

The mass equation law for binding of a protein P to its DNA

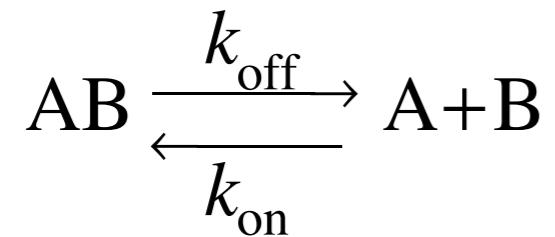


binding of the first proteins with the dissociation constant K_1

D_{free} , concentration free DNA; P_{free} , concentration free protein

$$\text{binding constant } K_B = \frac{1}{\text{dissociation constant } K_D}$$

How fast is binding or dissociation



k_{off} in s^{-1} is the reaction rate constant for dissociation

k_{on} in $\text{M}^{-1} \text{s}^{-1}$ is the reaction rate constant for binding

$$\frac{k_{\text{off}}}{k_{\text{on}}} = K_{\text{d}}$$

relation to the equilibrium dissociation constant

$$\frac{1}{k_{\text{off}}} = \tau$$

life time of the complex

$$\frac{d[AB]}{dt} = k_{\text{on}} \cdot [A] \cdot [B] - k_{\text{off}} \cdot [AB]$$

rate equation for complex formation,

can be solved but it is already difficult

k_{on} cannot be higher than $10^8 - 10^9 \text{ M}^{-1} \text{ s}^{-1}$ for a diffusion controlled reaction

What is the meaning of the dissociation constant for binding of a single ligand to its site?

1. K_d is a concentration and has units of mol per liter
2. K_d gives the concentration of ligand that saturates 50% of the sites (when the total site concentration is much lower than K_D)
3. Almost all binding sites are saturated if the ligand concentration is $10 \times K_d$
4. The dissociation constant K_d is related to Gibbs free energy ΔG by the relation $\Delta G = - R T \ln(K_d)$

Our energy and time coordinate system

K (M)	concentration scale	ΔG (kcal/mol)	k_{off} (s⁻¹)	complex life time	Binding interaction
			for k		
10	1 mM	-4.1	10	10 ms	ion-DNA ion-protein
10	0.1 mM	-5.5	10	0.1 sec	
10	10 μ M	-6.8	1	1 sec	enzyme-ligand (weak)
10	1 μ M	-8.2	10	10 sec	protein-DNA, unspecific
10	0.1 μ M	-9.5	10	100 sec	enzyme-ligand (strong)
10	10 nM	-10.9	10	16.7 min	
10	1 nM	-12.3	10	2.8 hours	protein-DNA specific
10	0.1 nM	-13.6	10	28 hours	
10	10 pM	-15	10	11.6 days	antibody-antigen
10	1 pM	-16.4	10	116 days	

