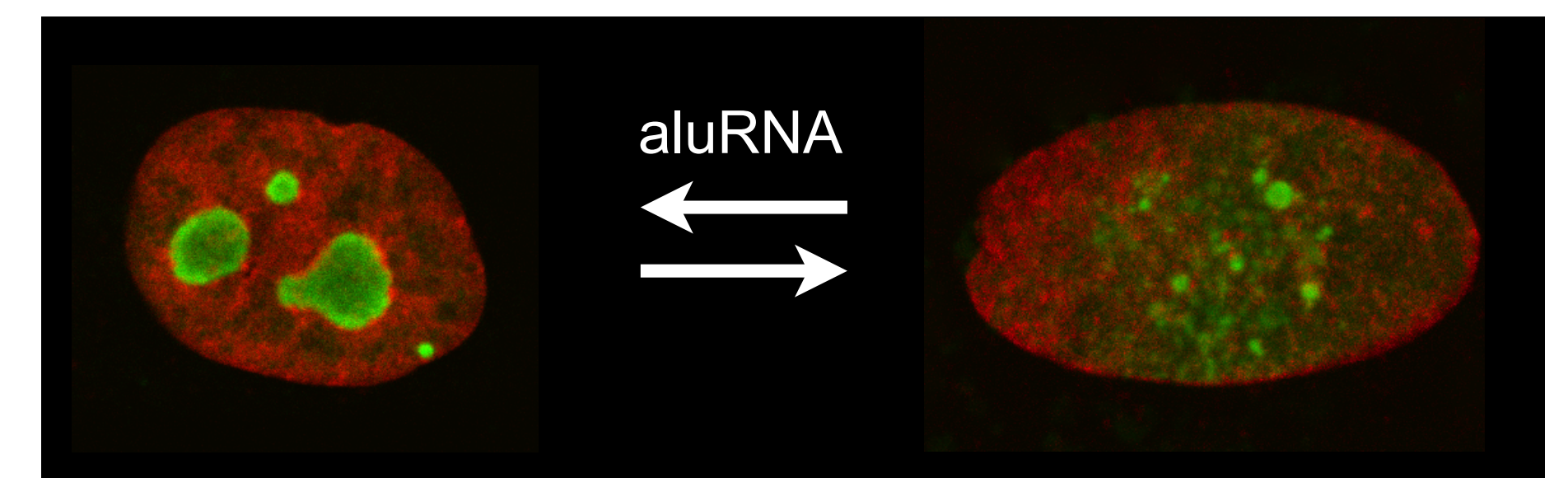
Lafontaine 2020 *Nat Rev Mol Bio*

Nucleoli fusion



Caragine 2019 *eLife*

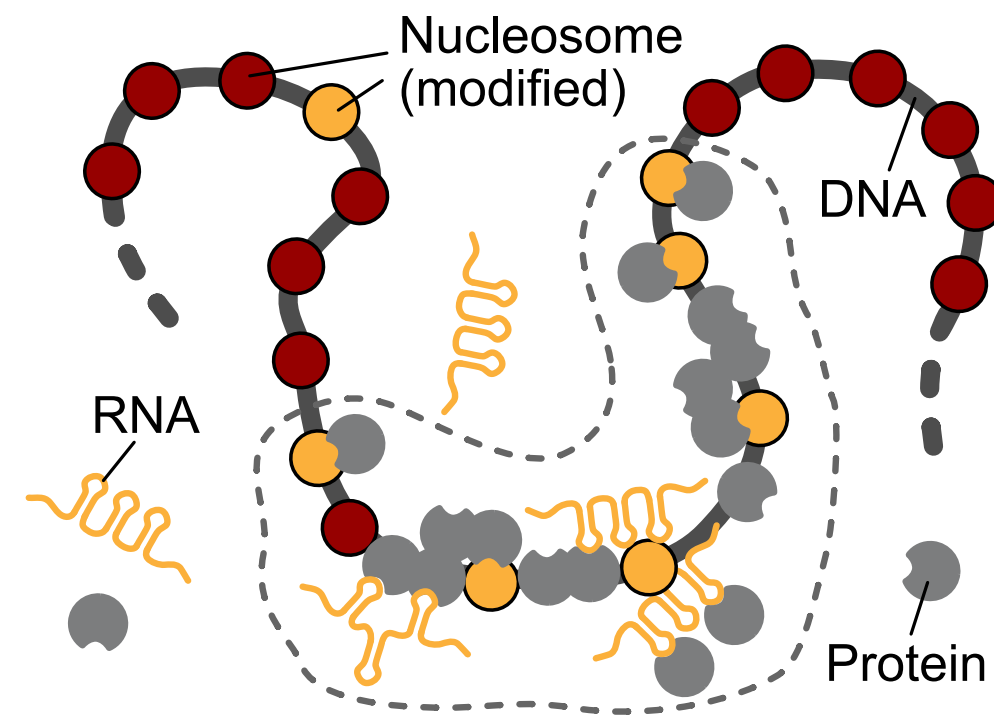
