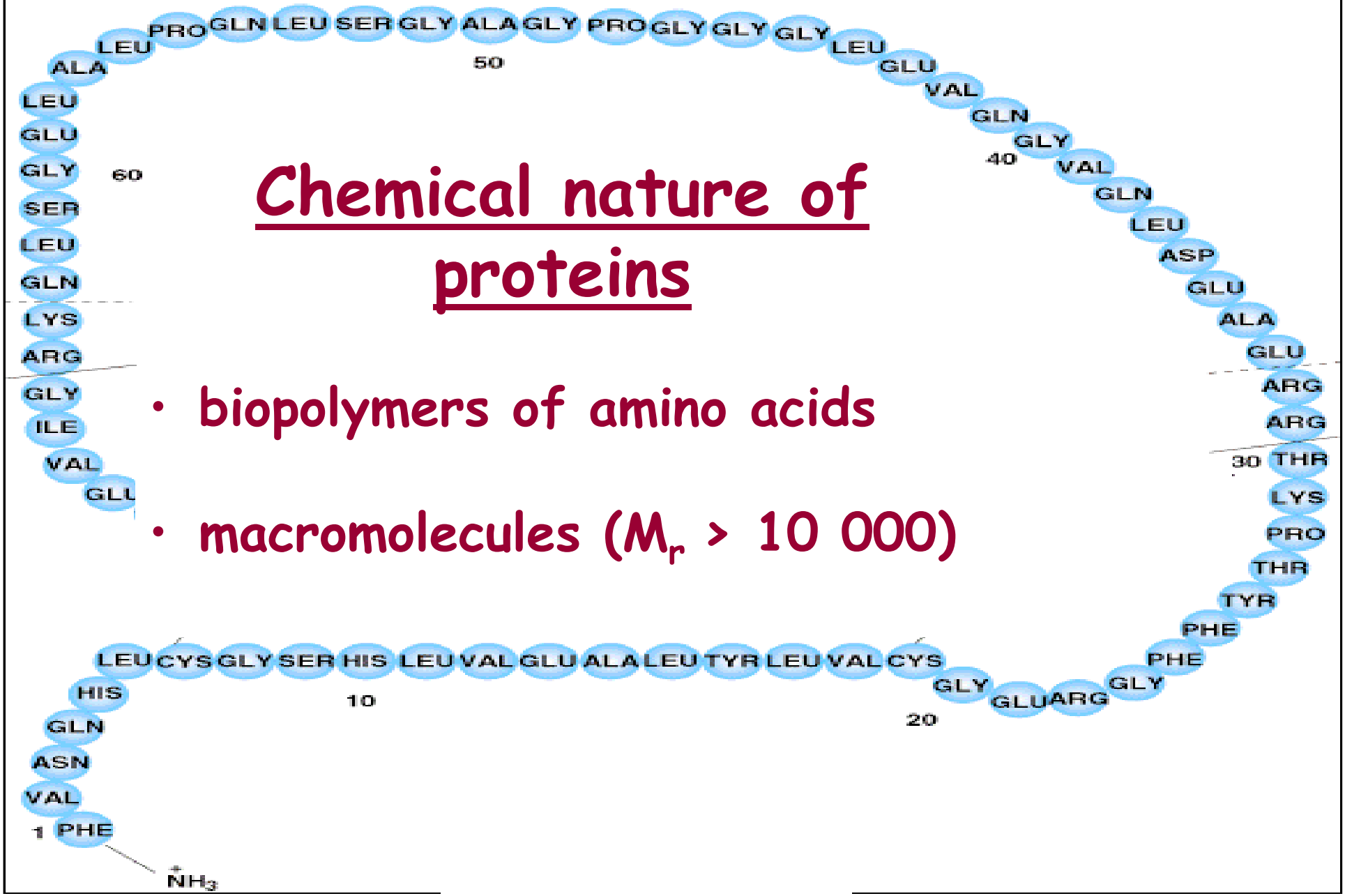
Structure and properties of proteins

Vladimíra Kvasnicová

Chemical nature of proteins

- biopolymers of amino acids
- macromolecules (M_r > 10 000)



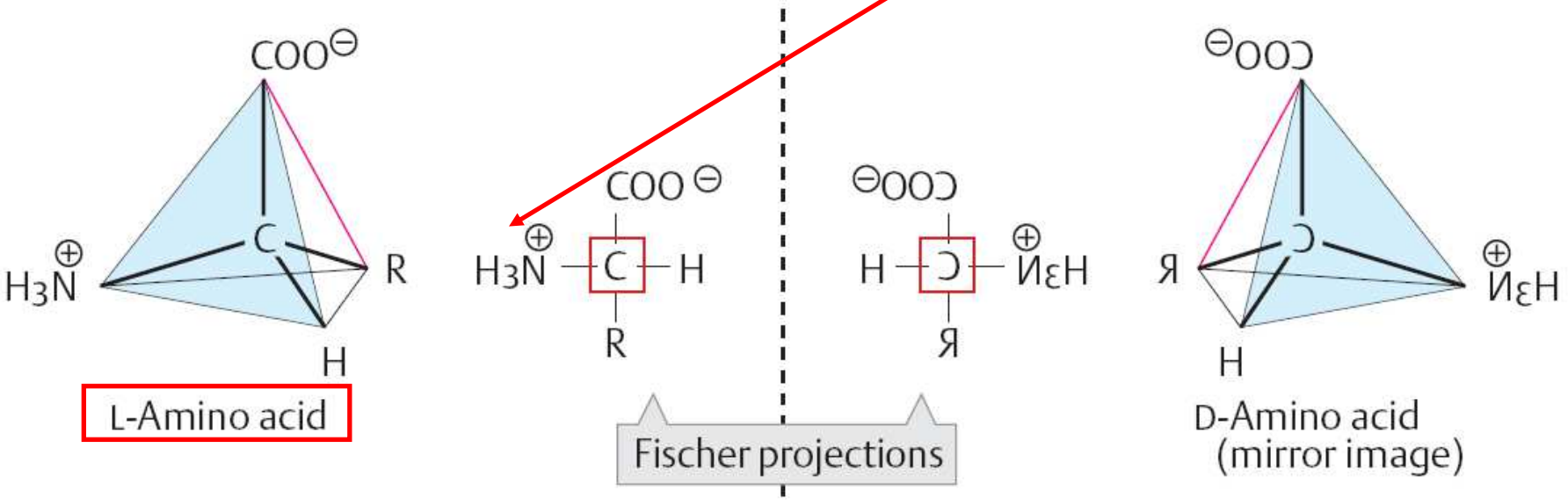
Classification of proteins

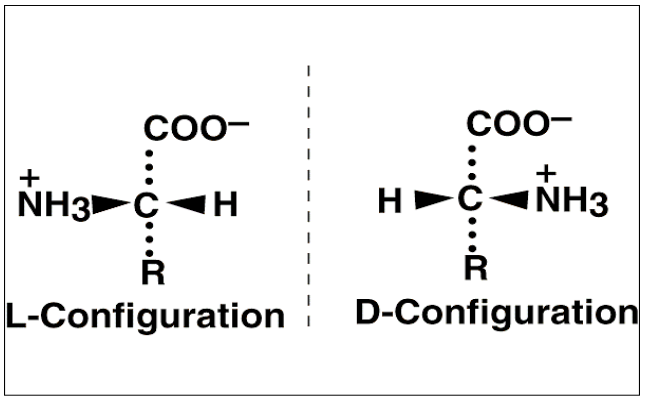
1) by localization in an organism
   - intra- / extracellular
2) by function
   - structural / biological active
3) by shape
   - globular / fibrous
4) by chemical composition
   - simple / complex (conjugated) proteins

→ conjugated proteins contein **polypeptide chain**
+ prosthetic group:

- **glycoproteins** + saccharide
- **metalloproteins** + metal ion
- **hemoproteins** + heme
- **phosphoproteins** + phosphoric acid
- **nucleoproteins** + nucleic acid
- (lipoproteins) + lipids

Proteins are synthesized from L-α-amino acids





- 21 proteinogenic AAs
- other AAs are non-proteinogenic

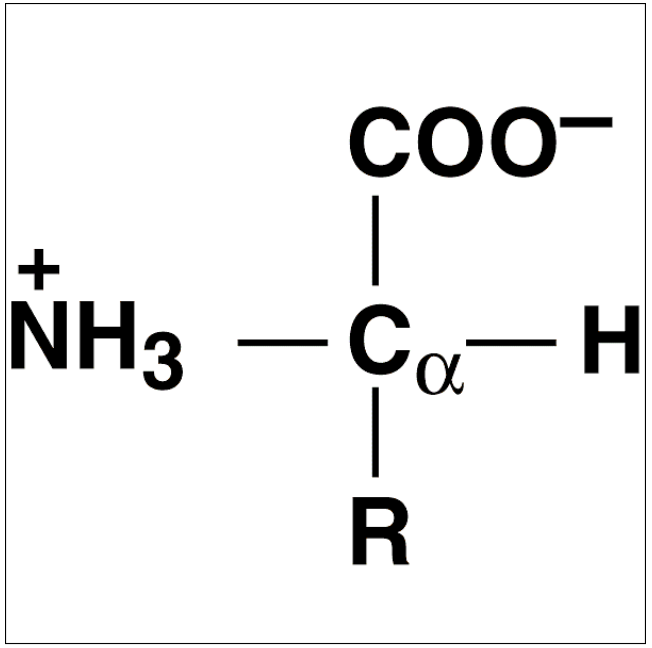
The figure was adopted from: J.Koolman, K.H.Röhm / Color Atlas of Biochemistry, 2nd edition, Thieme 2005

Side chains of AAs determine final properties of proteins

Isoelectric point (pI)