Biophysical Concepts and Theoretical Descriptions

Oct 16: Intro protein-DNA/RNA interactions

Oct 23: The energy, length and time coordinate system

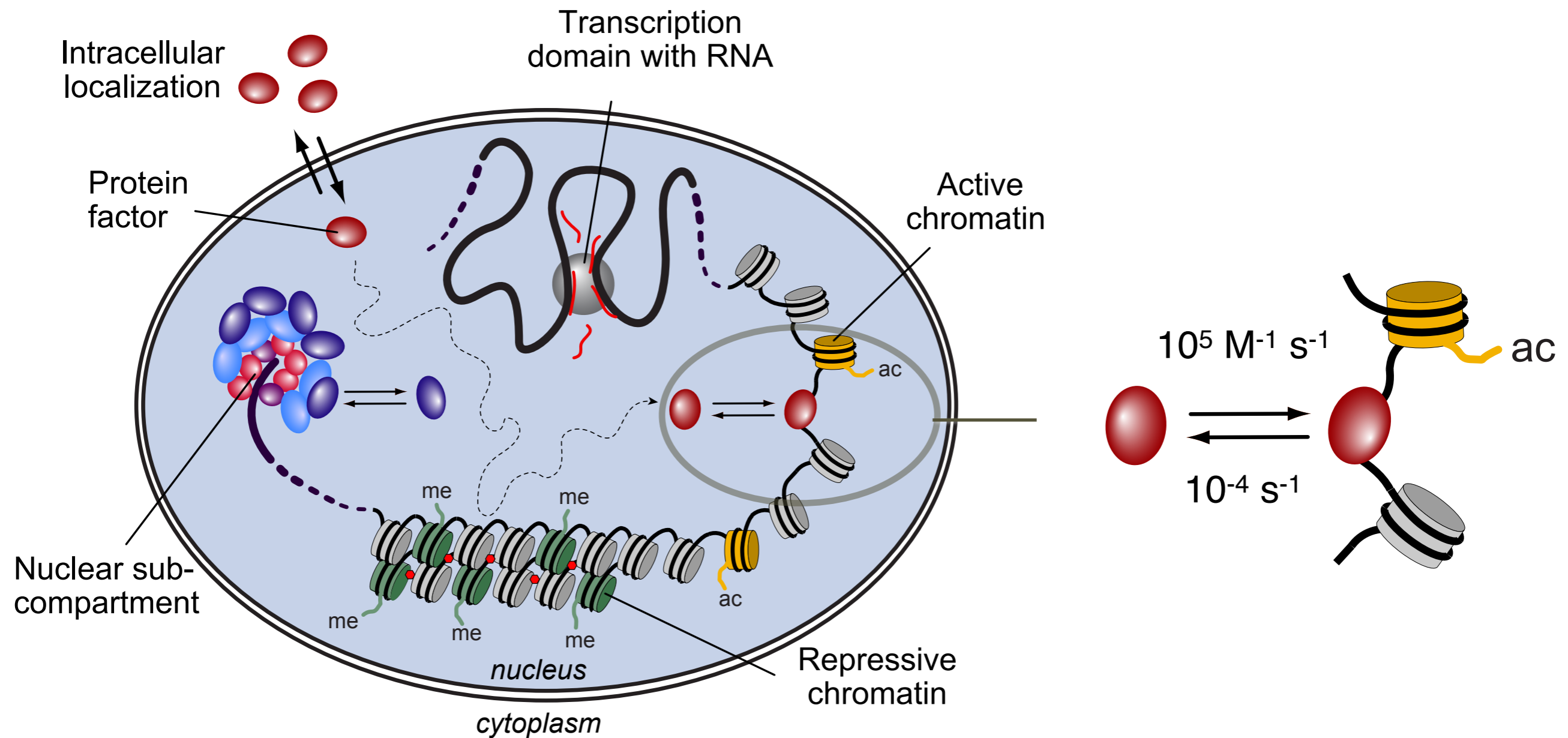
Oct 30: Diffusion (Fabian Erdel)

