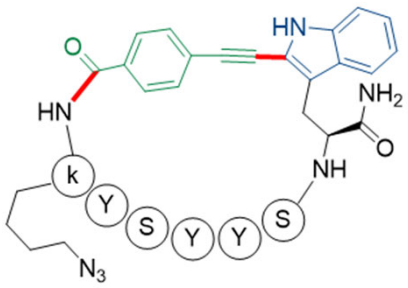
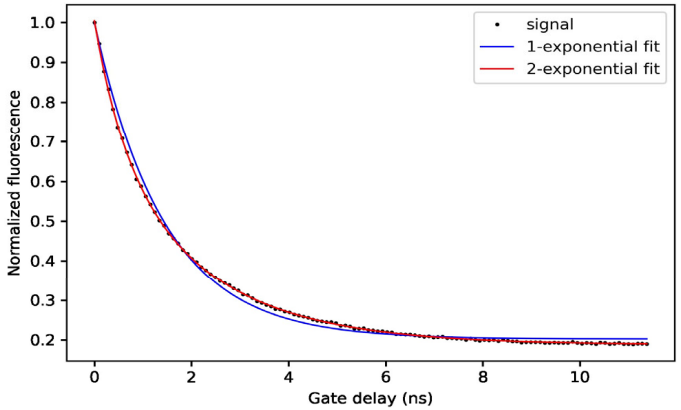
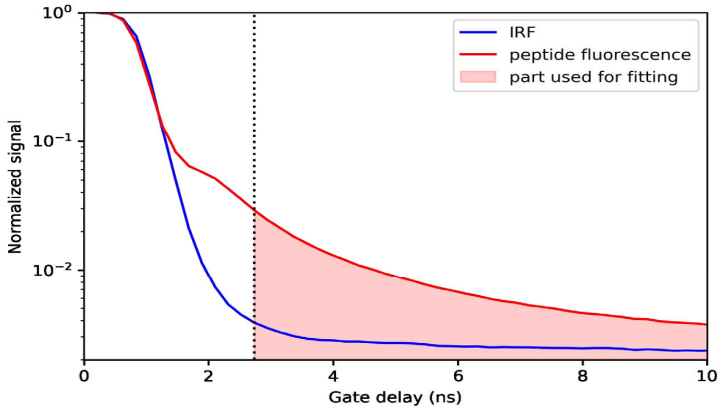
Fluorescence lifetime



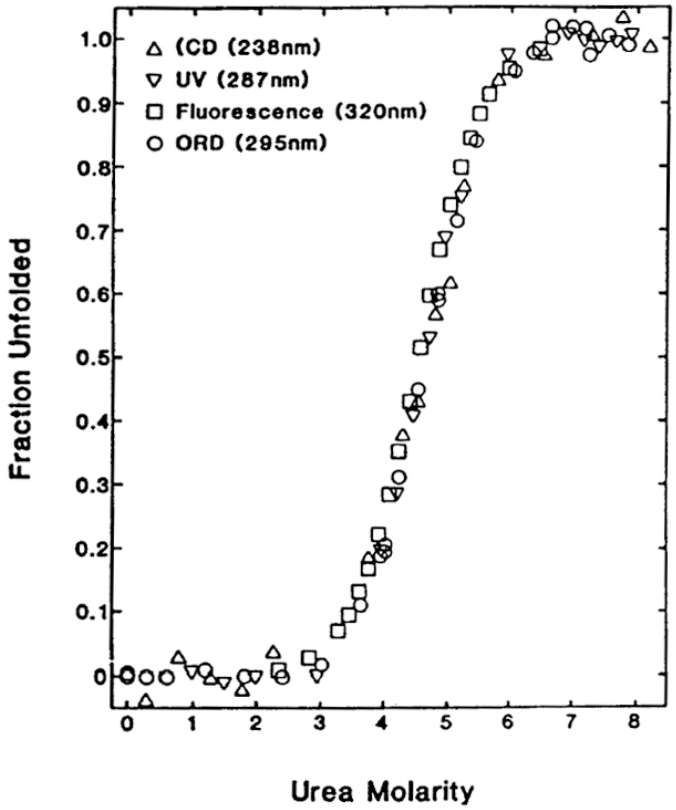
kYSYYSW-NH$_2$
2aa, 53%, 95:5





Xing-Yu Liu, Nathan Ronceray

Denaturation of globular, monomeric protein : RNase T1



$$N \rightleftarrows D$$

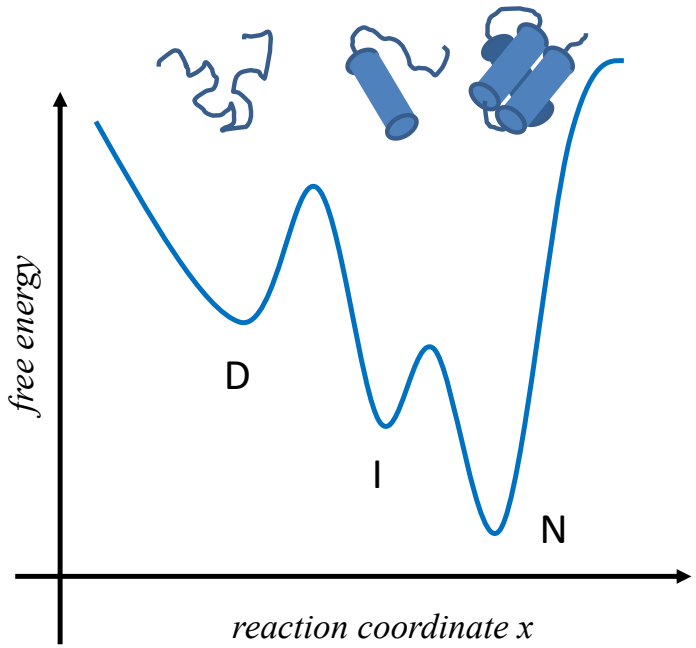
$$y = [\mathrm{N}]\,\mathrm{y}_\mathrm{N} + [D]\,\mathrm{y}_D$$

$$K_D = \frac{[\mathrm{D}]}{[N]} = \frac{\mathrm{y}_N - y}{y - y_D}$$

different parameters completely overlap

normalized transitions ($\theta_N = [N] / ([N] + [D])$) overlap

Three (or more) state equilibrium transitions

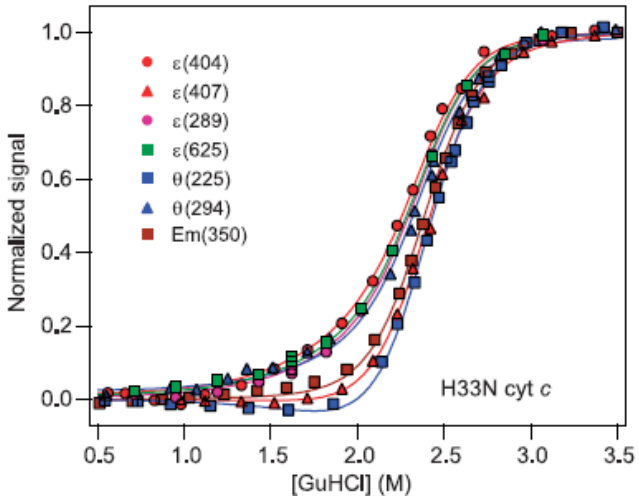


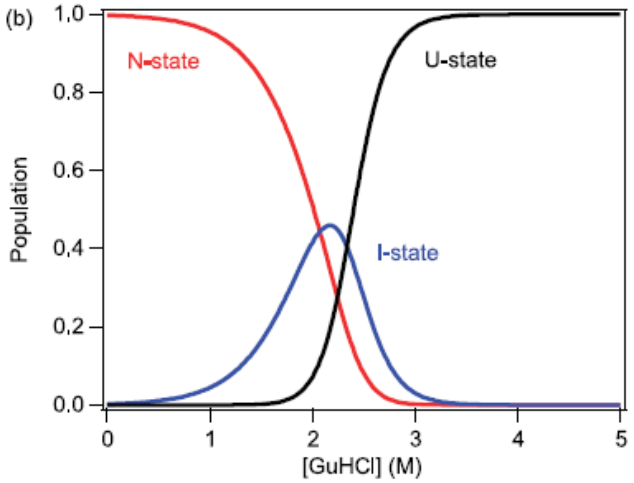
In many proteins, intermediates are populated.

Intermediates include proteins, where only partial structure has formed.

This complicates the analysis.

Multistate transitions in cytochrome c unfolding



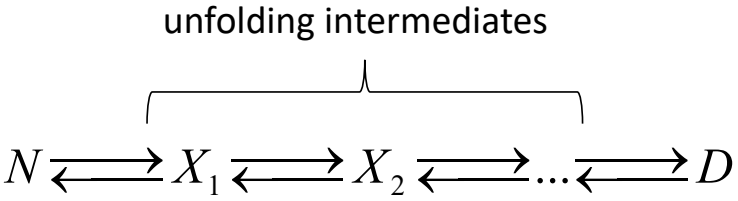


Latypov et al.
JMB 2006

If different parameters are observed, unfolding traces do no longer coincide.

Intermediates accumulate during the unfolding transition

Multi-state transition



apparent stability, eludicated by summing the individual contributions

$$K_{app} = K_D \frac{1 + \sum d_i \frac{K_i}{K_D}}{1 + \sum (1 - d_i) K_i} = \frac{K_D + \sum d_i K_i}{1 + \sum (1 - d_i) K_i}$$

$$d_i = \frac{y_i - y_N}{y_D - y_N}, \quad 0 < d_i < 1$$

$$K_i = \frac{[\mathrm{X_i}]}{[\mathrm{N}]} \qquad K_D = \frac{[D]}{[\mathrm{N}]}$$

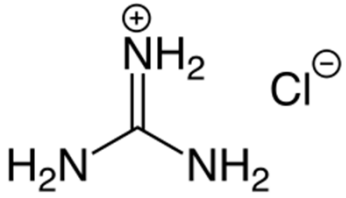
Denaturation with chemical agents

Molecular mechanism of denaturant action:

1. Direct effect:

   H-bonding to polar groups, mostly the protein backbone, thereby competing with internal H-bonds

   If charged: Interaction with ionic groups

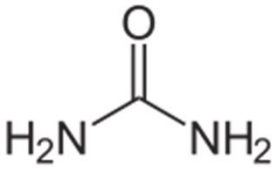


guanidinium chloride

2. Indirect effect:

   Alteration of water structure and thus diminishment of the hydrophobic effect

   Facilitation of the exposure of hydrophobic groups.



urea

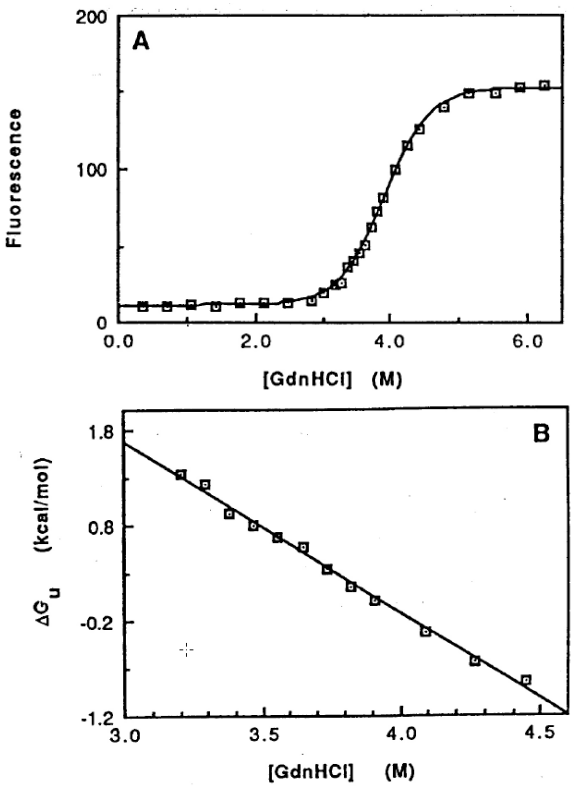
Protein denaturation with denaturants

The **effect of denaturants** on the free energy is linear (empirical finding)

$$\Delta G^0 = \Delta G^0_{H_2O} - m\ [\text{denaturant}]$$

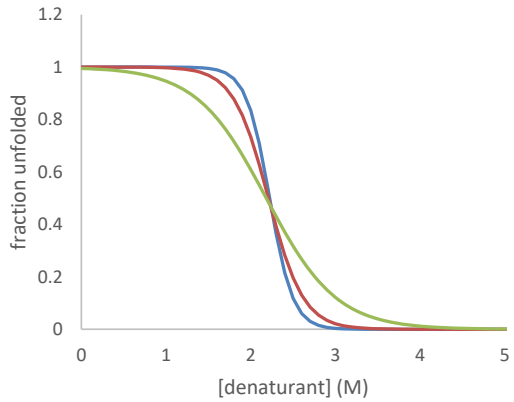
The **free energy of unfolding** can thus be determined by an extrapolation to **0 M denaturant**

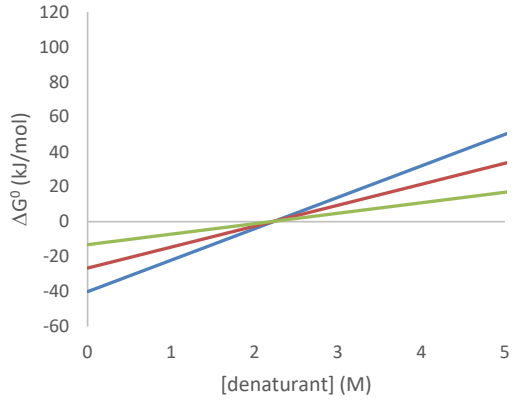
Example: Chymotrypsin inhibitor 2 (CI2)



Sensitivity to denaturant

simulated unfolding curves





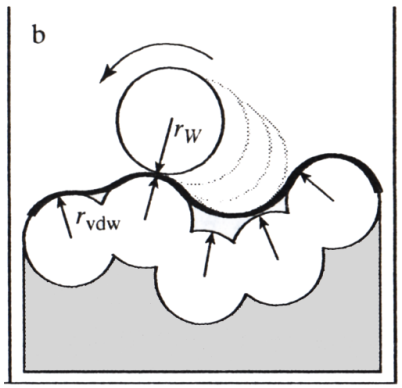
Parameters

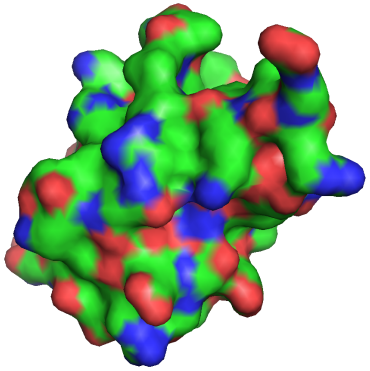
- ΔG_0 = -40 *kJ/mol*, m = 18 *kJ/mol/M*
- ΔG_0 = -26.5 *kJ/mol*, m = 12 *kJ/mol/M*
- ΔG_0 = -13.1 *kJ/mol*, m = 6 *kJ/mol/M*

molecular meaning of m-value:

- proportional of buried ASA
- proteins with large hydrophobic core exhibit high m-value
- the higher the m-value the stronger the dependence of a folding transition to denaturant (steepness)

M-values are proportional to change in ASA





Calculating ASA

- a water-sized sphere is rolled across the chemical structure keeping VdW radii
- the accessible surface corresponds to the ASA

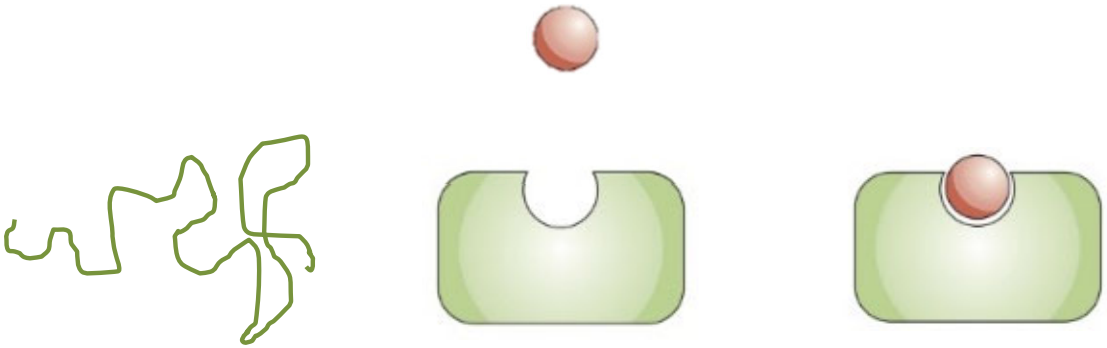
molecular meaning of m-value:

- proportional to change in ASA
- proteins with large hydrophobic core exhibit high m-value
- the higher the m-value the stronger the dependence of a folding transition to denaturant (steepness)

Small quiz:

- We have a small protein, whose standard free energy of folding (stability) is $\Delta G^{o}_{U} = 20\ kJ/mol$
- Upon addition of guanidinium hydrochloride (GdmHCl), the protein denatures reversibly
- Fluorescence measurements determined a mid-point of the transition at 2 M GdmHCl
- What is the *m-value* for this protein?
- If we compare this to a different protein with $m = 5\ kJ/mol/M$, what can we say about its structure?

