

Biochemistry 2

- send answer to iClicker Question 14A now.
- Polysaccharides (a.k.a carbohydrates)
 - blood type
- Proteins I
 - amino acids (polymerization animation)
 - side-chain properties
 - proteins & folding demo
- iClicker Question 14B

Be sure you have a piece of wire.

⇒ Due in lab NEXT week:

- Pre-lab for Lab 06 (Lab Manual p 85 and on-line)

Exam I: Monday 10/19 (info in Chemistry 2 handout)

- Last names starting with A through E: 11th floor of Healy Library
- Last names starting with F through Z: Lipke Auditorium (here)
(1 bonus point for going to right room)

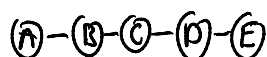
Polysaccharides (aka carbohydrates)

* monomers = sugars (100's of different kinds)

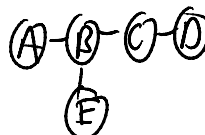
* all monomers have many $\text{H}-\text{C}-\text{OH}$ groups \therefore 'philic

* polymers can be

a) linear



or b) branched



due to differences in lipo polysaccharides

red blood cell



surface molecule

A, B, or O

- anchored in 'phobic core of membrane by via 'phobic effect

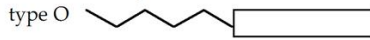
Bio 111 Macromolecules Handout

Blood type

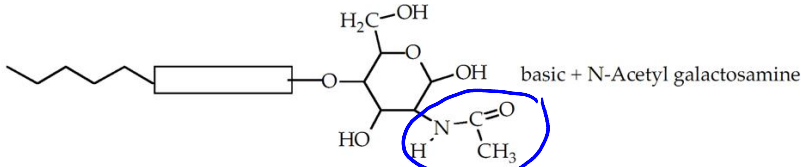
lipid tail

"basic" polysaccharide (4 sugars)

type O

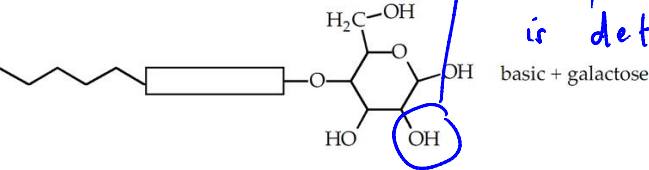


type A



- tiny difference is detectable by your immune system

type B



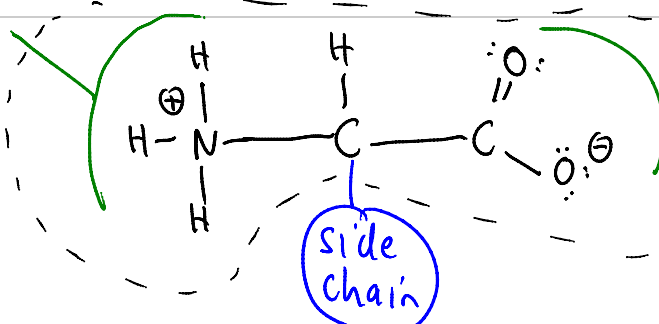
type AB = mixture of BOTH A and B

Proteins : monomer : amino acid * 20 different types
polymer : never branched

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"generic" amino acid

amino group



"backbone"

same for all 20

carboxyl group

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R different in each

Properties of amino acids depend on side chain structure
(rare exceptions)

ex

<u>Property</u>	<u>alanine (ala)</u>	<u>aspartic acid (asp)</u>
- side chain	- CH ₃	- CH ₂ -C(=O)O ⁻
x bonds it can make	'phobic int.	H-bonds ionic bond
x phobic or philic	'phobic	'philic
x size / shape	small	medium

Protein folding demo

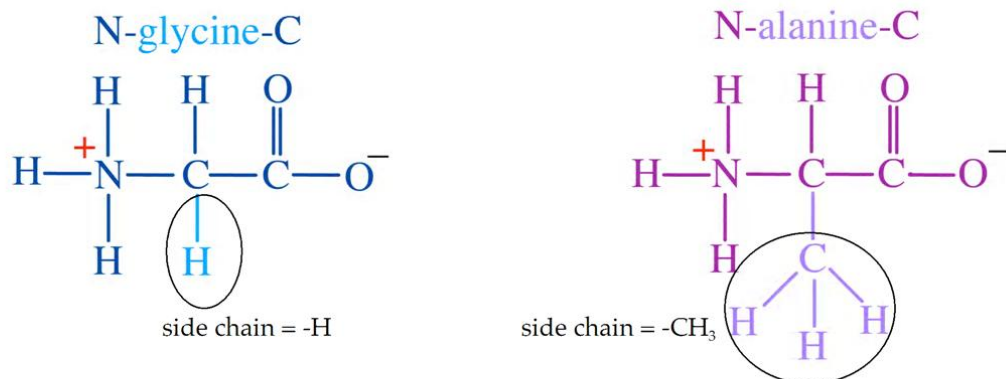
* all proteins "born" as linear chain of amino acids
then fold into complex 3d shapes