Nov 6: Kinetics

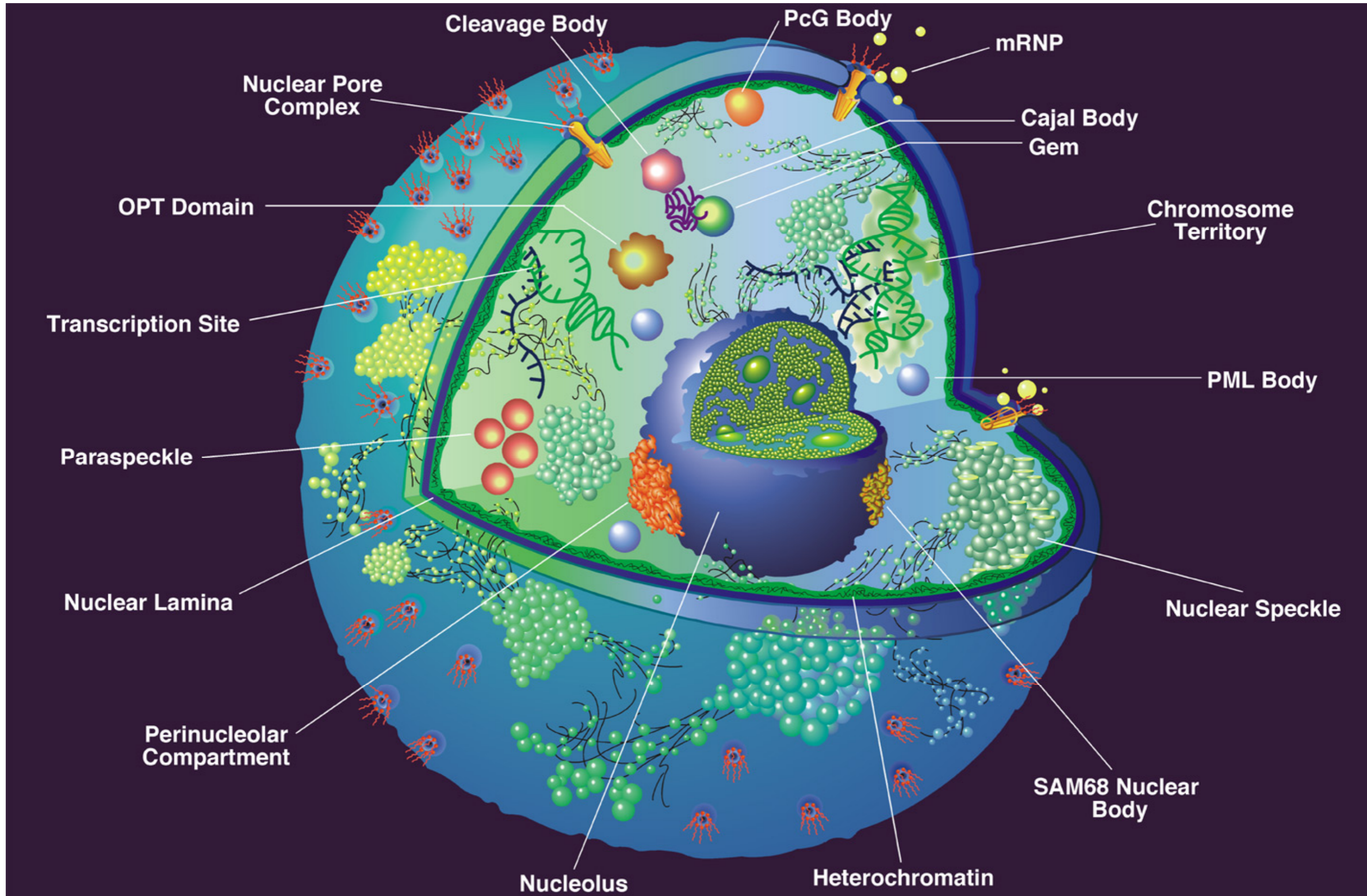
Nov 13: Essentials of protein-DNA/RNA interactions

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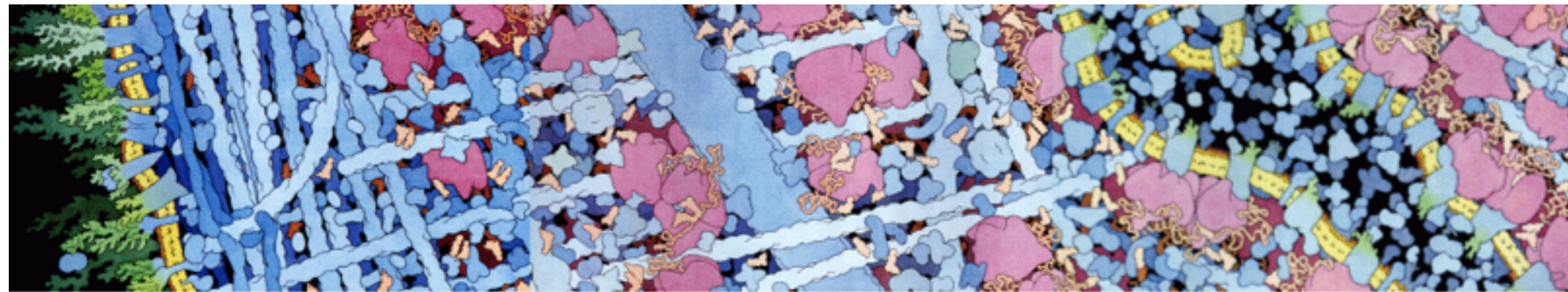
How to link in vitro measurements to interactions in the cell?