Proteins are stabilized by ligand binding

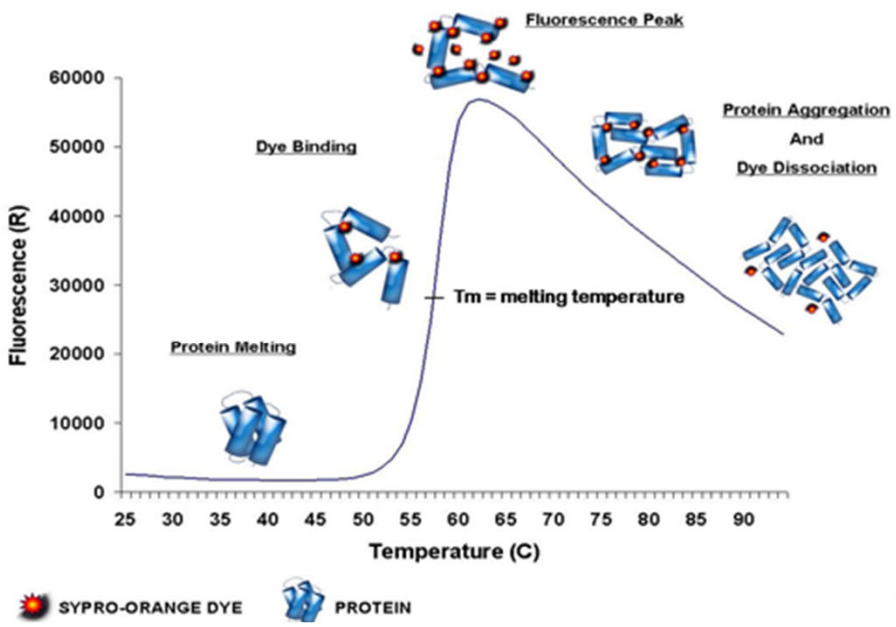


$$R_D \rightleftharpoons R_N + L \rightleftharpoons R_N : L$$

Protein stabilization by
free energy of ligands

→ measuring protein stability as a
screening tool

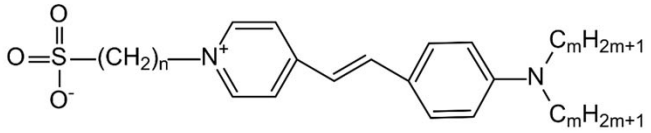
Differential Scanning Fluorimetry: A high-throughput assay to determine protein stability



source: Wikipedia

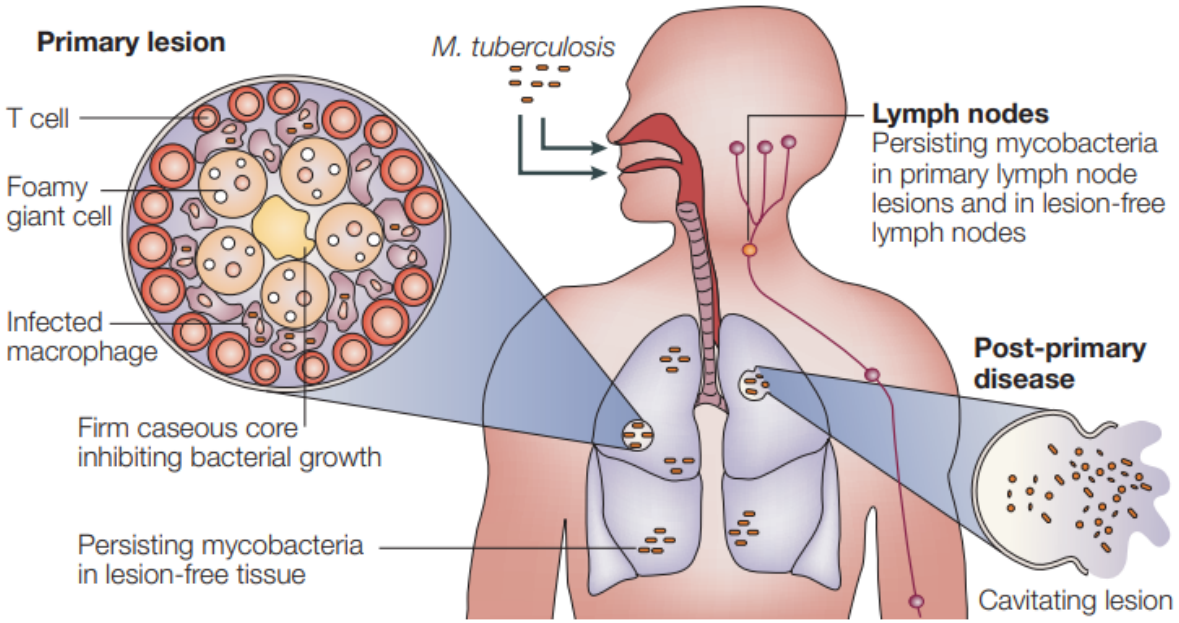
Differential Scanning Fluorimetry: Thermal shift assay

- Addition of a fluorophore
- binding to exposed hydrophobic sites: increase in fluorescence
- dyes: SYPRO orange
- High-throughput method
- ligand binding shifts Tm
- DSC: binding thermodynamics



SYPRO Orange

Case study: protein stability and pharmaceutical research for Tuberculosis



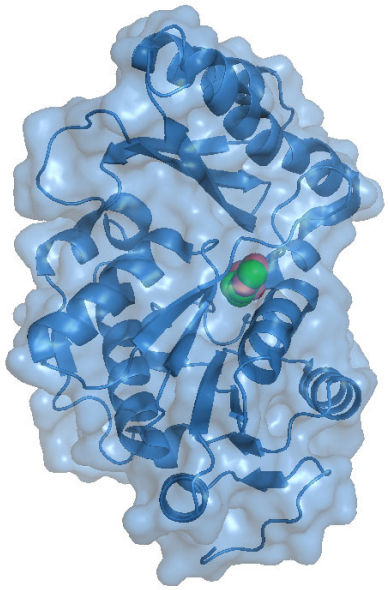
Nat Rev Microbiology 2003

Screening for pantothenate synthetase inhibitors

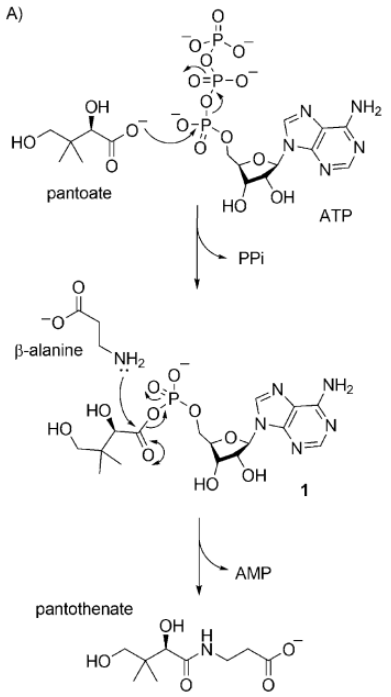
Pantothenate (vitamin B5)

- essential precursor to coenzyme A
- all enzymes absent in mammals
- de novo synthesis important for bacteria, including **M. tuberculosis**
- mutant can get pantotheate through salvage pathway, but no disease

→ **pantotheate synthase is a good target**

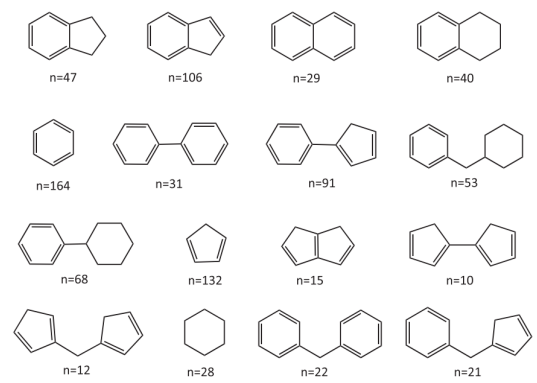


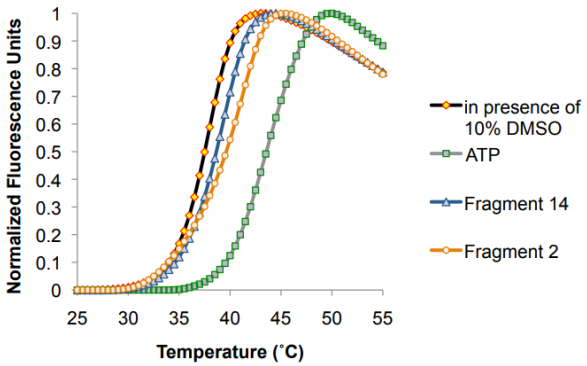
pantothenate synthetase: new target



Ciulli et al. ChemBioChem 2008

Fragment screen to identify binders





Silvestre et al. PNAS 2013

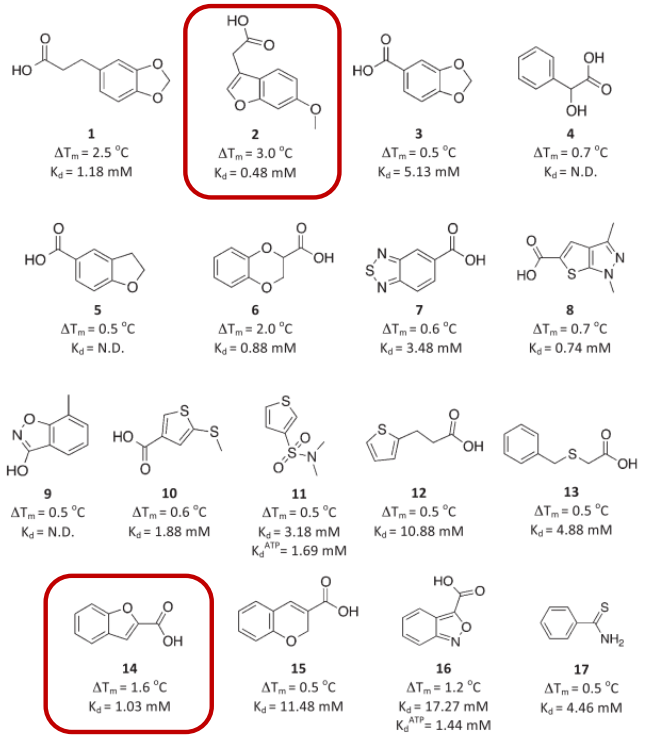


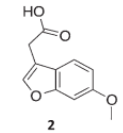
Fig. 1. The hits identified in the primary thermal shift screen and validated by secondary NMR spectroscopy screen, with K_d determined by ITC. The fragments exhibited a varied range in both ΔT_m (from 0.5 to 3.0 °C) and affinities (K_d from 480 μM to 17.3 mM).

Follow – up on hits to obtain thermodynamics of binding

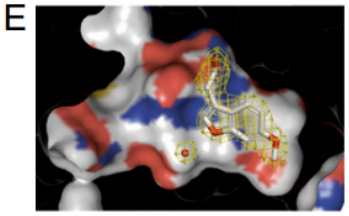
Table 1. Thermodynamic binding parameters determined by ITC

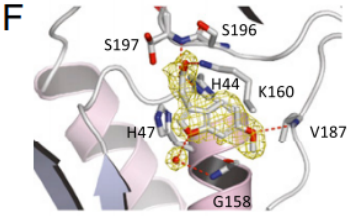
Fragment	ΔH, kcal/mol	ΔG, kcal/mol	K_d, mM	*LE*
1	−13.9 ± 0.1	−4.0 ± 0.1	1.2 ± 0.01	0.29
2	−10.1 ± 0.2	−4.5 ± 0.3	0.5 ± 0.01	0.30
3	−11.6 ± 0.2	−3.1 ± 0.3	5.1 ± 0.2	0.26
6 (racemate)	−10.3 ± 0.05	−4.2 ± 0.1	0.9 ± 0.04	0.32
6 (R-enantiomer)	−7.9 ± 0.1	−4.1 ± 0.1	0.9 ± 0.02	0.32
6 (S-enantiomer)	−12.3 ± 0.2	−4.3 ± 0.2	0.7 ± 0.02	0.33
7	−9.4 ± 0.1	−3.3 ± 0.1	3.5 ± 0.04	0.28
8	−7.51 ± 0.1	−4.2 ± 0.1	0.7 ± 0.02	0.32
10	−7.2 ± 0.1	−3.7 ± 0.1	1.9 ± 0.03	0.37
11	−16.2 ± 0.8	−3.4 ± 0.9	3.2 ± 0.2	0.31
11 (in the presence of ATP)	−1.5 ± 0.05	−3.8 ± 0.1	1.7 ± 0.08	0.34
12	−21.2 ± 1.0	−2.7 ± 1.0	10.9 ± 0.6	0.27
13	−10.7 ± 0.3	−3.1 ± 0.3	4.9 ± 0.2	0.26
14	−8.7 ± 0.2	−4.0 ± 0.2	1.0 ± 0.01	0.33
15	−12.3 ± 0.7	−2.3 ± 0.7	11.5 ± 0.8	0.18
16	−11.3 ± 0.02	−2.6 ± 0.1	17.3 ± 0.8	0.22
16 (in the presence of ATP)	−1.8 ± 0.4	−3.8 ± 0.4	1.4 ± 0.02	0.32
17	−5.3 ± 0.2	−3.1 ± 0.2	4.5 ± 0.2	0.34

