Lecture of October 24, 2018
Chapter 5: Energy and Equilibrium

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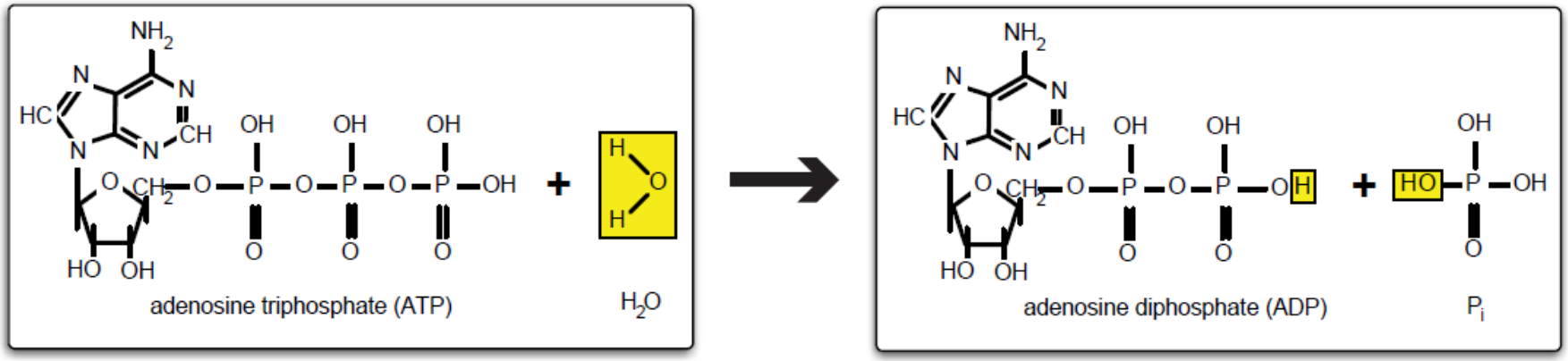
Energy of Living Cells derived from ATP Hydrolysis



- $\Delta G = -30.5kJ \cdot mol^{-1} \rightarrow \sim 12.5k_BT$ at room temperature

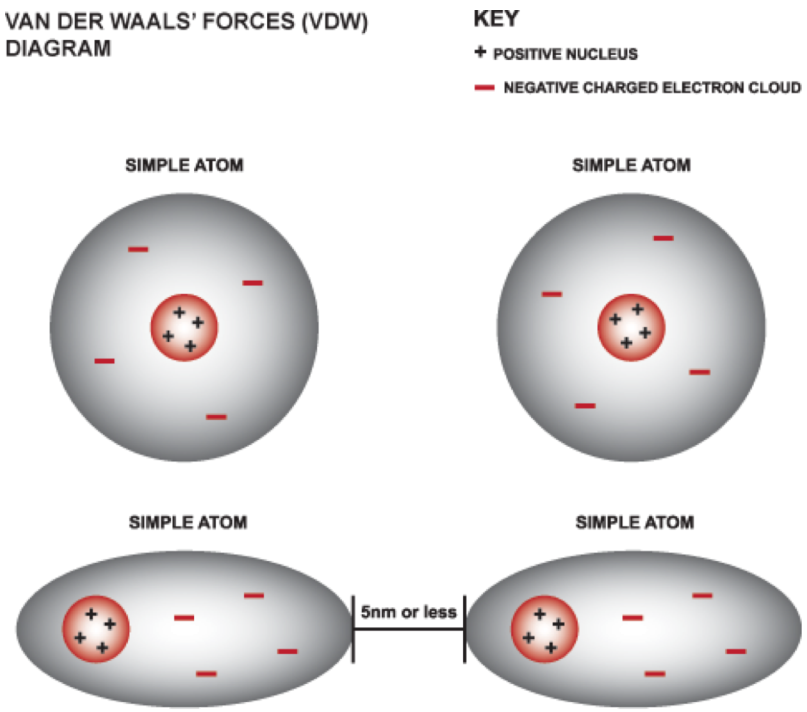
However textbook states that for *in vivo* systems it is $\rightarrow \sim 25k_BT$

