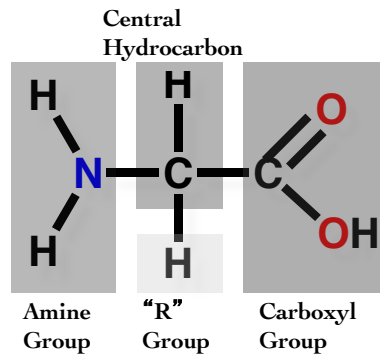
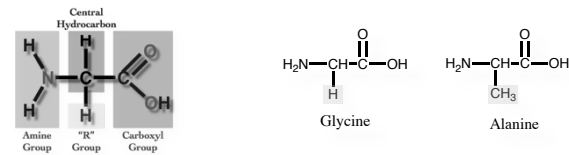


Proteins are composed of monomers called **amino acids**

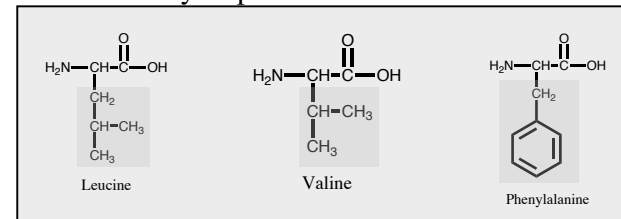


• ALL amino acids have the exact same structure *except* for the "R" Group

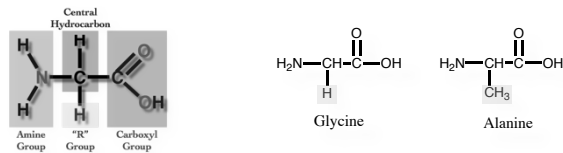
There are **20** different amino acids



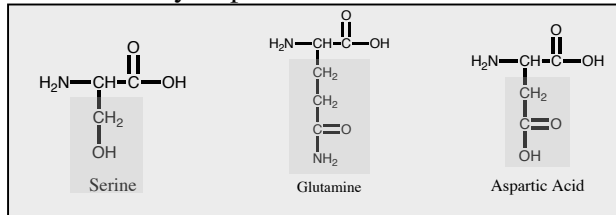
### Hydrophobic Amino Acids



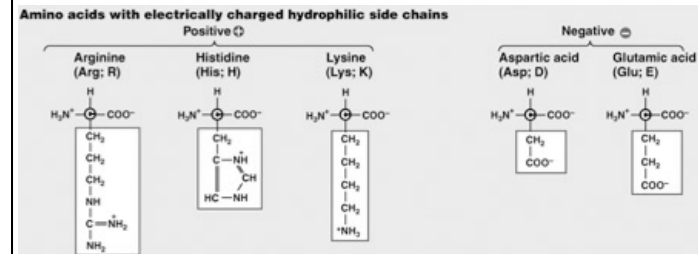
There are **20** different amino acids



### Hydrophilic Amino Acids

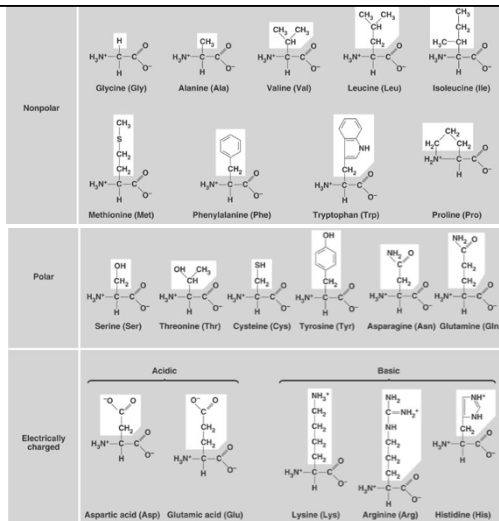


### Charged amino acids (side-chains)



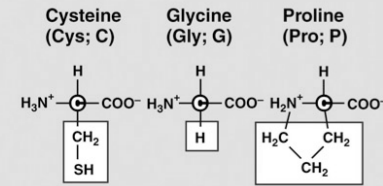
Are these polar or nonpolar side chains??