binding mode of **2**

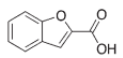


2
ΔT_m = 3.0 °C
K_d = 0.48 mM

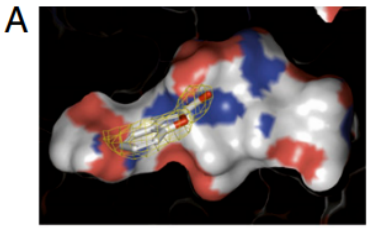


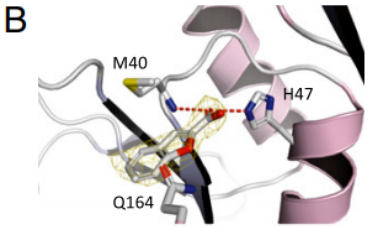


binding mode of **14**

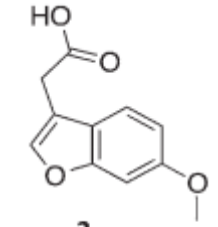


14
ΔT_m = 1.6 °C
K_d = 1.03 mM





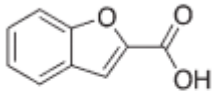
From fragments to inhibitors



2

$\Delta T_m = 3.0\ ^{\circ}C$

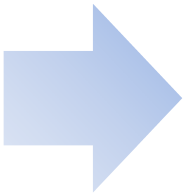
$K_d = 0.48$ mM

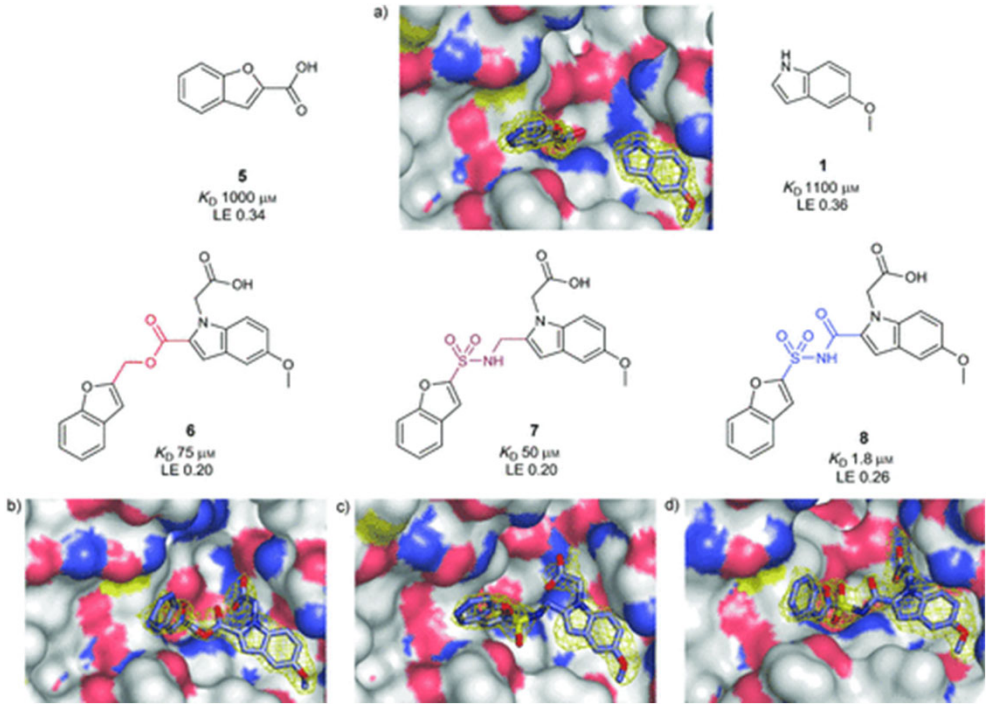


14

$\Delta T_m = 1.6\ ^{\circ}C$

$K_d = 1.03$ mM

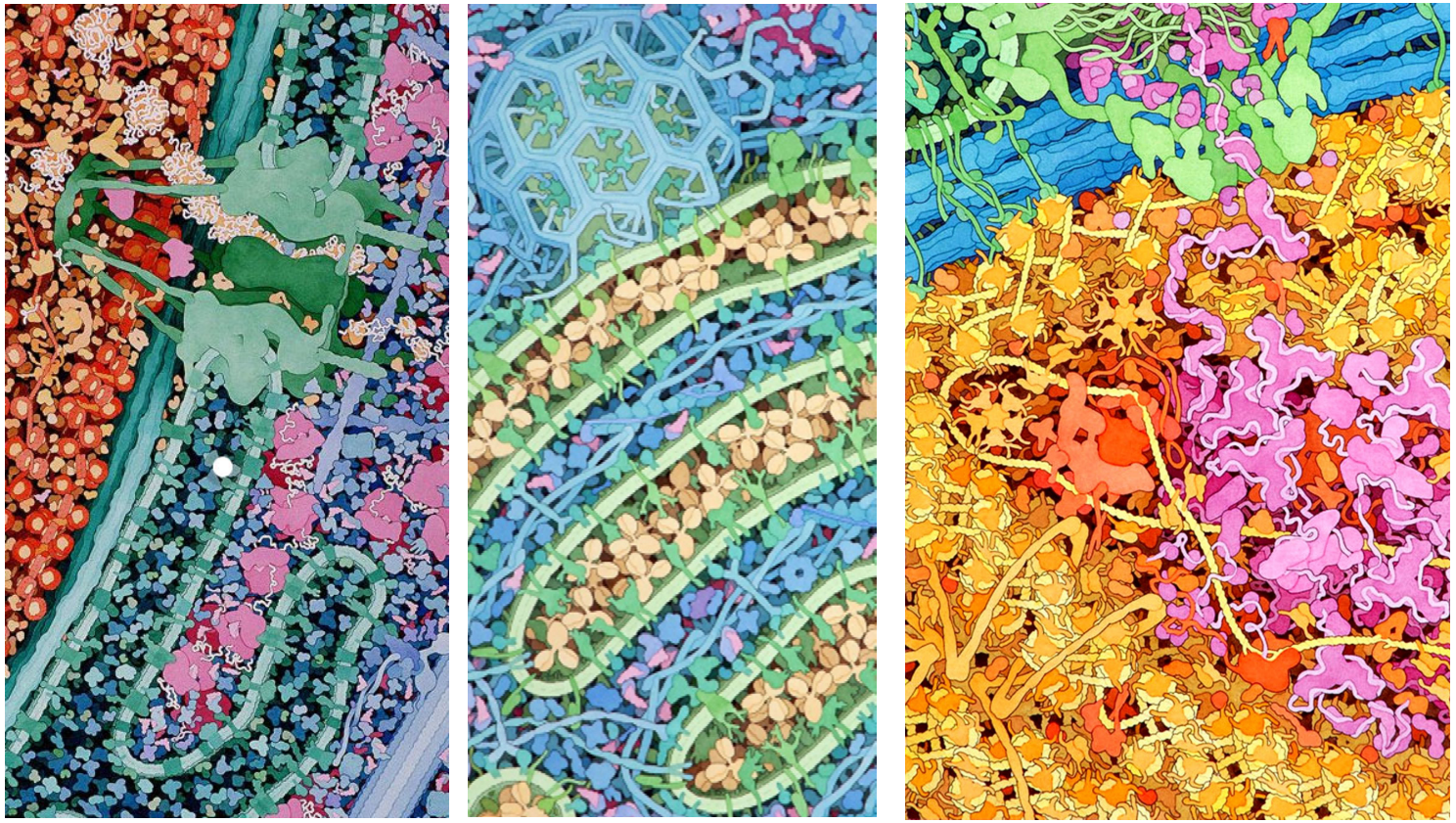




A fragment-linking strategy designed for *M. tuberculosis* pantothenate synthetase

Hung et al. Angew Chem 2009

Binding interactions are the foundation of biology



David Goodsell

Cellular signaling – Receptor ligand interactions

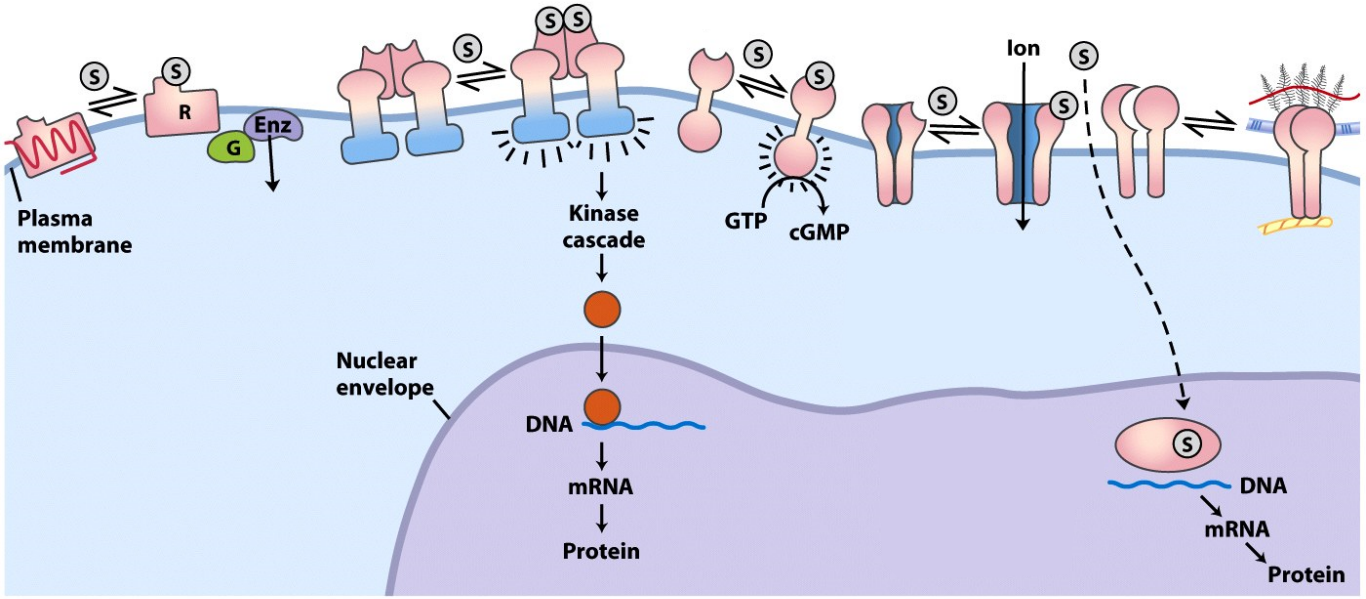
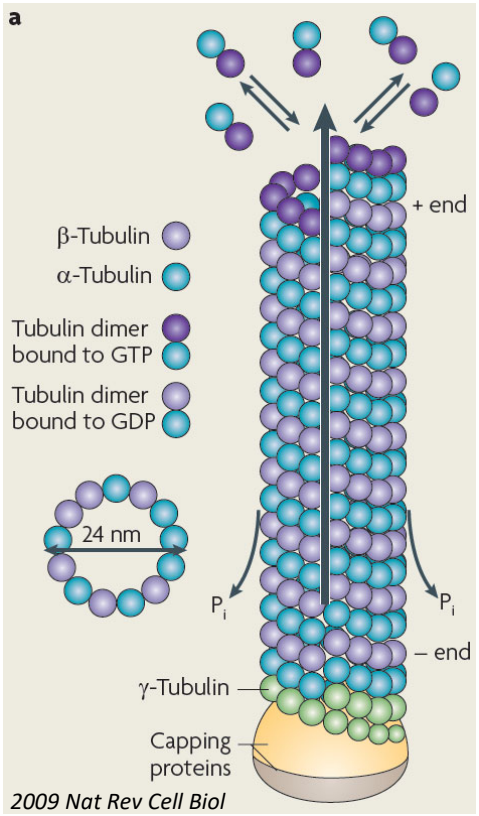
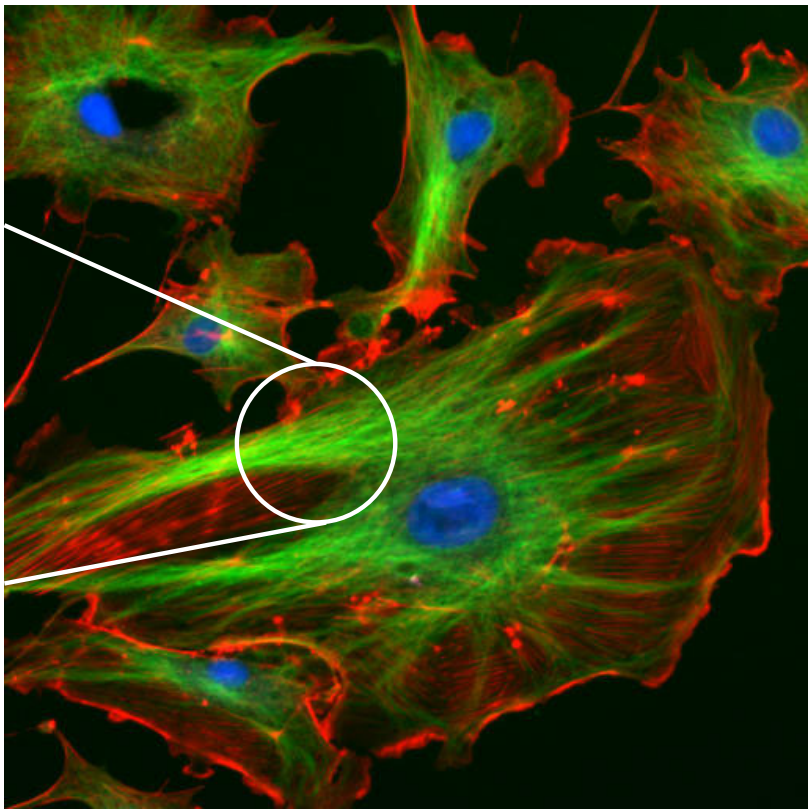


Figure 12-2
Lehninger Principles of Biochemistry, Fifth Edition

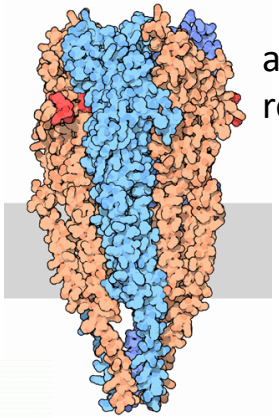
Protein – protein association: Large structures



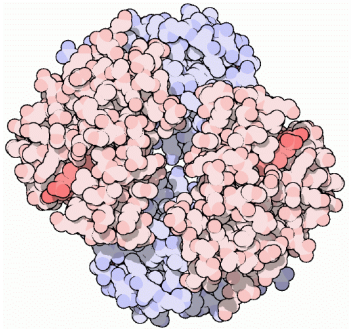


Types of association reactions

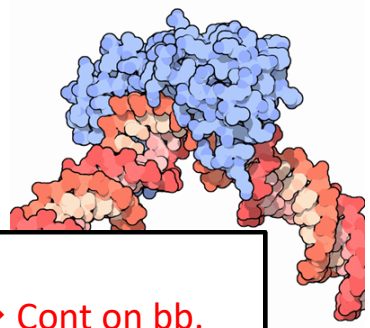
- **Protein – protein binding (homo-oligomers, hetero-oligomers)**
  - oligomeric enzymes
    - metabolic enzymes
    - ribosomes
    - channel proteins and pores
    - molecular machines
  - structural proteins
    - cytoskeleton
    - extracellular proteins
- **Receptor – ligand interactions**
  - signaling and import
  - cell surface receptors
  - intracellular receptor
- **Protein – DNA binding**
  - transcription factors
  - chromatin
  - DNA enzymes



acetylcholine receptor



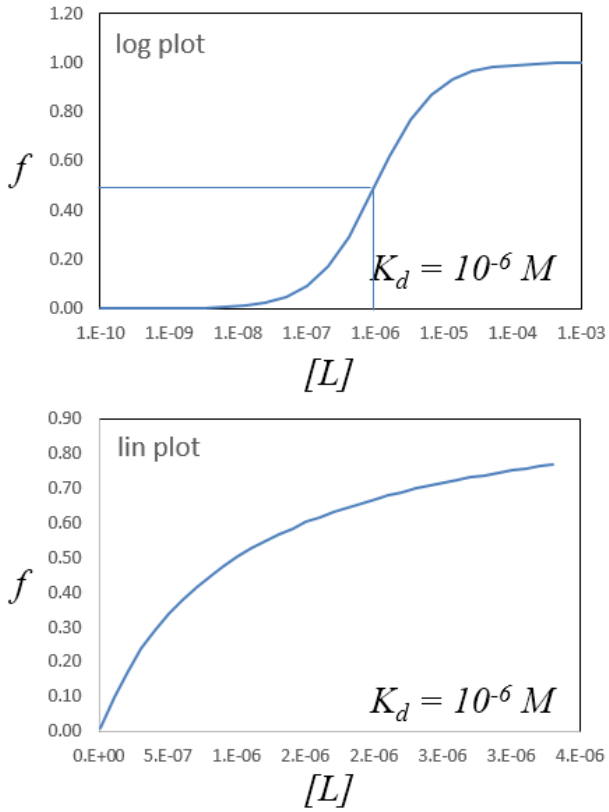
hemoglobine



TATA-bin
pro

→ Cont on bb.