= pH value at which the net charge of a compound is zero

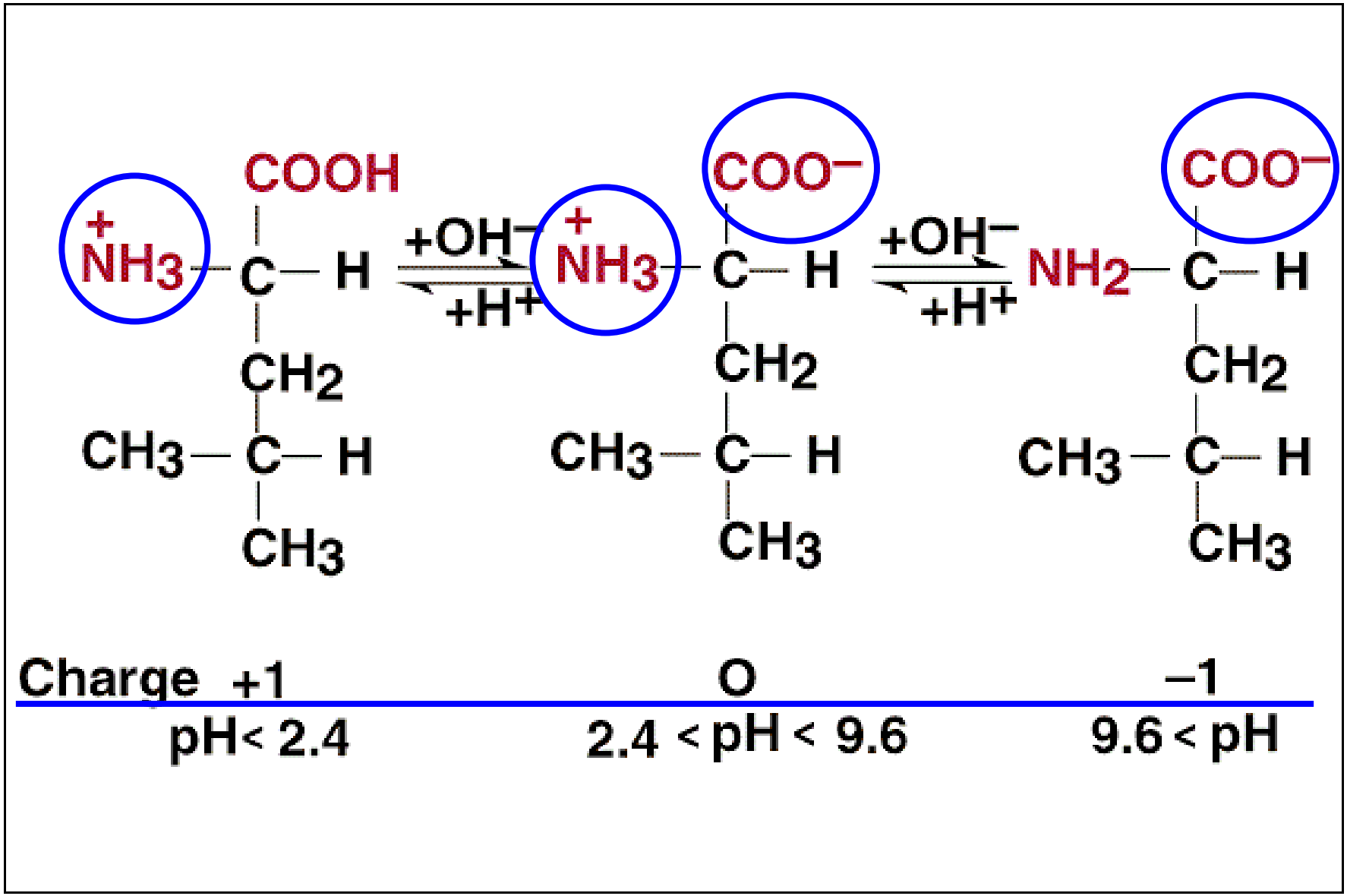
$$pI = (pK_{COOH} + pK_{NH3+}) / 2$$

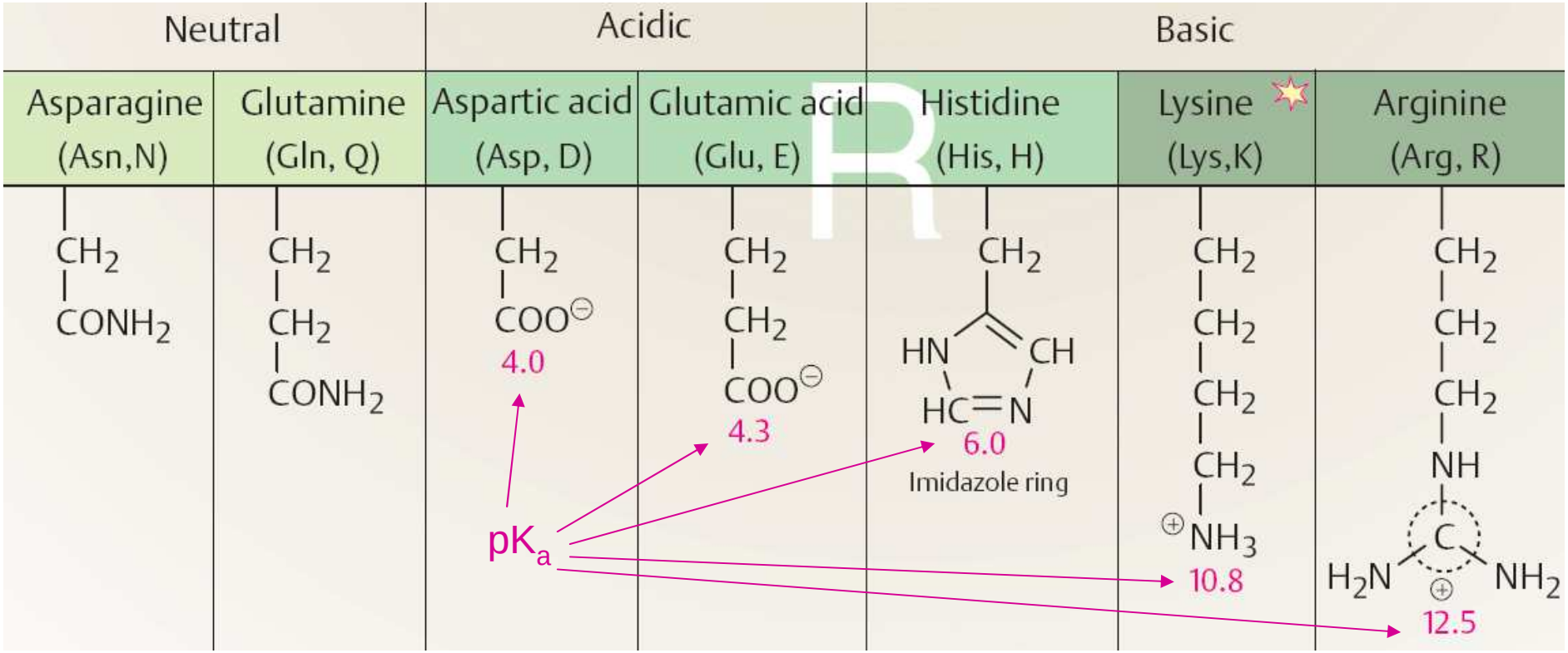


Solutions of AAs belong among ampholytes

(= amphoteric electrolytes)

„AMPHION"





Henderson-Hasselbalch equation:

$$pH = pK_a + \log \frac{[base]}{[acid]}$$

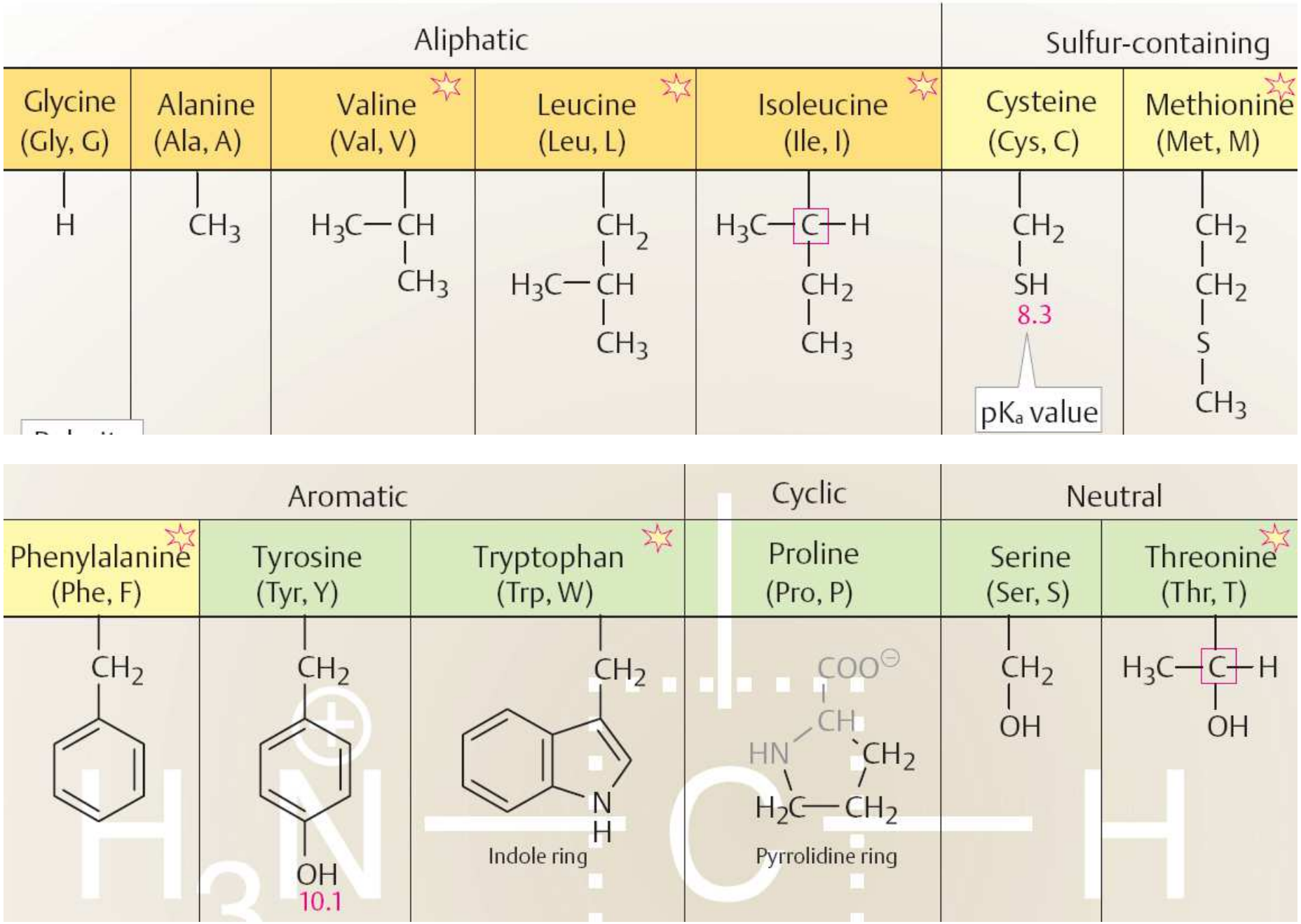
„acid" ↔ „base" + H^+

(for example: R-COOH ↔ R-COO^- + H^+)

If pH of a solution (e.g. cytosol) is higher than pK_a (i.e. more basic) the structure of „base" predominates:

„acid" → „**base**" + H^+

The figure was adopted from: J.Koolman, K.H.Röhm / Color Atlas of Biochemistry, 2nd edition, Thieme 2005



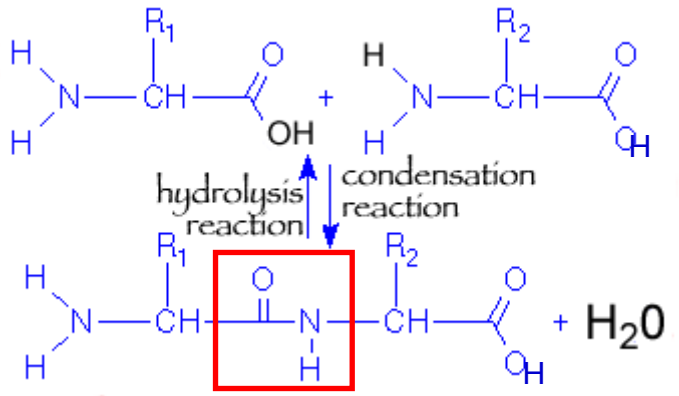
The figure was adopted from: J.Koolman, K.H.Röhm / Color Atlas of Biochemistry, 2nd edition, Thieme 2005

Functional groups of amino acids

• **-COOH** ↔ -COO^- + H^+	carboxyl group → anion
• -COOH → -CO-	carboxyl group → acyl
• **-NH_2** + H^+ ↔ -NH_3^+	amino group → cation
• **-$CONH_2$** (not basic)	amide group
• **-OH** (not acidic in H_2O)	alcohol group
• **-SH** (not acidic in H_2O)	thiol group
• -SeH	selenol group
• **-S-**	sulfide group
• -HN-C(=NH)-NH_2	guanidine group

Important reactions of AAs

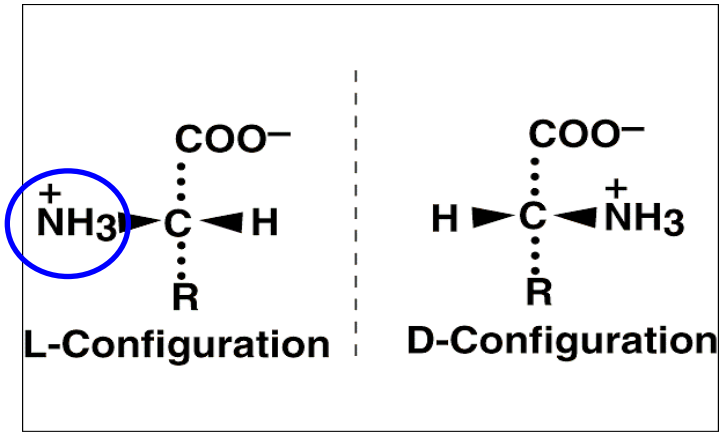
1) dissociation → „bases"
2) decarboxylation → biogenic amines
3) transamination → 2-oxoacids
4) deamination → 2-oxoacids
5) formation of peptide bonds → peptides or proteins



