

# Structural Biology – a concept

**structure & dynamics**



***In vivo*  
function**

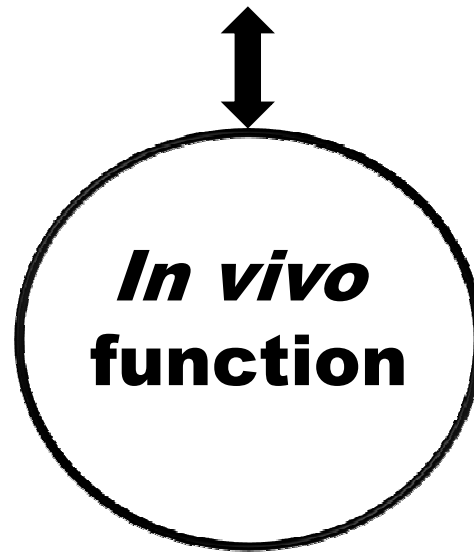
## Where the structural information comes from ....

### PDB Statistics – by method

Molecular Type ↓	X-ray ↓↑	NMR ↓↑	EM ↓↑
Nucleic acid (only)	2054	1296	35
Other	460	49	117
Protein (only)	136930	11383	3848
Protein/NA	6615	264	1069
Total	146059	12992	5069

## ***In vitro* structure & dynamics**

buffered solutions, crystalline state, or deposited isolated molecules on the surface



~~***In vivo* structure & dynamics**~~

Complex environment of living cells

X-ray diffraction

# approximation

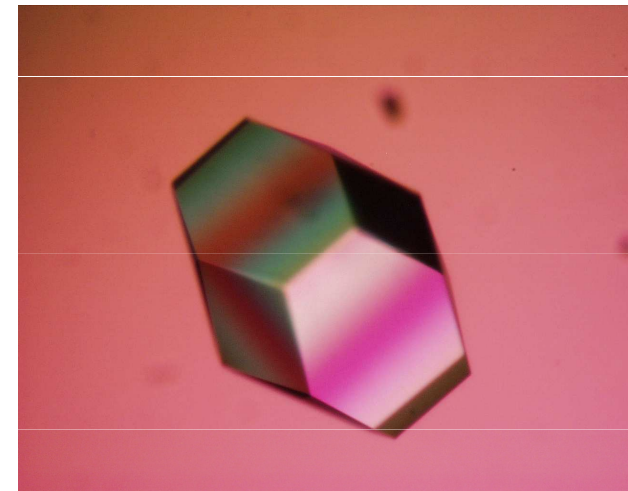
**Complex heterogenous aqueous env.**



**37 °C**

**Simple homogenous anhydrous env.**

vs.

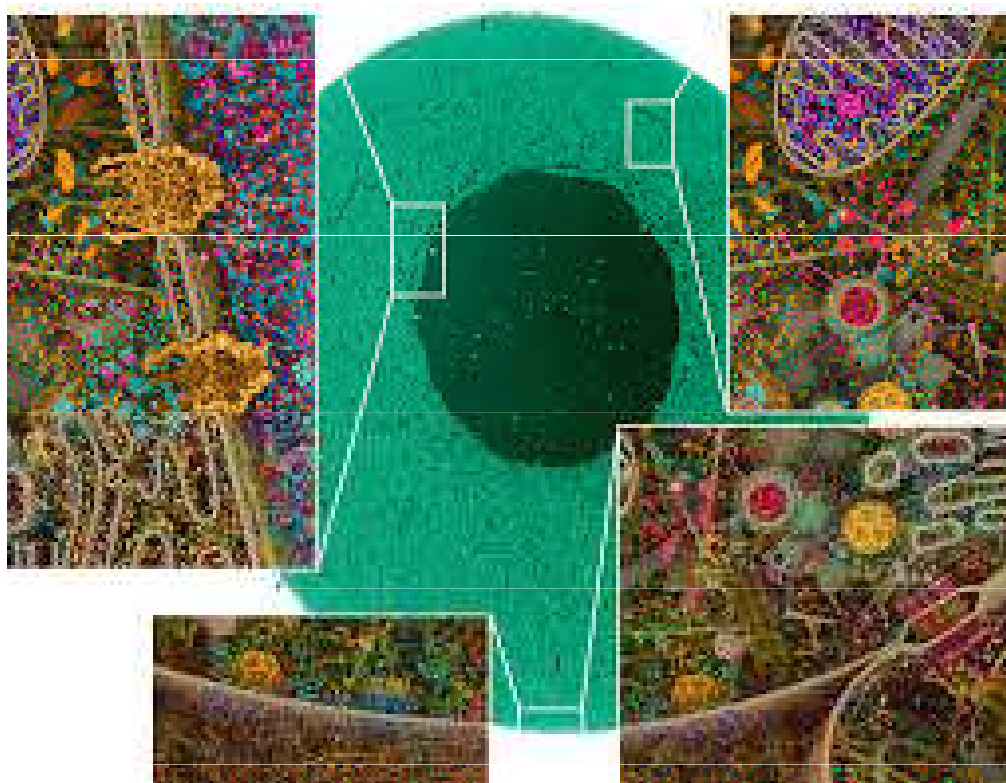


**-180 °C**

# NMR spectroscopy

## approximation

**Complex heterogenous aqueous env.**



**37 °C**

**Simple homogenous aqueous env.**

vs.