The mammalian cell nucleus



The cell is a very crowded place (David Goodsell)



from left to right:

cell surface

cytoplasm

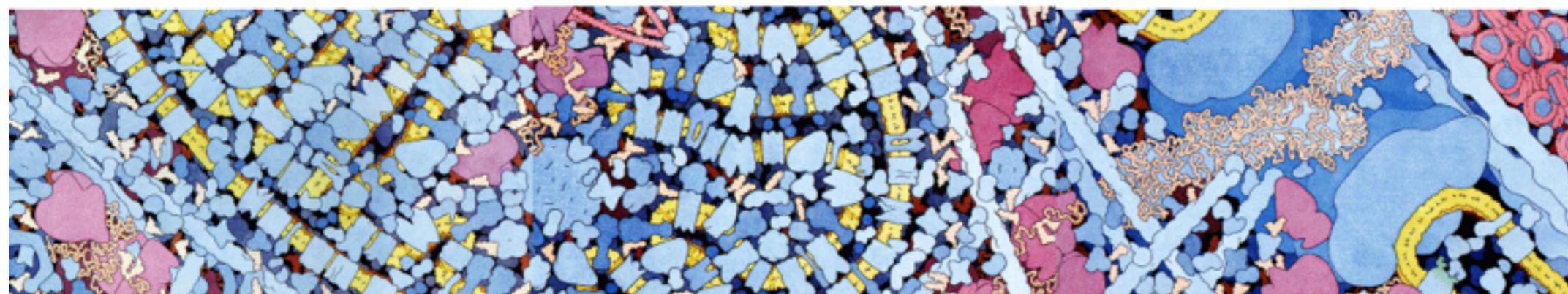
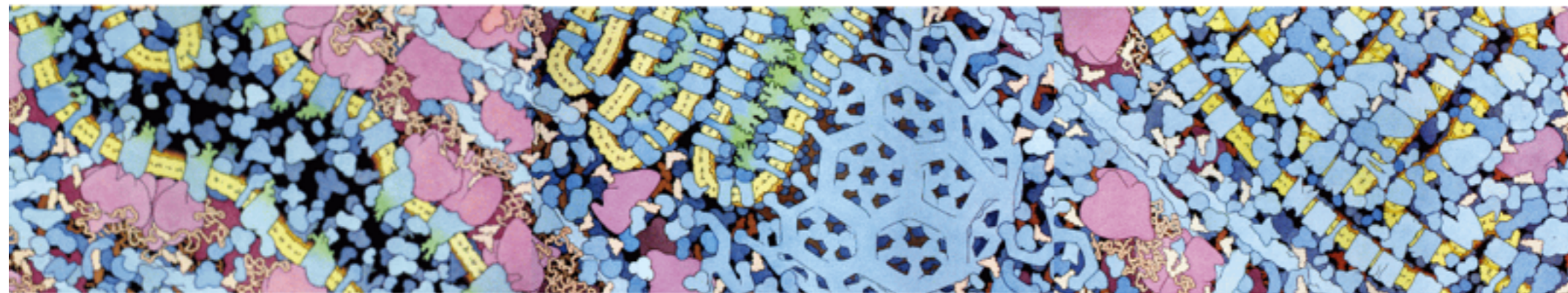
synthesis of
proteins from the
endoplasmic
reticulum

