4th John, Xuni
3rd Scott
2nd Craig
1st Buy

Chem 728    S12

# I. | Diffusion Controlled Reactions |

$$A + B \rightleftarrows AB$$
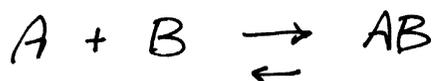
Molecules A and B react every time they collide.
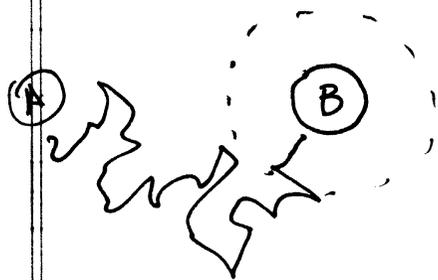
## How fast are these reactions?

$$J_A = -D_A \nabla C_A \qquad \text{flux of } A \text{ to } B$$

$$J_A = -D_A \, \partial C_A / \partial r \qquad \text{radial dep.}$$

$J_A$ = number of molecules flowing across 1 cm²/s

$r$ is the separation distance betw. molecular centers

flux across spherical surface of radius r and surface area $4\pi r^2$ :

$$\mathcal{J}_A = -4\pi r^2 J_A = -4\pi r^2 D_A \, \partial C_A / \partial r$$

steady state flow $\mathcal{J}_A$ is constant for all values of r.

$\mathcal{J}_A$ = number of A molecules that flow into surface of B per unit time.

Cast into a better form:

i $r_0$ = distance of closest approach

(1)

Boundary Conditions @ $r = r_0$ and $r = \infty$

ii  $r_0$ (cm)

iii  $C_A = 0$  at  $r = r_0$  (all molecules react upon collision)

iv  $C_A = \tilde{C}_A$ (bulk)  at  $r_\infty$   $r = \infty$

Integrate betw. boundary conditions

$$J_A \int_{r_0}^{\infty} r^{-2} dr = 4\pi D_A \int_0^{\tilde{C}_A} dC_A$$

$$J_A / r_0 = 4\pi D_A \tilde{C}_A$$

$$J_A = 4\pi r_0 D_A \tilde{C}_A$$

number of molecules of A that collide with B per second

* Molecules of B actually move with $D_B$ diffusion $D_B$ – diffusion coefficient of B.

* Rate scales with bulk concentration of B.

$$\text{Rate} = 4\pi (D_A + D_B) r_0 \, C_A C_B = k \, C_A C_B$$

$k'$   $cm^3$ molecule$^{-1}$ sec$^{-1}$

   $M^{-1}$   multiply by $10^{-3} N_0$

$$k = 10^{-3} N_0 k'$$

(2)

$$k' = 4\pi(D_A + D_B)r_o$$

$r_o$ = distance of close
approach

We'll take this to be
the diameter of the molecule colliding    (2 × radius)



$$r_A + r_B = r_o \simeq 30\,\text{Å}$$
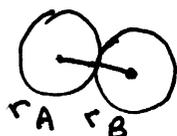
Suppose, as an example, we calculate
the collision rate, of a 15 kDa protein (globular).

A 15 kDa globular protein ($\bar{v} = 0.73\ cm^3/g$),
which is spherical, has a radius of
15 Å and a diffusion coefficient of $1.4\cdot10^{-6}\ cm^2/s$

Then $k' = 4\cdot\pi\ (2\cdot1.4\cdot10^{-6}\ cm^2/s)\ 30\,\text{Å}\cdot10^{-8}\ cm/\text{Å}$

$$k' = 1.05\cdot10^{-11}\ cm^3/s/molecule$$

$$k = \cancel{\qquad} k'\cdot10^{-3}\ dm^3/cm^3 \times 6\cdot10^{23}\ molecules/mole$$

$$k = 1.05\cdot10^{-11}\ cm^3/s/molecule \cdot 10^{-3}\ dm^3/cm^3 \cdot 6\cdot10^{23}\ \frac{mole}{molecule}$$

$$k = 6.3\cdot10^{9}\ M^{-1}s^{-1}$$

Reaction rate constant for for diffusion-
controlled reaction of a 15 kDa protein

# Features of Diffusion Controlled Reaction Rate Constant

- No activation energy
  - 100 % react every collision
    (no orientation effect)
  - collision rate determine by diffusion
    (no attractive or repulsive interactions)
    - van der Waals
    - charge charge
    - H-bond
    - etc.