# 20 Amino Acids



## Special amino acids

### C. Special cases



Cysteine has  $-\text{SH}$  that can react with another to form disulfide bridge. Controls peptide folding.

Glycine- small side chain allows it to pack tightly and fit in tight corners

Proline- ring structure limits its ability to rotate and form bonds. Stabilizes bends and loops.

## There are **20** different amino acids

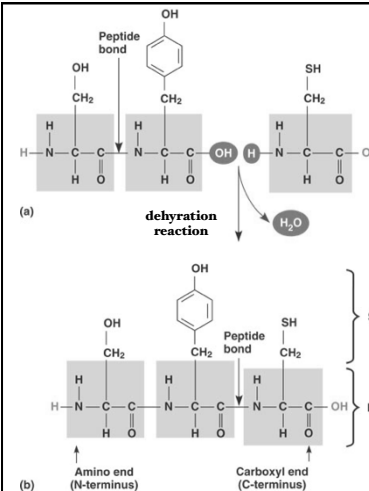
The type of *R*-Group will affect the 3-dimensional structure of the protein

AMINO ACID	SIDE CHAIN	AMINO ACID	SIDE CHAIN
Aspartic acid Asp D	negative	Alanine Ala A	nonpolar
Glutamic acid Glu E	negative	Glycine Gly G	nonpolar
Arginine Arg R	positive	Valine Val V	nonpolar
Lysine Lys K	positive	Leucine Leu L	nonpolar
Histidine His H	positive	Isoleucine Ile I	nonpolar
Asparagine Asn N	uncharged polar	Proline Pro P	nonpolar
Glutamine Gln Q	uncharged polar	Phenylalanine Phe F	nonpolar
Serine Ser S	uncharged polar	Methionine Met M	nonpolar
Threonine Thr T	uncharged polar	Tryptophan Trp W	nonpolar
Tyrosine Tyr Y	uncharged polar	Cysteine Cys C	nonpolar

POLAR AMINO ACIDS

NONPOLAR AMINO ACIDS

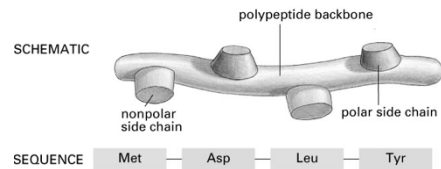
## Peptide bonds



link amino acids together to form a polypeptide chain

The peptide bond does NOT occur between the "R" groups. Is between the amino and carboxyl group of the "backbone"

## Peptide Bonds Form Chains (Primary Structure)

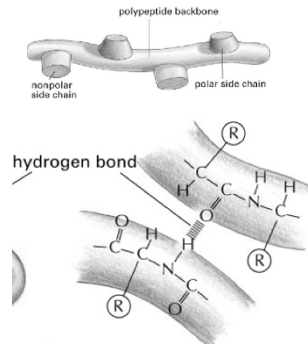


The **sequence** of amino acids constitutes the **primary structure** of a protein.

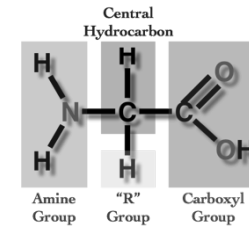
Held together by covalent peptide bonds.



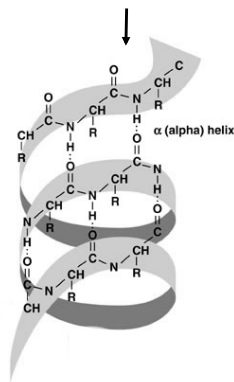
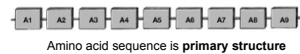
## Protein Secondary Structure



Secondary Structure Arises From the Hydrogen Bonds Between the Peptide Backbone



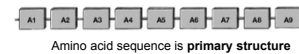
## Protein Secondary Structure



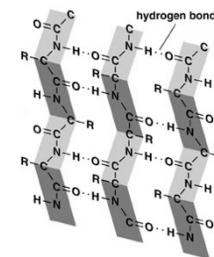
The **alpha helix** arises from hydrogen bonds within the amino acid chain itself.

