

Chem 109 C

Bioorganic Compounds

Armen Zakarian
Office: Chemistry Bldn 2217

<http://labs.chem.ucsb.edu/~zakariangroup/courses.html>

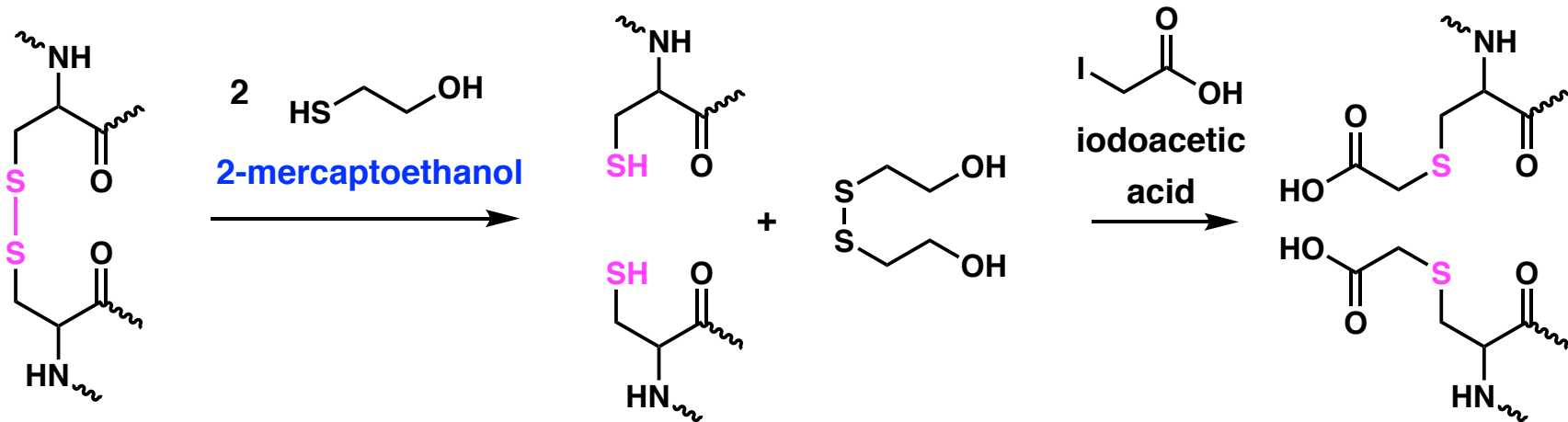
Primary structure is the sequence of amino acids in a protein and the location of disulfide bridges

strategy for determining the primary structure:

- 1. break down peptide into individual amino acids to determine composition**
- 2. use selective reagents to determine sequence**

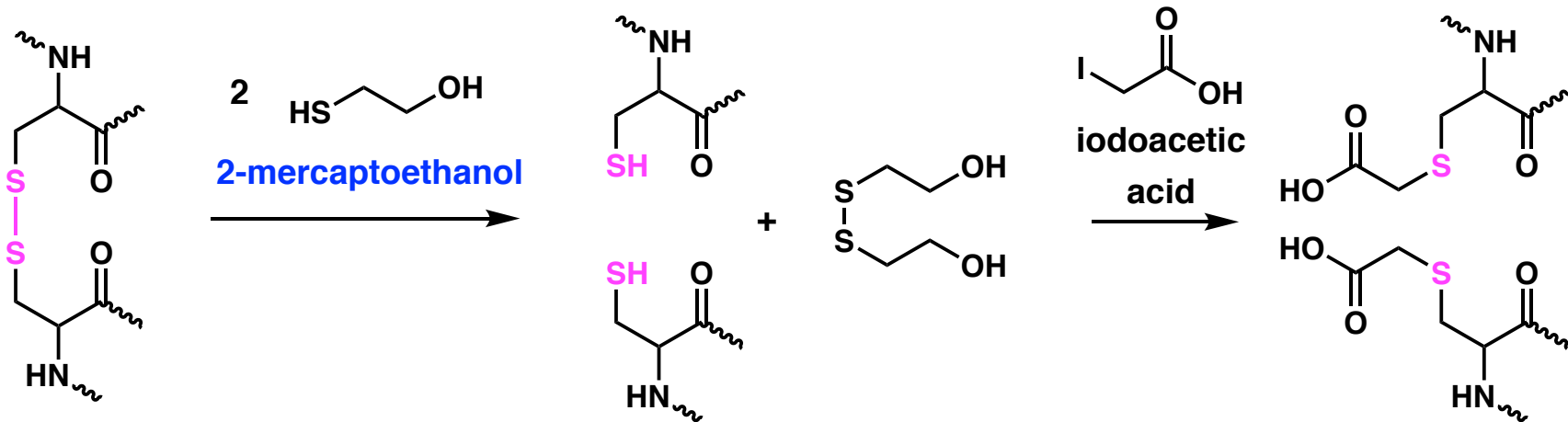
first steps - overall composition:

cleaving disulfide bridges: $\text{HSCH}_2\text{CH}_2\text{OH}$

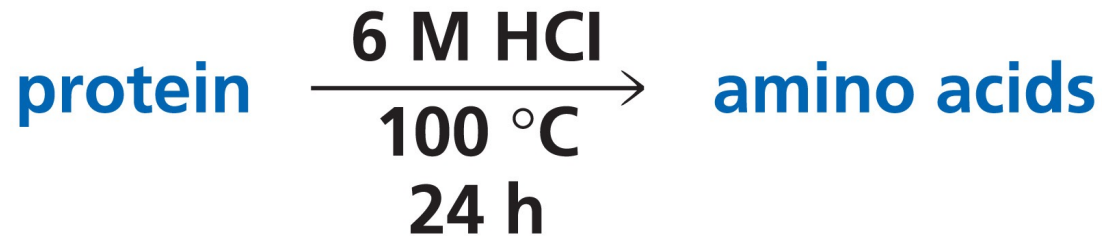


first steps - overall composition:

cleaving disulfide bridges: $\text{HSCH}_2\text{CH}_2\text{OH}$



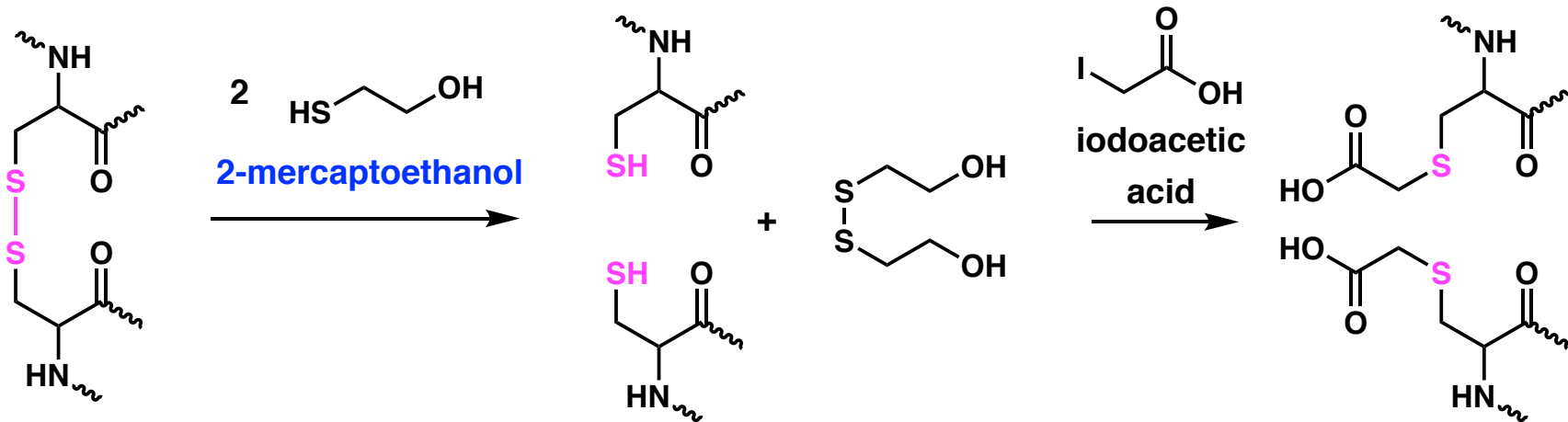
complete hydrolysis: 6 M HCl, H₂O, 100 °C, 24 h



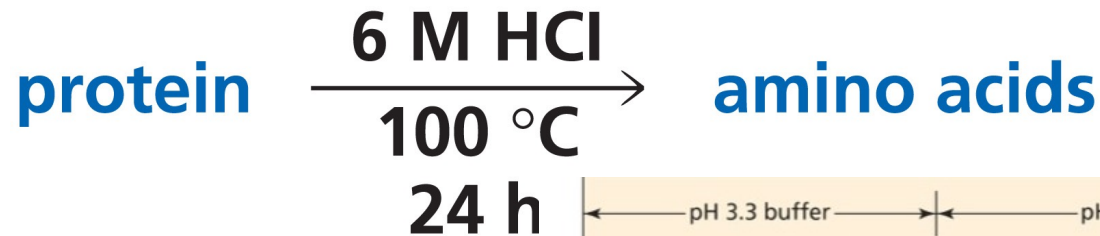
Proteins: Structure

first steps - overall composition:

cleaving disulfide bridges: $\text{HSCH}_2\text{CH}_2\text{OH}$

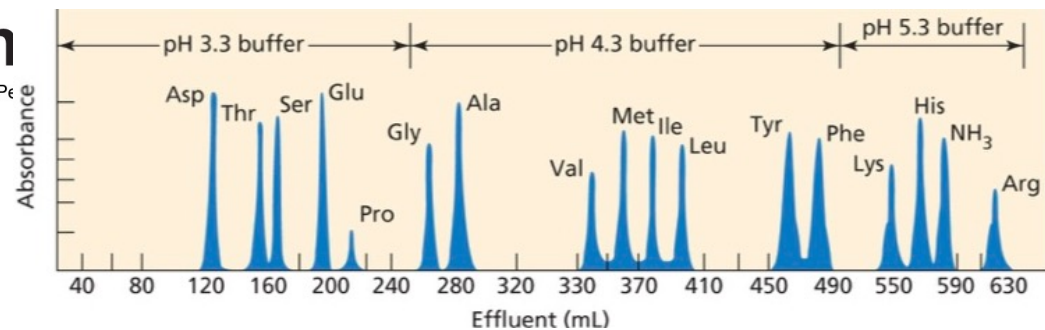


complete hydrolysis: 6 M HCl, H_2O , 100 °C, 24 h



Copyright © 2007 PerkinElmer

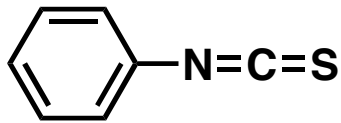
then use amino acid analyzer...



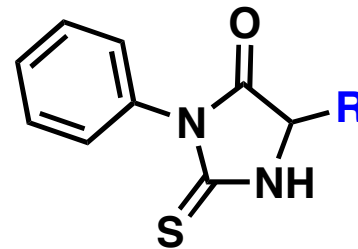
selective reagents to break amide bonds:

for *N*-terminal amino acid

Edman's reagent:



phenyl isothiocyanate



PTH-amino acid

from *N*-terminal amino acid

can be repeated up to 50 times in sequencer

selective reagents to break amide bonds:

partial hydrolysis with dilute acid into smaller pieces

Ala-Lys-Phe-Gly-Asp-Trp-Ser-Arg-Met-Val-Arg-Tyr-Leu-His

Sequencing an oligopeptide...

PRACTICE PROBLEM

A decapeptide undergoes partial hydrolysis to give peptides whose amino acid compositions are shown. Reaction of the intact decapeptide with Edman's reagent releases PTH-Gly. What is the sequence of the decapeptide?

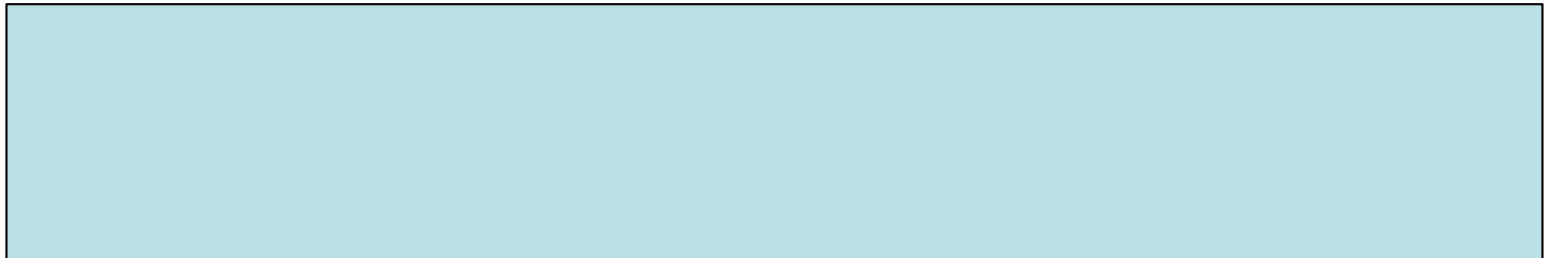
- | | | | |
|------------------|-------------|------------------|-----------------------|
| 1. Ala, Trp | 3. Pro, Val | 5. Trp, Ala, Arg | 7. Glu, Ala, Leu |
| 2. Val, Pro, Asp | 4. Ala, Glu | 6. Arg, Gly | 8. Met, Pro, Leu, Glu |

Sequencing an oligopeptide...

