

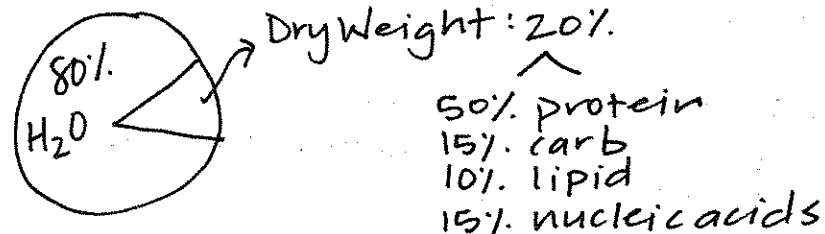
# Biochemistry

**Organization/Scale:** atom → molecules → macromolecule → cell → tissue → organ → ...

**What is your atomic composition?**

H: 63%.      N: 14%.  
 O: 24%.      P: 0.2%.  
 C: 10%.      S: <0.1%.

**What is your molecular composition?**



## Covalent Bonds

→ shared e<sup>-</sup> bonds  
 → relatively stable (80 kilocal/mol to break)

atom	H	C	O	N	P
Max # Bonds	1	4	2	3 (4)	5

## Electronegativity & Polarity

→ How tightly an atom holds onto the e<sup>-</sup>

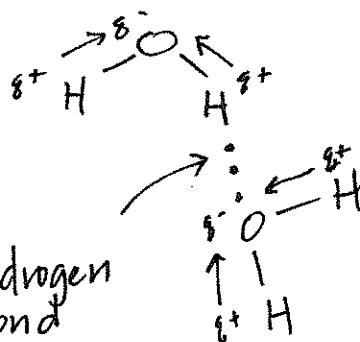
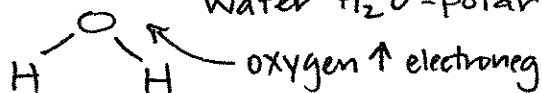
C-C = non-polar, same pull.

O-H = polar, oxygen δ<sup>-</sup> ← δ<sup>+</sup> pulls @ e<sup>-</sup> stronger

N-H = polar, N pulls e<sup>-</sup> ← δ<sup>+</sup> stronger

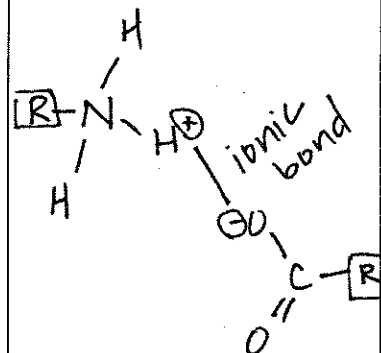
## Hydrogen Bonds

Water H<sub>2</sub>O = polar



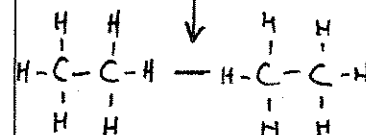
- COHESION: surface tension
  - Water - water
- ADHESION: plants + towels
  - water - other stuff

## Ionic Bonds



• stable bonds

## Van Der Waals Interactions

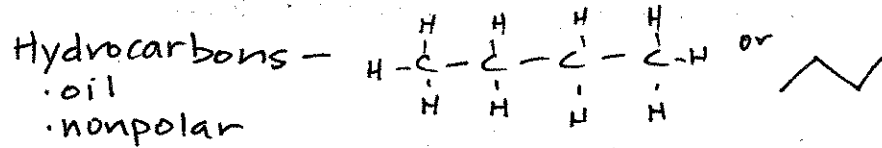


slight interactions  
 (1 kilocal/mol to break)

If you have a large macromolecule (say a protein), the sum of all these interactions and bonds can result in very stable molecules.

### Hydrophobic Interactions

Water · fear/hate



oil + water don't mix because nonpolar molecules cannot bond w/ polar molecules.

