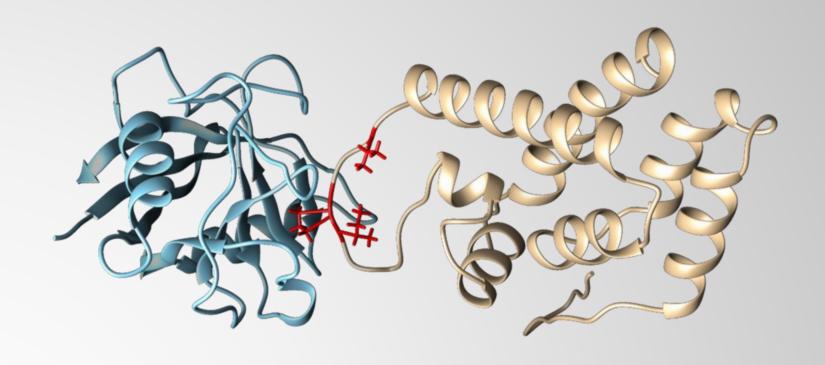
# Seminar 8: exercises on protein binding and energetics



#### A reminder from last year chemistry...

$$aA + bB \rightleftharpoons cC + dD$$

The equilibrium constant

$$K = \frac{[\mathbf{C}]^c[\mathbf{D}]^d}{[\mathbf{A}]^a[\mathbf{B}]^b}$$

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$$\Delta G = \Delta G^{\circ} + R \cdot T \cdot ln(Q)$$

$$At$$
equilibrium:
$$0 = \Delta G^{\circ} + R \cdot T \cdot ln(K)$$

$$\Delta G^{\circ} = -R \cdot T \cdot ln(K)$$

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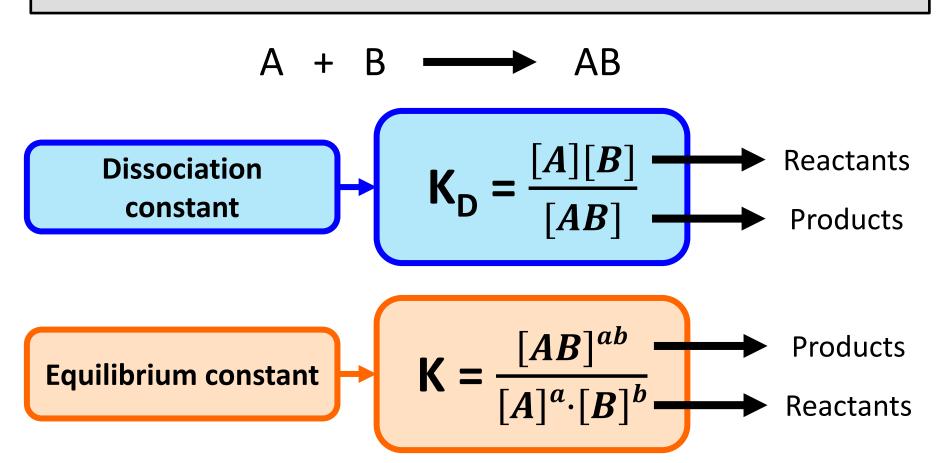
$$\Delta G^{\circ} = -R \cdot T \cdot ln(K)$$

The dissociation constant represents the concentration of protein and ligand at which 50% of the proteins are involved in a complex

$$A + B \longrightarrow AB$$

$$K_{D} = \underbrace{[A][B]}_{[AB]} \longrightarrow \text{Reactants}$$
Products

The dissociation constant represents the concentration of protein and ligand at which 50% of the proteins are involved in a complex



For PPIs, the equilibrium constant is the inverse of the dissociation constant, their logarythm has opposite sign

**Equilibium constant** 

**Dissociation constant** 

$$\mathbf{K} = \frac{[AB]^{ab}}{[A]^a \cdot [B]^b}$$

$$\mathbf{K}_{\mathsf{D}} = \frac{[A][B]}{[AB]}$$

For interactions between proteins:  $ln(K) = ln(K_D) \cdot (-1)$ 

We can relate the equilibrium constant to the disociation constant from protein-protein interactions

$$\Delta G = -R \cdot T \cdot \ln(K)$$

$$\ln(K) = \ln(K_D) \cdot (-1)$$

$$\Delta G = R \cdot T \cdot \ln(K_D)$$

We can relate the equilibrium constant to the disociation constant from protein-protein interactions

$$\Delta G = -R \cdot T \cdot ln(K)$$

$$ln(K) = ln(K_D) \cdot (-1)$$

$$\Delta G = R \cdot T \cdot ln(K_D)$$

$$\text{We can use this formula for mutations in protein-protein interactions}$$

$$\Delta \Delta G = R \cdot T \cdot ln(K_D^{\text{mut}}) - R \cdot T \cdot ln(K_D^{\text{wt}})$$

Also, remember that the  $\Delta G$  of a protein-protein interaction can be decomposed into different terms

$$\Delta G = \Delta G_{electrostatics} + \Delta G_{VanDerWaals} + \Delta G_{Solvation}$$