Binding curves for one site binding



$$R + L \rightleftarrows RL$$

sigmoidal binding curve

advantage of semilogarithmic plot:
both baselines are available

The free energy of binding

The energy of a ligand-receptor interaction is determined by ΔG :

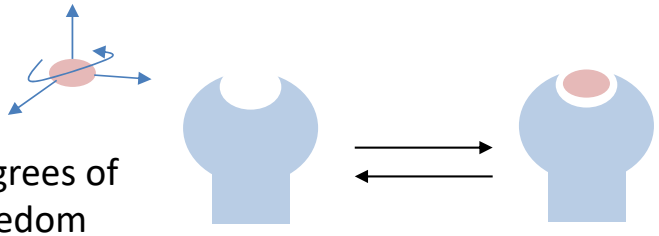
$$\Delta G = RT \ln K_D$$

... whereas ΔG itself can be separated into enthalpy and entropy

$$\Delta G = \Delta H - T\Delta S$$

+ ionic
+ vdW
+ H-bonds

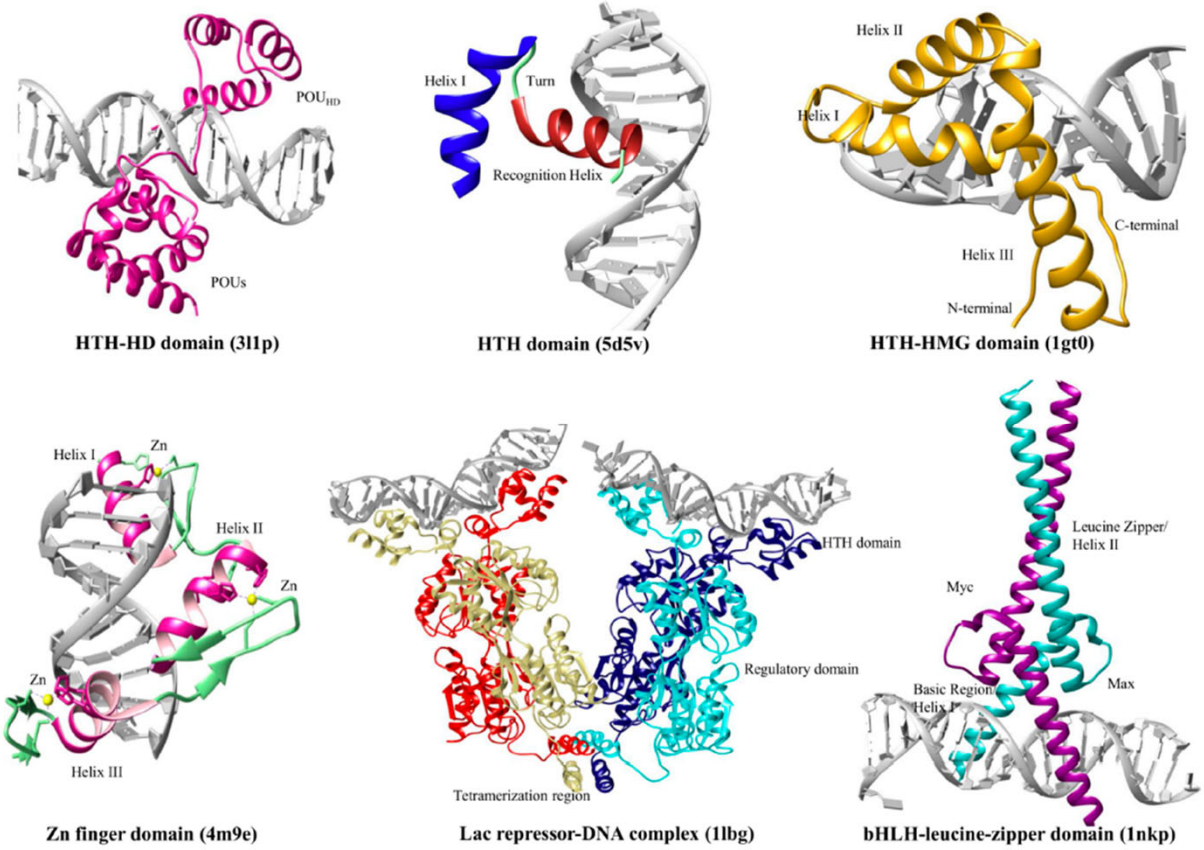
+ hydrophobic effect
- loss of ligand entropy!



degrees of freedom

degrees of freedom fixed!

Calculation example

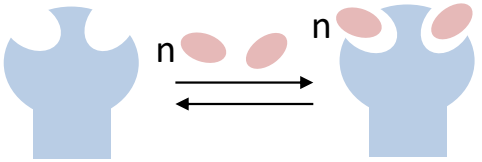


- You have a protein (transcription factor) binding to a particular DNA sequence with a dissociation constant of 10^{-9} M.
- Now, you test a different sequence and find that the protein binds tenfold (10x) better
- what is the **free energy difference** between the two interactions?
- Could you suggest what molecular interaction could account for that difference?

https://doi.org/10.3390/genes8080192

Binding to multiple non-interacting sites

$$R + nL \rightleftarrows \rightleftarrows \ldots \rightleftarrows RL_n$$



for a single site: $L + s \rightleftarrows L_b$ $\quad K_d = \dfrac{[s][L]}{[L_b]}$

s: free binding site

L_b: bound ligand

$$f = \frac{RL + 2RL_2 + 3RL_3 + \ldots}{R + RL + RL_2 + \ldots} = \frac{\sum_{i=1}^{n} iRL_i}{\sum_{i=0}^{n} RL_i}$$

fraction of ligand bound per macromolecule

$$f = \frac{\sum_{i=1}^{n} i[R][L]^i / K'_i}{\sum_{i=0}^{n} [R][L]^i / K'_i} = \frac{\sum_{i=1}^{n} i[L]^i / K'_i}{\sum_{i=0}^{n} [L]^i / K'_i}$$

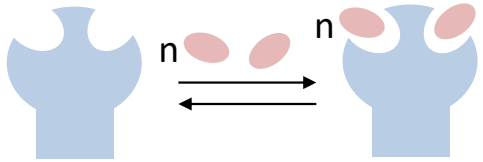
$$\boxed{f = \frac{n[L]}{[L] + K_d}}$$

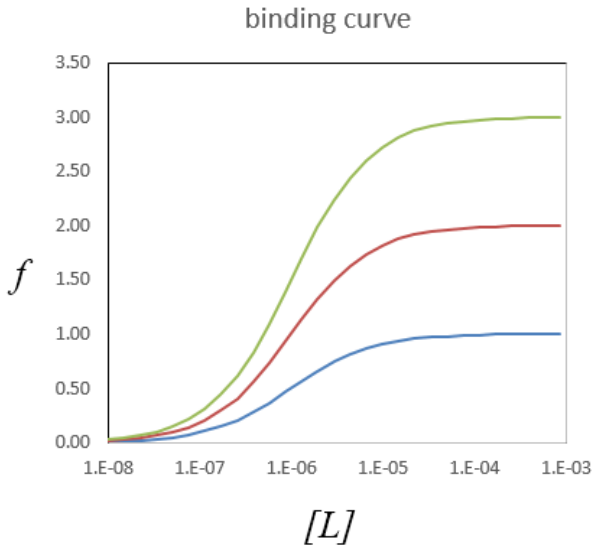
Binding isotherm for multi-site binding

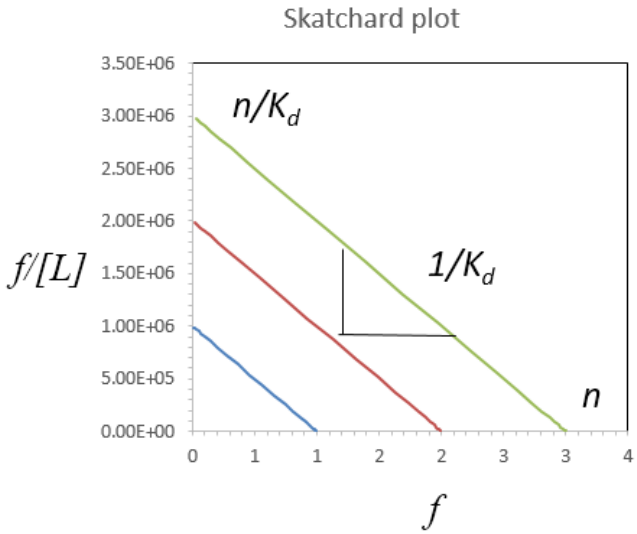
$$K'_i = K_1 \cdot K_2 \cdot K_3 \cdot \ldots K_i = \prod_i K_i$$

Scatchard plot for multisite binding

Linearization method







Plot of the ratio of bound ligand, L_b and unbound ligand, L vs. L_b

Cooperative binding

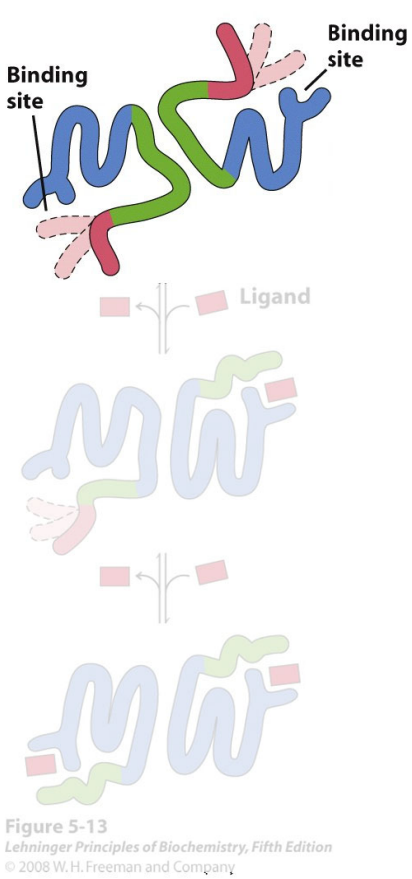


Figure 5-13
Lehninger Principles of Biochemistry, Fifth Edition

no ligand, flexible regions at binding site, interior low stability regions

one site bound
protomer converted into high affinity conformation
second binding site stabilized

second ligand bound with higher affinity
→ positive cooperativity

Cooperativity: Hemoglobin

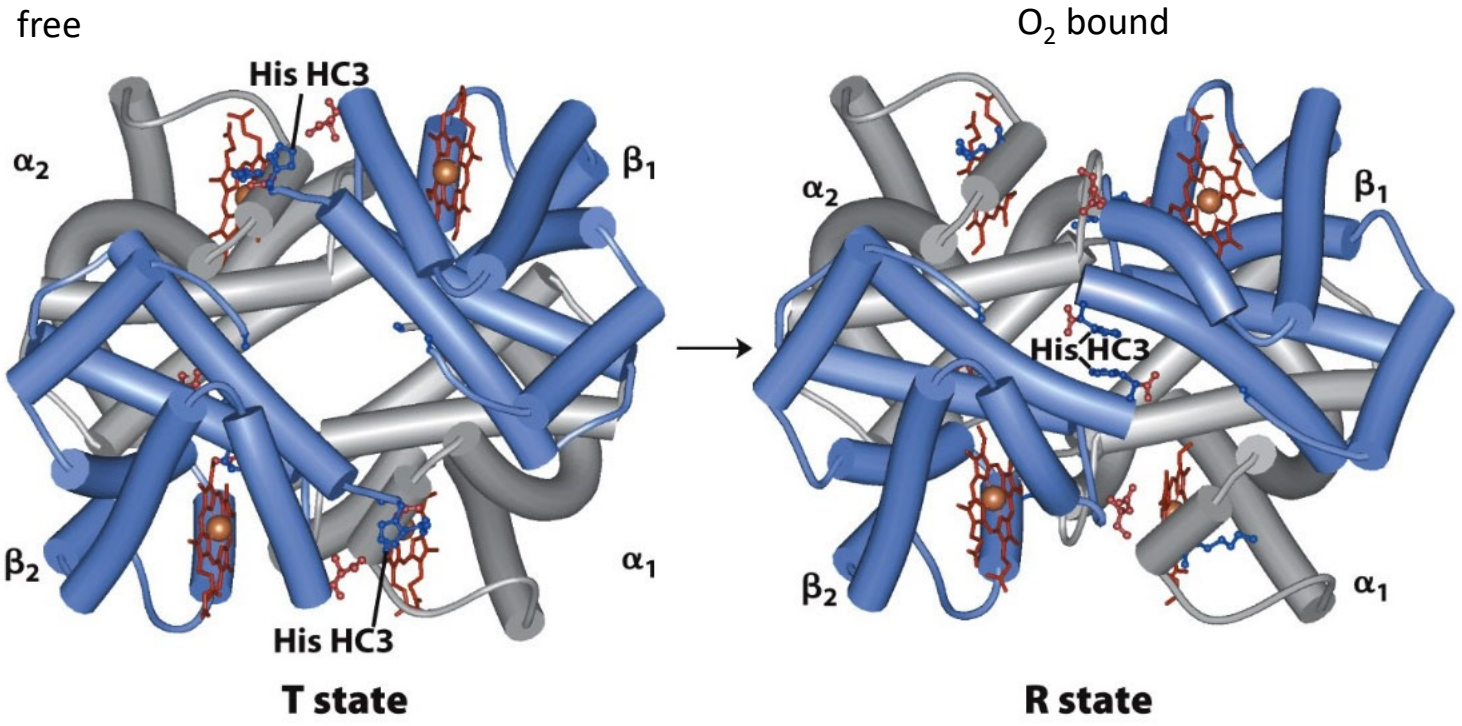
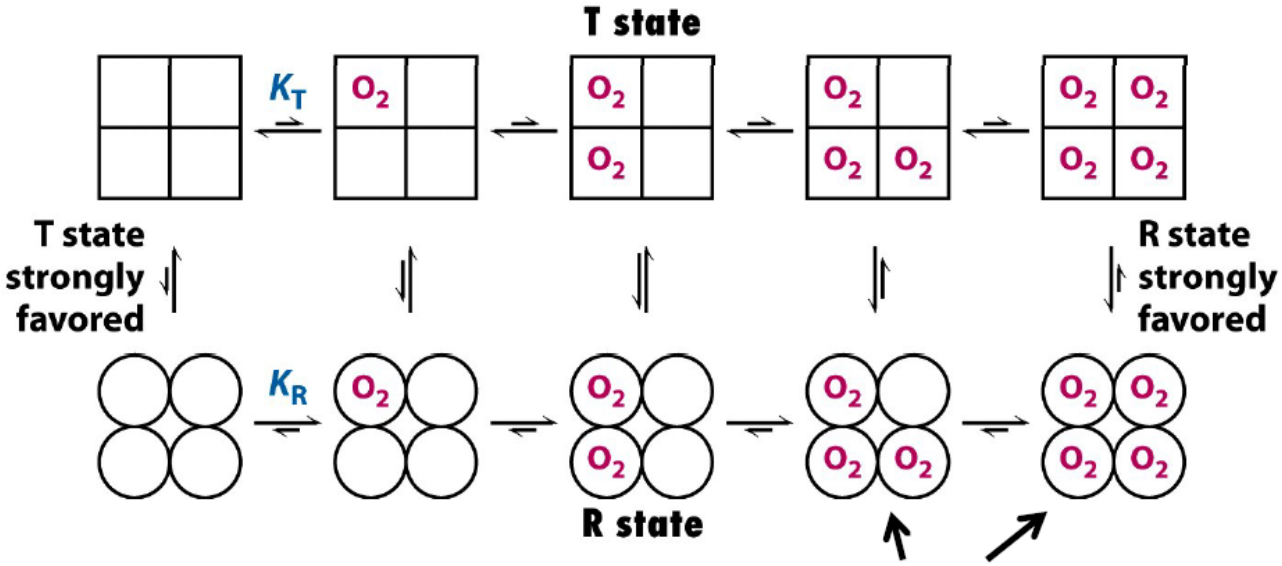


Figure 5-10
Lehninger Principles of Biochemistry, Fifth Edition

Fun fact: 750 g hemoglobin per adult, 10^{22} molecules (10^{8} molecules per blood cell).