### Hydrophilic Interactions

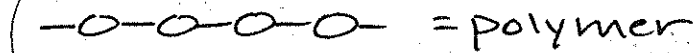
water love

· polar molecules

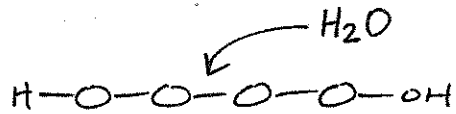
Amphipatic: molecule with hydrophobic + hydrophilic regions.

### Macromolecules

#### Hydrolysis Reactions



Water · break



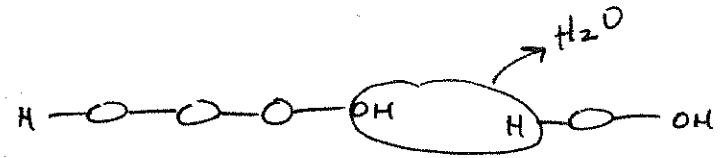
Water splits the polymer into smaller pieces.



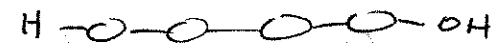
breakdown

#### Dehydration Reactions

remove Water



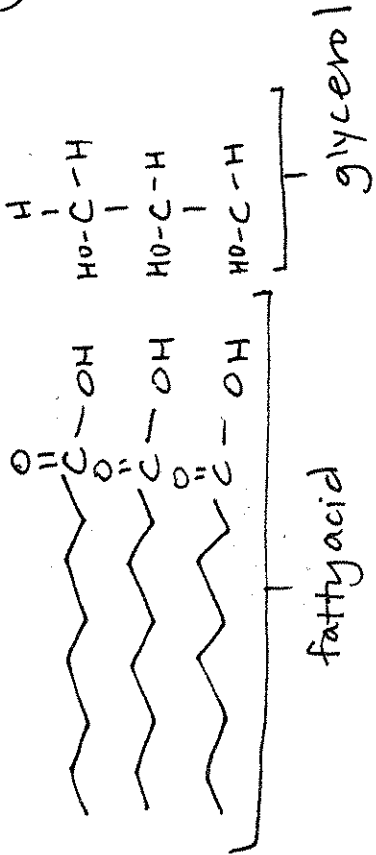
remove water to link together



build/link

**Lipids**

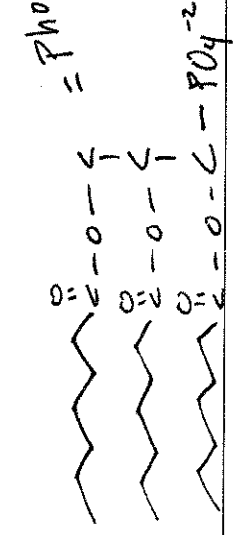
- oils, waxes, fats
- fat is stored in adipose tissue
- makes membranes, insulates, stores energy



Q: How do we link these?  
 - Dehydration Rxns

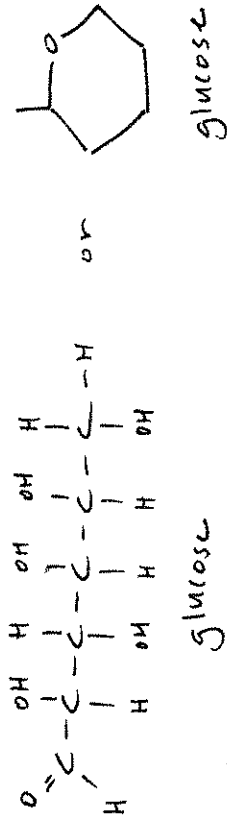
→ forms a triglyceride

"fat in the blood"