**20 °C**

# Electron microscopy

## approximation

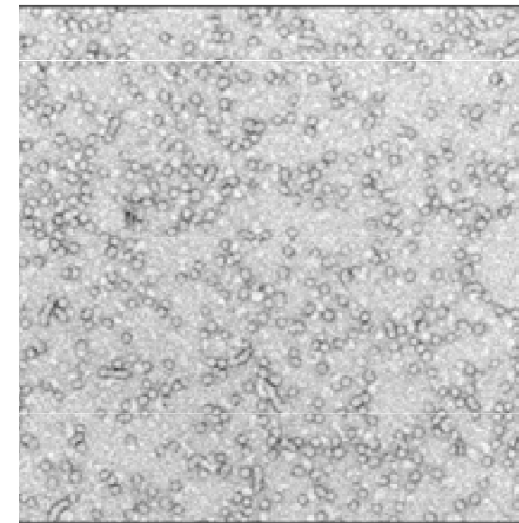
**Complex heterogenous aqueous env.**



**37 °C**

**Simple homogenous aqueous env.**

vs.



**-180 °C**

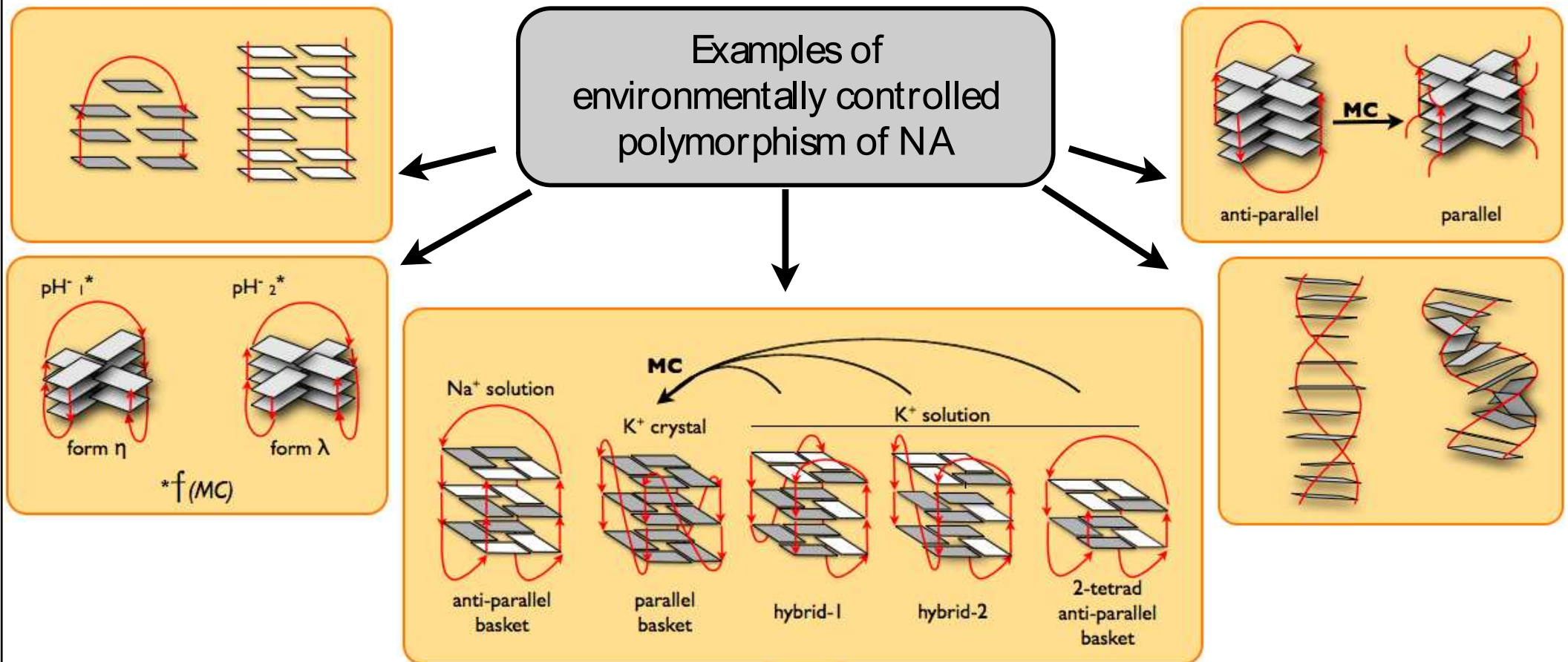
# The use of these techniques imposes ...