On the other hand most rate constants are much smaller that the 'upper limit' defined by the analysis for Diffusion Controlled Reactions. Why?

II | **Activation Energy** | . In transforming from reactants to products, there are often high energy intermediates, referred to as transition states.



Energy | Reactant

$E(r)$   $E_a(f)$

$E_a(r)$   Products $E(p)$

Reaction Coordinate

④
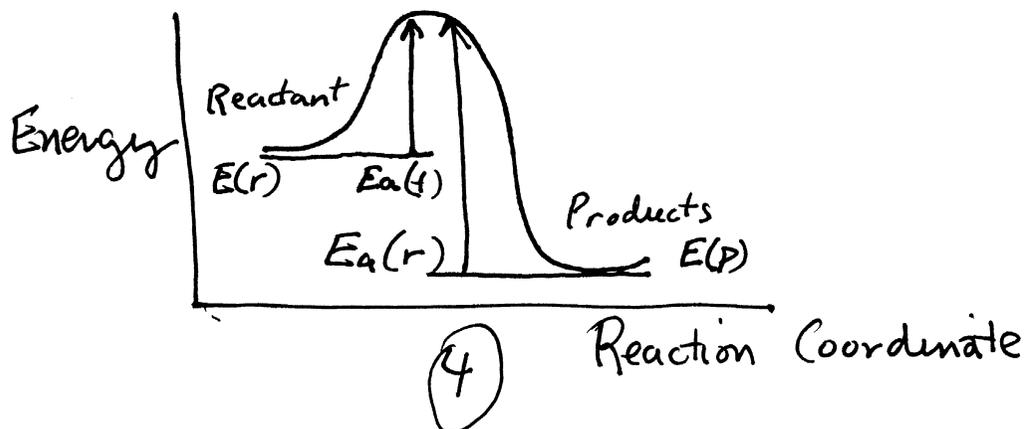
- Reactants and Products have energies associated with ~~ten~~ them.

- The transform from Reactant to Product proceeds along a reaction coordinate. The diagram implies this as an independent variable, of which the system energy is a function

- The difference in energy between Reactants and products determines the Reaction equilibrium, $\Delta E = E(P) - E(R)$

- The pathway from Reactant to Product (or Product to Reactant) involves passage through a high energy state. The difference in Energy of the transition state and either the reactant or product state defines the Activation energies $E_{act}(f)$, $E_{act}(R)$

  (f forward; r, reverse)

$$E_{act}(f) = E(TS) - E(R)$$

$$E_{act}(r) = E(TS) - E(P)$$

- <u>By definition</u>, there is <u>one</u> transition state in an <u>elementary reaction step</u>. For multi-step reaction schemes, the largest activation energy defines the rate-limiting step.

The Arrhenius Equation, even in its simplest form, gives the activation energy

$$k = A \exp\left(-\frac{E_a}{RT}\right)$$

here $E_a$ is a <u>molar</u> energy since $R$ (instead of $k_B$) is used.

Again, ~~the E activat~~ an energy (here $\bar{E}_a$) relative to thermal energy, $RT$, ($k_B T$) ~~has an~~ gives an exponential ~~depends~~ dependence to $k$.

- The pre-exponential factor, $A$, is sometimes regarded as a frequency factor, since it can represent the number of collisions per unit time (as in a diffusion controlled reaction) and the term $\exp(-E_a/RT)$ reduces the number of collisions to the number of collisions that result in a reaction. The larger $E_a$ is, relative to $RT$, the smaller this fraction is.

