Thermodynamics + protein modeling

4 laws

first law : Energy is neither created nor destroyed
(conservation of energy)

Enthalpy (heat) → ΔH
→ heat a process generates or absorbs

$+\Delta H$ → system absorbs heat
↳ endothermic ← gets cold

$-\Delta H$ → system generates heat and gives
off heat to surroundings
↳ exothermic ← gets hot

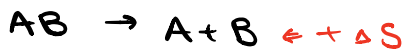Second law : The Universe tends towards maximum disorder
spontaneous processes
↳ order → disorder

Entropy (disorder) → ΔS

$+\Delta S$ when disorder ↑
$-\Delta S$ when disorder ↓

more order
$A + B \rightarrow \overset{\frown}{AB}$ ← $-\Delta S$

$AB \rightarrow A + B$ ← $+\Delta S$

A process is spontaneous if
it does not need to be
driven by outside energy

● 1 ● 2 ● 1 ● 2

| 1 2 | 1 2 | | 1 1 | 2 2 |
| 1 2 | 2 1 | | 1 2 | 2 1 | etc...
| 2 1 | 1 2 | | 2 1 | 1 2 | 24 combos
| 2 1 | 2 1 | | 2 2 | 1 1 |

*more ways for less
organized combos
to occur

Gibbs Free Energy (constant T, P)

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

heat - temp·entropy

$\Delta G \leq 0$ ← spontaneous
↳ the binding happens

$\Delta G > 0$ ← not spontaneous

} @ temp T

$\Delta G = 0$ at equilibrium

← standard conditions

$$\Delta G^{0)} = -RT \ln k_{eq}$$

Equilibrium:

$$AB \underset{}{\overset{K_d}{\rightleftharpoons}} A + B$$ ← in equilibrium when amt AB and amt A+B stay constant
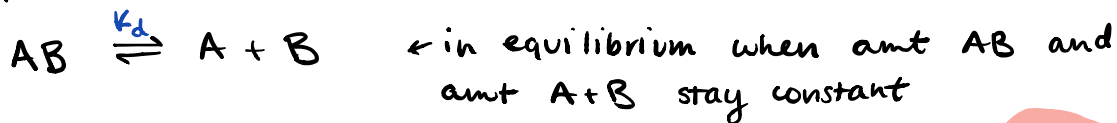
K_d = dissociation constant

$$= \frac{[A][B]}{[AB]} = \frac{Products}{Reactants}$$

K_d = [ligand] at which $\frac{1}{2}$ of the protein binding sites are occupied (for 1:1 reaction)

$[\ ] =$ concentration (molarity

$M = \frac{mol}{L}$)

$mol = 6.02 \times 10^{23}$

Smaller $K_d \rightarrow$ there is greater affinity between the protein and ligand
→ smaller conc. ligand in order for $\frac{1}{2}$ sites to be bound

K_d in:
nM   μM
↑
higher affinity

smaller K_d , greater affinity

→ less ligand required to have ½ sites bound

ΔG binding → ΔG_{bind} (in kcal/mol or J or kJ)

Example: $\Delta G_{bind \#1}$ = − 50 kcal/mol

$\Delta G_{bind \#2}$ = − 150 kcal/mol ← more spontaneous

at eq → $K_d = K_{eq}$