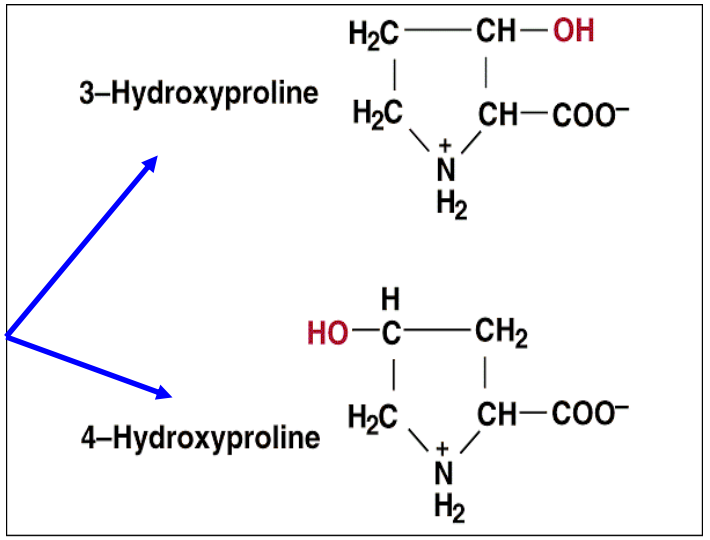
peptide bond

Amino acids in proteins

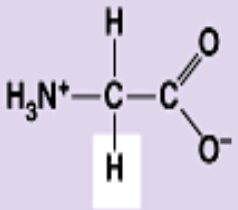
L-α-**amino**carboxylic acids



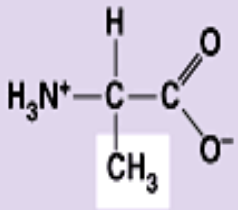
- **21 proteinogenic *AAs***
- other *AAs* are formed by a posttranslational modification



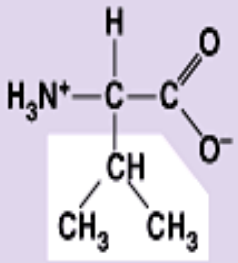
Nonpolar



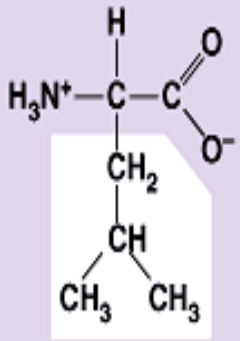
Glycine (Gly)



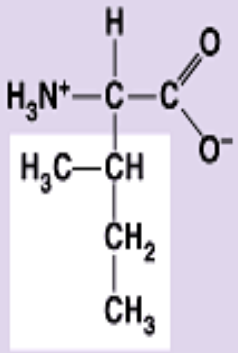
Alanine (Ala)



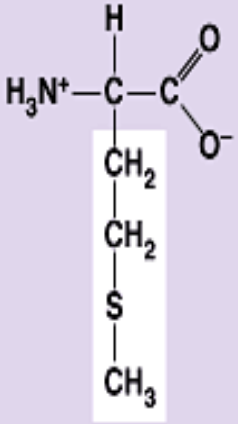
Valine (Val)



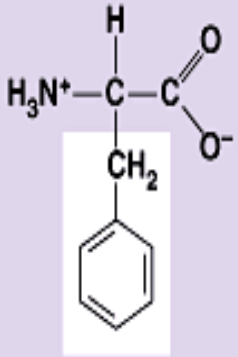
Leucine (Leu)



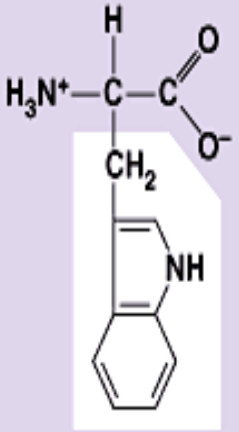
Isoleucine (Ile)



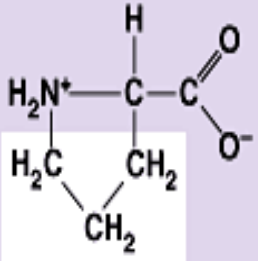
Methionine (Met)



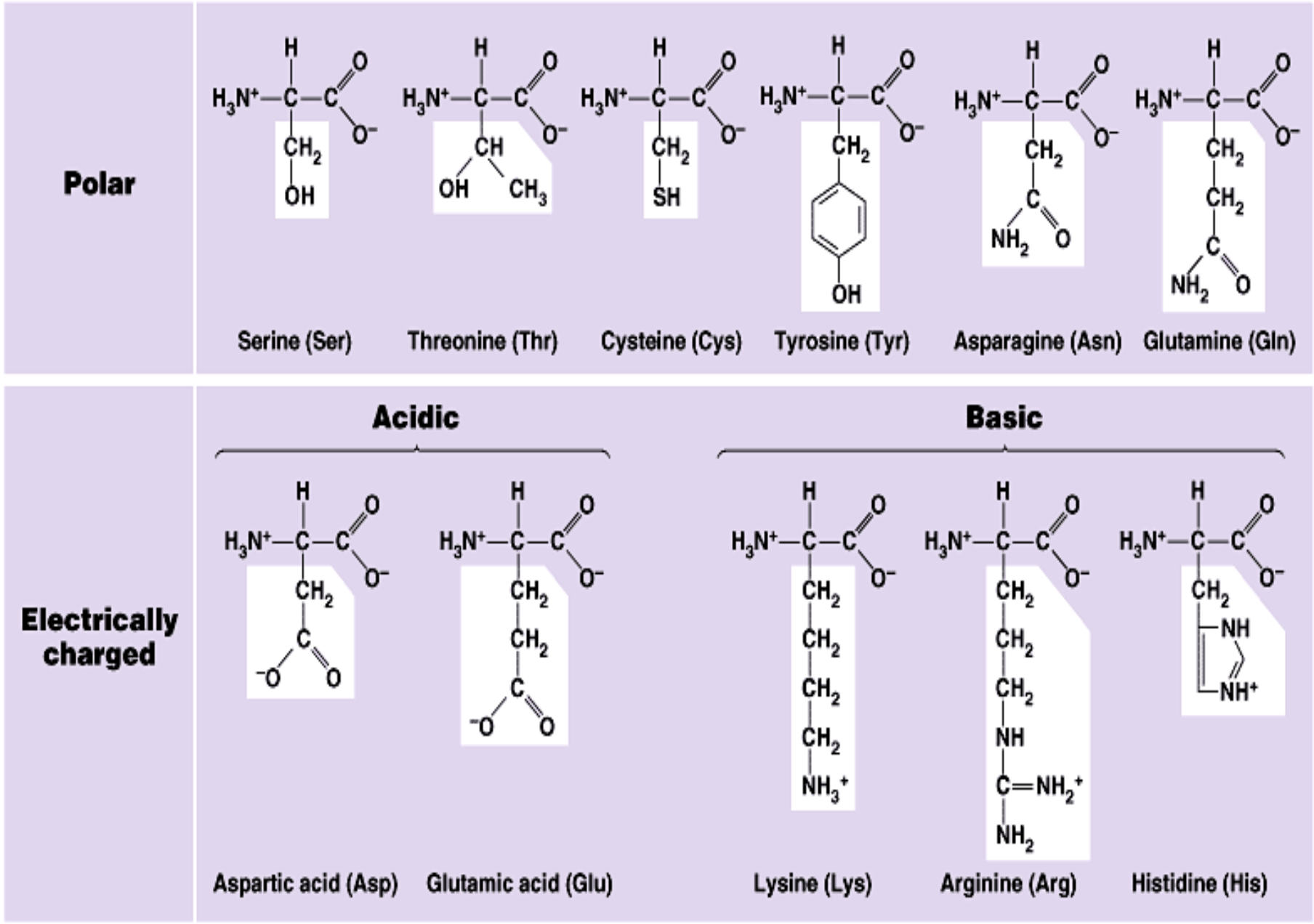
Phenylalanine (Phe)



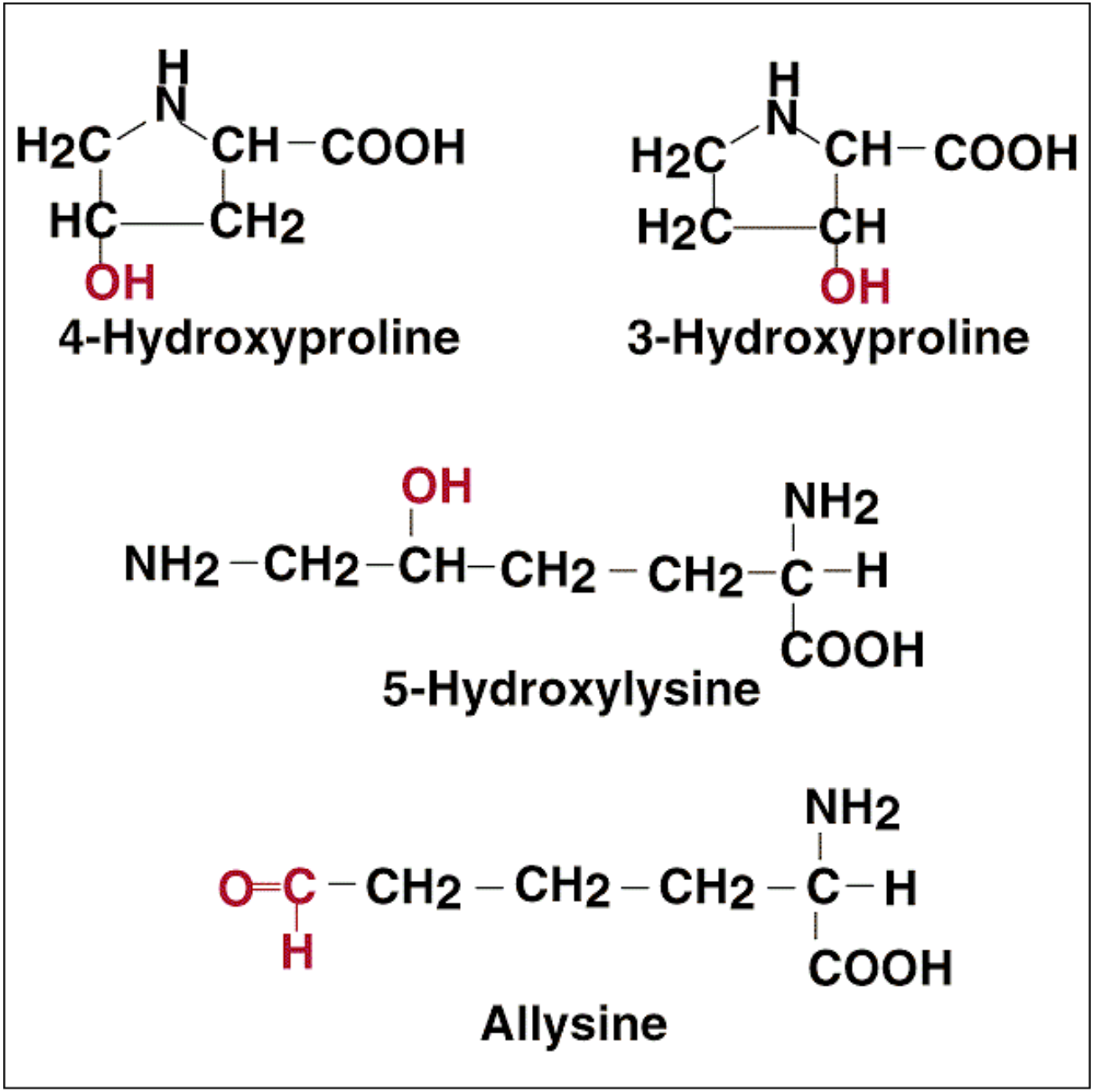
Tryptophan (Trp)