... underlying assumptions in STRUCTURAL BIOLOGY

- **structure is independent of environmental conditions**
- **thermodynamically NOT kinetically preferred conformation is responsible for biological activity.**
- **biologically active specie = lowest (free) energy structure**

➤ structure is independent of environmental conditions

...not entirely true, particularly for DNA

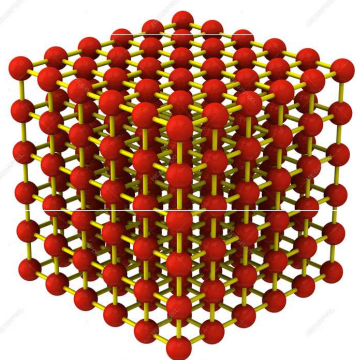


( $\Delta \text{pH}$ ,  $\Delta$  ion strength, ion type, MC, hydration)



# X-ray – particularly prone to env. artifacts

...monocrystal production



Crystal Screen™

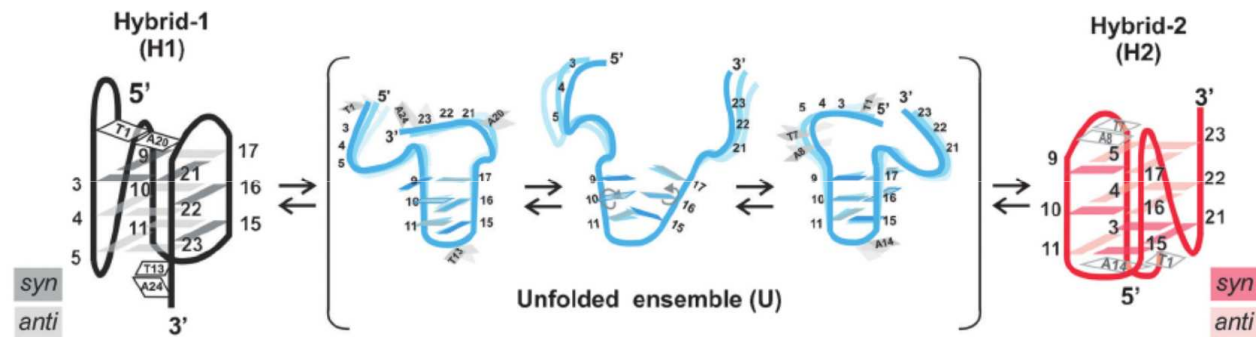
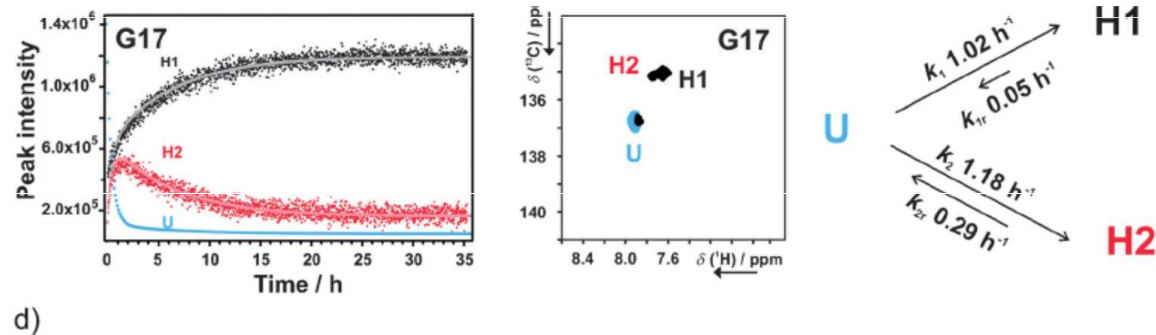
HR2-110 Reagent Formulation

Tube #	Salt	Tube #	Buffer ◊	Tube #	Precipitant
1.	0.02 M Calcium chloride dihydrate	1.	0.1 M Sodium acetate trihydrate pH 4.6	1.	30% v/v (+/-)-2-Methyl-2,4-pentanediol
2.	None	2.	None	2.	0.4 M Potassium sodium tartrate tetrahydrate
3.	None	3.	None	3.	0.4 M Ammonium phosphate monobasic
4.	None	4.	0.1 M TRIS hydrochloride pH 8.5	4.	2.0 M Ammonium sulfate
5.	0.2 M Sodium citrate tribasic dihydrate	5.	0.1 M HEPES sodium pH 7.5	5.	30% v/v (+/-)-2-Methyl-2,4-pentanediol
6.	0.2 M Magnesium chloride hexahydrate	6.	0.1 M TRIS hydrochloride pH 8.5	6.	30% w/v Polyethylene glycol 4,000
7.	None	7.	0.1 M Sodium cacodylate trihydrate pH 6.5	7.	1.4 M Sodium acetate trihydrate
8.	0.2 M Sodium citrate tribasic dihydrate	8.	0.1 M Sodium cacodylate trihydrate pH 6.5	8.	30% v/v 2-Propanol
9.	0.2 M Ammonium acetate	9.	0.1 M Sodium citrate tribasic dihydrate pH 5.6	9.	30% w/v Polyethylene glycol 4,000
10.	0.2 M Ammonium acetate	10.	0.1 M Sodium acetate trihydrate pH 4.6	10.	30% w/v Polyethylene glycol 4,000
11.	None	11.	0.1 M Sodium citrate tribasic dihydrate pH 5.6	11.	1.0 M Ammonium phosphate monobasic
12.	0.2 M Magnesium chloride hexahydrate	12.	0.1 M HEPES sodium pH 7.5	12.	30% v/v 2-Propanol
13.	0.2 M Sodium citrate tribasic dihydrate	13.	0.1 M TRIS hydrochloride pH 8.5	13.	30% v/v Polyethylene glycol 400

- thermodynamically NOT kinetically preferred conformation is responsible for biological activity.