PRACTICE PROBLEM

A decapeptide undergoes partial hydrolysis to give peptides whose amino acid compositions are shown. Reaction of the intact decapeptide with Edman's reagent releases PTH-Gly. What is the sequence of the decapeptide?

- | | | | |
|-------------------------|--------------------|-------------------------|------------------------------|
| 1. Ala, Trp | 3. Pro, Val | 5. Trp, Ala, Arg | 7. Glu, Ala, Leu |
| 2. Val, Pro, Asp | 4. Ala, Glu | 6. Arg, Gly | 8. Met, Pro, Leu, Glu |



Wednesday, October 16, HFH 1104, 8 – 8:50 am

- **Chapter 20. Carbohydrates.**

All Sections except 20.13, 20.17, 20.19

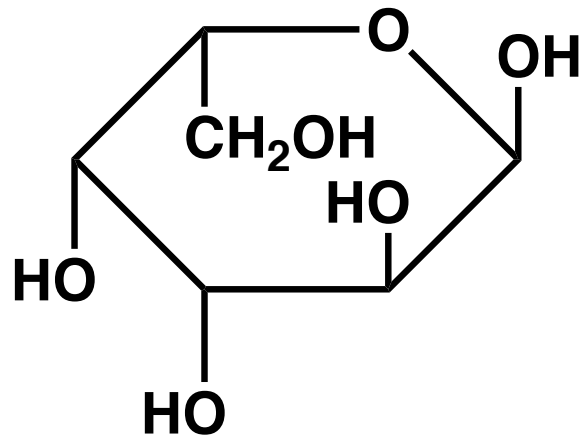
- **Chapter 21. Amino acids, Proteins.**

All sections Up to 21.11, including 21.11

structures of carbohydrates (except glucose, mannose, and galactose) and amino acids will be provided

PRACTICE PROBLEM

Name the following monosaccharide and draw a Fischer projection for the open form



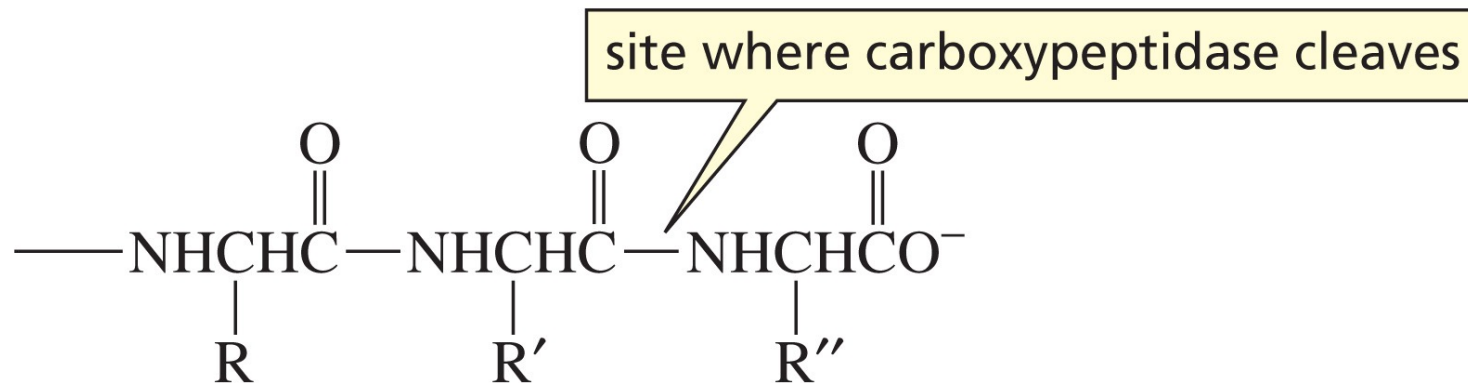
selective reagents to break amide bonds:

for C-terminal amino acid:

exopeptidases:

carboxypeptidase A: all but **Arg** and **Lys**

carboxypeptidase B: only **Arg** and **Lys**

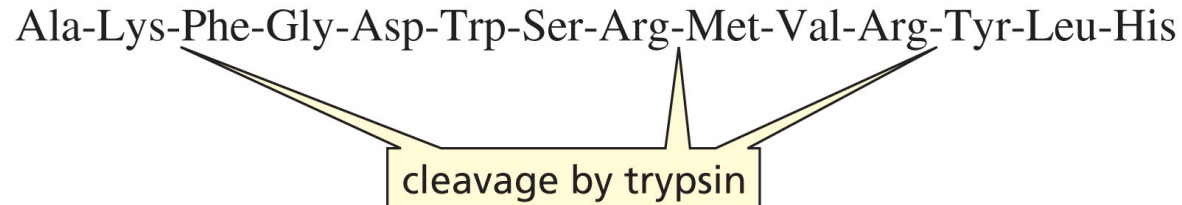


selective reagents to break amide bonds:

partial hydrolysis with endopeptidases:

Trypsin: C-side of Arg and Lys

Ala-Lys-Phe-Gly-Asp-Trp-Ser-Arg-Met-Val-Arg-Tyr-Leu-His

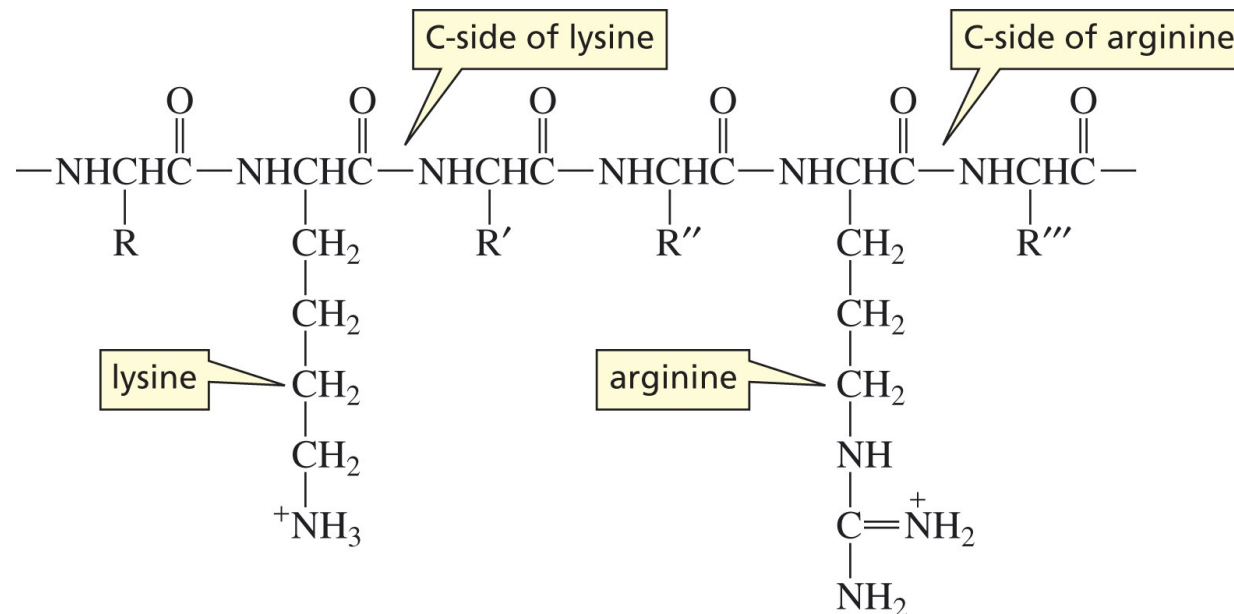


cleavage by trypsin

selective reagents to break amide bonds:

partial hydrolysis with endopeptidases:

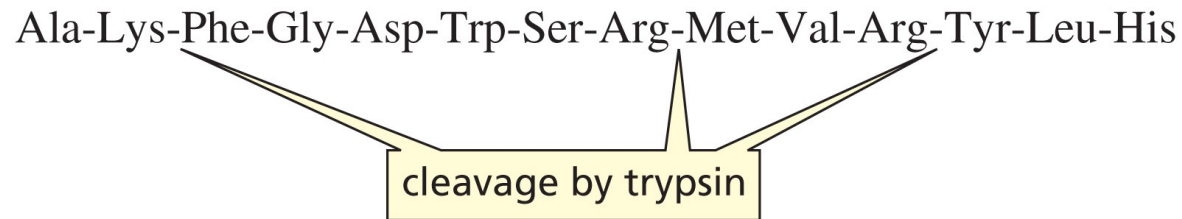
Trypsin: C-side of **Arg** and **Lys**



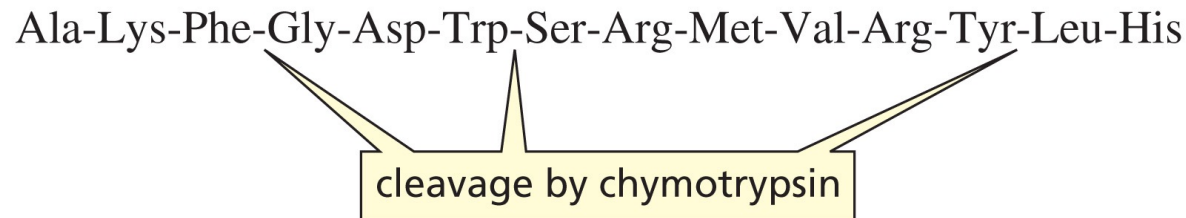
selective reagents to break amide bonds:

partial hydrolysis with endopeptidases:

Trypsin: C-side of **Arg** and **Lys**



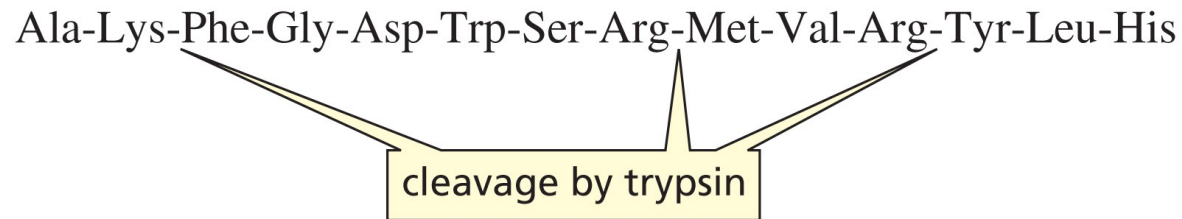
Chymotrypsin: C-side of **Phe**, **Tyr** and **Trp**



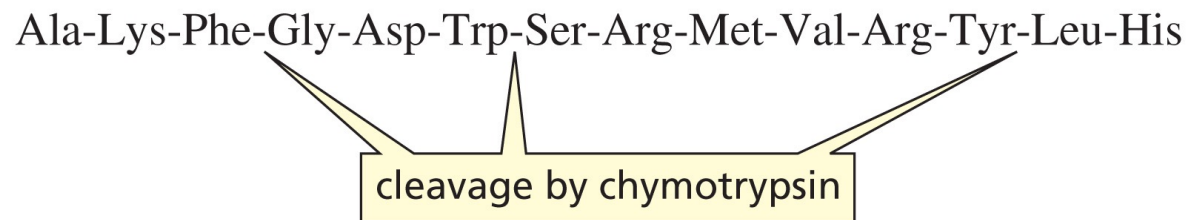
selective reagents to break amide bonds:

partial hydrolysis with endopeptidases:

Trypsin: C-side of **Arg** and **Lys**



Chymotrypsin: C-side of **Phe**, **Tyr** and **Trp**



Elastase: C-side of **Gly** and **Ala**



Proteins: **Structure**

selective reagents to break amide bonds:

**for endo- and exopeptidases,
no reaction at Pro:**

Ala-Lys-Pro

trypsin will not cleave

Leu-Phe-Pro

chymotrypsin will not cleave

Pro-Phe-Val

chymotrypsin will cleave

selective reagents to break amide bonds:

cyanogen bromide: BrCN,

C-side of Met

Ala-Lys-Phe-Gly-Asp-Trp-Ser-Arg-Met-Val-Arg-Tyr-Leu-His

BrCN will cleave next to proline (Pro)

Table 21.4 Specificity of Peptide or Protein Cleavage

| Reagent | Specificity |
|--------------------|--|
| Chemical reagents | |
| Edman's reagent | removes the N-terminal amino acid |
| Cyanogen bromide | hydrolyzes on the C-side of Met |
| Exopeptidases* | |
| Carboxypeptidase A | removes the C-terminal amino acid (not Arg or Lys) |
| Carboxypeptidase B | removes the C-terminal amino acid (only Arg or Lys) |
| Endopeptidases* | |
| Trypsin | hydrolyzes on the C-side of Arg and Lys |
| Chymotrypsin | hydrolyzes on the C-side of amino acids that contain aromatic six-membered rings (Phe, Tyr, Trp) |
| Elastase | hydrolyzes on the C-side of small amino acids (Gly and Ala) |

* Cleavage will not occur if Pro is on either side of the bond to be hydrolyzed.