Proline (Pro)



Modified amino acids



The figure was adopted from: Devlin, T. M. (editor): Textbook of Biochemistry with Clinical Correlations, 4th ed. Wiley-Liss, Inc., New York, 1997. ISBN 0-471-15451-2

Important groups of proteinogenic amino acids

- branched chain *AAs*: valine, leucine, isoleucine
- aromatic *AAs*: phenylalanine, tyrosine, tryptophane, histidine
- sulfur-containing *AAs*: methionine, cysteine
- alcohol group containing *AAs*: serine, threonine, tyrosine
- basic *AAs*: lysine, arginine, histidine
- acidic *AAs*: aspartic acid (aspartate), glutamic acid (glutamate)
- amide group containing: asparagine, glutamine
- not optically active: glycine
- rare amino acid: selenocysteine
- abundant in blood: glutamine, alanine

Essential amino acids

- essential in a diet, they are not synthetized in a human body

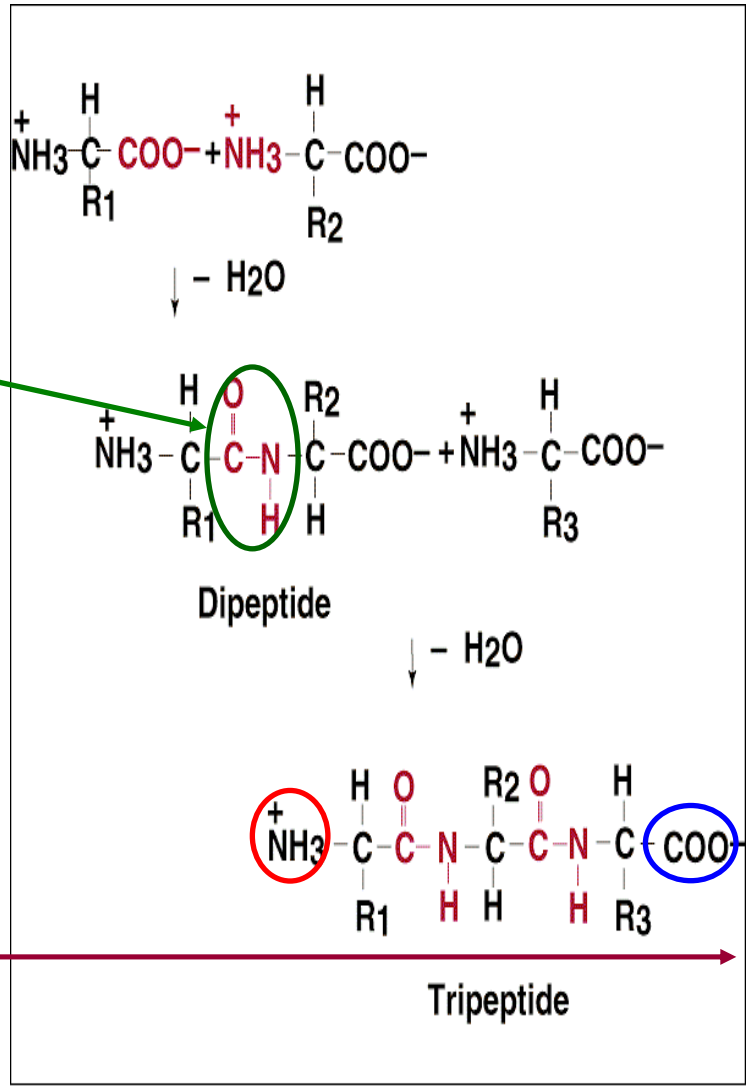
1) branched chain AAs (Val, Leu, Ile)
2) aromatic AAs (Phe, Trp)
3) basic AAs (Lys, Arg, His)
4) secondary-OH (Thr), sulfide group (Met)

Peptides and proteins

- contain 2 or more AAs bound by peptide bond(s)
- common names are used
- systematic names: AA_1-yl-AA_2-yl-AA_3

oligopeptides:	2 – 10 AA
polypeptides:	> 10 AA
proteins:	polypeptides of M_r > 10 000

- border: **polypeptide /protein** is not sharp **(~ 50 *AAs*)**
- *AAs* are bound by **peptide bonds**
- **the order of *AAs*** in a chain *(= primary structure)* is given by a **genetic information**
- the order of *AAs* is reported **from N- to C- terminal**



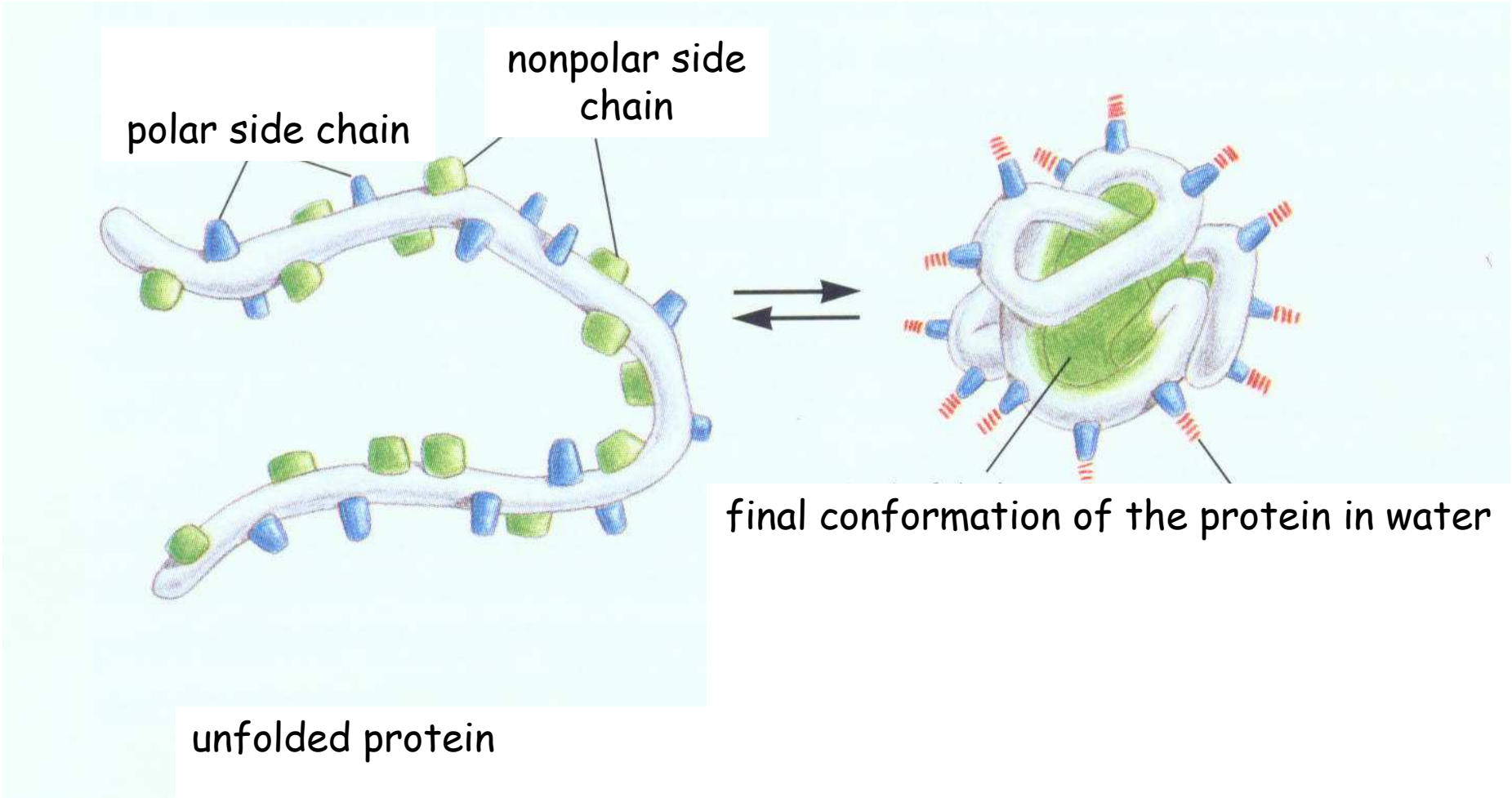
Description of structure of proteins

- the macromolecule contains various *AAs*,
  in an exactly defined order and quantity

- spacial arrangement and biological function
  are DEPENDENT
  on the amino acid composition

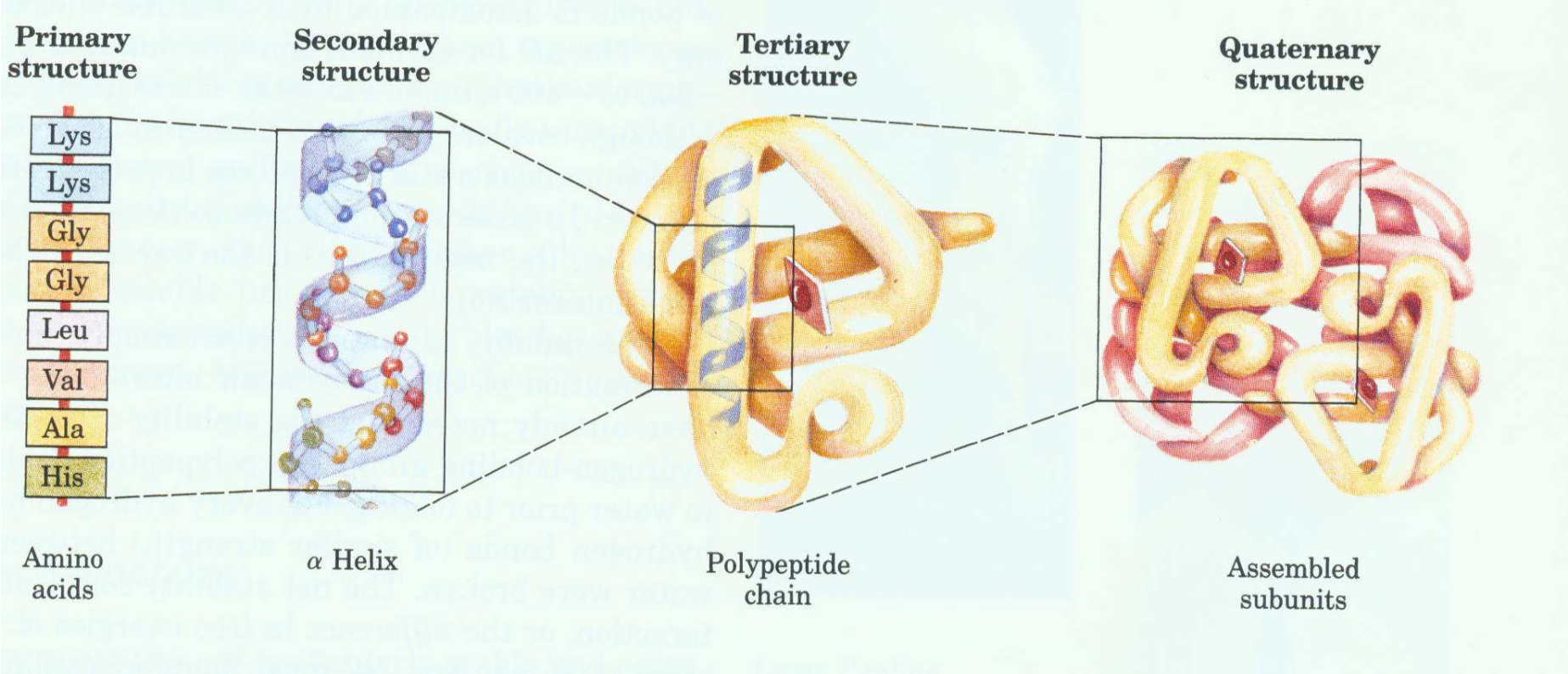
- native protein ~ biological active conformation