... not generally true

Biological processes (folding, interactions)  $t \ll \tau$



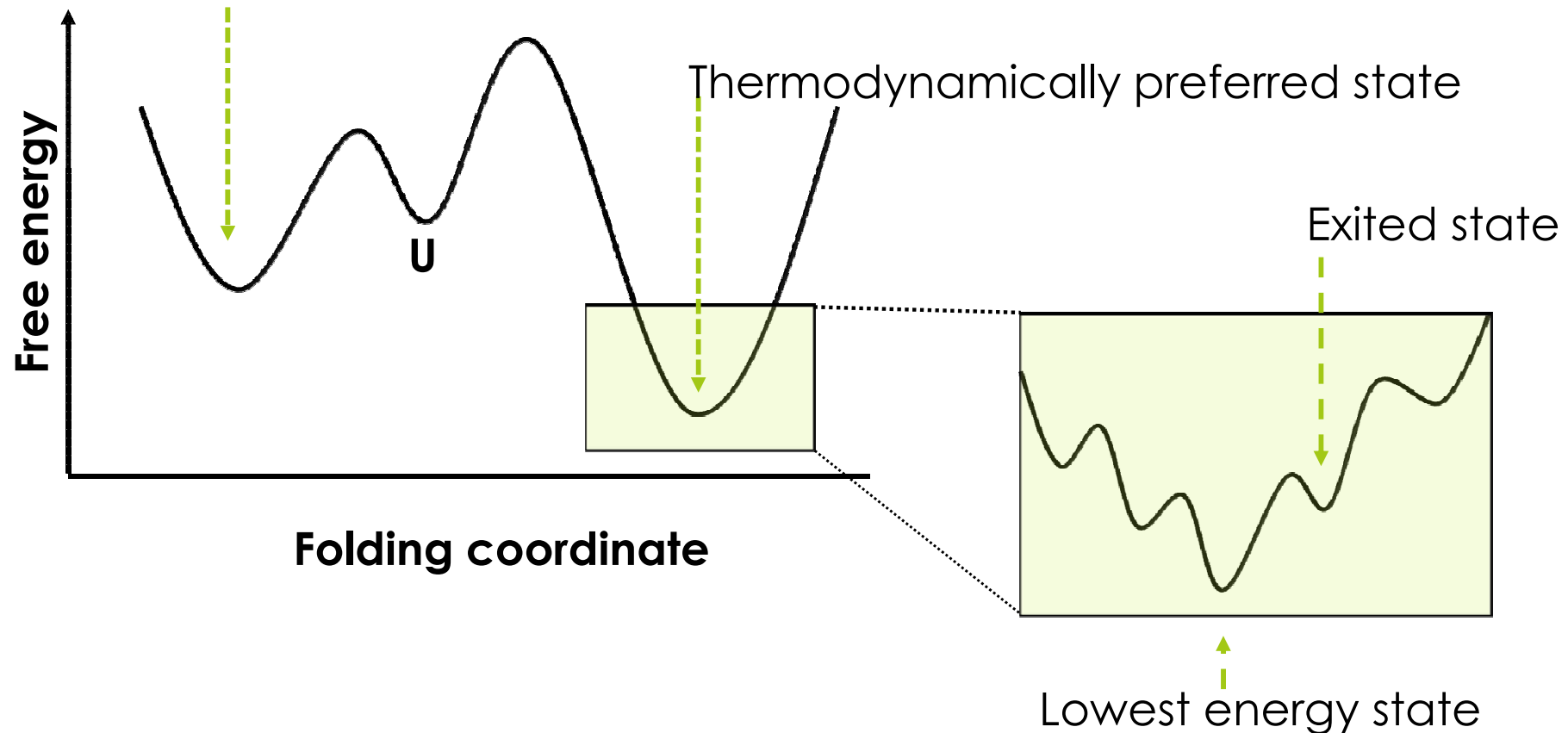
Only H2 would be observed in conventional X-ray, NMR experiment

➤ **biologically active specie = lowest (free) energy structure**

...not entirely true

...number of processes happens via conformational selection  
(from excited/non-visible states)