- **Covalent bonds** has energy $\sim 200kJ \cdot mol^{-1} \sim 80k_BT$, and **cannot be broken** by **ATP hydrolysis**

Major Forces in Biological System

Weak Intermolecular Interactions		
Force	**Strength (kJ/mol)**	**Distance (nm)**
Van der Waals	0.4-4.0	0.3-0.6
Hydrogen Bonds	12-30	0.3
Ionic Interactions	20	0.25
Hydrophobic Interactions	<40	varies

Van der Waals forces (non-bonded) between atoms and molecules

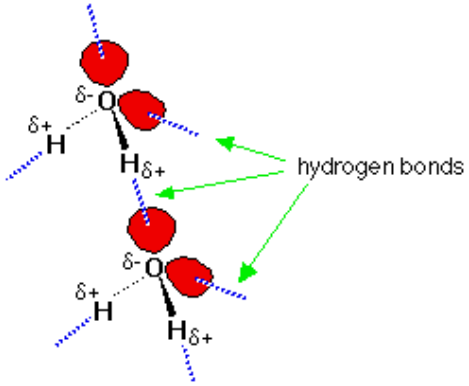


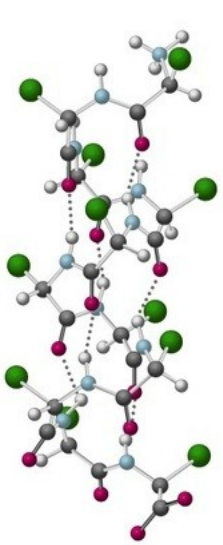
When two atoms come within 5 nanometers of each other, there will be a slight interaction between them, thus causing polarity and a slight attraction.

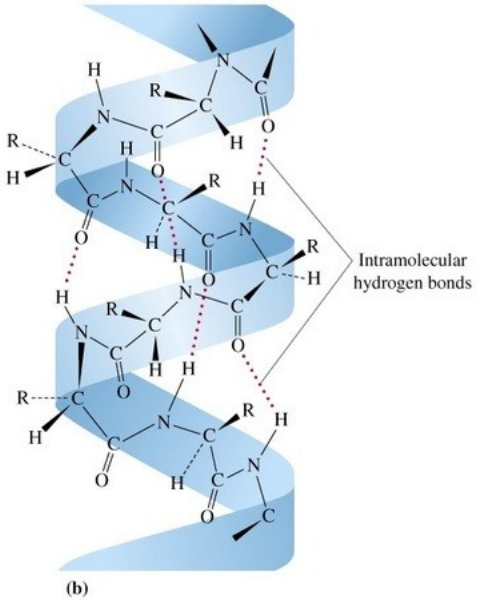
$\sim 1.5 k_B T$

van der Waals contacts between atoms and molecules can be **thermally** broken.

Hydrogen Bonds (HB)