Side chains of AAs influence a final structure of proteins:



- the peptide chain has a special

spatial arrangement:



- only some proteins are composed of **subunits**

(= quaternary structure)

Bonds found in proteins

1) **covalent**
   - peptide bond — *-CO-NH-*
   - disulfide bond — *-S-S-*

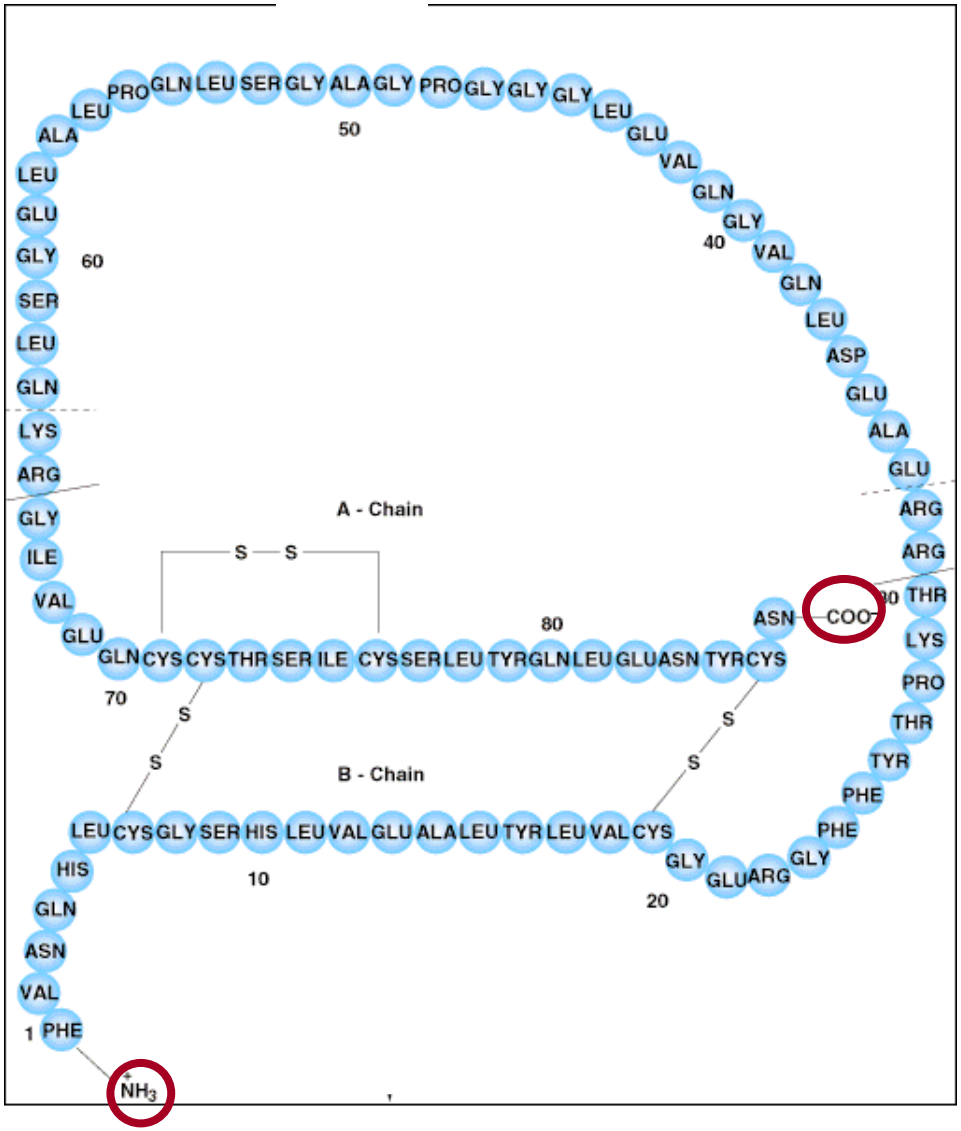
2) **noncovalent interactions**
   - hydrogen bonds — *-H···O-* *-H···N-*
   - hydrophobic interactions — *nonpolar side chains*
   - ionic interactions — *$-COO^-$ / $^+H_3N-$*

Primary structure of proteins

= order of amino acids

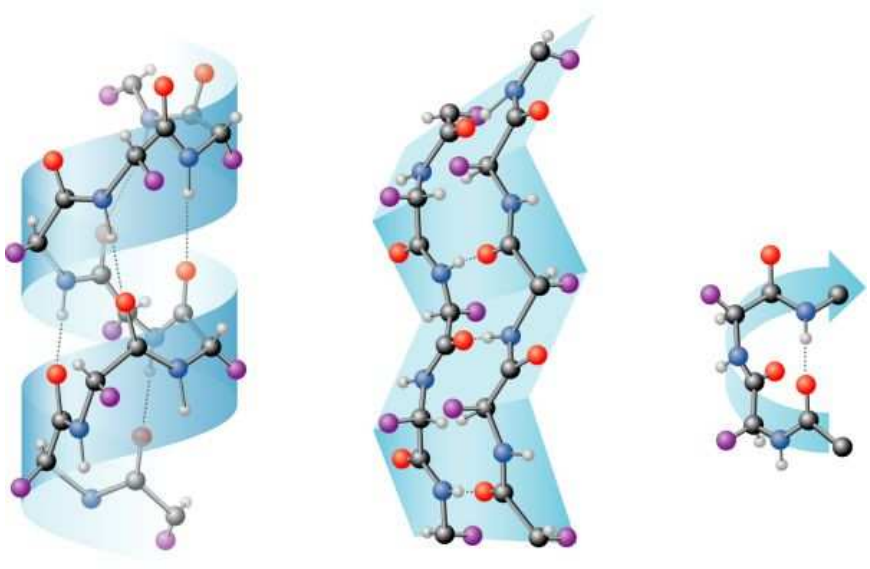
- read: from N-to C- end
- it is coded on a genetic level
- <u>stabilization</u>:

  peptide bonds



Secondary structure of proteins

= spatial arrangement of the polypeptide chain given by rotation of the planar peptide bonds around α-carbons



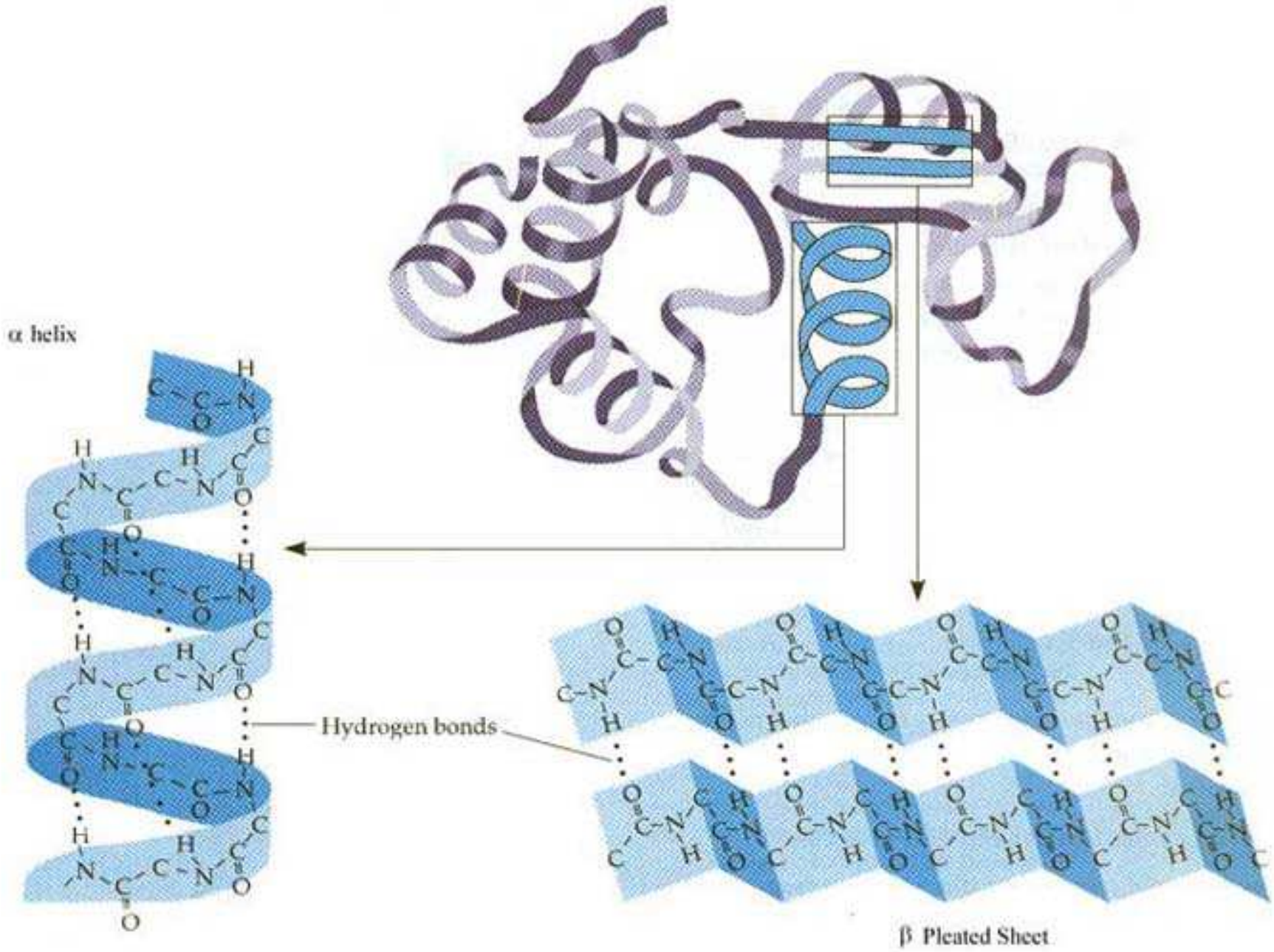
α-helix β-pleated sheet β-turn

stabilization:

hydrogen bonds

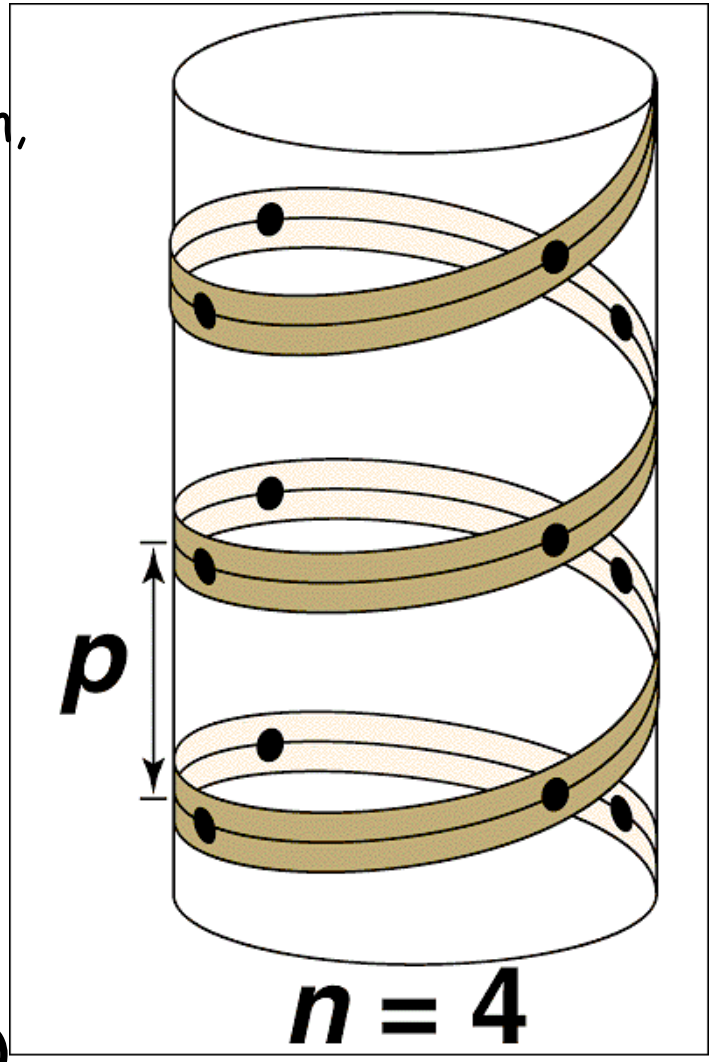
between –CO- and -NH- of the peptide bonds

real proteins: different parts of the polypeptide chain exist in various secondary structures