Kinetically preferred state



Folding coordinate

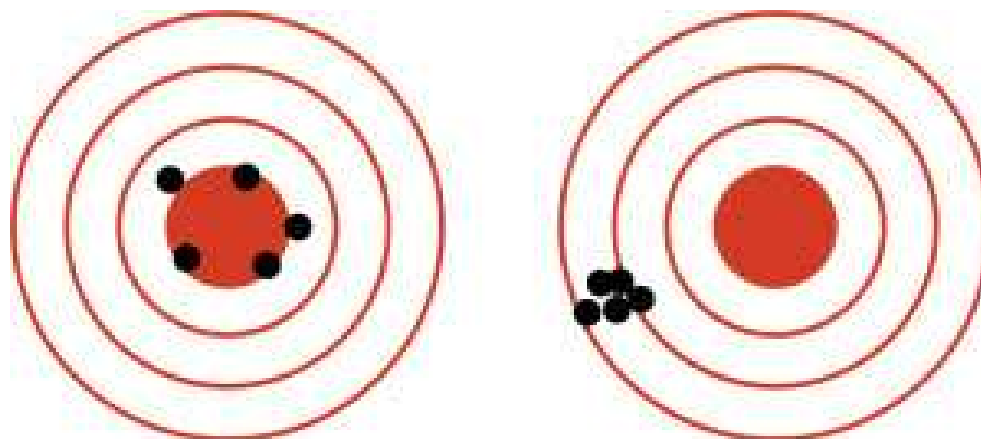
Lowest energy state

## ➤ Summary

...X-ray, NMR, cryoEM structures

...are biased

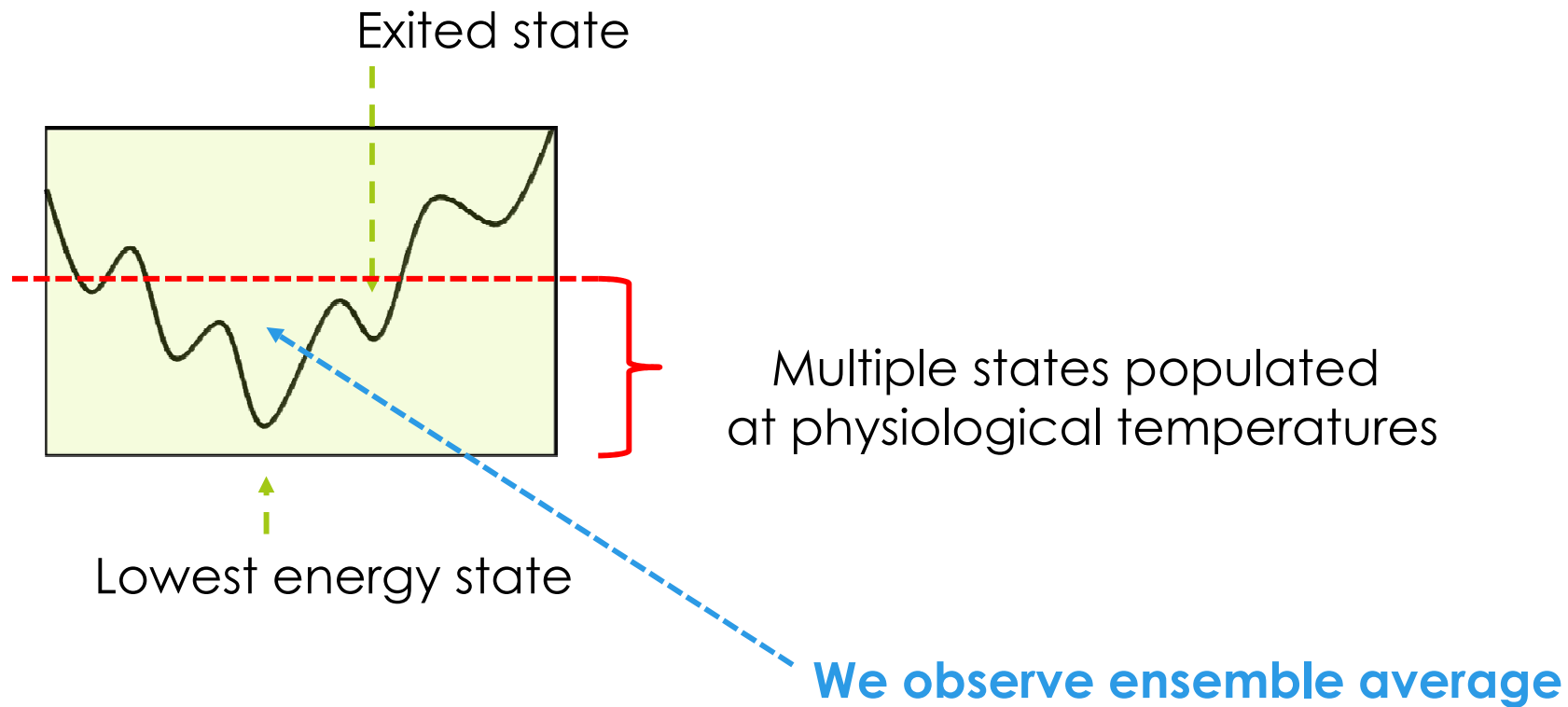
- **Towards thermodynamically preferred (lowest energy) conformation**, which is not necessarily biologically active; the bias is a function of  $T$  [°C]
- **Towards conformation specific to selected environmental conditions**
- **Parameters used to assess structure quality refers only to precision not accuracy**