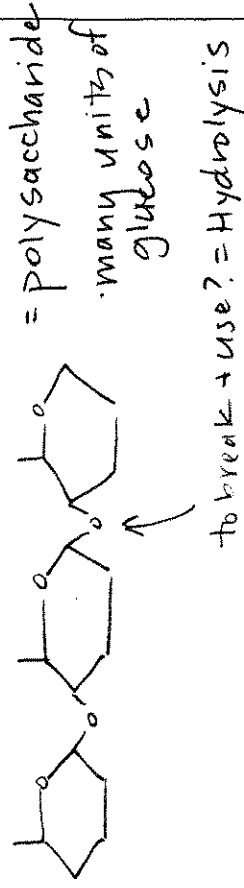


**Carbohydrates**

- store energy (starch/glycogen)
- structure (cellulose, chitin)



- \* named "-ose"
- \* length (mono/di/poly saccharides)



Non-polar (Hydrophobic)

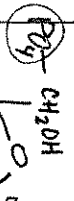
Polar (Hydrophilic)

**Nucleic Acids**

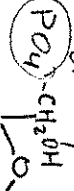
• Stores genetic information

• RNA + DNA

↓  
ribose



↓  
deoxyribose

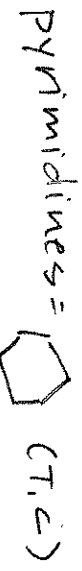


No oxygen at the 2' carbon  
"deoxy"ribose



called a nucleotide

Bases: A T C G



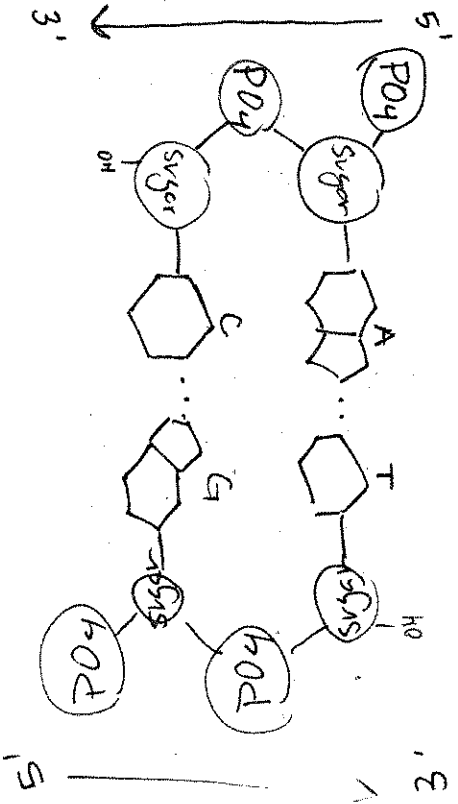
Where does "U" go?  
(RNA)

DNA

• antiparallel structure

• A-T

• C-G

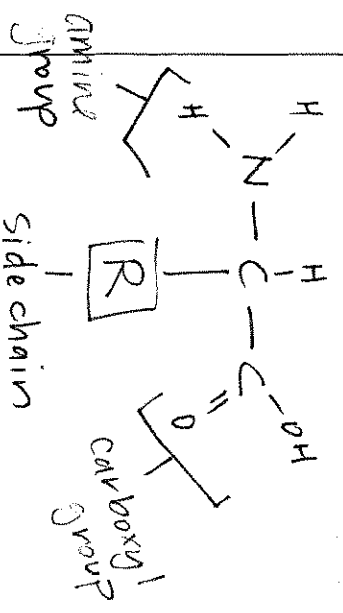


**Proteins**

• Do everything!