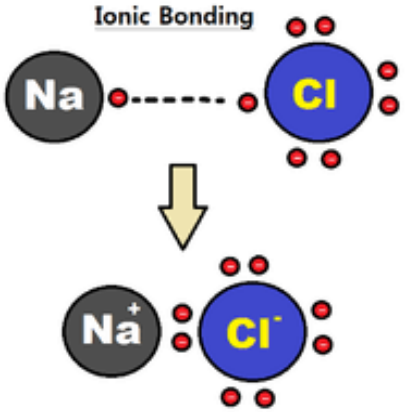






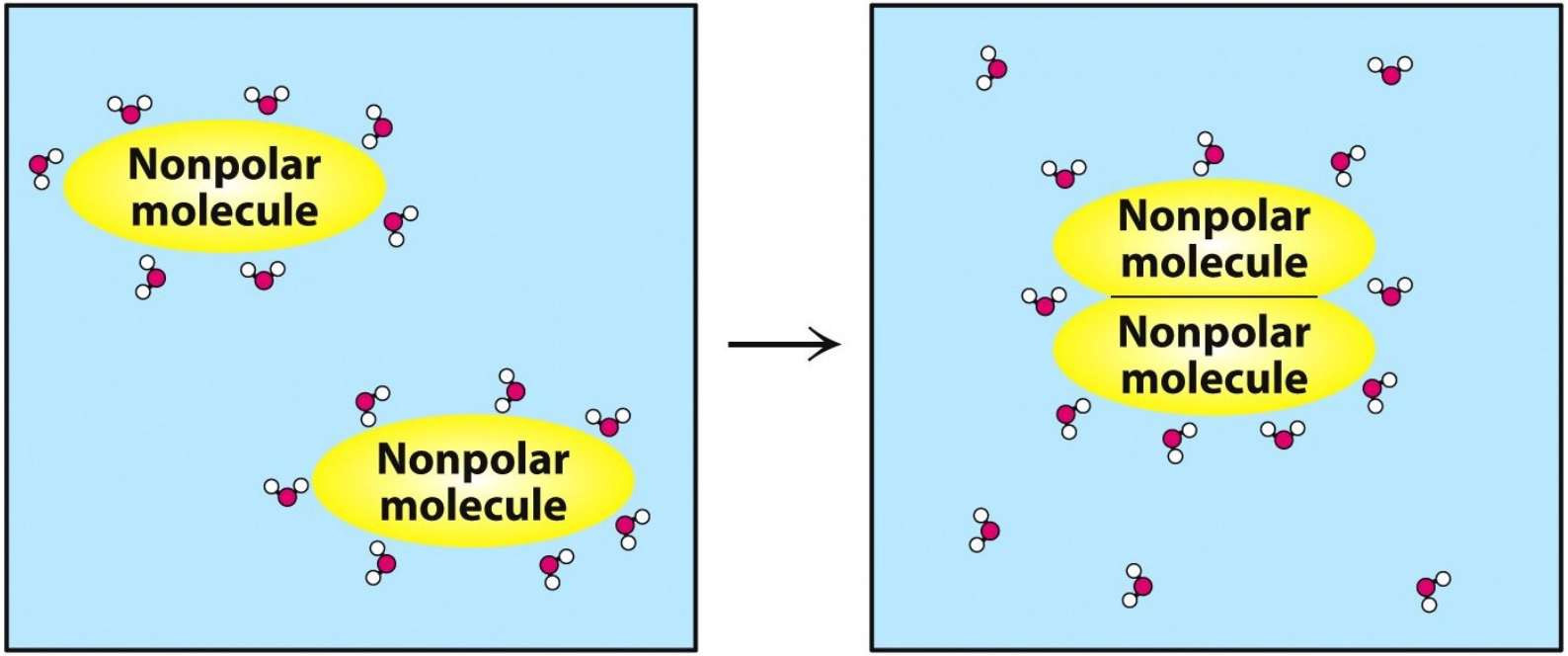
- Stabilizes protein structures such as $\alpha - helix$ and $\beta - sheet$
- $\sim 10 k_B T$ HB can broken by ATP hydrolysis

Ionic Bonds



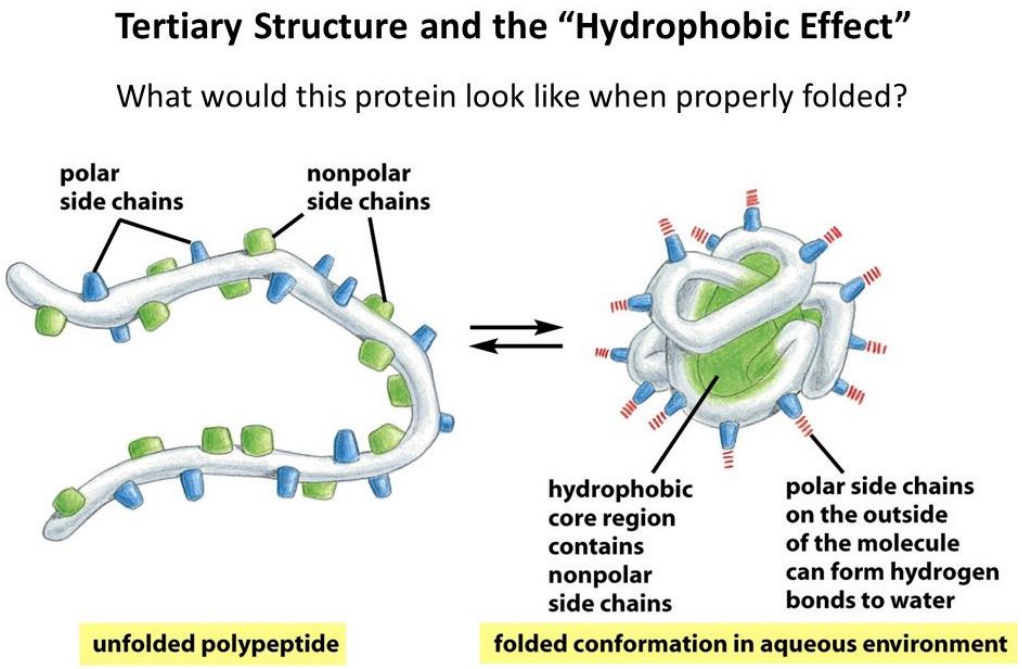
- $\sim 10 k_B T$ HB can broken by ATP hydrolysis