## ➤ Summary

...in addition, NMR

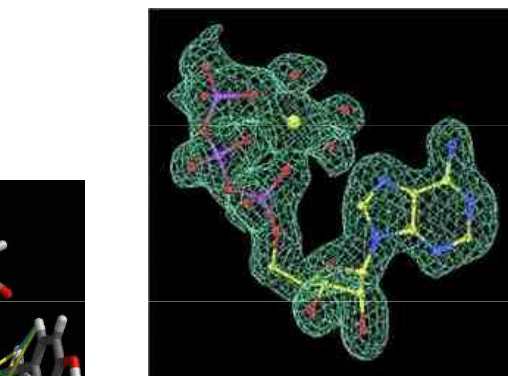
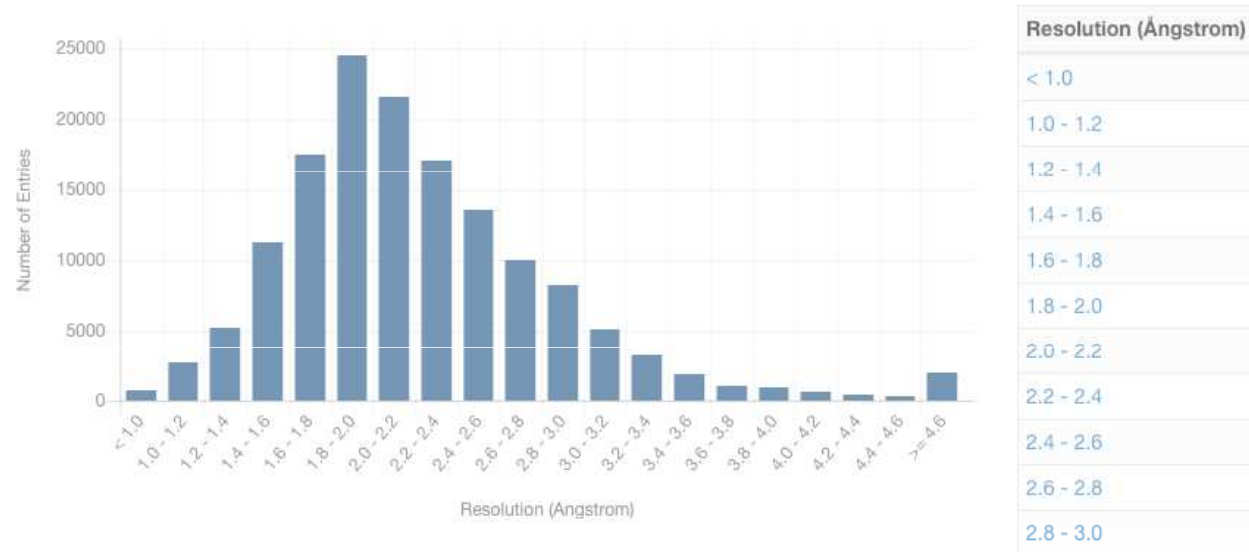
...is biased by **averaging**



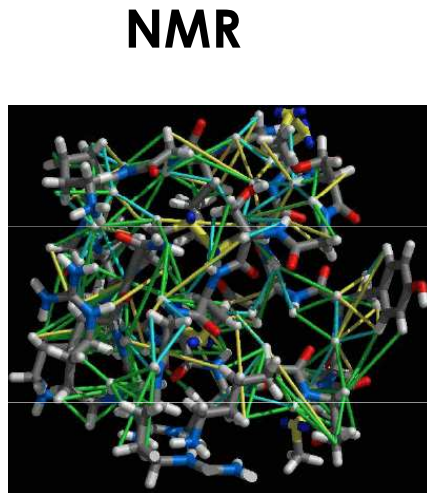
# Bias from external information on local structure

## PDB Statistics: PDB Data Distribution by Resolution

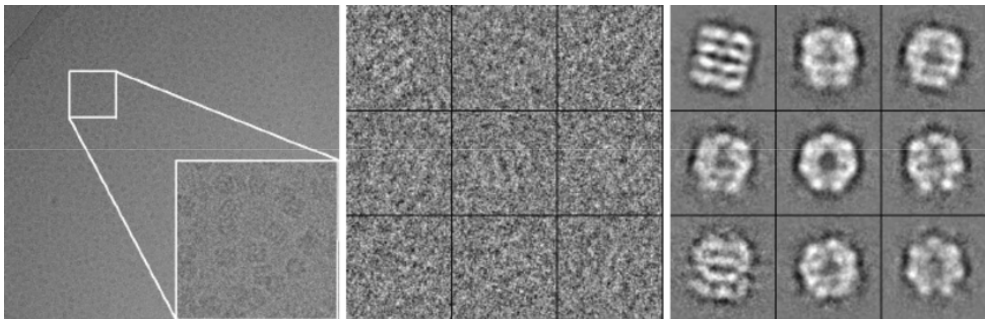
Distribution by structure resolution. Data shown include structures solved by X-ray crystallography or electron microscopy.