RNA dependent dispersion of nucleoli



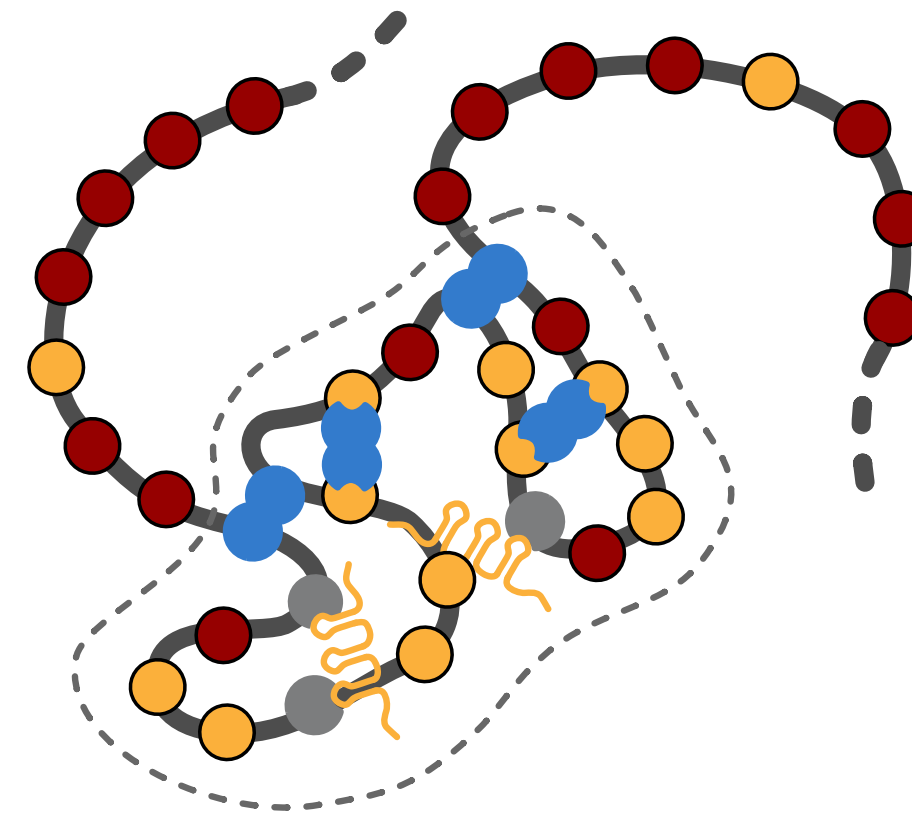
Caudron-Herger 2015 *EMBO J*; 2016 *Nucleus*