• Very diverse + specific in function

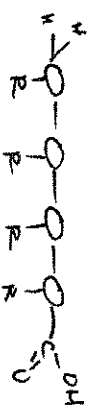
Amino Acids (peptide)



↳ 20 different amino acids

Structure:

1° primary: a.a.'s linked by dehydration rxns



2° secondary: basic folding or mix + sheet

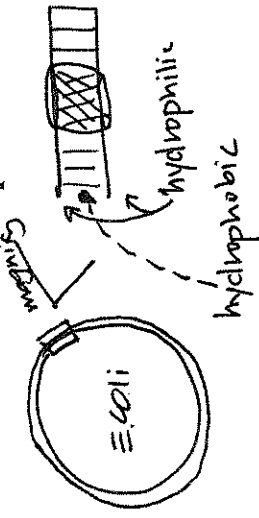


3°/4° structure: more complex folding

\* if it's not folded correctly, it will not work

Chaperonin (helps fold correctly)

**E. Coli OMPF Example:**



\* create a protein that allows molecules through

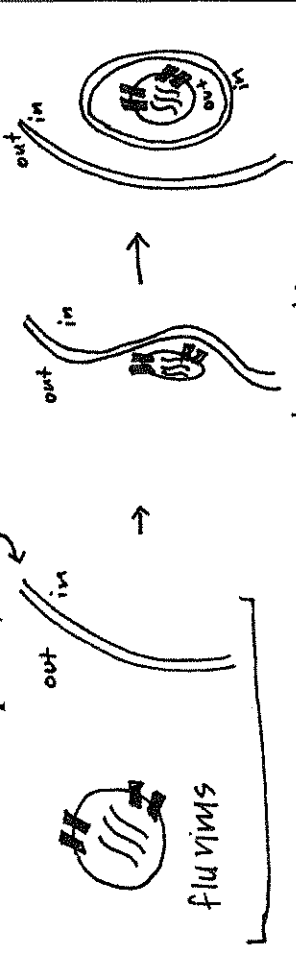
→ nothing big, nothing charged or hydrophobic

→ allow small polar molecules in.

→ "beta barrel": need hydrophobic side chains on the outside to keep it between the bilayer.

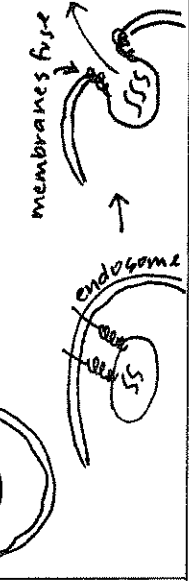
→ inside the hole: need charged side chains to keep charged ions out.

**Influenza Example: Your cell membrane**



\* when the body recognizes an endosome, "push into" it lowers the pH (more acidic) and destroys the endosome. But...

flu virus has long  $\alpha$  helix chains, as pH ↓ the endosome collapses, but the virus coils spring open + fuse with the membrane of the endosome.



flu virus is now officially in your cell and starts reproducing.

**Enzymes**

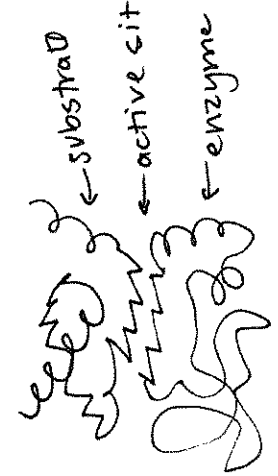
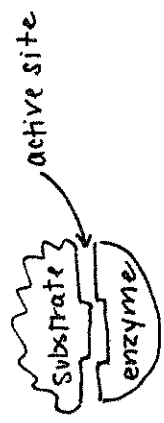
→ speed up chemical reactions by ↓ the activation energy

→ examples:

- catalase (liver) +  $H_2O_2$
- amylase (spit) + starch
- lactase + lactose
- polymerase + DNA

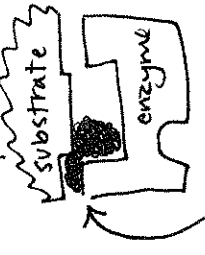
→ Reactions:

- catabolic → break apart ( $A \rightarrow AD$ )
- anabolic → build up ( $AD \rightarrow A$ )



→ Turn enzyme off? Inhibitors

competitive



inhibitor directly blocks the active site. No rxn.

non-competitive



inhibitor binds to a different part of the enzyme, which causes the active site to  $\Delta$  shape.