Cooperativity: Hemoglobin



Cooperativity: Hemoglobin

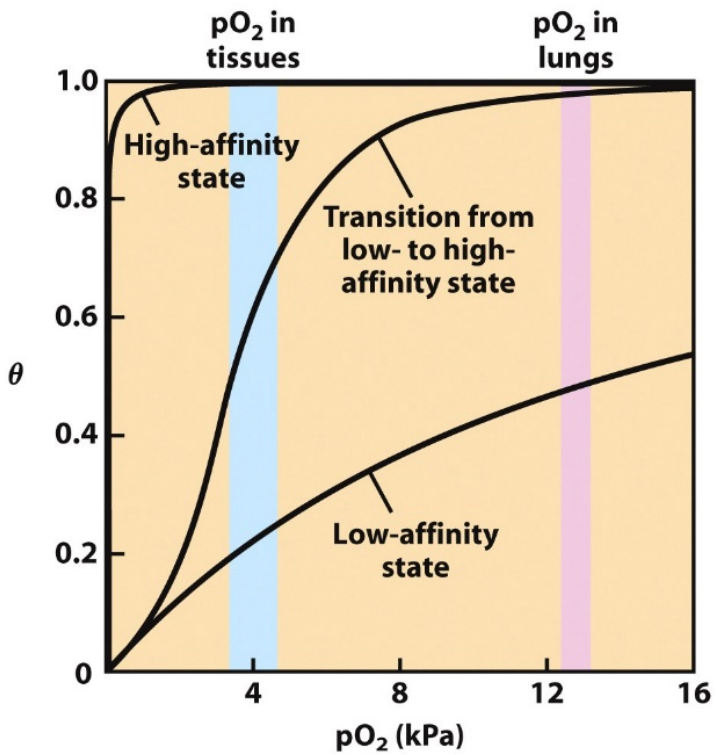


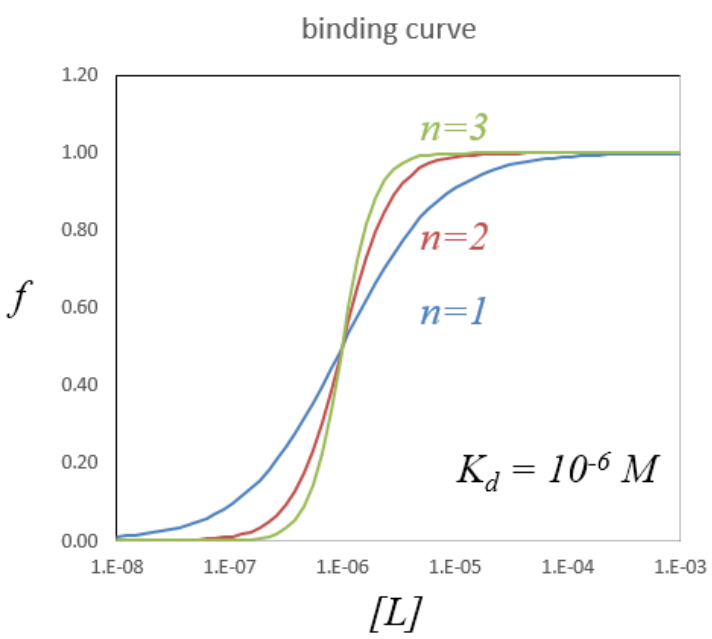
Figure 5-12
Lehninger Principles of Biochemistry, Fifth Edition

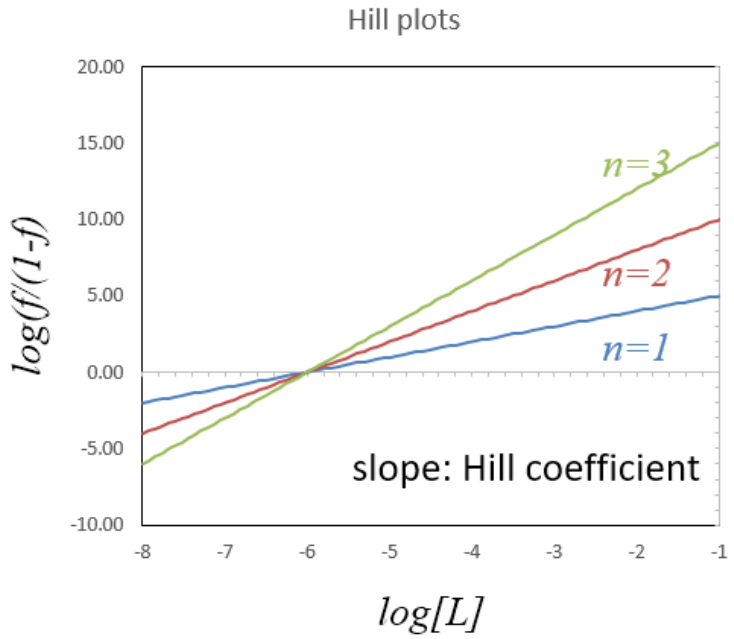
Finely tuned transition between high- to low affinity state

- transport function of hemoglobin
- transfer to myoglobin (only high affinity state)
- blood O2 saturation: critical parameter

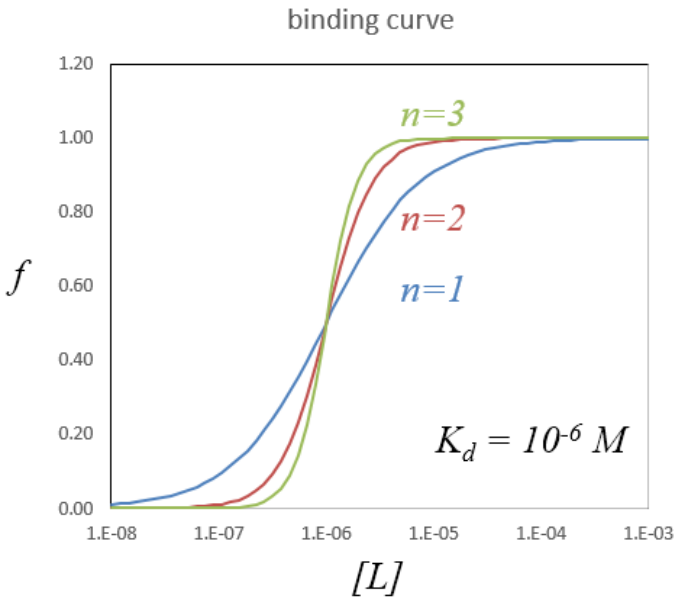
discussion on bb

The Hill plot





Interpretation of the Hill coefficient



For a receptor / protein with x binding sites:

Total cooperativity (all-or-none transition): $n = x$

No cooperativitiy: $n = 1$

All other cases: $1 < n < x$

Empirical description of the behavior

Effect of the receptor concentration

$$R + L \underset{K_d}{\rightleftharpoons} RL$$

Up to this point, we have assumed that [R] is much lower than the K_d

discussion on bb

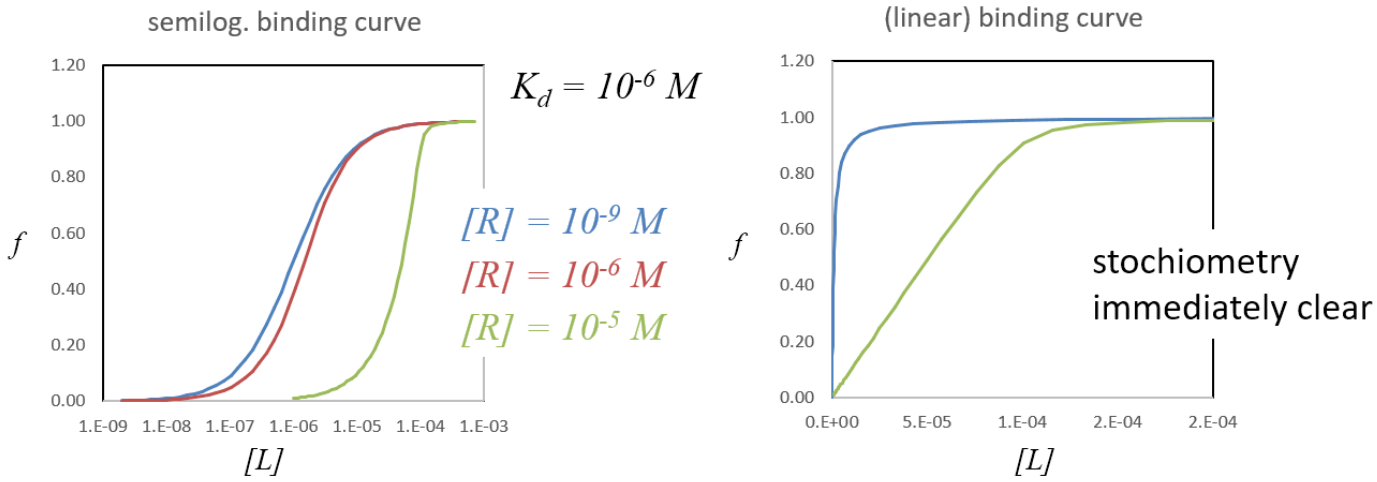
Effect of the receptor concentration

$$R + L \underset{K_d}{\rightleftharpoons} RL$$

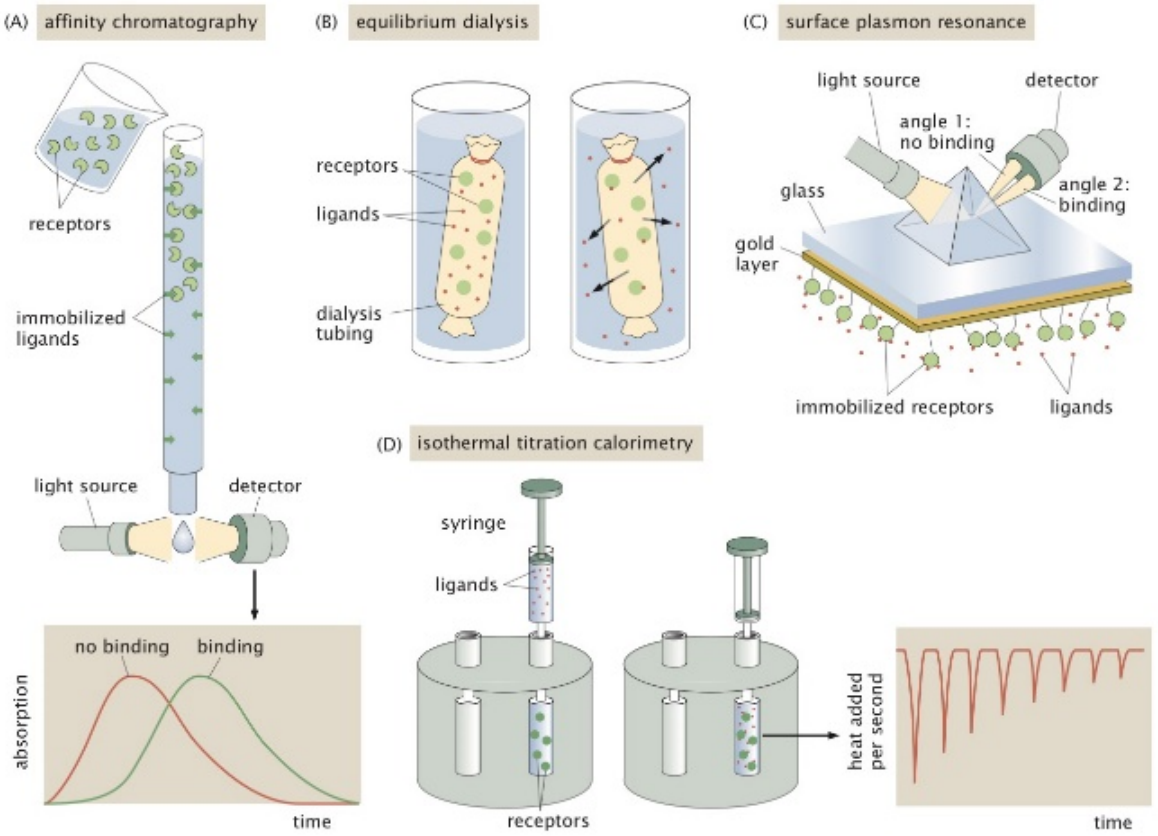
Up to this point, we have assumed that [R] is much lower than the K_d

if this is not the case the fraction bound ligand is expressed as:

$$\frac{[RL]}{[R_{tot}]} = \frac{K_d + [R_{tot}] + [L_{tot}]}{2} - \frac{\sqrt{(K_d + [R_{tot}] + [L_{tot}])^2 - 4[R_{tot}][L_{tot}]}}{2}$$



Measuring binding interactions



Fluorescence anisotropy: Transition dipole moment

Interaction with light:
Incident light ***E*** induces a dipole μ_{ind}:

$$\mu_{ind} = \alpha \bullet E$$

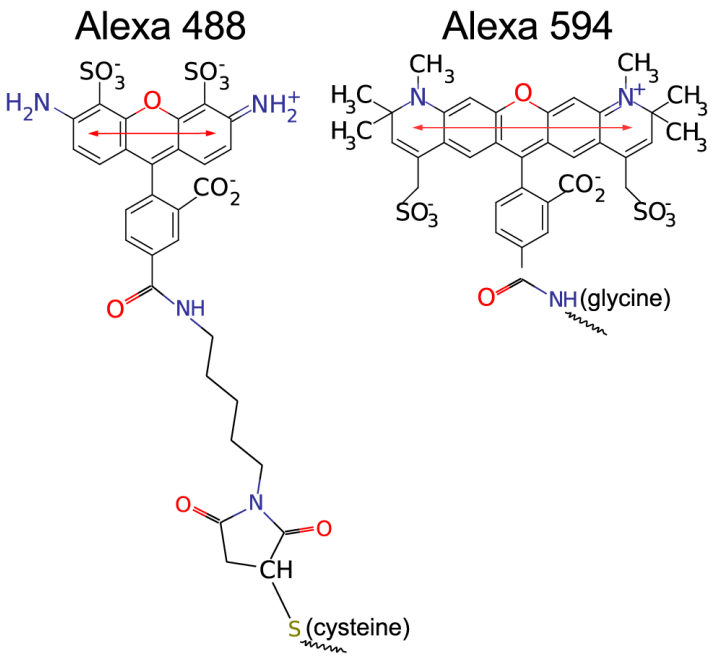
α : polarisability

Transition dipole moment:

Ground state wave funct.: ψ_a
Excited state wave funct.: ψ_b

$$\left\langle \psi_b \left| \underline{\boldsymbol{\mu}} \right| \psi_a \right\rangle$$

can be interpreted as a vector



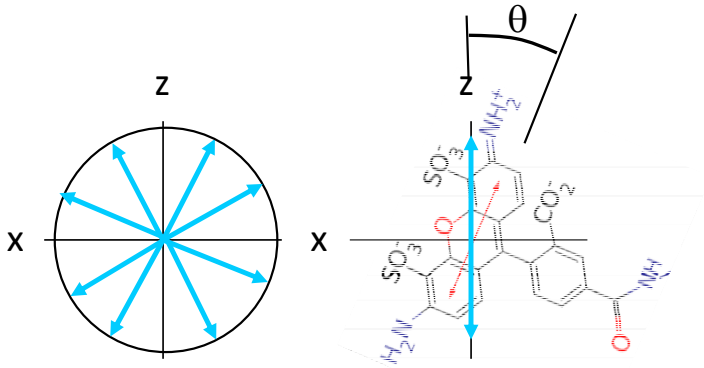
Hoefling et al. PLOS ONE 2011

Excitation of chromophore subpopulation

Conditions:
Immobile chromophores (e.g. embedded in a glass)

Excitation light **vertically polarized**

Probability of absorption: $p \sim cos^2\theta$



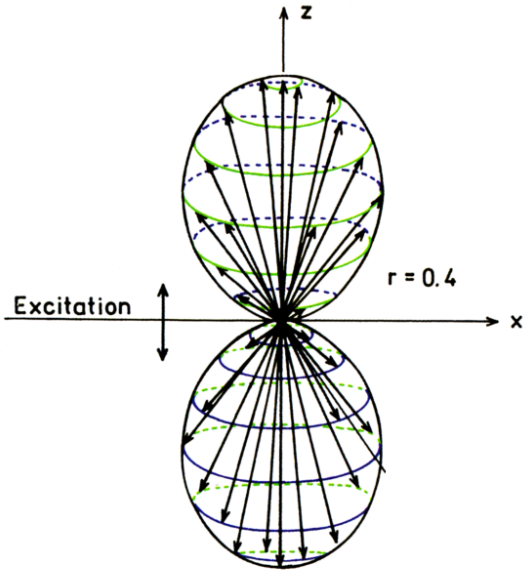


Figure 10.6. Excited-state distribution for immobile fluorophores with $r_0 = 0.4$.