The **R-groups** play only minor roles, if any, in stabilizing secondary structure

## Protein Secondary Structure



$\beta$ -pleated sheet

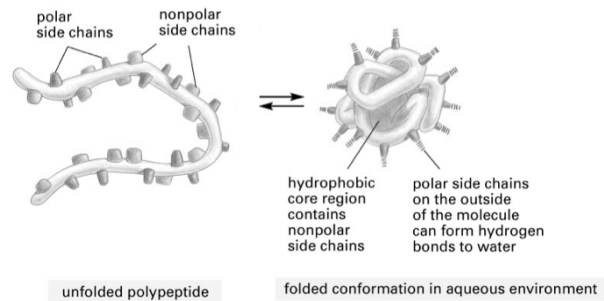


The **beta sheet** arises from hydrogen bonds within the amino acid chain itself.

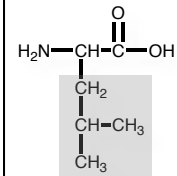
The **R-groups** play only minor roles, if any, in stabilizing secondary structure

## Protein Tertiary Structure

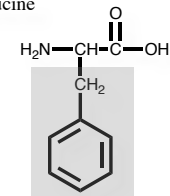
Tertiary Structure Arises From Folding of the  
*Amino Acid Sidechains (R groups)*



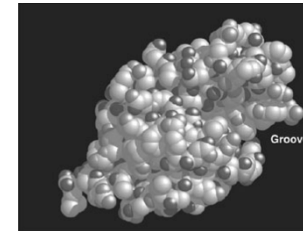
## The Hydrophobic Effect



Leucine

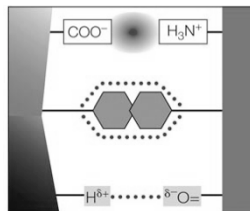


Phenylalanine



Hydrophobic side-chains will be near the center, stabilized by van der Waals forces.

## Protein Tertiary Structure, continued:

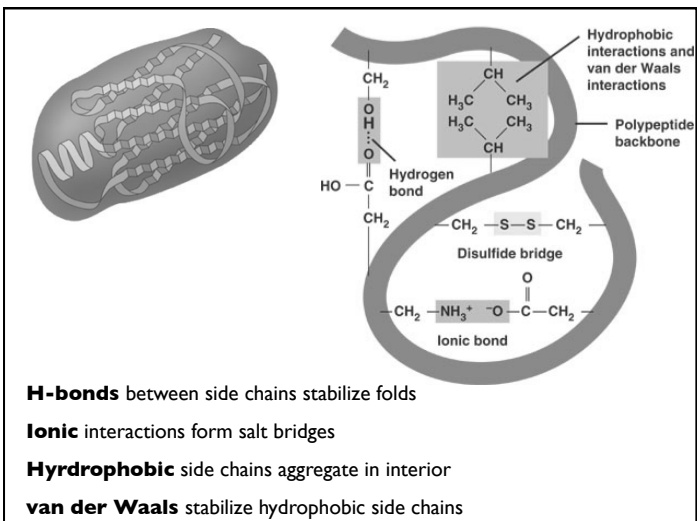
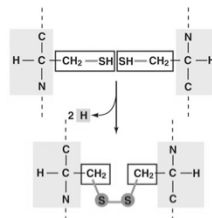