X-ray



NMR

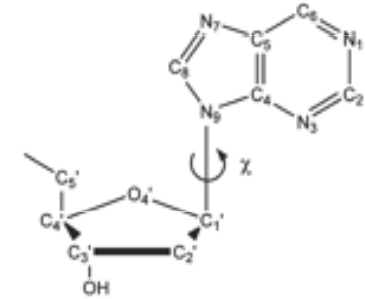


cryoEM

## Bias from external information on local structure

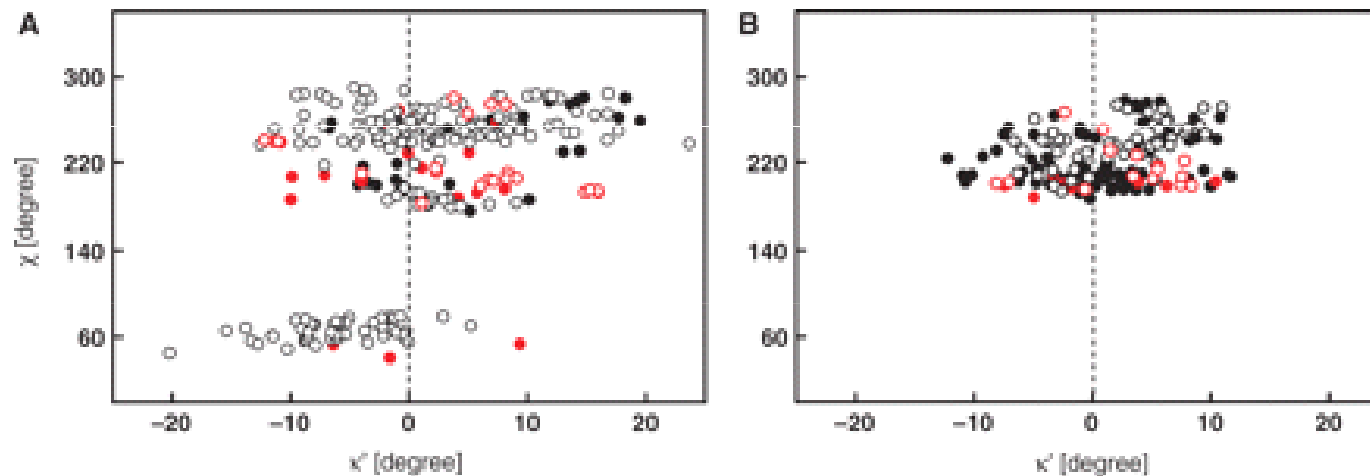
### Example: Implicitly used assumption of planarity of nucleic acid bases

However, NA bases are planar only when isolated and when at 0 K.



### Data from ultra-high resolution structures of nucleotides

*Nucleic Acids Res*, Volume 37, Issue 21, 1 November 2009, Pages 7321–7331



During structure determination we presume planarity

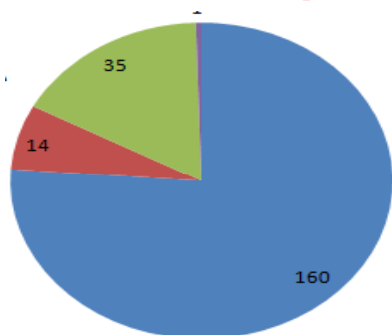
... source of the artefact in NMR – affects interpretation of NOEs, Js, RDCs

# Historically based artifacts

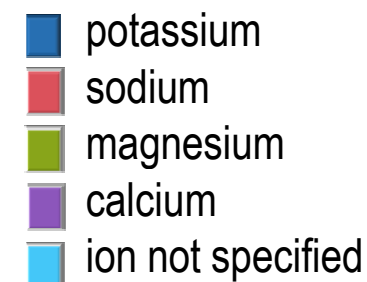
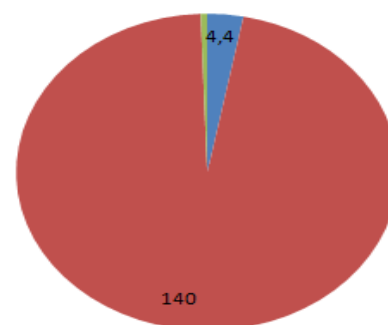
... which can be easily fixed

## Ionic composition of:

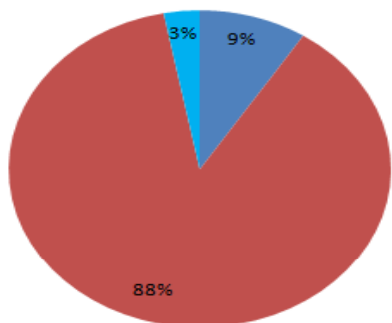
### *Intracellular space*



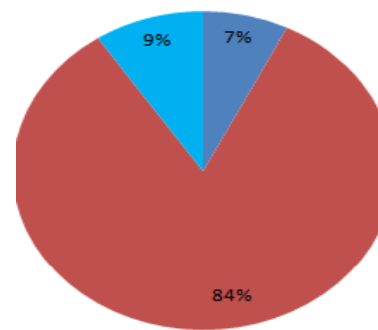
### *Extracellular space*



## Ionic composition of buffers used for NMR studies of:



### *DNA*



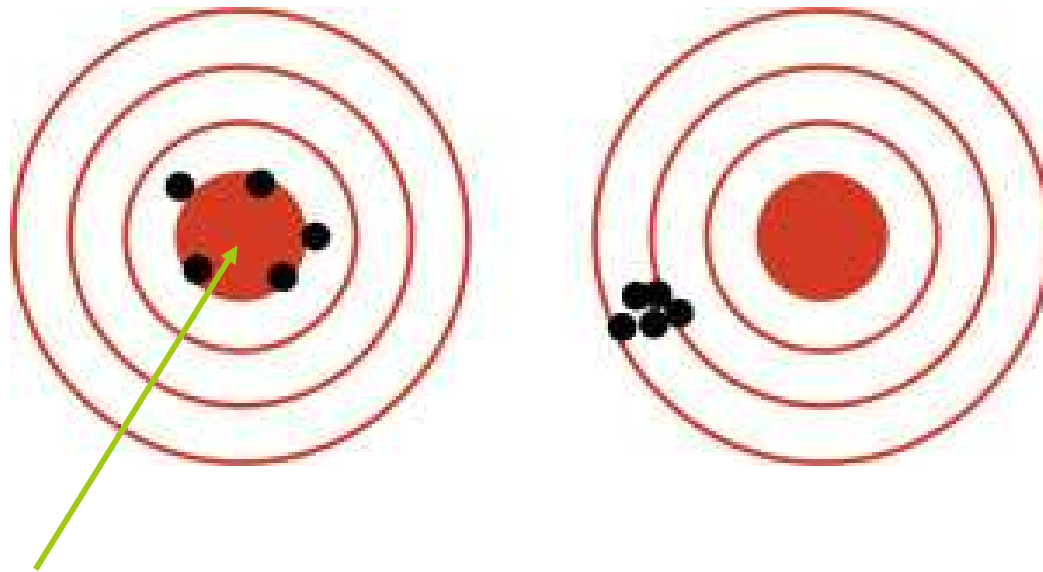
### *RNA*

Statistics based on PDB data



# Structural Biology – an issue

How to recognize physiologically relevant (accurate) structure?