α helix
Hydrogen bonds
β Pleated Sheet

Helical structure (helix)

- **various types of the spiral:**
  different steepness, direction of rotation, number of AAs per turn
- **peptide bond planes are parallel to the axis of the helix with R- perpendicular to it**
- **H-bonds are formed between AAs found above and below themselves**

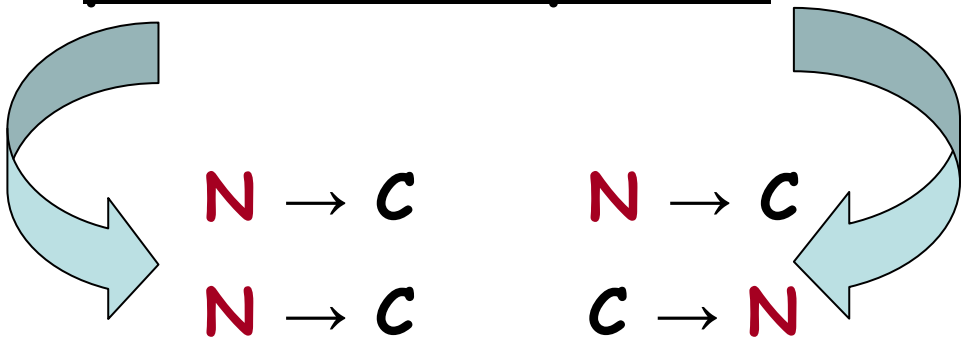


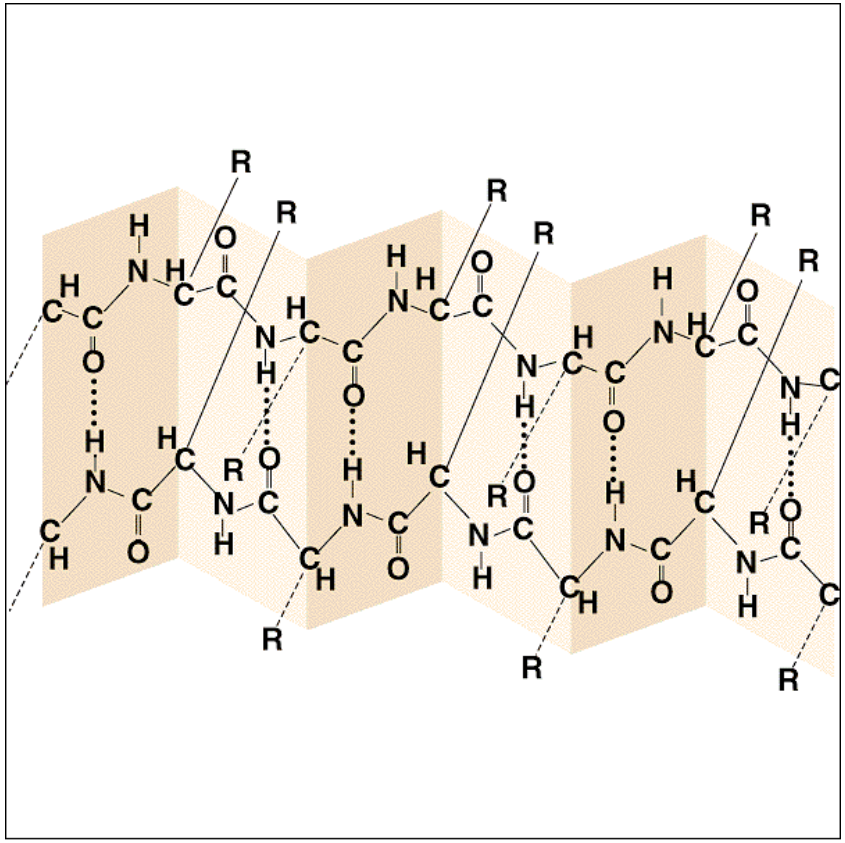
***the most common*:**

- α-helix (right-handed)
- collagen helix (left-handed, steeper)

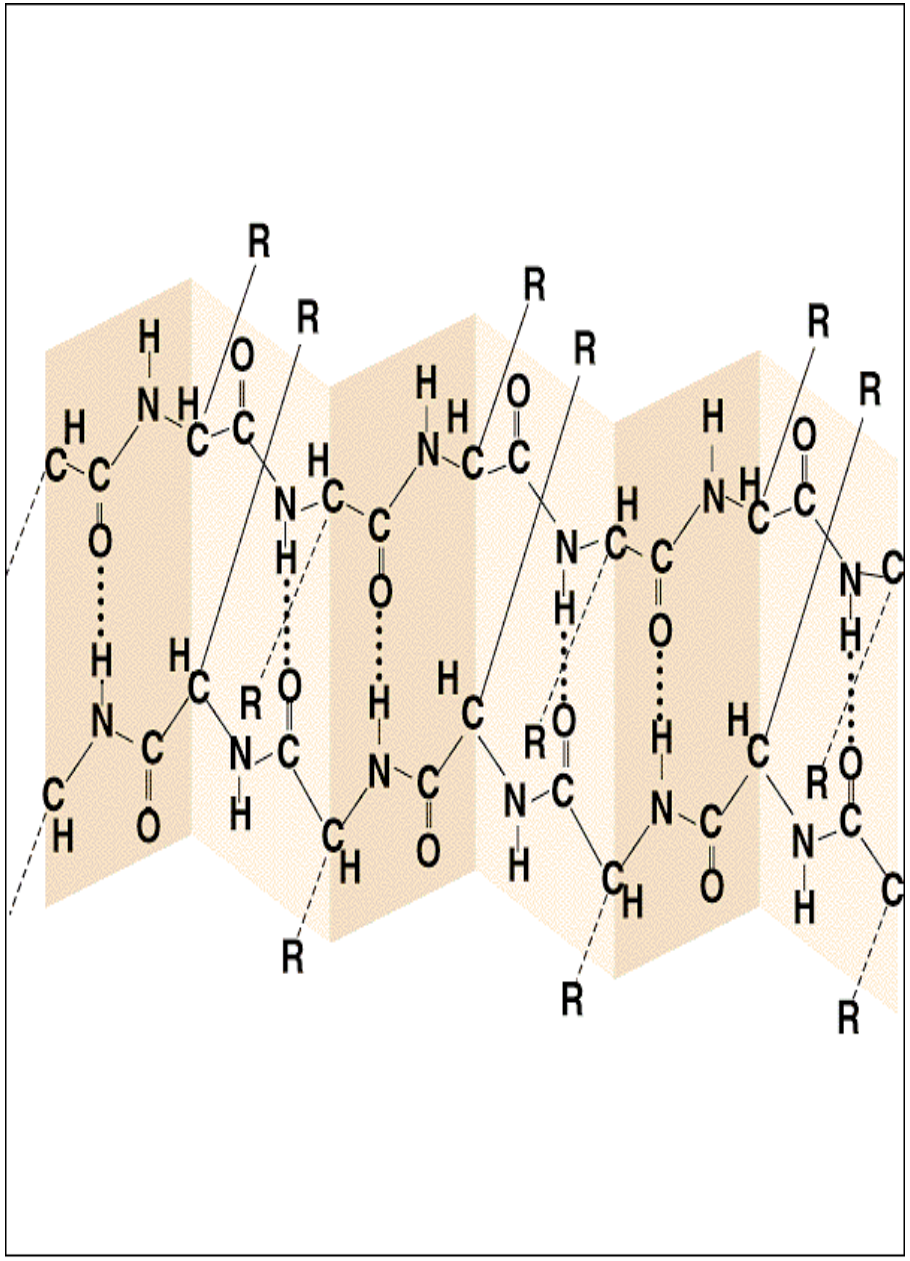
β-pleated sheet (β-structure)

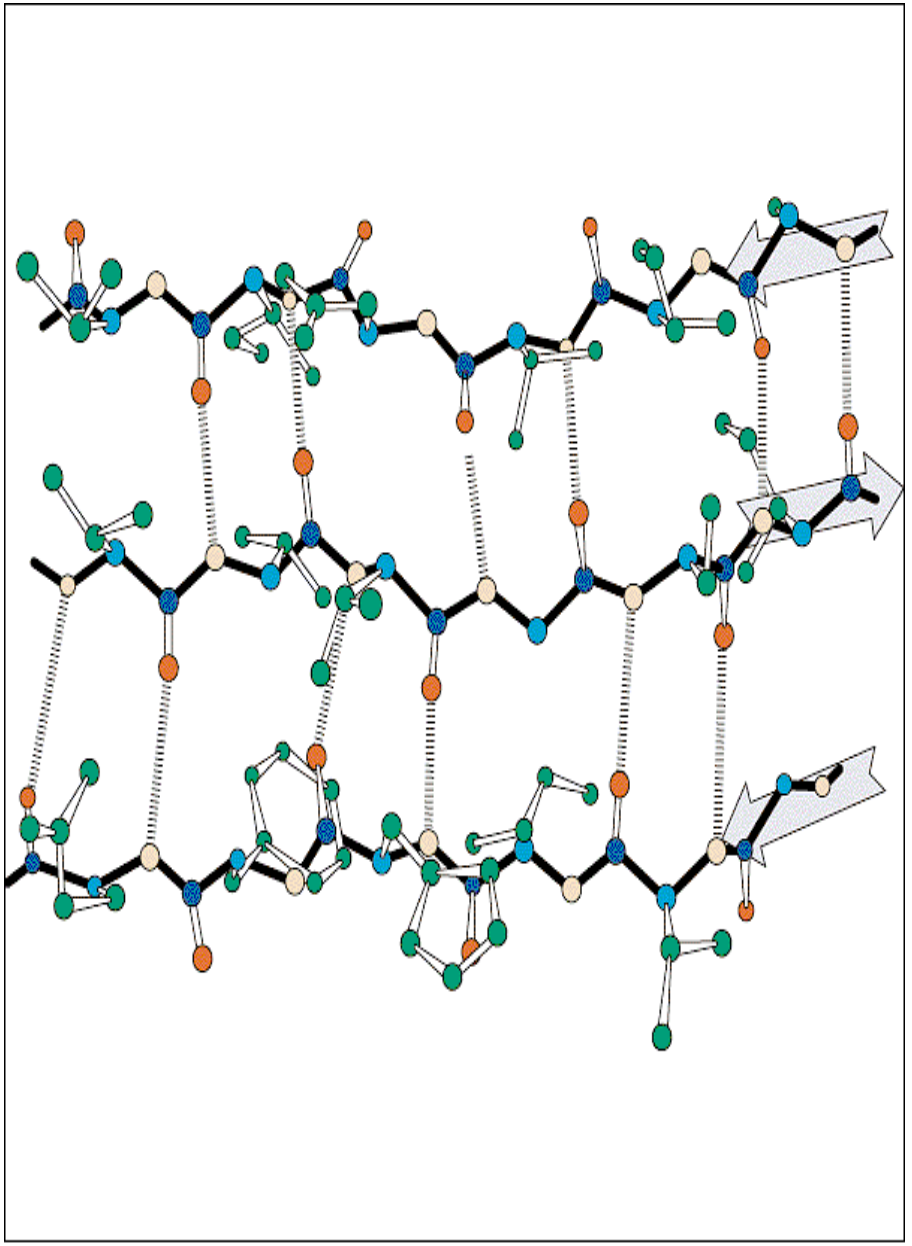
- direction of parts of the polypeptide chain is either parallel or antiparallel