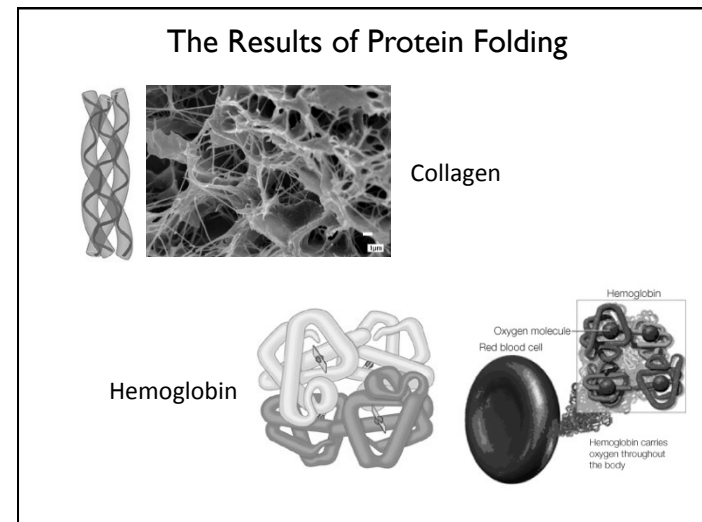
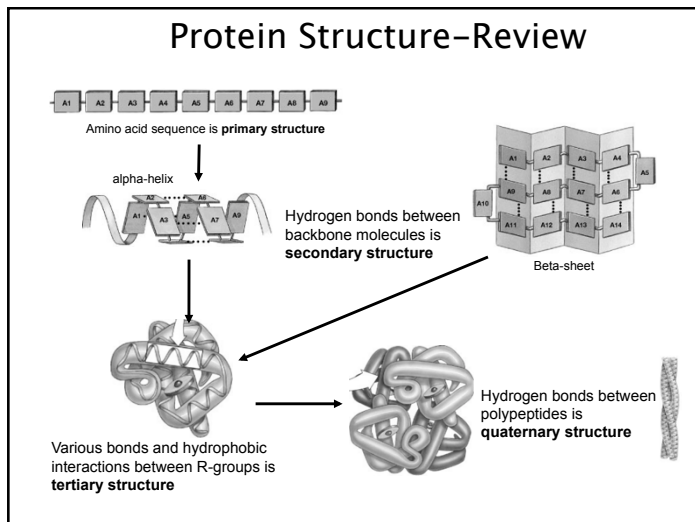
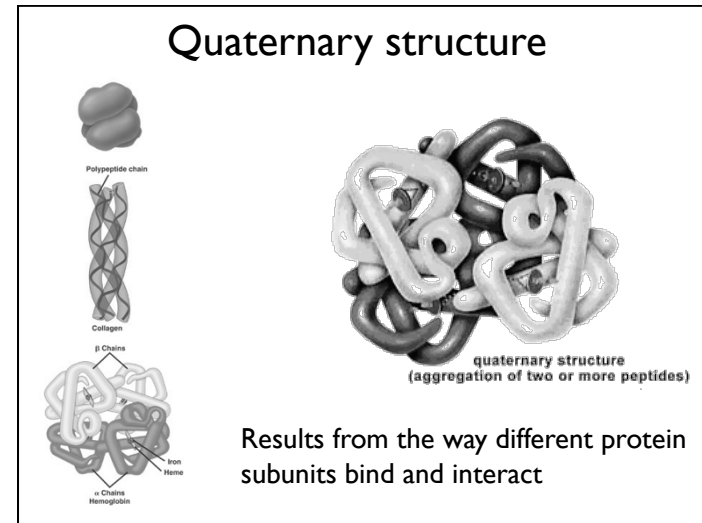
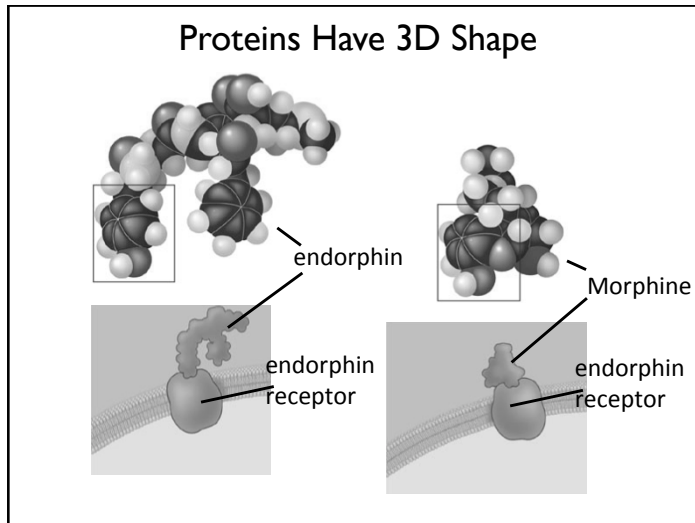
Ionic interactions occur between charged R groups.