Lakowicz, Principles of fluorescence spectroscopy

Fluorescence emission anisotropy

Conditions:

Emission dipole colinear absorption dipole

No molecular motion

Emission **is polarized**

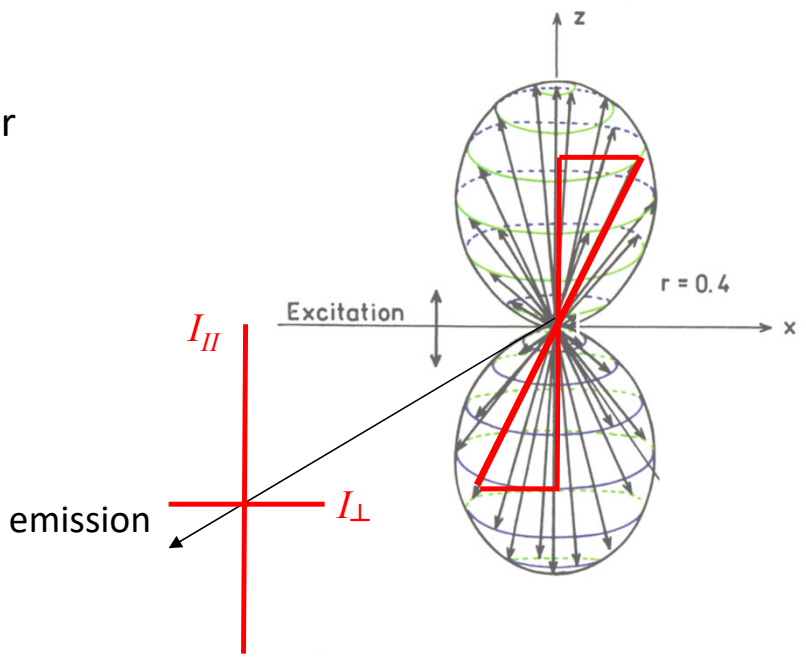
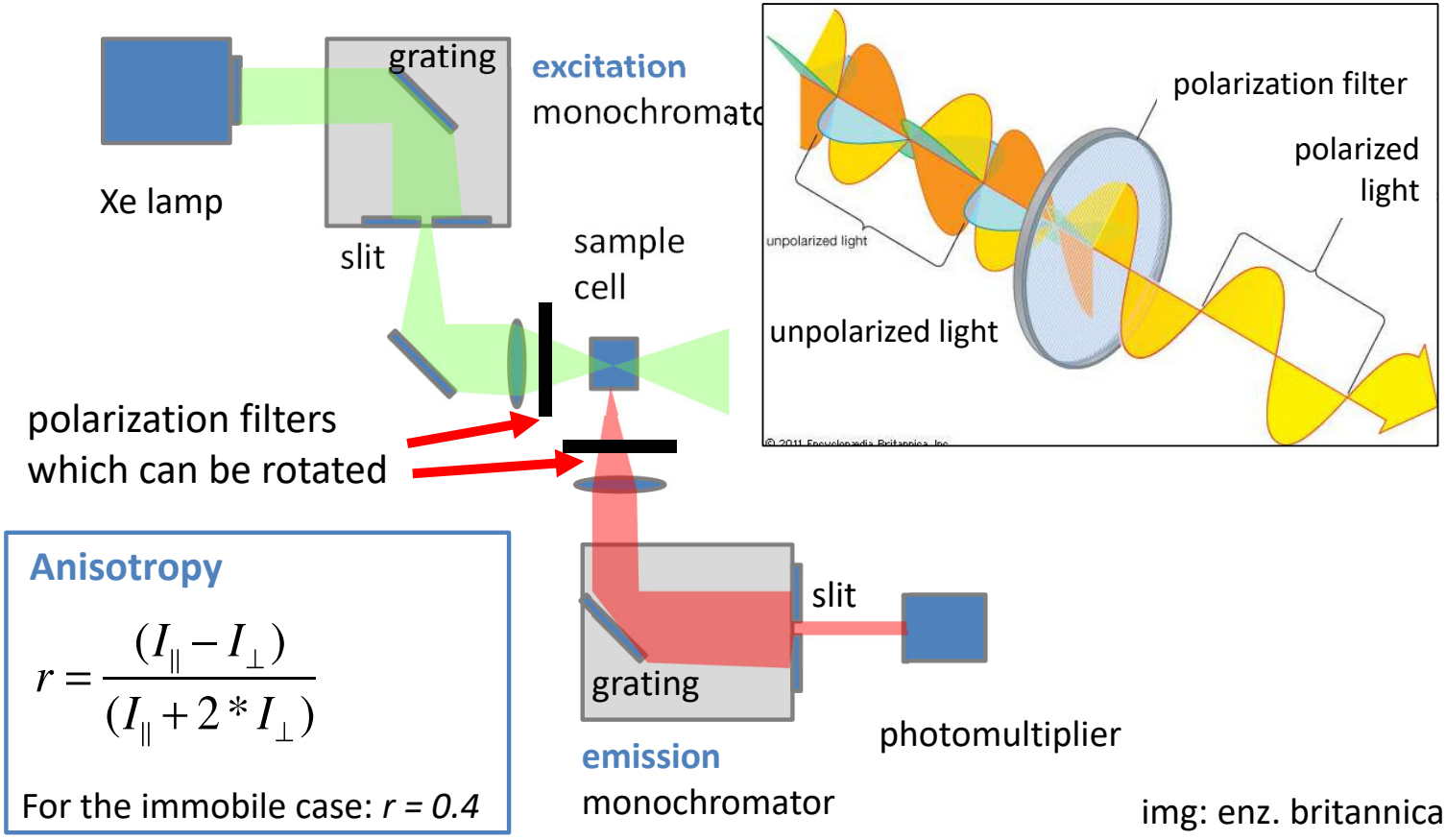


Figure 10.6. Excited-state distribution for immobile fluorophores with $r_0 = 0.4$.

Lakowicz, Principles of fluorescence spectroscopy

Measuring fluorescence anisotropy



Anisotropy

$$r = \frac{(I_{\parallel} - I_{\perp})}{(I_{\parallel} + 2 * I_{\perp})}$$

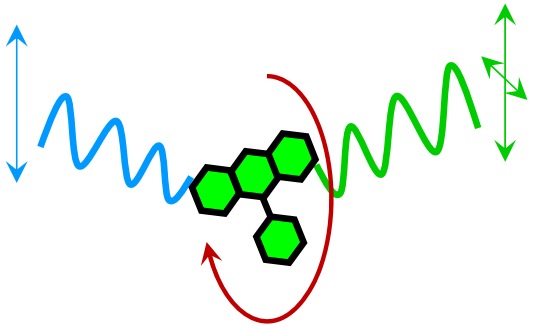
For the immobile case: *r = 0.4*

img: enz. britannica

Loss of fluorescence anisotropy

Anisotropy

$$r = \frac{(I_{\parallel} - I_{\perp})}{(I_{\parallel} + 2 * I_{\perp})}$$



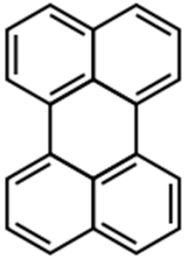
Rotational diffusion:

The Perrin equation

$$\frac{r_o}{r} = 1 + \frac{\tau}{\theta} = 1 + 6D\tau$$

r_0: anisotropy in the absence of motion
τ : fluorescence lifetime
θ : rotation correlation time
D : rotational diffusion coefficient

e.g.: Perylene



r_0: 0.36
τ : 6 ns
Anisotropy in solution (EtOH): 0.005

Loss of fluorescence anisotropy: Proteins

Rotational diffusion:

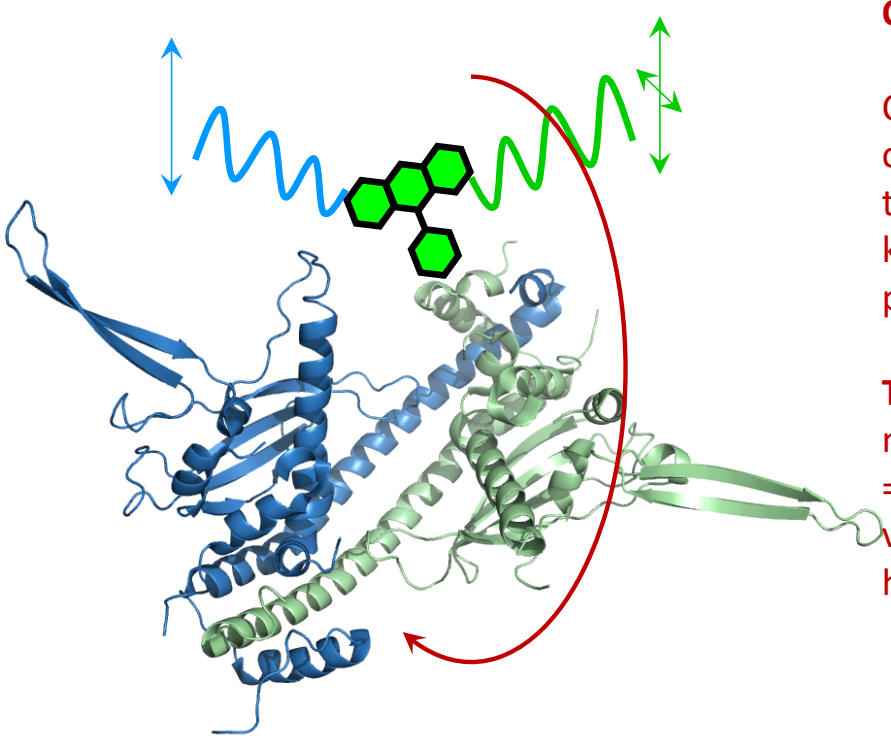
The Perrin equation

$$\frac{r_o}{r} = 1 + \frac{\tau}{\theta} = 1 + 6D\tau$$

For a 50 kDa protein the rotation correlation time θ = 14 ns

$$\theta = \frac{\eta V}{RT} = \frac{\eta}{RT} \cdot M(\bar{v} + h)$$

η = viscosity
V = volume
M = molecular weight
v = specific volume protein
h = hydration (g/g protein)



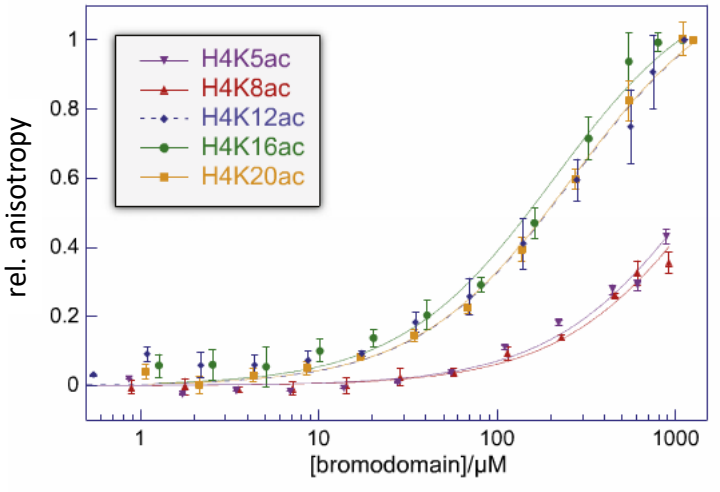
Quiz:

Calculate the anisotropy of a dye with r0 = 0.38 and tau = 5 ns attached to a 1 kDa peptide or 30 kDa protein.