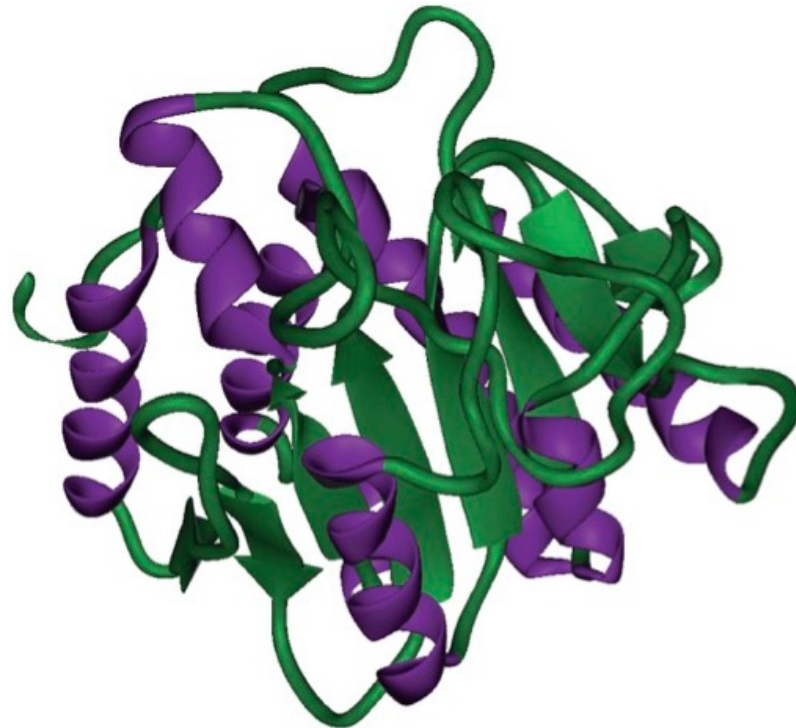
Proteins: **Structure**

Primary structure is the sequence of amino acids in a protein and the location of disulfide bridges

- **obtained from sequencing a protein**

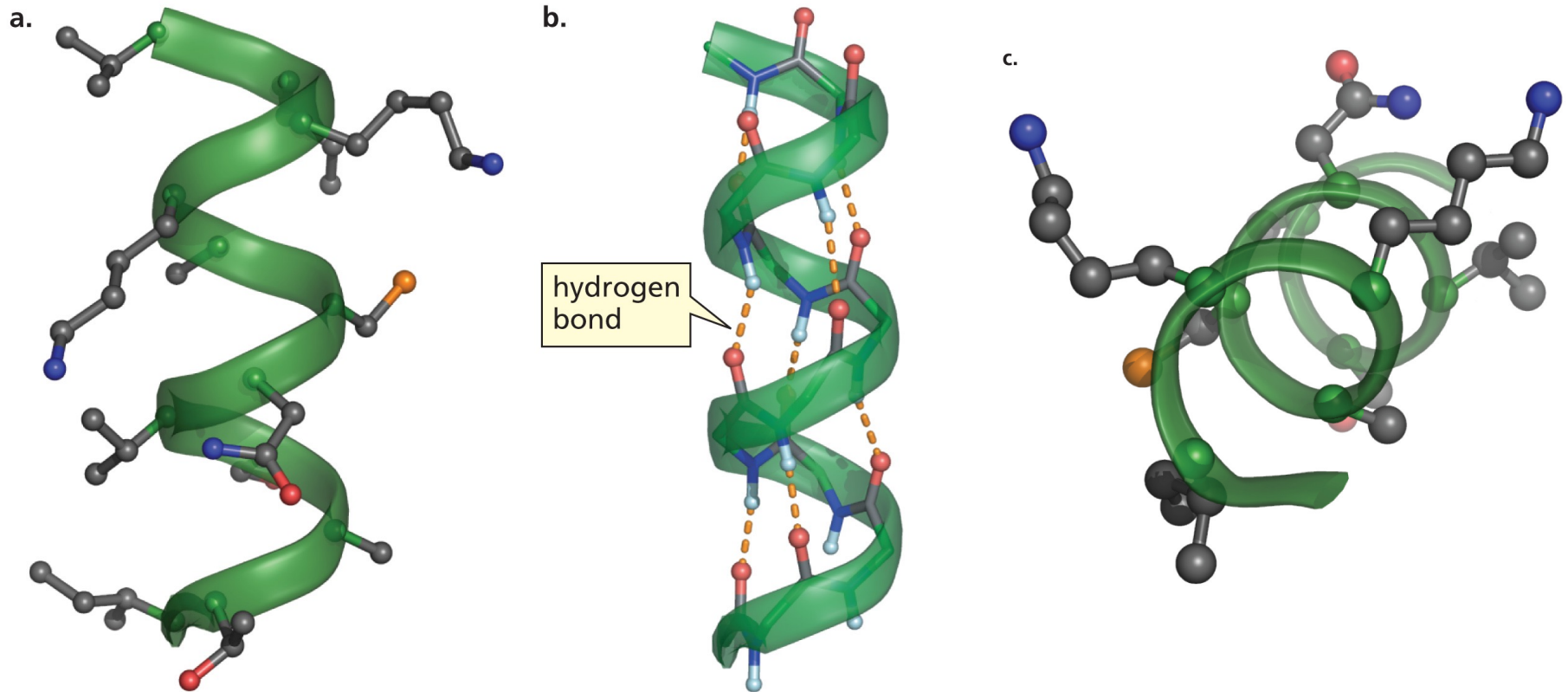
Secondary structure *describes the common conformations of segments of a protein*

three types:



Proteins: Secondary Structure

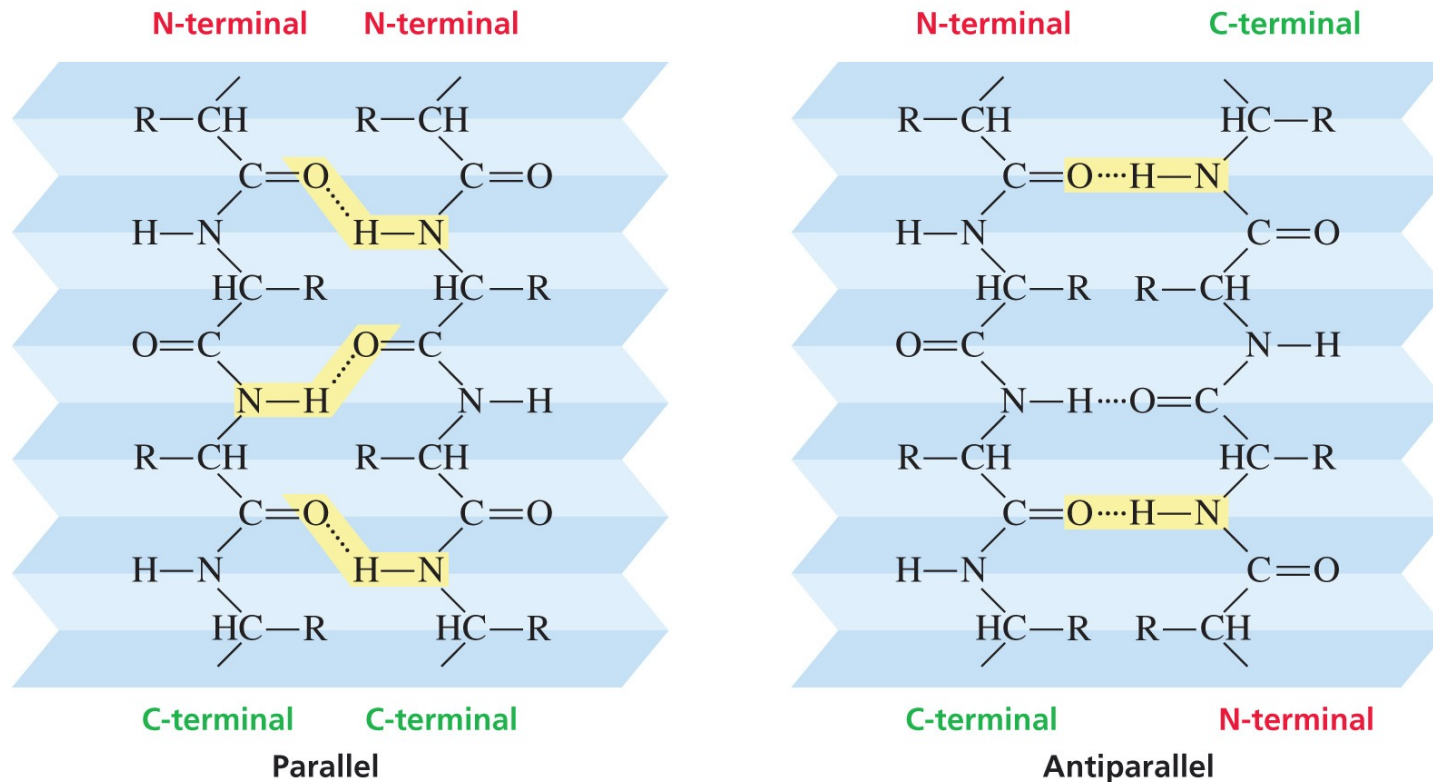
α -Helix



one turn: 3.6 aa, 5.4 Å repeat distance

Proteins: Secondary Structure

β -Pleated Sheet



average two residue repeat distance is 7.0 Å

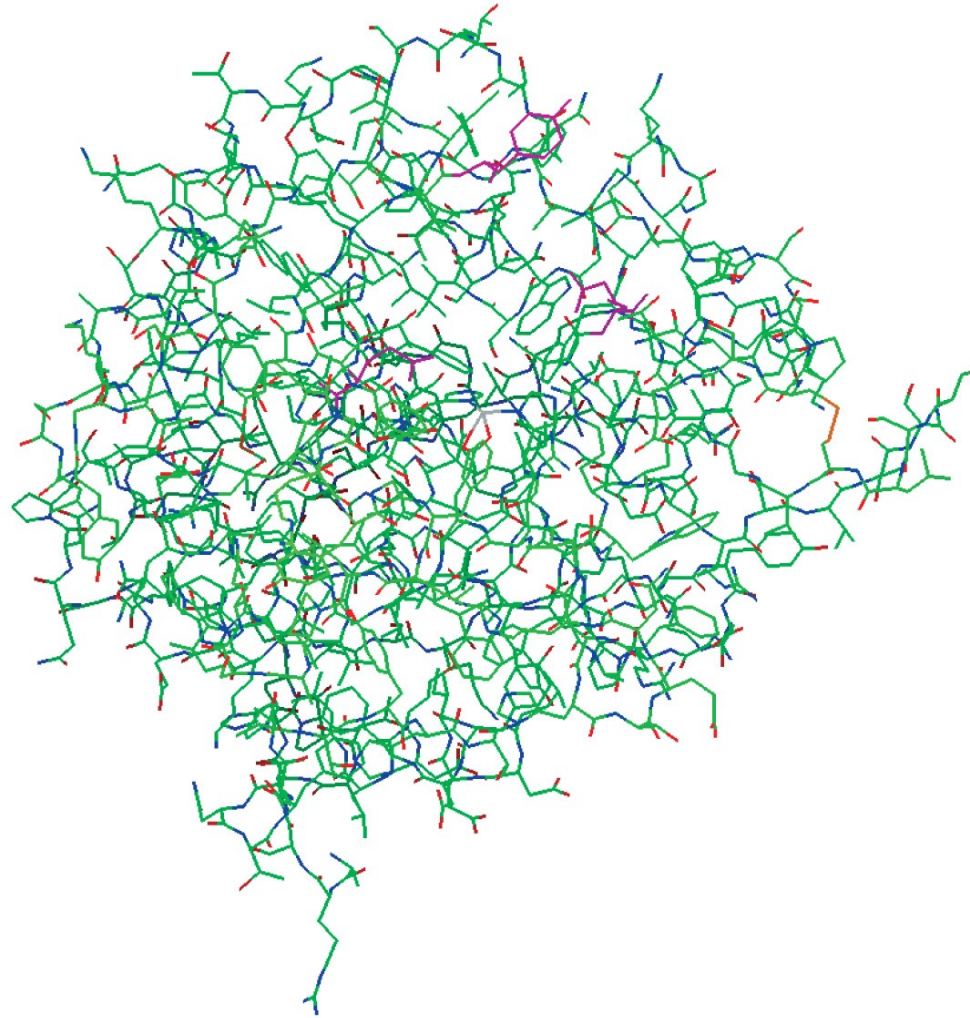
Proteins: **Secondary Structure**

Coils or Loops



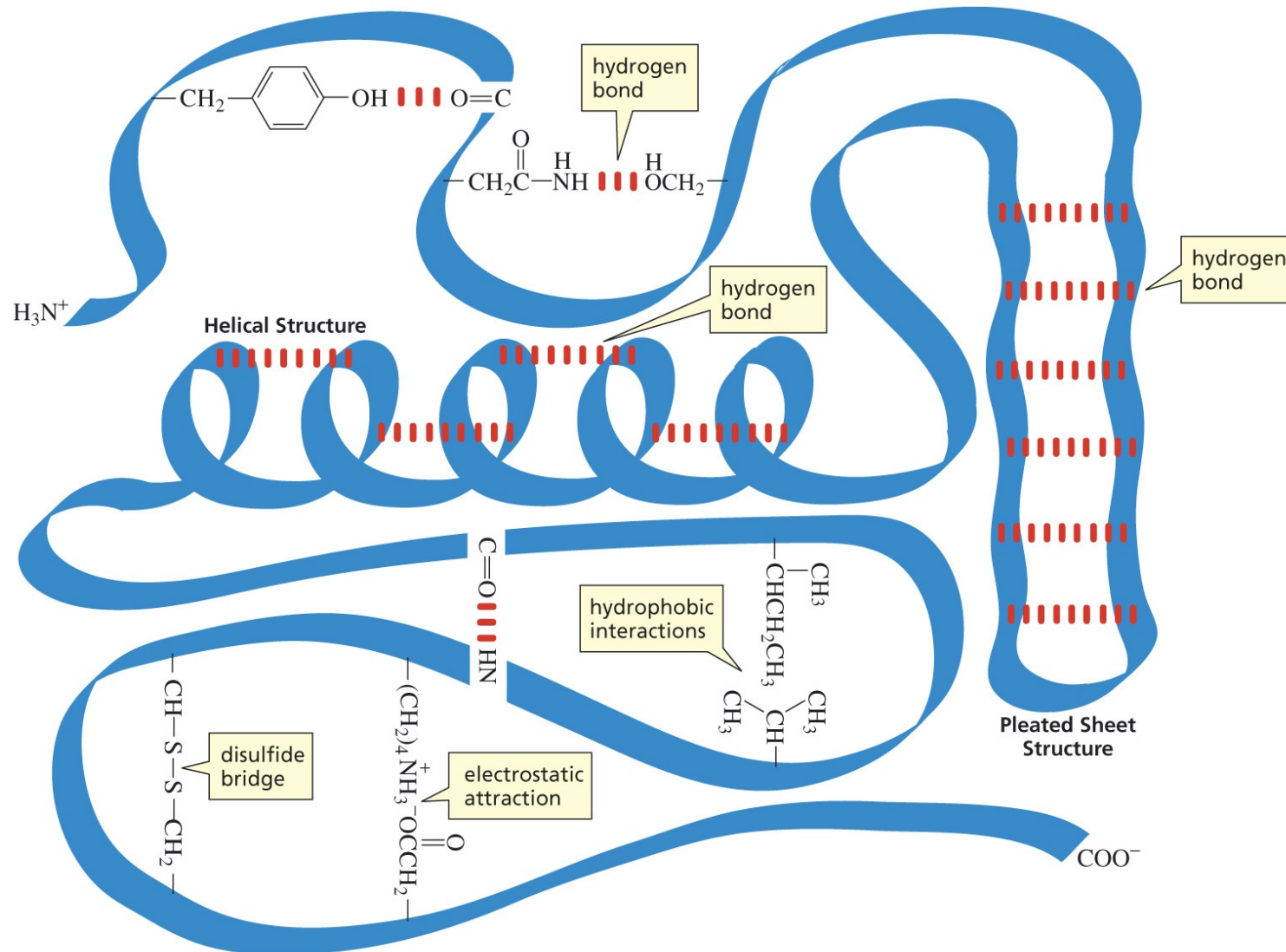
Proteins: **Tertiary Structure**

Tertiary structure describes the 3D arrangement of all the atoms in the protein



Proteins: Tertiary Structure

Tertiary structure describes the 3D arrangement of all the atoms in the protein

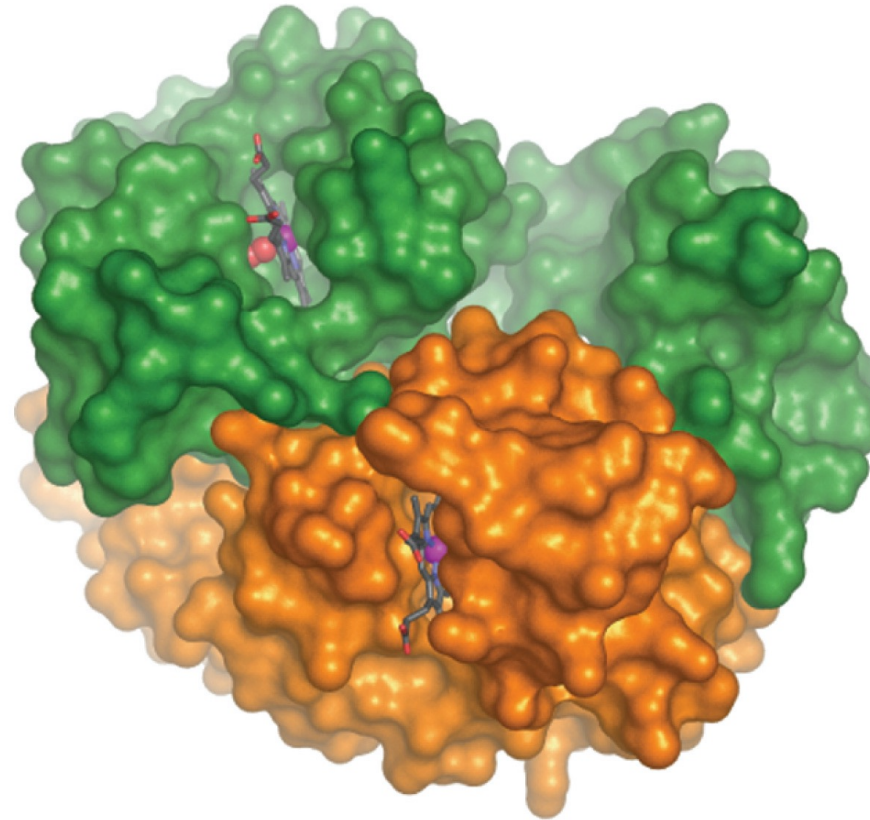