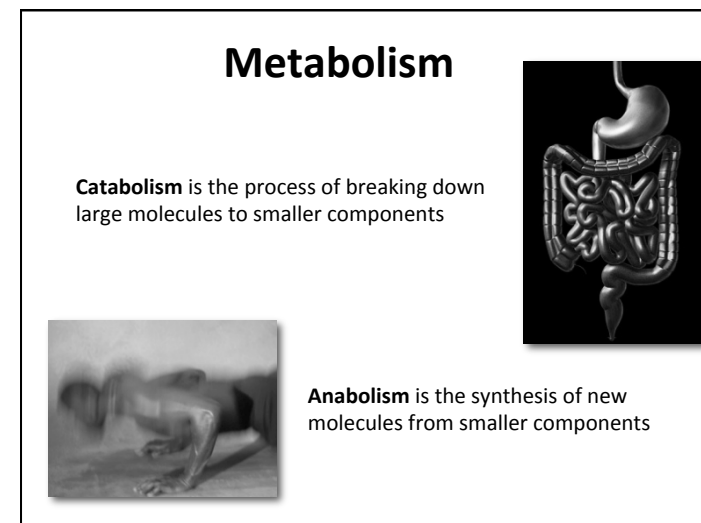
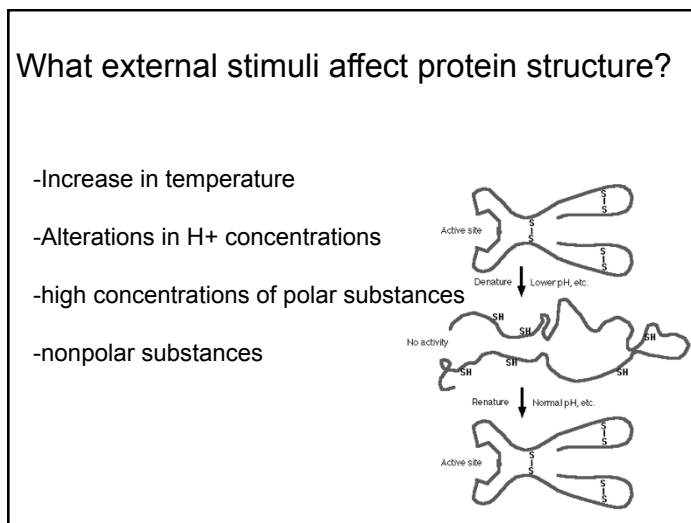
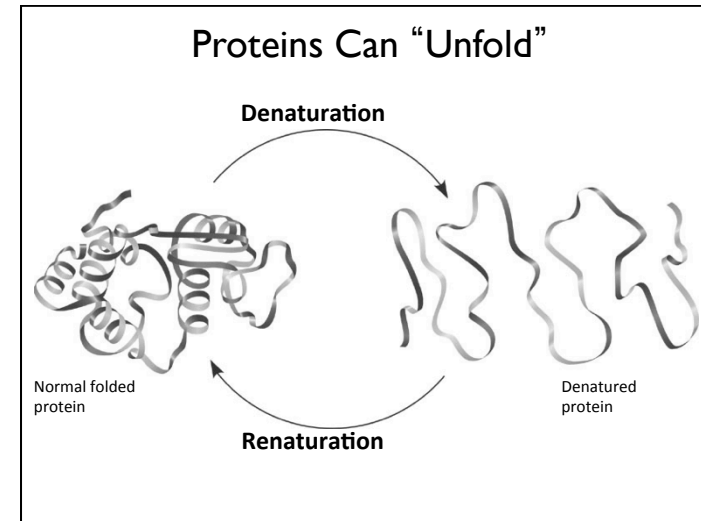
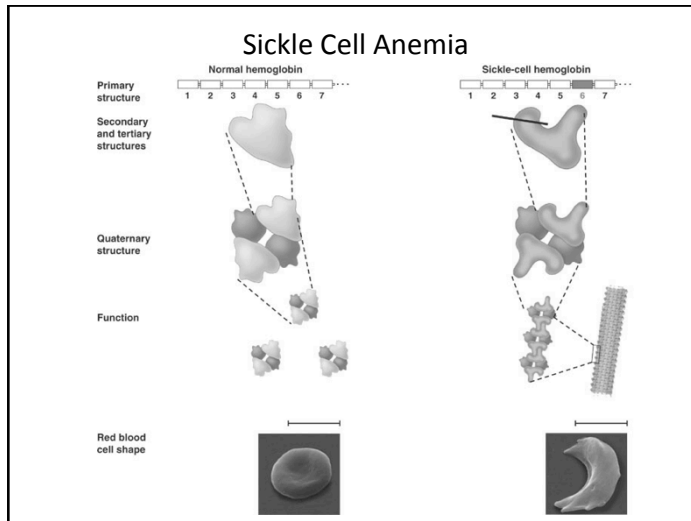
Two nonpolar groups interact **hydrophobically**.