Q: how? A: side-chain interactions (mostly)

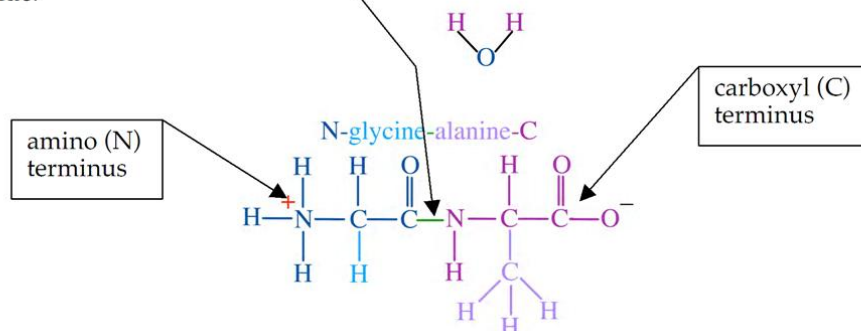
Protein Synthesis

= joining amino acids = peptide bond formation

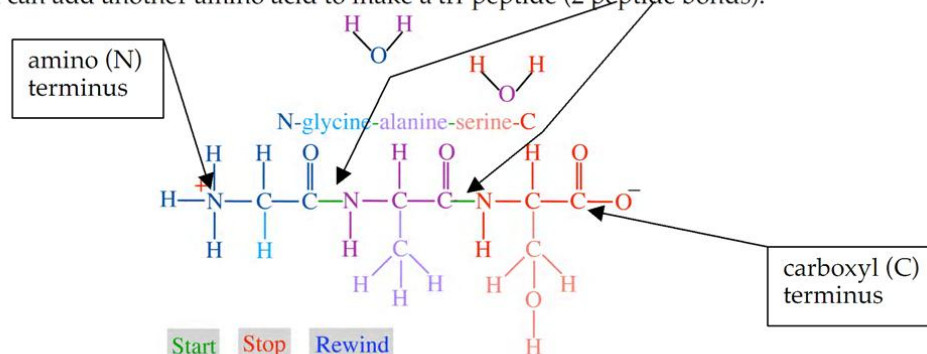
1) Start with 2 amino acids



2) Join them: lose H₂O and form a peptide bond (a kind of covalent bond). Now, you have a di-peptide:



3) You can add another amino acid to make a tri-peptide (2 peptide bonds):



Note that a protein always has only one N-terminus and one C-terminus and the (+) and (-) charges of the internal amino acids are no longer present.

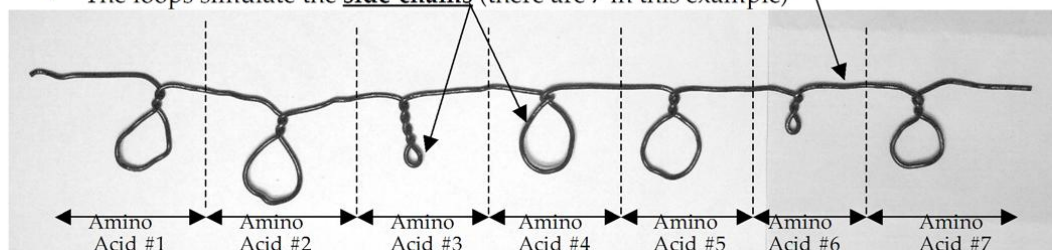
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Bio 111: Protein Folding Demonstration

Today in lecture, you will twist a piece of wire so that it simulates the behavior of a chain of amino acids (also known as a protein). We will then use this to explore protein folding in lecture.

A simulated 7-amino acid protein is shown below; your protein will be similar although it may have a different pattern of loops.




- The more-or-less straight part of the wire simulates the **backbone**
- The loops simulate the **side-chains** (there are 7 in this example)



- One end is the amino terminus; the other is the carboxyl terminus (for this demonstration, it does not matter which is which).

Side-chains

In the simplified world of this demonstration, there are three kinds of amino acids, each of which is represented by a different type of loop:

<u>Hydrophobic</u>	<u>Positively-charged</u>	<u>Negatively-charged</u>
		
A <u>large open loop</u> . Make it two finger-widths wide.	A <u>long closed loop</u> . Make it <u>four</u> twists long.	A <u>short closed loop</u> . Make it <u>two</u> twists long.

How to do it

Now you will twist your wire to make a protein of seven or eight amino acids. The sequence of amino acids is up to you, but it works best if your protein contains:

- More hydrophobic amino acids than charged ones.
- At least one positively-charged and one negatively-charged amino acid.

The measurements in this demonstration need not be precise; you will use the width of your fingers as a ruler.

- Leave two finger-widths of space un-twisted at the starting end.
- Leave three finger-widths of space between each amino acid.



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