Hydrophobic Forces



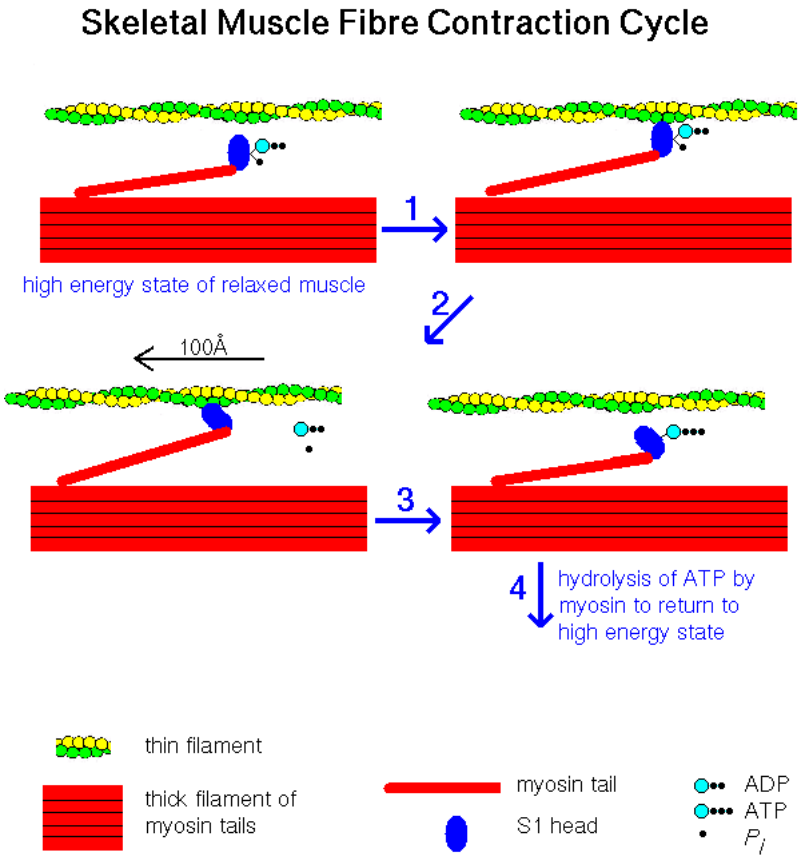
- Non-polar molecules tend to **aggregate** to reduce contacts with water molecules
- It is considered an entropic (depletion) effect
- $\sim 16 k_B T$ can broken by ATP hydrolysis

Hydrophobic Forces Stabilize Folded Protein Structiures



- **Side-chains** of **non-polar amino acids** form **hydrophobic core** to shield themselves from water creating compact folded proteins.
- $\sim 16 k_B T$ ATP hydrolysis can break **functional sites** of proteins

Myosin Power Stroke and Muscle Contractions



- **Myosin power** stroke of distance $\Delta x \sim 10nm$ with ATP hydrolysis energy $\sim 25 k_B T$
- This can be used to estimate the number of cells in a human body$\sim 10^{14}$