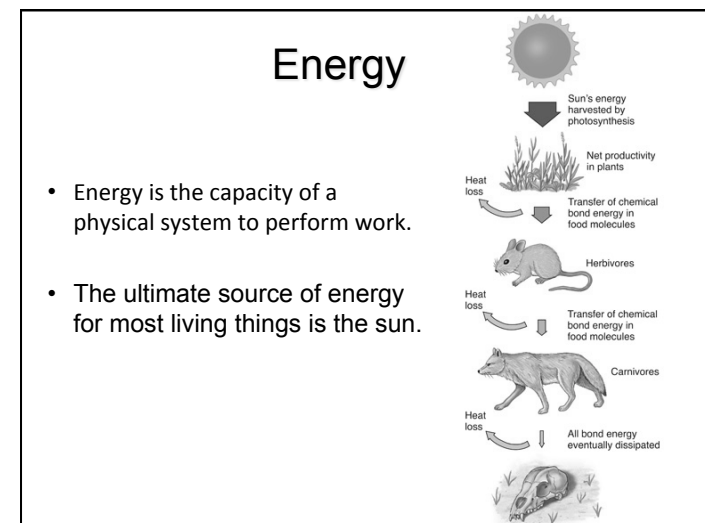
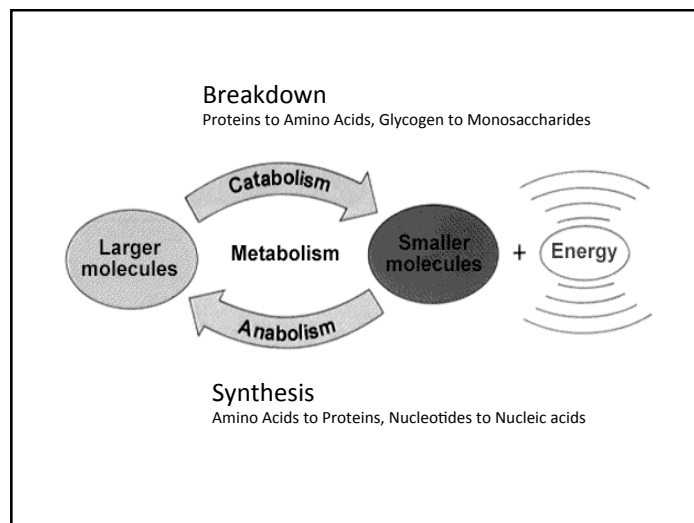
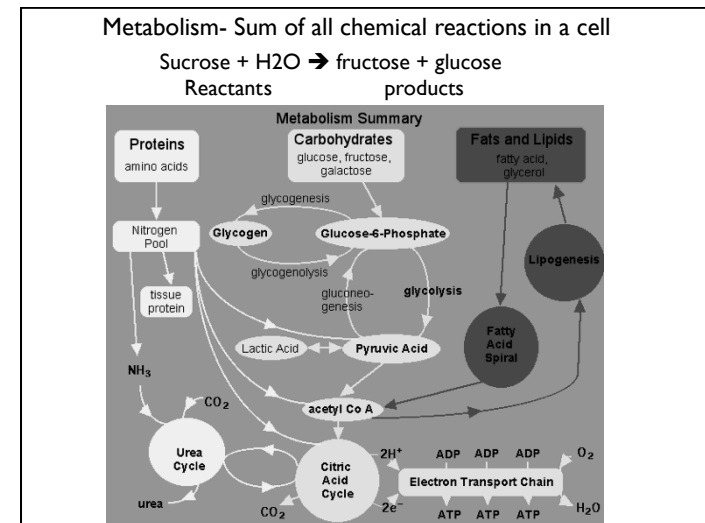
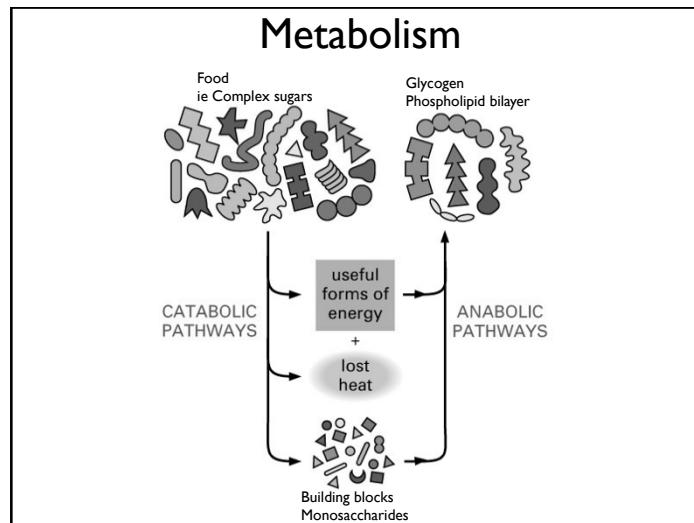
Hydrogen bonds form between two polar groups.