- R- are placed above or below the plane of the sheet
- H-bonds are formed between peptide bonds of the neighboring parts of the polypeptide chain
- it brings strength to proteins





β-bend (reverse or β-turn)

- reverse the direction of a polypeptide chain, helping it form a compact, globular shape
- often connect successive strands of antiparallel sheets

Nonrepetitive secondary structure

- loop or coil conformation
- not random but less regular structure than α- or β-
- one half of a protein molecule exist in it

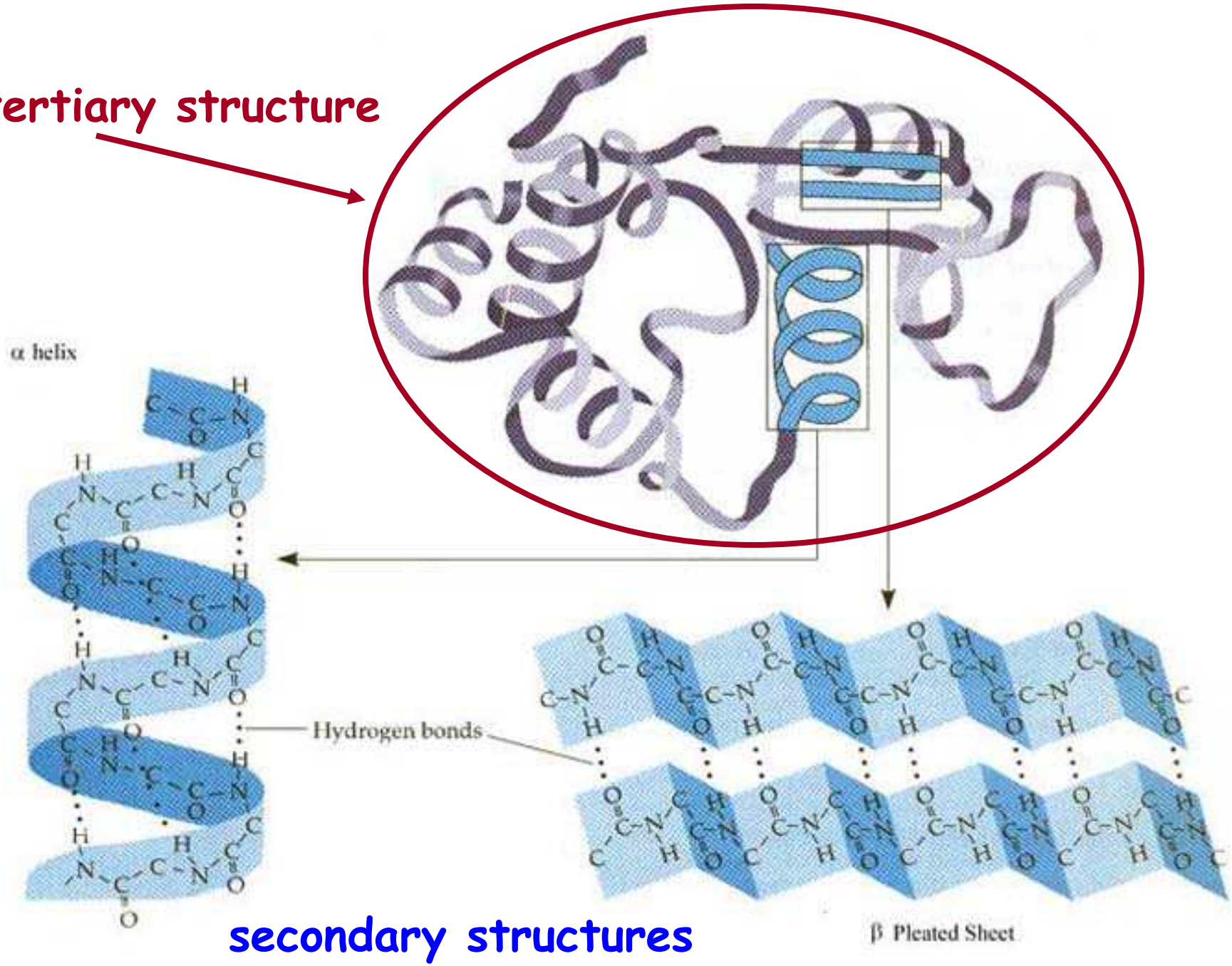
Tertiary structure of proteins

= spatial arrangement of the secondary structures (folding of domains)

stabilization: *between side chains of AAs*

1) hydrogen bonds
2) ionic (electrostatic) interactions
3) hydrophobic interactions
4) disulfide bonds

tertiary structure

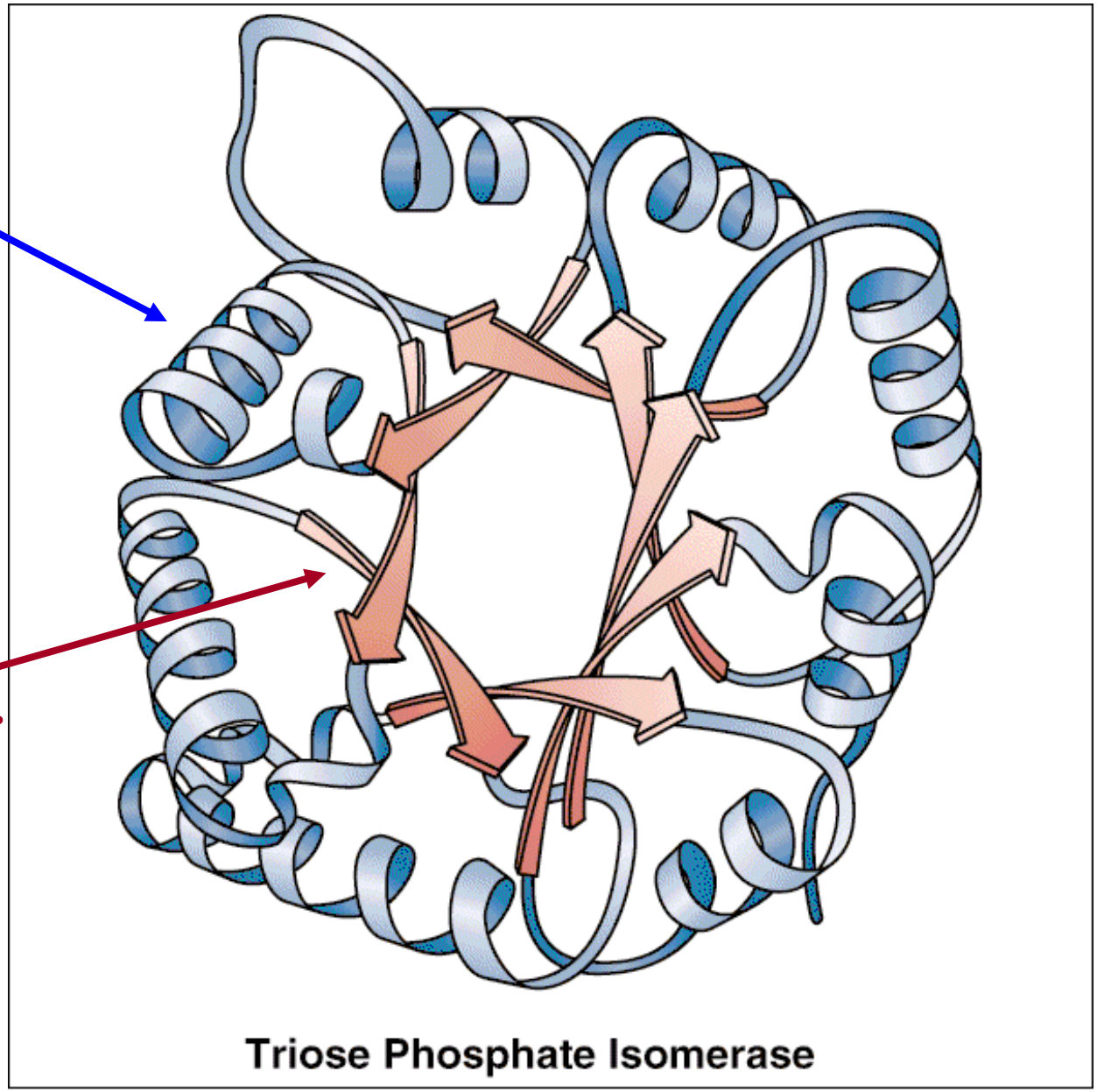


secondary structures

α-helix

β-sheet

motif:
barrel



Triose Phosphate Isomerase

Classification of proteins according to their tertiary structure

1) globular proteins (spheroproteins)

- spheroidal shape
- both secondary structures are abundant

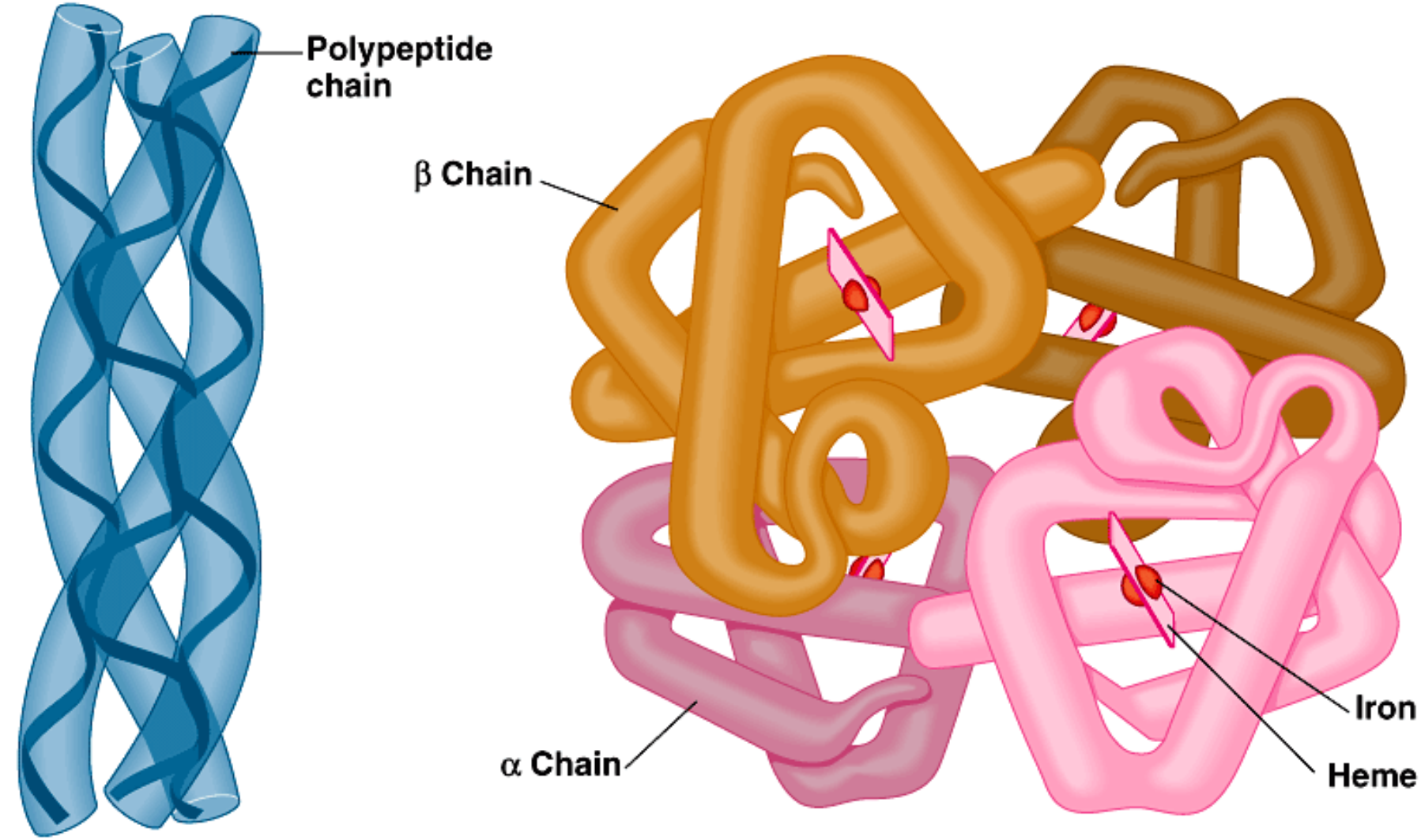
2) fibrous proteins (scleroproteins)