**... assessment of structural accuracy presumes knowledge of reference structure**

# Cellular Structural Biology – a concept

... characterization of structures at physiologically relevant env. conditions

*In vitro* structure & dynamics

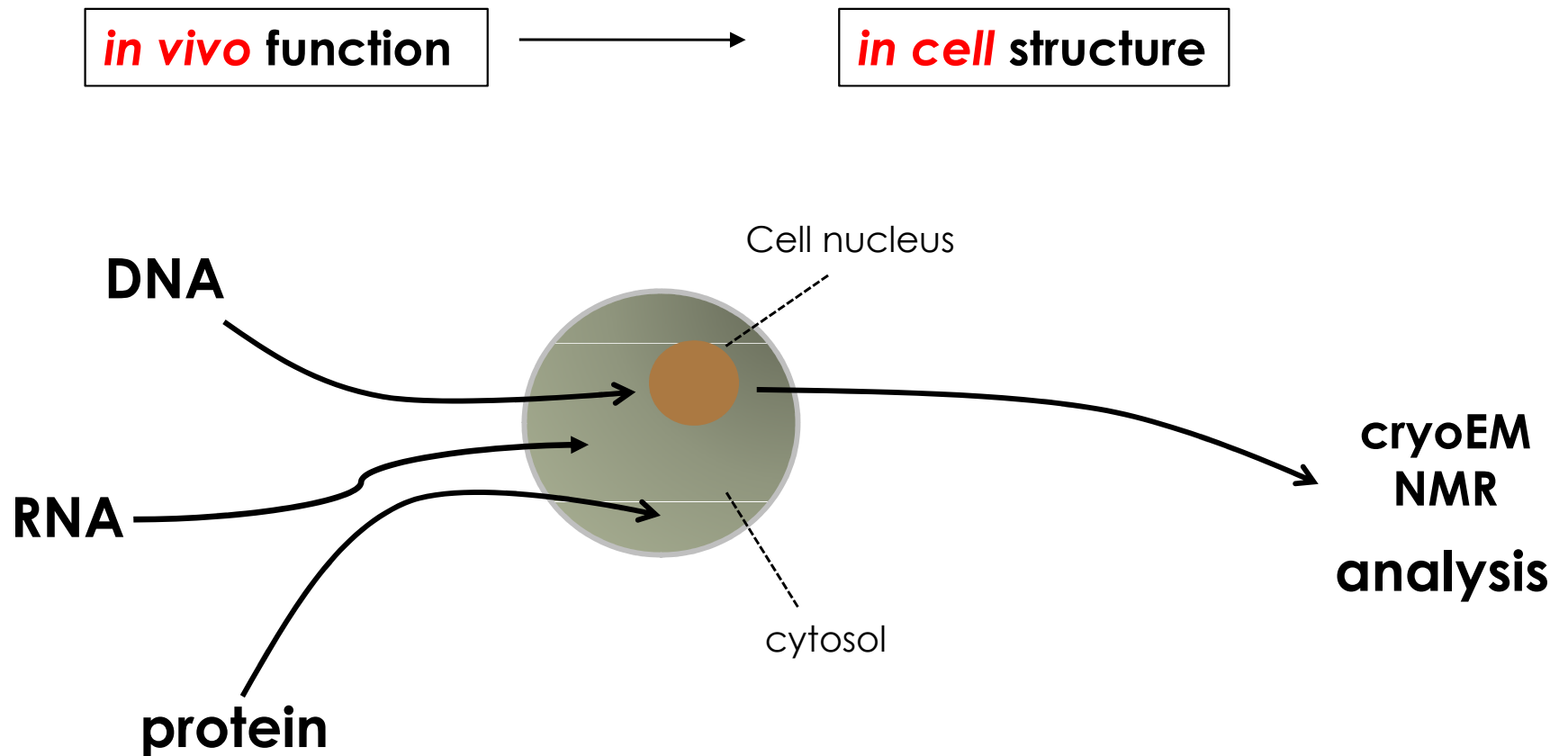
buffered solution **X** crystalline state



***In vivo* structure & dynamics**

Complex environment of living cells

## Cellular structural biology



### Homework – mandatory self-reading

Plitzko et al. Structural Biology Outside the Box-Inside the Cell.  
*Curr Opin Struct Biol.* **2017** Oct;46:110-121

## EXAM by homework

Model a 3D complex between TBA aptamer and FGF2 presuming that the TBA binds to the heparin binding site via electrostatic interactions.

Consider visualization of charge distribution on structural models of FGF2 and TBA.

e.g., Raček et al. Atomic Charge Calculator II: Web-Based Tool for the Calculation of Partial Atomic Charges. *Nucleic Acids Res.* 2020 May 13;gkaa367. doi: 10.1093/nar/gkaa367