Golgi apparatus,

coated vesicle

mitochondrion

nucleus



proteins: blue

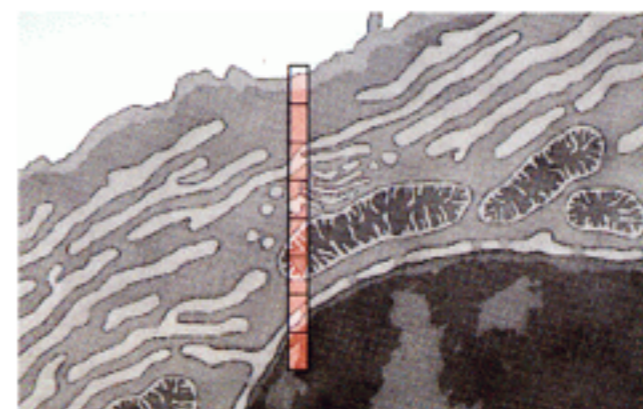
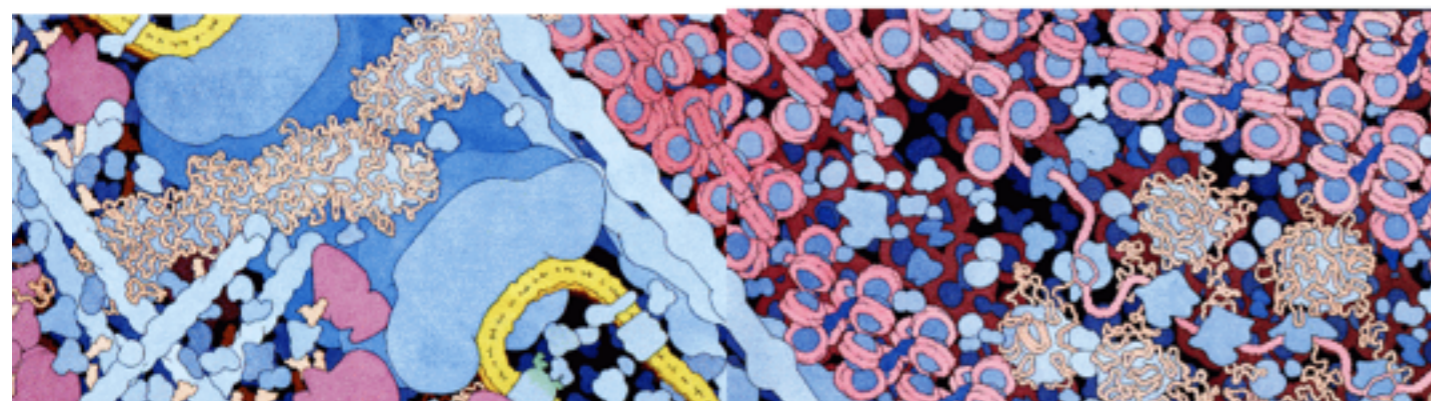
DNA and RNA: red
and orange

lipids: yellow

carbohydrates:

green

Ribosomes:
magenta



Concentration of proteins and DNA in the nucleus

DNA

~ **15mg/ml** (6pg DNA per cell,¹⁹ nucleus ~1/10 of cell volume 4×10^{-9} cm³ typical)²⁰

~**18.5mg/ml** (56mM nucleosome concentration,²¹ 200 bp/nucleosome, 2bases/bp, 1Mbase/30g.²²

~**19 mg/ml**²³

~**20-31 mg/ml** (8.1-12.5pg/cell,²⁴ nucleus ~1/10 of cell volume 4×10^{-9} cm³ typical)²⁰

RNA

~**11 mg/ml** (5-25pg RNA per cell,²⁵ 18% in nucleus,²⁶ nucleus ~1/10 of cell volume 4×10^{-9} cm³ typical).²⁰

~**12-15mg/ml** (27.1-33.1pg/cell,²⁴ 18% in nucleus,²⁶ nucleus ~1/10 of cell volume 4×10^{-9} cm³ typical).²⁰