Cysteine R group contains  $-\text{SH}$ .  
Can react with second  $-\text{SH}$  to form a **disulfide bridge**









## Energy

**Energy** - The capacity to do work (to move matter against an opposing force).

**Potential Energy** - The energy stored by matter as a result of its location or spatial arrangement.

*Potential Energy (gravitational)*



*Kinetic Energy*



**Kinetic Energy** - The energy of motion, which is directly related to the speed of that motion. Moving matter does work by imparting motion to other matter.

## Thermodynamics I

A. Energy cannot be created or destroyed

B. Energy can only be transformed into another form



## Thermodynamics II

A *closed* system moves toward entropy, increasing disorder.

Living systems are open systems that maintain organization and increase it during development



**ENTROPY**  
It's not so much 'letting yourself go' as it is 'succumbing to the inevitable'

Life increases **order**...  
but increases overall **disorder**  
(entropy) in the process

## Chaos will reign

Entropy is a measure of disorder in the system



**ENTROPY**

Eg. Anabolic reactions required to make 1kg of your body requires 10kg of food. Rest is "waste:."



## 5 principles governing metabolism

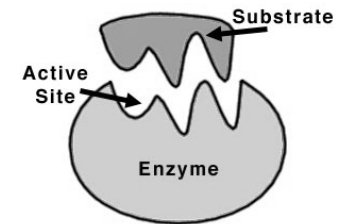
- Complex chemical transformations occur through a series of separate intermediate reactions.
- These reactions are catalyzed by specific enzymes.
- These enzymes are activated/inactivated to control reaction rate.
- Most metabolic pathways are similar between organisms.
- In eukaryotes these metabolic pathways are compartmentalized in organelles.