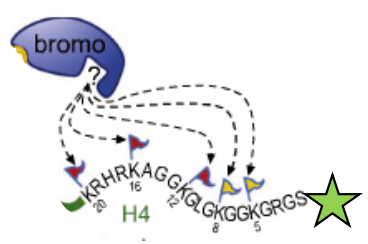
Tips:

η (water) = 0.01 Poise (1 P = 0.1 Pa s) @ 25°C
v: 0.73 mL/g
h: neglected

Measuring protein-protein interactions with anisotropy



Ruthenburg et al. Cell 2011



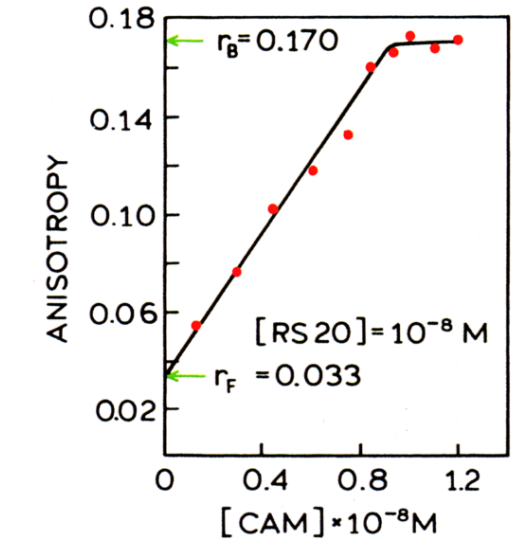
Protein domain (bromodomain) interacting with modified histone peptides

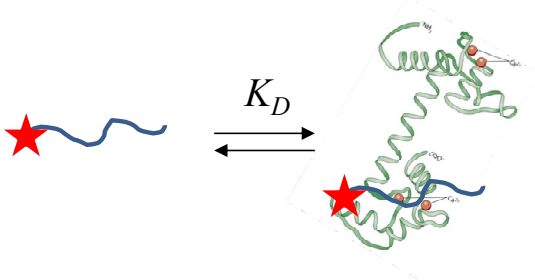
Peptides contain fluorophore, are kept at the same concentration

Protein is titrated and anisotropy is determiend for each concentration

→ Kd is obtained

Stochiometry determined by anisotropy measurement



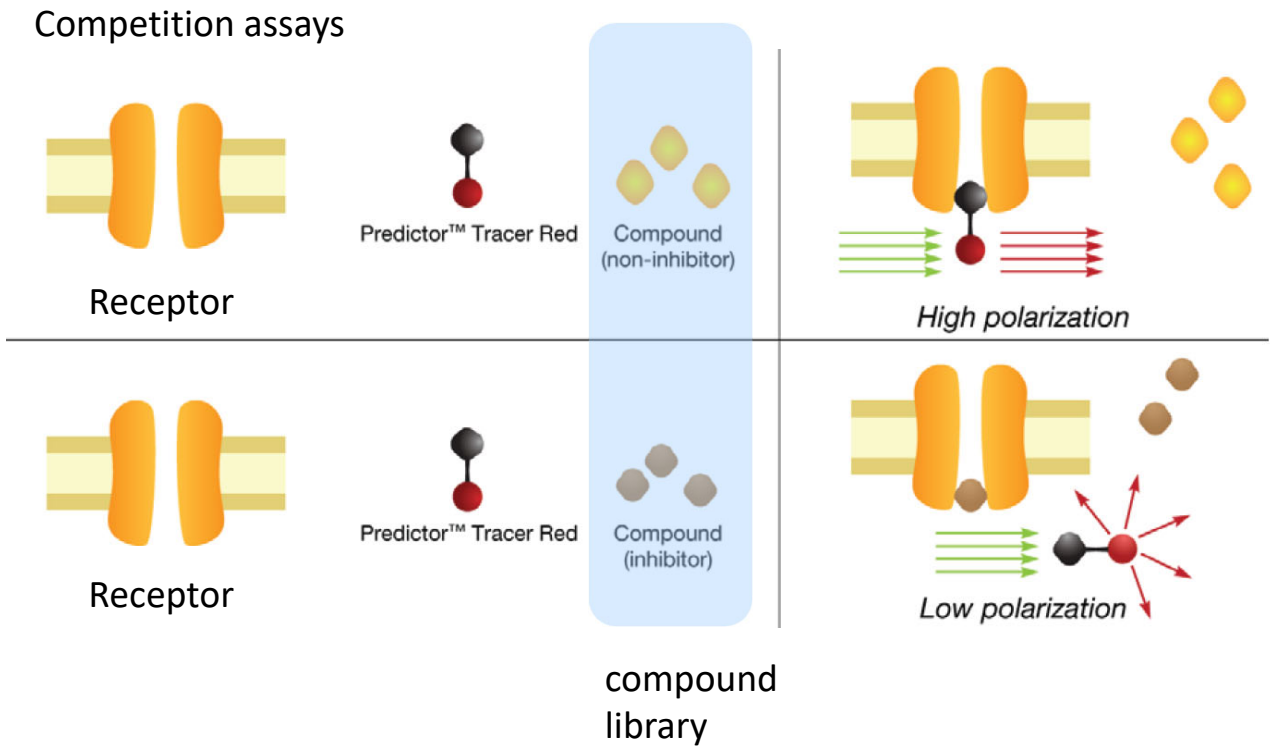


Fluorescence anisotropy measurements can be used to determine binding reactions

Example: MLCK peptide (RS20) binds calmodulin

Determining tryptophan **fluorescence anisotropy** in peptide, the binding constant can be determined in a **titration**.

Fluorescence anistropy in HTS

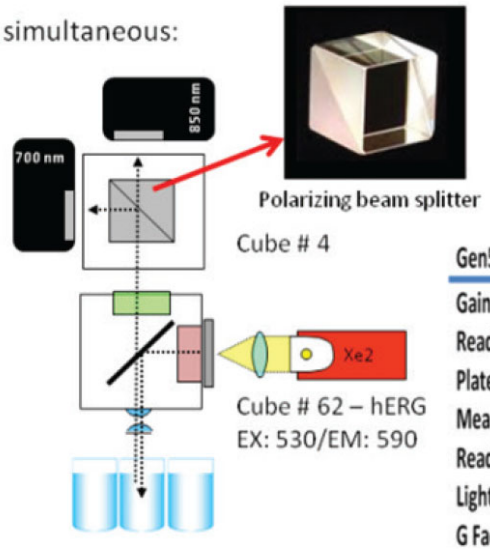


High throughput evaluation using plate readers

Fluorescence Polarization

- Specialized optics:
  - FP cube beam splitter
  - Non-standard high-transmission filters

Top simultaneous:



Polarizing beam splitter

Cube # 4

Cube # 62 – hERG
EX: 530/EM: 590

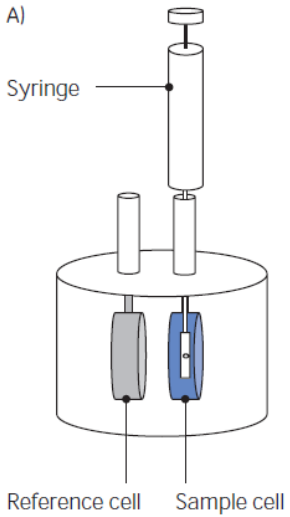
Gen5™ Protocol Parameters	Top PMT	Side PMT	
Gain*	97	119	–
Read Speed	–	–	Normal
Plate Movement Delay	–	–	0
Measurements/well**	–	–	10-200
Read Height (mm)	–	–	10.25
Light Source	–	–	Xenon, Low
G Factor	–	–	Fixed value: 1

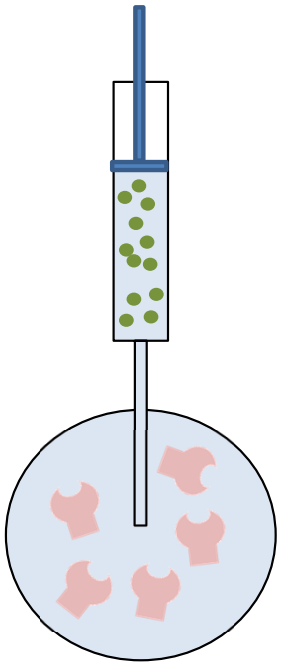
** It is recommended Gain be determined for each reader.*

***Higher measurements/well can result in greater precision & specificity but lower read times*

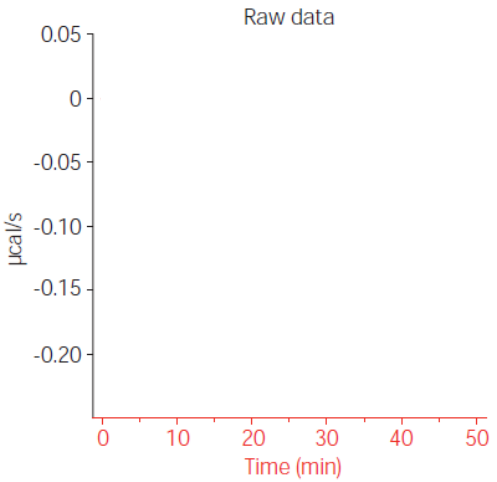
Source: Biotek

Isothermal titration calorimetry



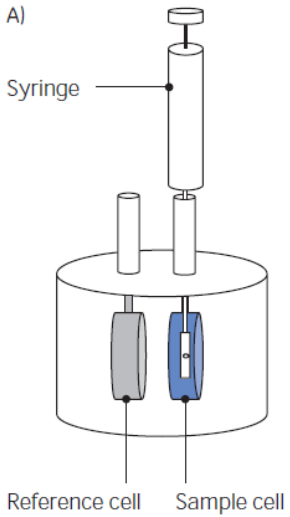


$$\Delta G = RT \ln K_D$$
$$\Delta G = \Delta H - T\Delta S$$

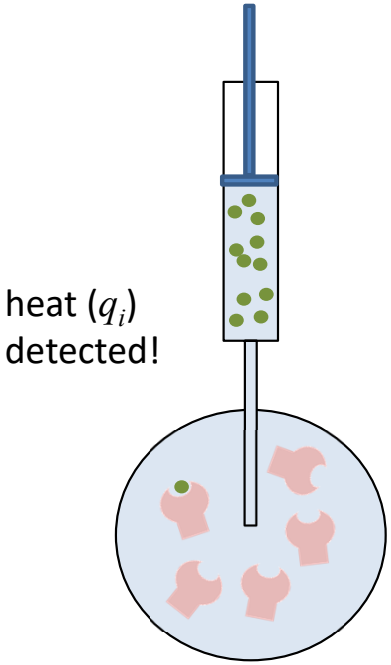


injection of ligand solution into receptor solution

Isothermal titration calorimetry

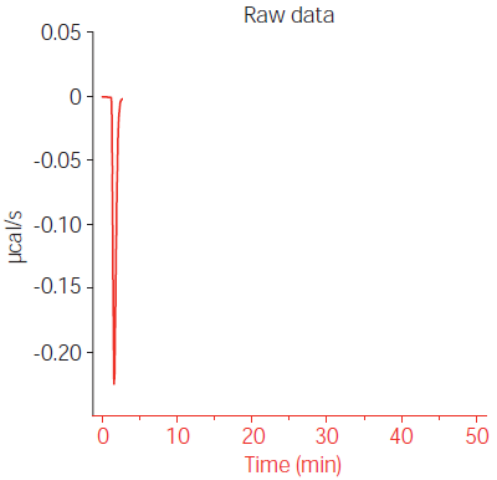


injection of ligand solution into receptor solution



heat (q_i) detected!

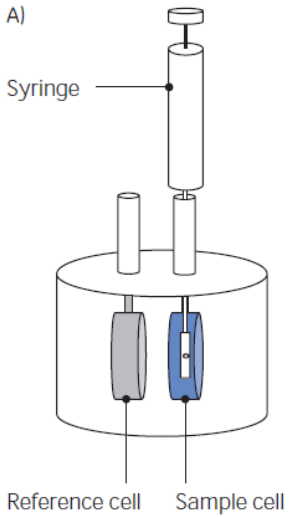
$$\Delta G = RT \ln K_D$$
$$\Delta G = \Delta H - T\Delta S$$



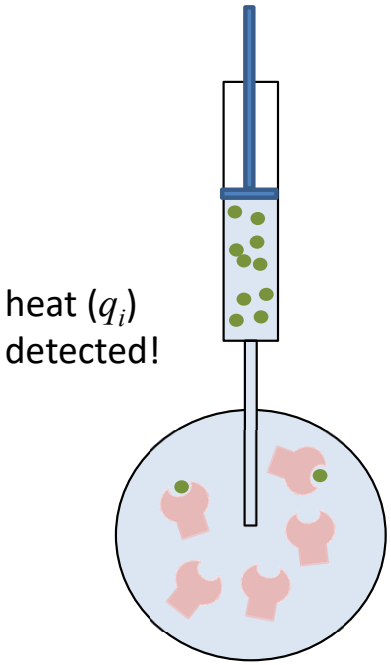
all injected ligand is bound

binding energy is released and is measured as heat

Isothermal titration calorimetry



injection of ligand solution into receptor solution



heat (q_i) detected!

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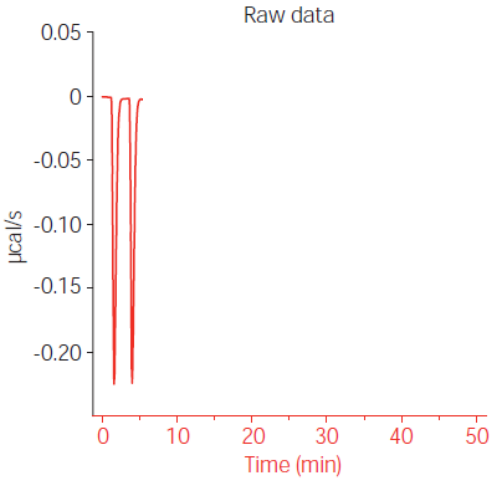
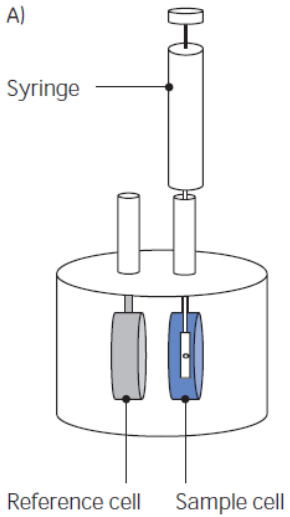


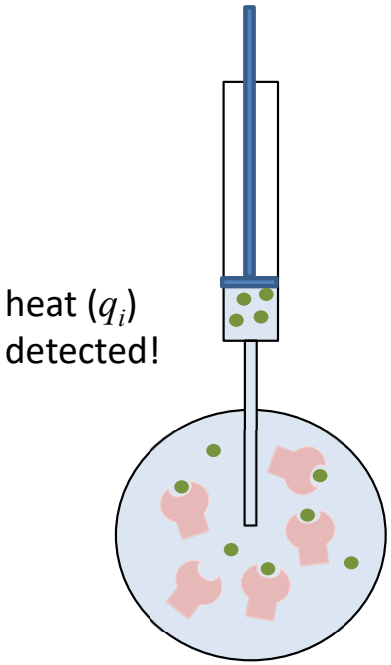
all injected ligand is bound

binding energy is released and is measured as heat

Isothermal titration calorimetry

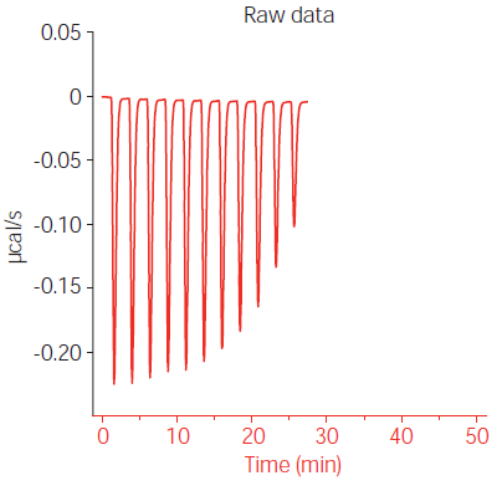


injection of ligand solution into receptor solution



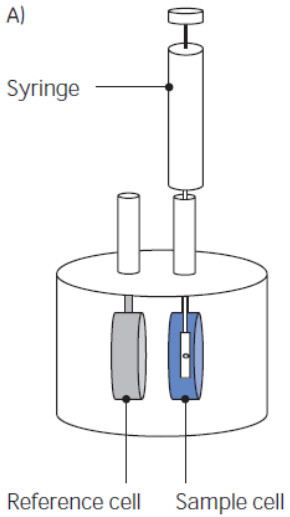
heat (q_i) detected!

$$\Delta G = RT \ln K_D$$
$$\Delta G = \Delta H - T\Delta S$$



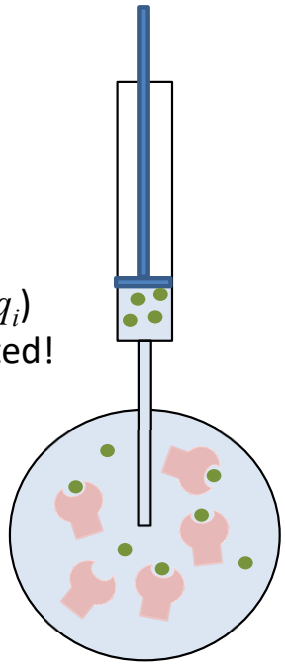
around the Kd, no longer all ligand is bound, less heat is released

Isothermal titration calorimetry

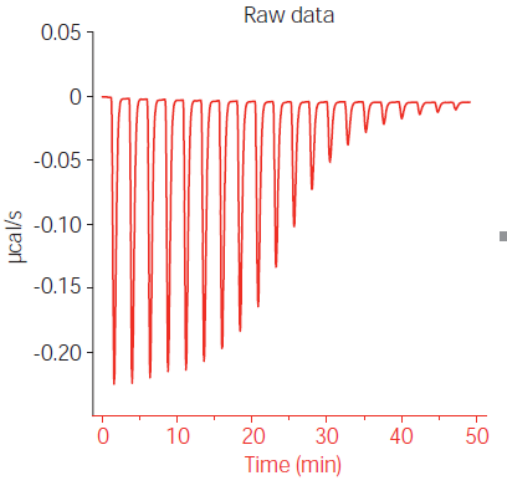


injection of ligand solution into receptor solution

heat (q_i) detected!