Proteins: **Quaternary Structure**

Quaternary structure aggregates of proteins: each is called a subunit

Proteins: **Quaternary Structure**

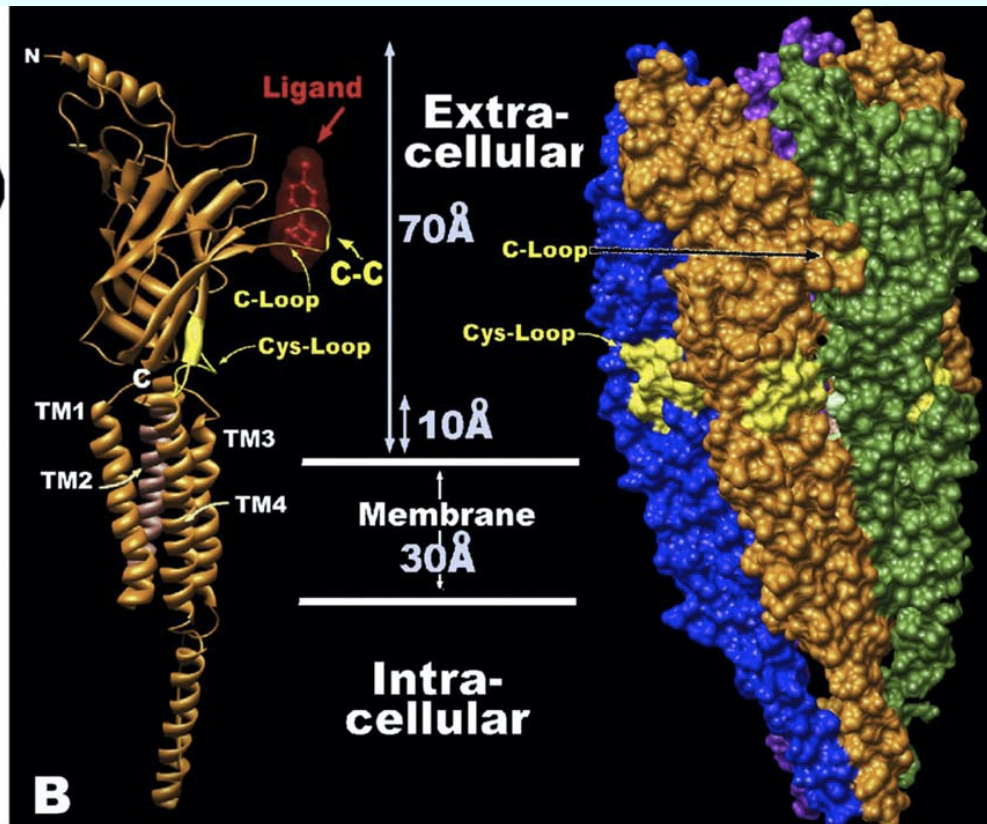
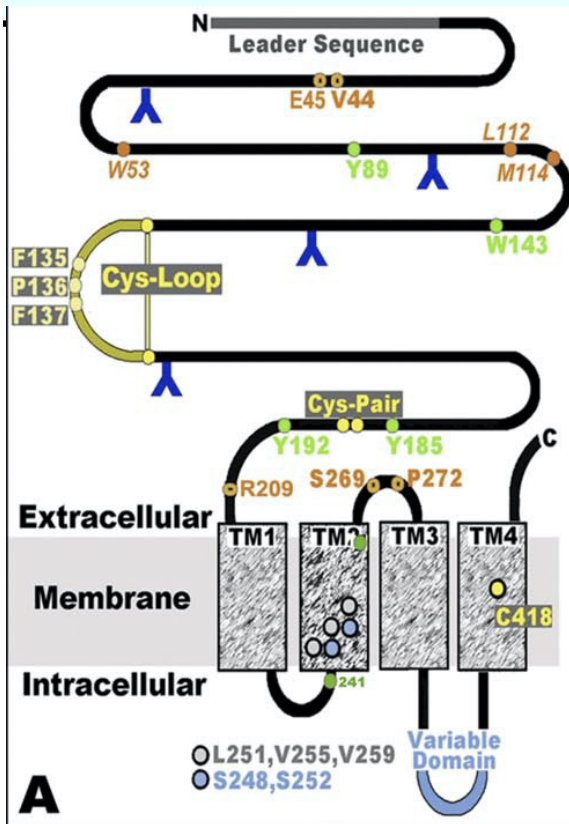
Quaternary structure aggregates of proteins: each is called a subunit



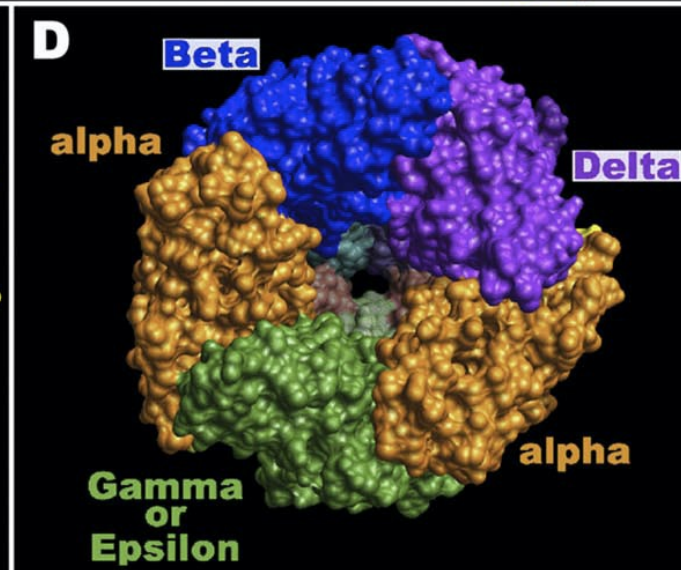
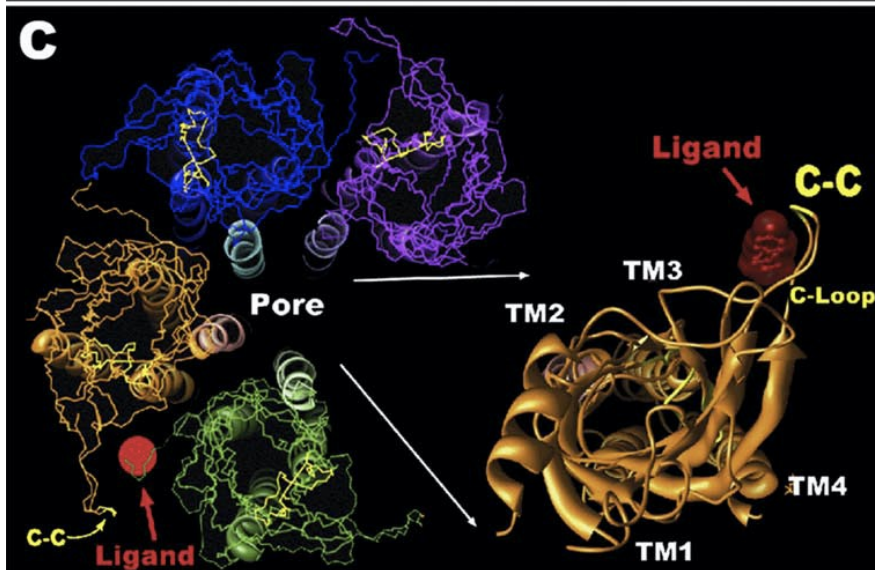
hemoglobin

mutation at position 6: glutamate → valine: sickle cell anemia

Proteins: Quaternary Structure



nicotinic
acetylcholine
receptor
(nAChR)



Proteins: Denaturation

Protein denaturation: is destruction of the highly organized tertiary structure, results in [irreversible] loss of function

factors that can cause denaturation:

- changing acidity (pH)
- temperature
- some reagents (urea, guanidine)
- detergents
- organic solvents

summary of previous sections

Protein Structure and Analysis

structure: primary, secondary, tertiary, quaternary
parameters of alpha-helix, beta sheet, loops/coils
and tertiary structures

structure determination, reagents:

$\text{HSCH}_2\text{CH}_2\text{OH}$

6M HCl

Edman's reagent

cyanogen bromide BrCN

exopeptidases: carboxypeptidase A
carboxypeptidase B

endopeptidases:
trypsin
chymotrypsin
elastase