Also, remember that the ΔG of a protein-protein interaction can be decomposed into different terms

$$\Delta G = \Delta G_{\text{electrostatics}} + \Delta G_{\text{VanDerWaals}} + \Delta G_{\text{Solvation}}$$

$$\Delta G_{\text{interaction}}$$

Also, remember that the ΔG of a protein-protein intermediate be decommon be d

# Now try to solve exercise 1 from the protein-protein interactions section

In protein-protein or in protein-drug interactions we usually distinguish between receptor (R) and ligand (L)

#### **Protein-protein interactions:**

Receptor ------ Bigger protein

Ligand → Smaller protein

#### **Protein-drug interactions:**

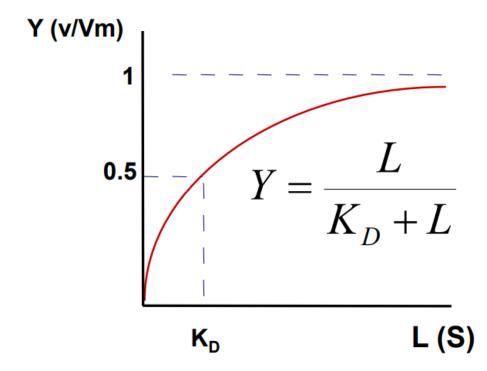
Receptor —— Protein

Ligand → Drug

We no longer use A and B to represent the binding process, now we use:

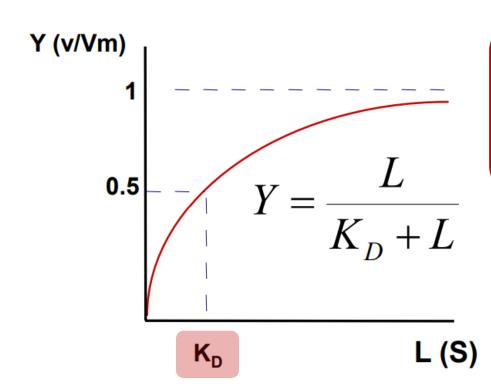
The saturation degree (Y) measures the percentage of receptor molecules that are involved in the interaction with a ligand

We can calculate the saturation degree from the value of the  $K_D$  and the concentration of ligand (L)



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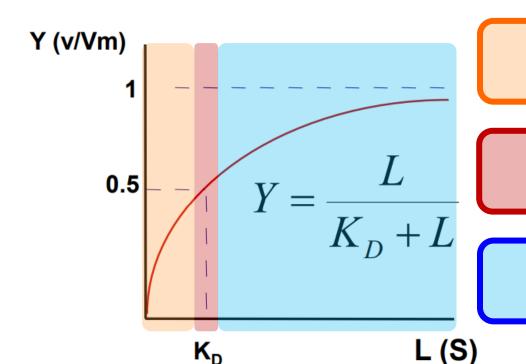
We can calculate the saturation degree from the value of the  $K_D$  and the concentration of ligand (L)



K<sub>D</sub> equals the concentration of ligand at which the saturation degree (Y) is 0.5

The saturation degree (Y) measures the percentage of receptor molecules that are involved in the interaction with a ligand

We can calculate the saturation degree from the value of the  $K_D$  and the concentration of ligand (L)



When  $L < K_D$ ; Y < 0.5

When  $L = K_D$ ; Y = 0.5

When  $L > K_D$ ; Y > 0.5

# If we introduce mutations in this system what will change? The K<sub>D</sub> or L?

$$Y = \frac{L}{K_D + L}$$

$$K_D \qquad \qquad L \text{ (S)}$$

When  $L = K_D$ ; Y = 0.5

When  $L > K_D$ ; Y > 0.5

# With that in mind, try to solve exercise 2 from the protein-protein interactions section

$$Y = \frac{L}{K_D + L}$$

When  $L = K_D$ ; Y = 0.5

When  $L > K_D$ ; Y > 0.5

## The inhibition constant (K<sub>i</sub>) indicates the affinity between a protein (R) and a drug (L)

It is calculated exactly as the dissociation constant (K<sub>D</sub>), the only difference is that it is used to describe protein-drug interactions.

$$R + L \longrightarrow RL$$

$$\mathbf{K_{i}} = \frac{[R][L]}{[RL]}$$

When 50% of the protein is binding the ligand

The inhibition constant (K<sub>i</sub>) indicates the affinity between a protein (R) and a drug (L)

Imagine that we keep the concentration of protein constant and we measure the K<sub>i</sub> of two drugs, estimate the affinity of the drugs for

The drug with higher K<sub>i</sub>

The drug with lower K<sub>i</sub>

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Tip: since the concentration of protein is constant, the  $K_i$  is going to be proportional to the concentration of drug.

The inhibition constant (K<sub>i</sub>) indicates the affinity between a protein (R) and a drug (L)

Imagine that we keep the concentration of protein constant and we measure the K<sub>i</sub> of two drugs, estimate the affinity of the drugs for

The drug with higher K<sub>i</sub>

The drug with lower K<sub>i</sub>

**Lower affinity** 

You need a higher amount of drug to achieve the 50% of binding

**Higher affinity** 

You need a lower amount of drug to achieve the 50% of binding

## With that in mind, try to solve exercise 1 from the protein-drug interactions section

achieve the 50% of binding

rou need a lower amount of drug to achieve the 50% of binding