Protein

~**106-215 mg/ml** in various regions of the nucleus.²⁷

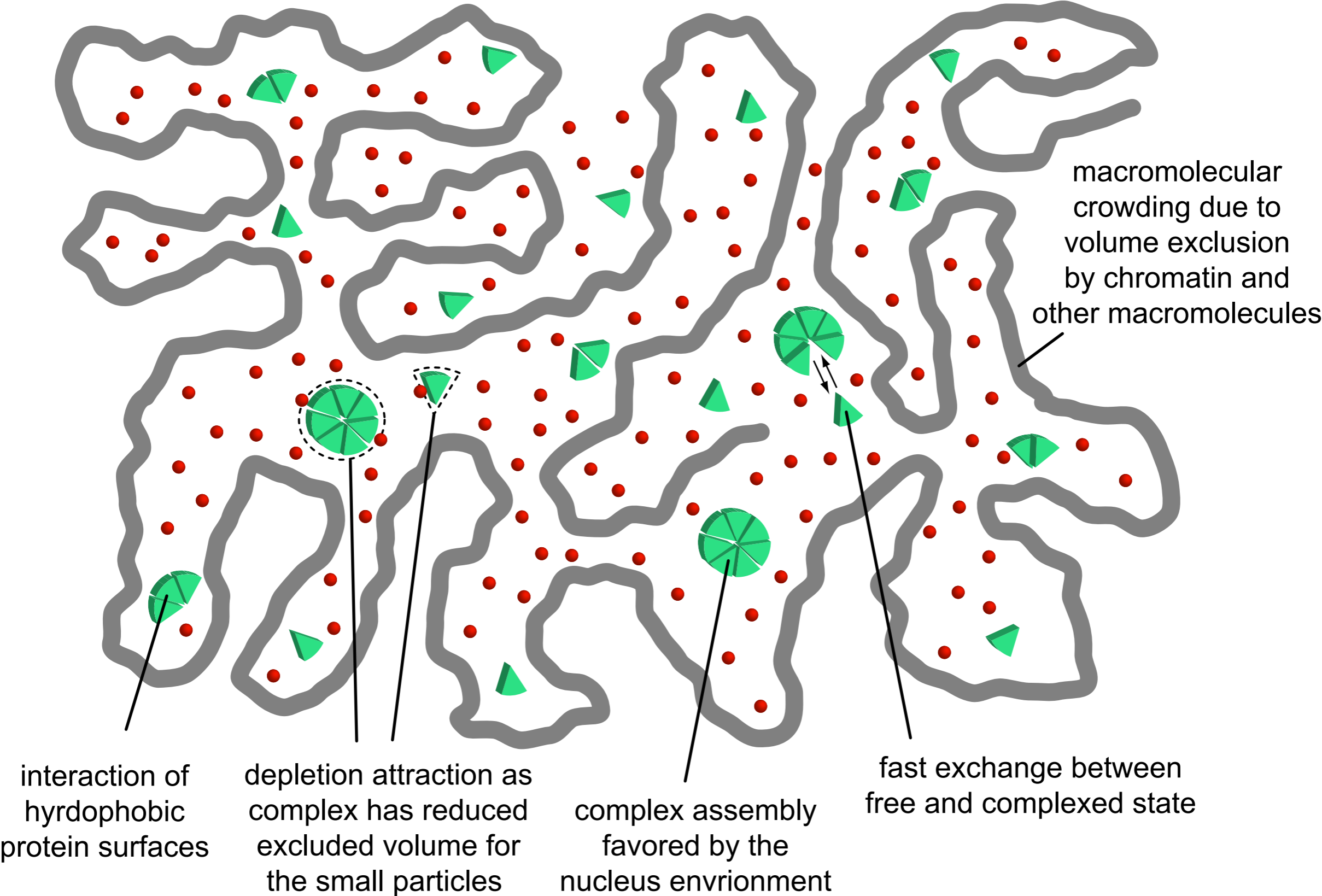
~**108mg/ml** (6pg DNA per cell,²⁰ protein mass 72X DNA mass and cell volume 4×10^{-9} cm³ typical).²⁰

~**200-300mg/ml** in E.coli.²⁸

Concentration of ions in the nucleus

- ▶ ~0.1 M K^+/Na^+ ($K^+ > Na^+$)
- ▶ 0.5-1 mM Mg^{2+}
- ▶ low μM values of Ca^{2+}
- ▶ 3.1 times higher apparent viscosity than water measured for the mobility of GFP ($D = 25 \mu m^2 cm^{-1}$)
- ▶ inorganic cations are significantly more abundant than the corresponding mobile anions nucleic phosphate groups and negative protein charges are in excess of the positive protein charges
- ▶ high Cl^- concentration (in vitro!) can significantly disturb protein-protein or protein-DNA interactions

Macromolecule interactions in the nucleus are different from in vitro conditions



macromolecular crowding due to volume exclusion by chromatin and other macromolecules

interaction of hydrophobic protein surfaces

depletion attraction as complex has reduced excluded volume for the small particles

complex assembly favored by the nucleus environment

fast exchange between free and complexed state

Measuring binding via protein mobility has a problem: many things affect the observed mobility