Different mechanisms to form chromatin subcompartments

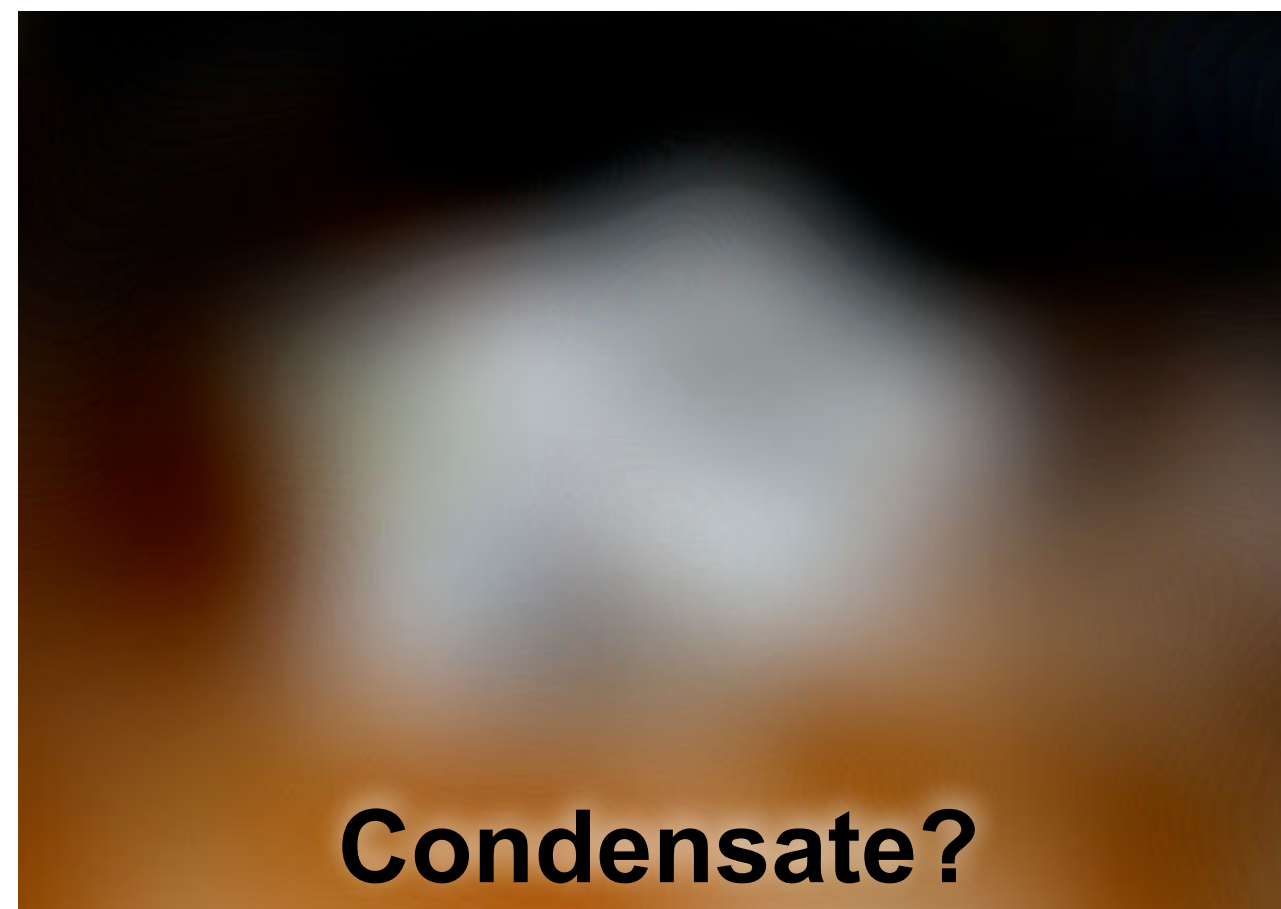
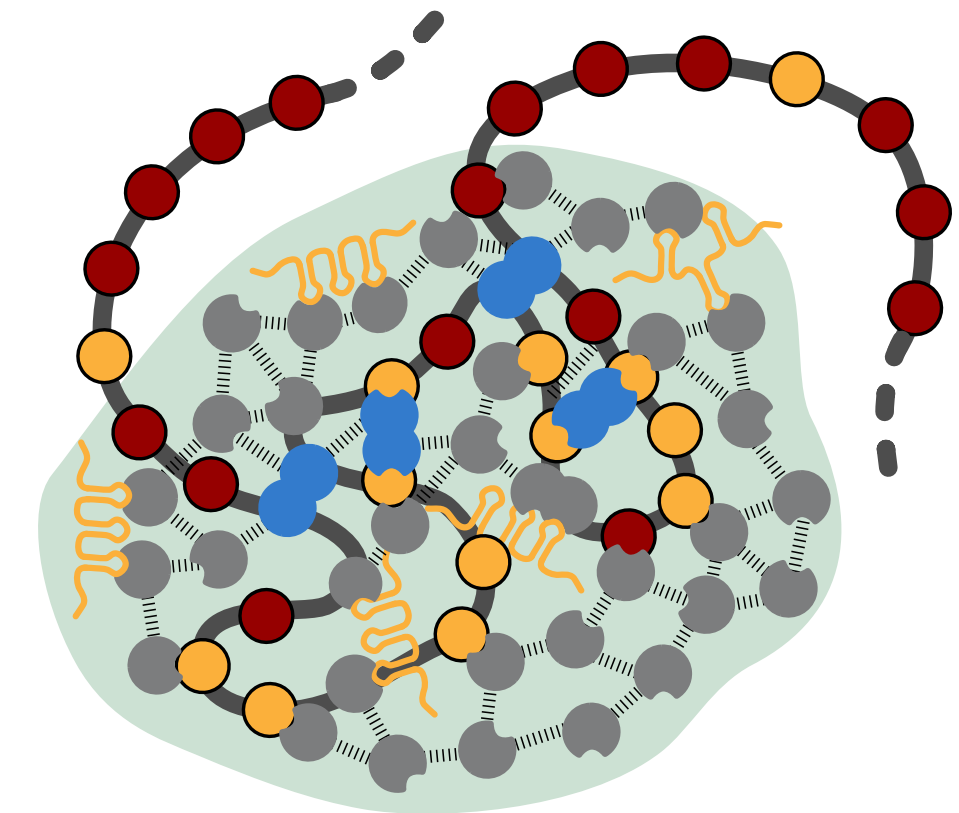
Binding site cluster