# III   Transition State Theory



Reaction Coordinate
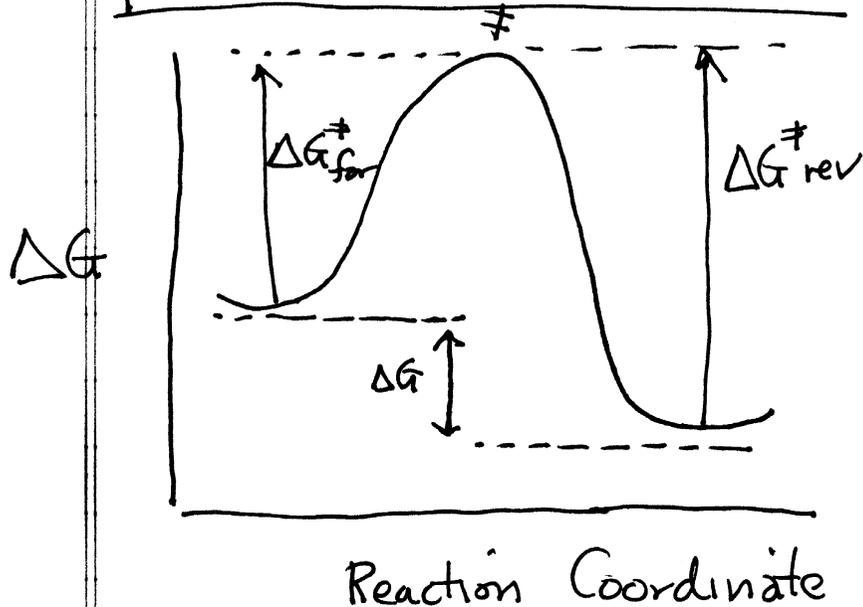
$$\Delta G(for)^{\ddagger} = \Delta G^{\ddagger}_{rev} - \Delta G^{\ddagger}_{for}$$

Transition state theory assigns thermodynamic significance to the $\ddagger$ transition state, a Gibbs energy, and an analysis of the pre-exponential factor to a universal rate constant.

To illustrate with specific reaction:

$$2A \rightleftharpoons AA^{\ddagger} \Longrightarrow A_2$$
$$K^{\ddagger} \qquad \overrightarrow{k^{\ddagger}}$$
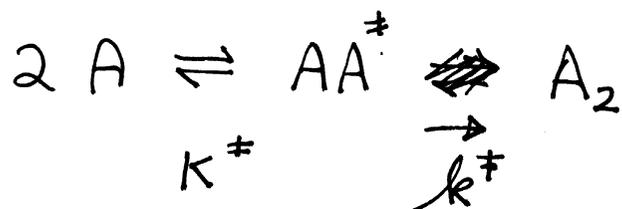
consider protein (A) dimerization ($A_2$)

The rate constant, $k$, is given by

$$k = k^{\ddagger} K^{\ddagger}$$

(7)

in transition theory.

$K^{\ddagger}$ is the equilibrium between the
reactant state and transition state
$k^{\ddagger}$ is the rate constant for the
decomposition of the transition state
to product

$$K^{\ddagger} = \frac{[AA^{\ddagger}]}{[A]^2} \qquad k^{\ddagger} = \frac{k_B T}{h}$$

With the definition of $K^{\ddagger}$, the
usual relation to $\Delta G^{\ddagger}$ can be applied

$$k = \frac{k_B T}{h} K^{\ddagger} = \frac{k_B T}{h} \exp\left[-\frac{\Delta G^{\ddagger}}{RT}\right]$$

$$k = \frac{k_B T}{h} \exp\left[\frac{\Delta S^{\ddagger}}{R}\right] \exp\left[-\frac{\Delta H^{\ddagger}}{RT}\right]$$

~~In principle, the value~~

$\Delta H^{\ddagger}$ is analogous to $E_{act}$ of the Arrhenius
equation.

$\Delta H^{\ddagger}$ and $\Delta S^{\ddagger}$ provide thermodynamic information about the weighting factor $\left( \exp\left(-\Delta G^{\ddagger}/RT\right)\right)$, the extent to which ~~bond~~ bonding may change $(\Delta H^{\ddagger})$ and configurational effects $(\Delta S^{\ddagger})$ are involved in the formation of the transition state.

IS this of any use to ~~broken~~ biochemical reactions?

Problem Set 7 investigates how it might be.