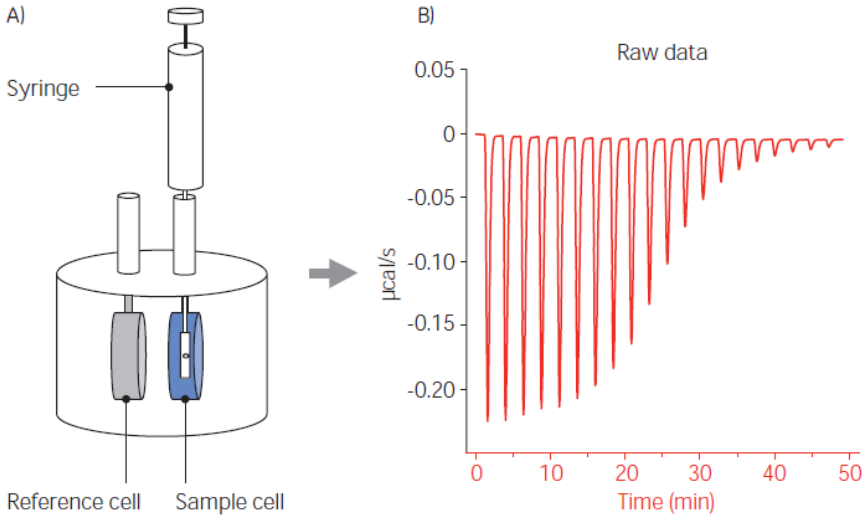


$$\Delta G = RT \ln K_D$$
$$\Delta G = \Delta H - T\Delta S$$



around the Kd, no longer all ligand is bound, less heat is released

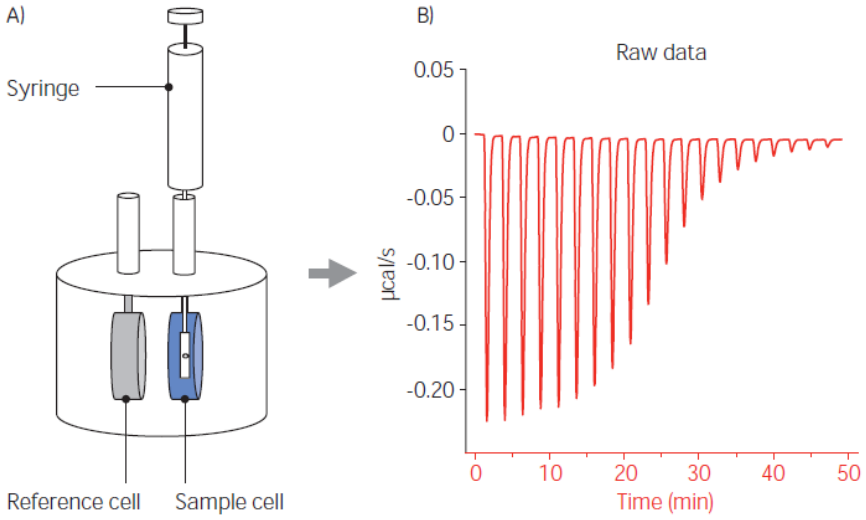
Isothermal titration calorimetry



injection of ligand solution into receptor solution

measurement of heat of binding

Isothermal titration calorimetry



injection of ligand solution into receptor solution

measurement of heat of binding

Analysis:

heat released (absorbed) for each injection

$$q_i = \Delta H_{app} \cdot V_C \left([RL]_{b,i} - [RL]_{b,i-1} \right)$$

Vc : volume of the cell

using binding isotherm for multisite binding:

$$f = \frac{\mathrm{n}[L]}{[L] + K_d} = \frac{[RL]}{[R_{tot}]}$$

$$q_i = \Delta H_{app} \cdot V_C \left(f_i [R_{tot}]_i - f_{i-1} [R_{tot}]_{i-1} \right)$$

ITC: Binding to n independent, equal sites

total heat released
(complete integral of curve):

$$Q = \sum_{i=1}^{N} q_i = \Delta H_{app} \cdot V_C \cdot [RL] = \Delta H_{app} \cdot V_C \cdot [R_{tot}] \cdot f$$

using the general solution, as shown before:

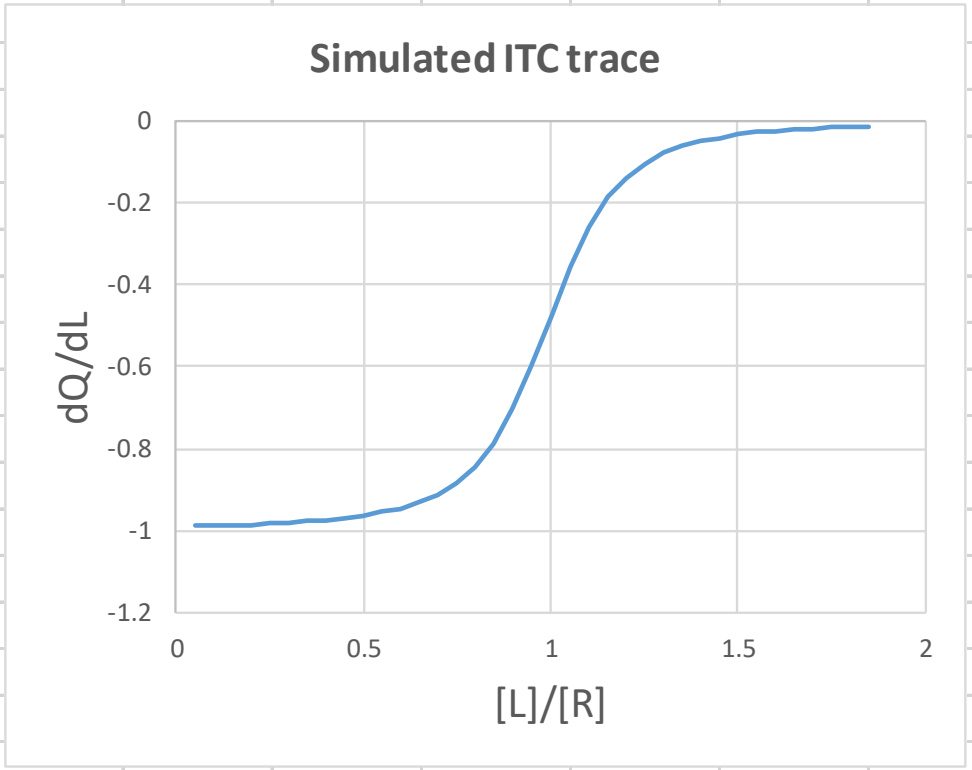
$$Q = \frac{\Delta H_{app} \cdot V_C}{2} \left([L_{tot}] + n[R_{tot}] + K_D - \sqrt{([L_{tot}] + n[R_{tot}] + K_D)^2 - 4n[R_{tot}][L_{tot}]} \right)$$

differentiate for $[L_{tot}]$:

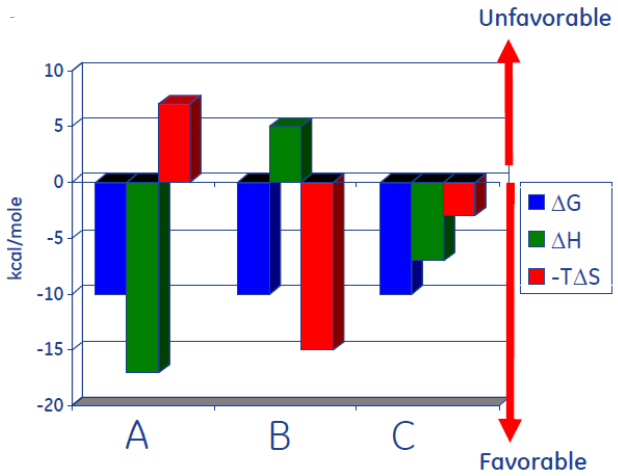
$$\frac{dQ}{d[L_{tot}]} = \frac{\Delta H_{app} \cdot V_C}{2} \left(1 - \frac{[L_{tot}] + K_D - n[R_{tot}]}{\sqrt{([L_{tot}] + n[R_{tot}] + K_D)^2 - 4n[R_{tot}][L_{tot}]}} \right)$$

Simulated ITC traces

Kd	1.00E-09
L (start)	5.00E-09
R	1.00E-07
n	1



ITC can give informations about binding mechanisms



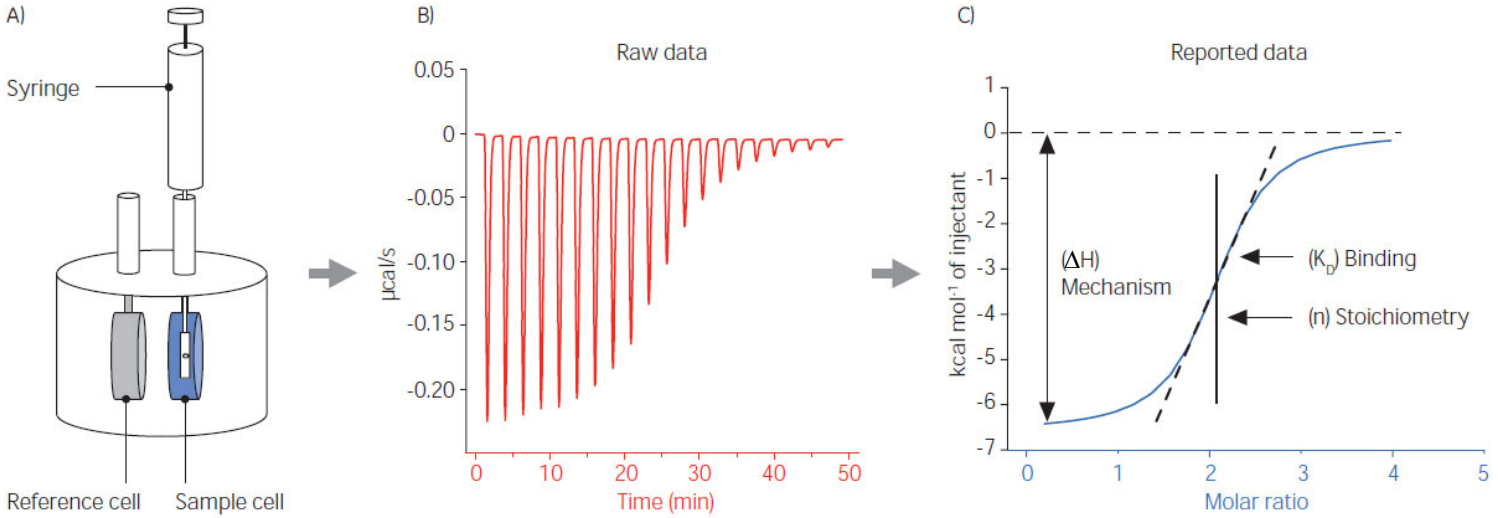
…all three binding reactions have the same ΔG.

A) good hydrogen bonding (enthalpy) and unfavorable conformational changes.

B) Hydrophobic interactions drive binding

C) both favorable enthalpic interactions and hydrophobic interactions

Isothermal titration calorimetry



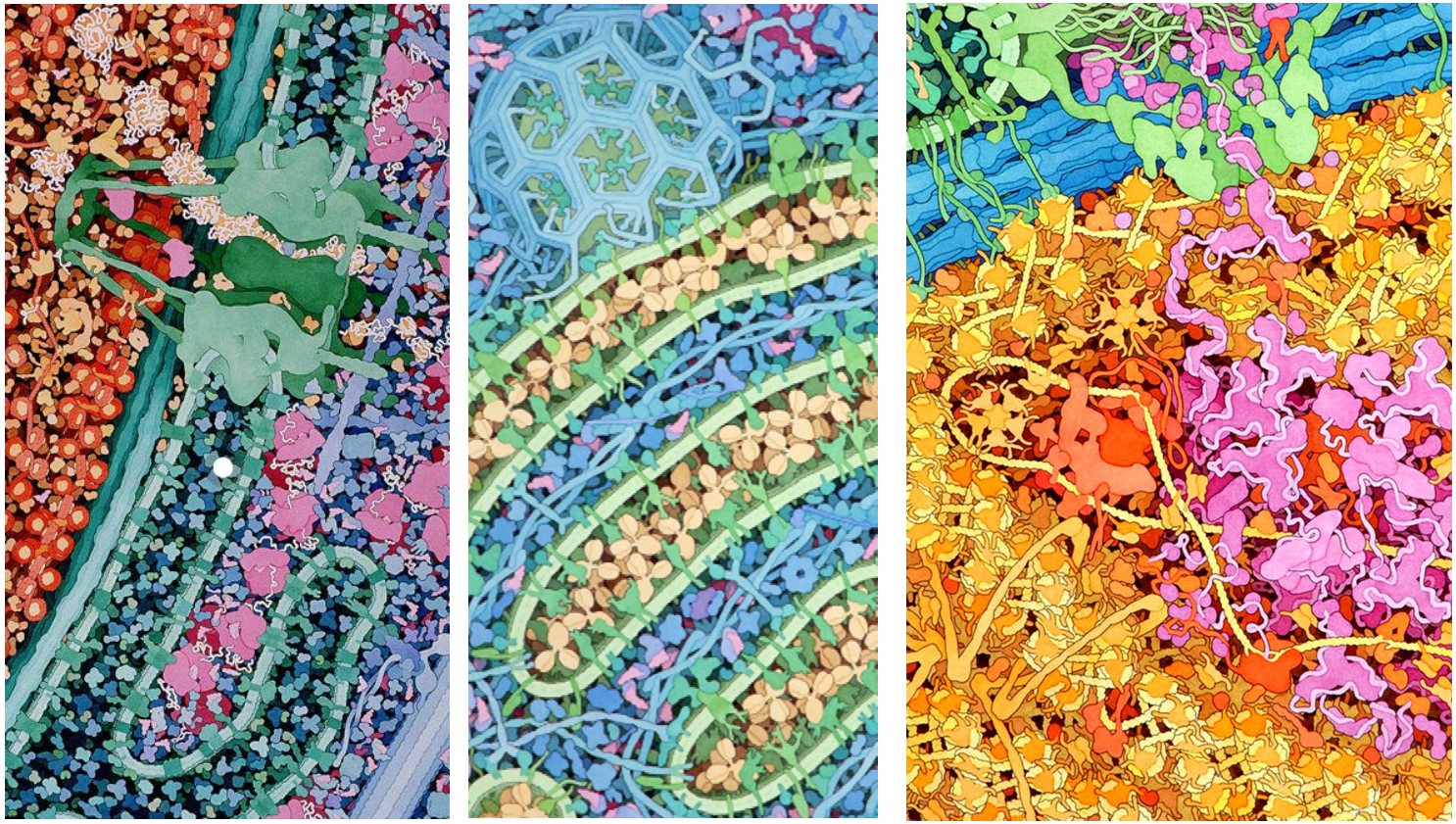
injection of ligand solution into receptor solution

measurement of heat of binding

Fitting to **appropriate model:** determination of all parameters of a binding reaction

for useful traces, $[R_{tot}]/K_D * n$ = 5 to 500 (10 to 100 ideal)

In cells, interactions are managed by compartmentalization



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