## Biological catalysts: Enzymes....

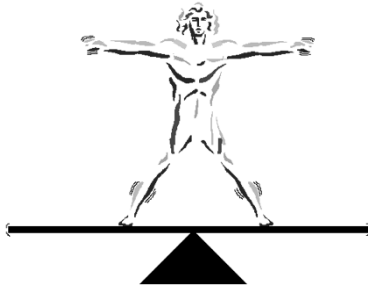
**Catalysts:** Proteins that speed up biochemical reactions  
Increase reaction rates without themselves being altered

these reactions may occur without catalysts, but too slowly

**Enzyme:** most common type of catalyst



Enzymes catalyze metabolic reactions  
and maintain **homeostasis**

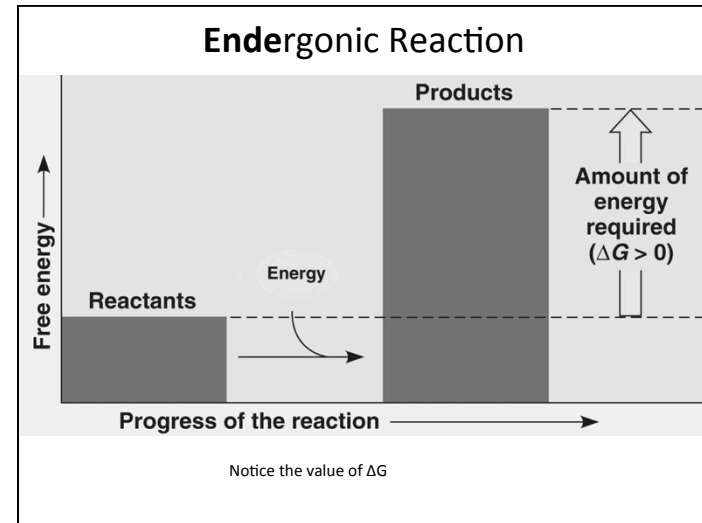
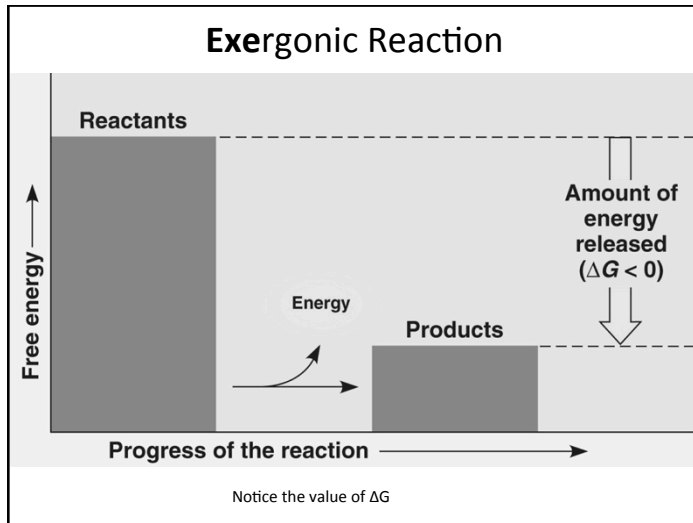


How do cells create this balance?

- regulation of enzyme expression levels
- regulation of enzyme activity

## Free Energy ( $\Delta G$ )

- **Free energy** – the energy available for doing work.
  - Most chemical reactions release free energy
    - they are **exergonic**.
      - Downhill
    - Some reactions require the input of free energy
      - they are **endergonic**.
        - Uphill



### Exergonic Reactions can perform Work

A reaction that releases energy ( $-\Delta G$ ) can “change” a system

**Equilibrium** has  $\Delta G$  of 0

Exergonic and endergonic reactions are often “coupled”