Chromatin bridging interactions



Liquid-liquid phase separation



Original image by Sean McGrath

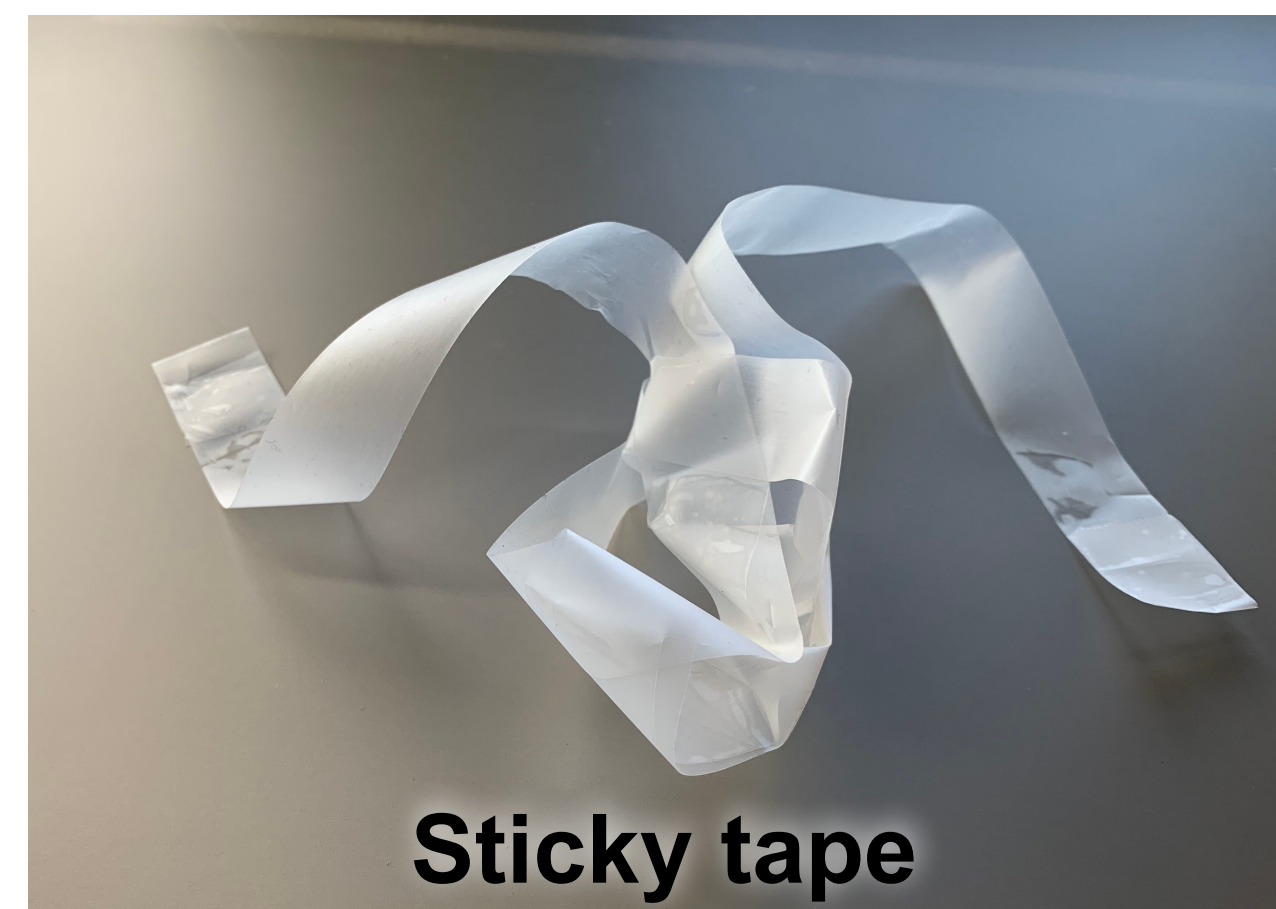


Image by Mathew Spolin