- rod-like shape
- one secondary structure predominates
- e.g. α-keratin, collagen

Quaternary structure of proteins

= oligomeric structure of a protein (2 or more subunits ~ monomers)

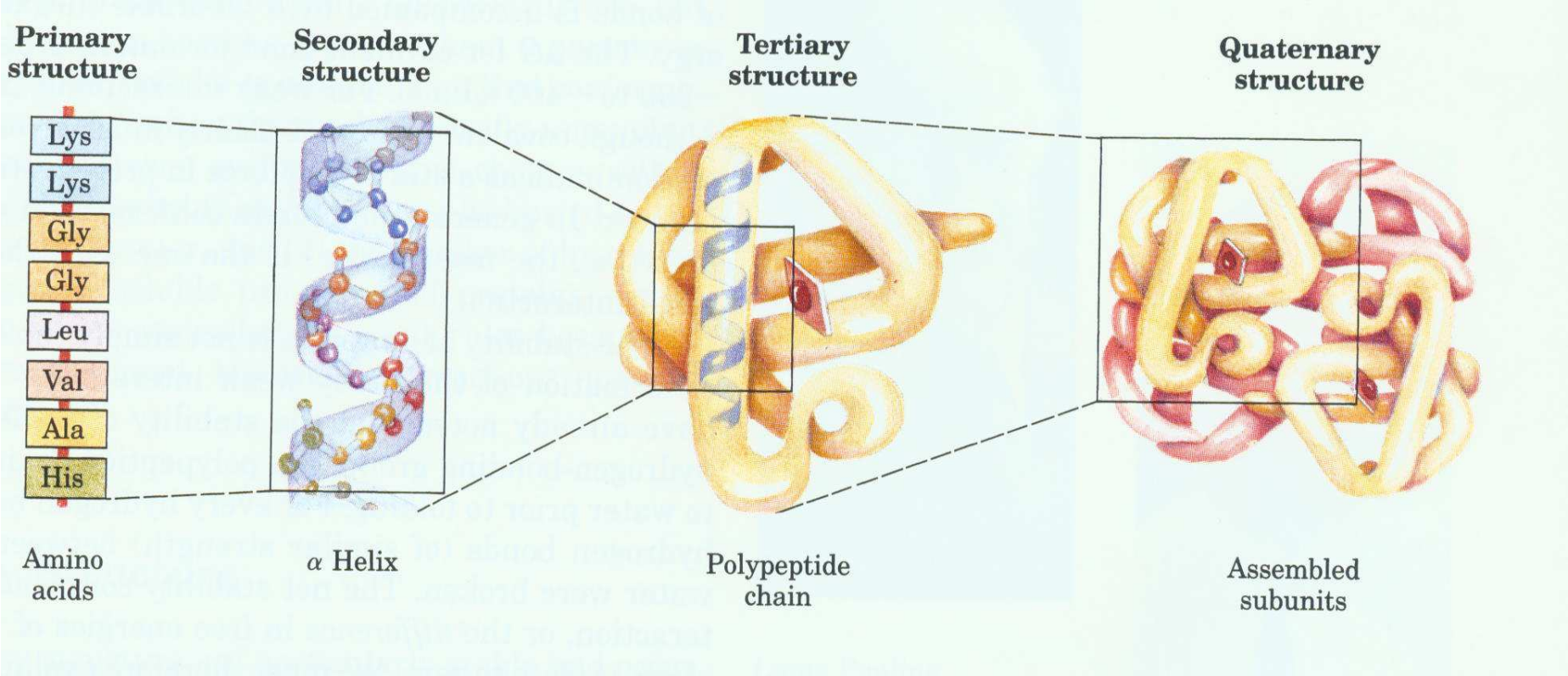
- i.e. the structure is found only in proteins composed from 2 or more chains (subunits)
- stabilization: noncovalent interactions
- the proteins have an „allosteric effect"



(a) Collagen

(b) Hemoglobin

SUMMARY
of
protein structure description



properties and functions of proteins

are related to their spatial arrangement

IT DEPENDS ON AMINO ACIDS COMPOSITION

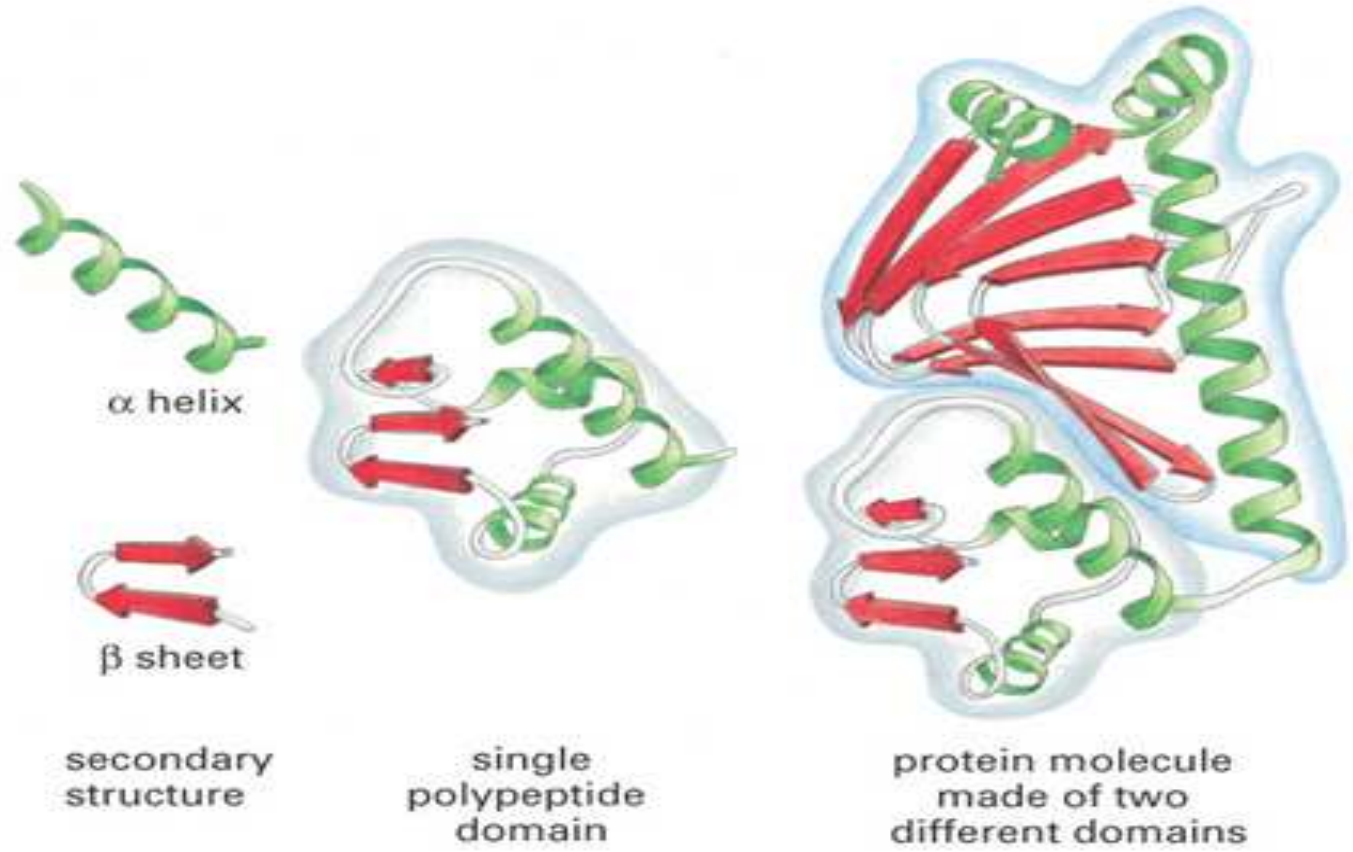
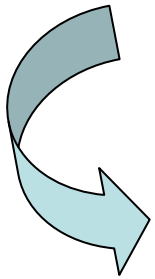


Figure 4-19 Essential Cell Biology, 2/e. (© 2004 Garland Science)

Physicochemical properties

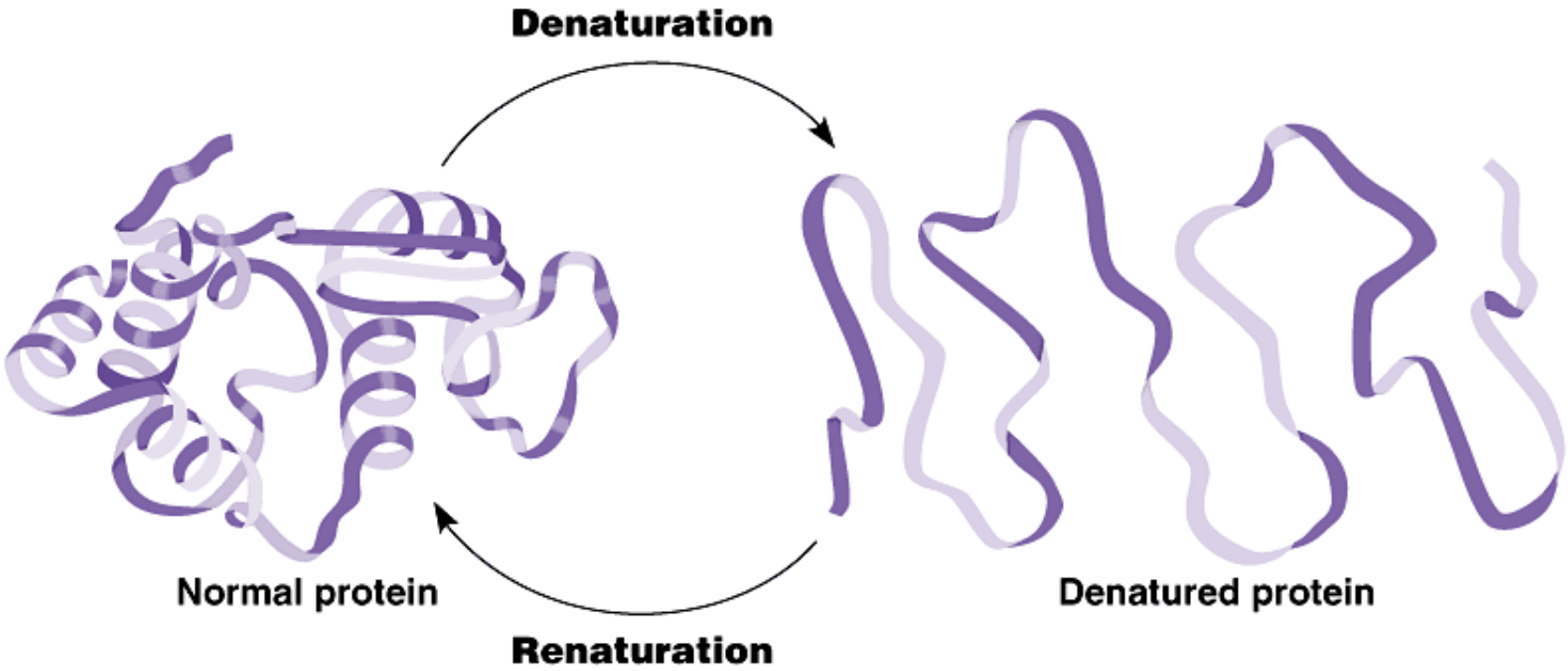
- water solubility depends on the structure
- proteins form colloidal solutions
  (viscosity, sedimentation, light dispersion)



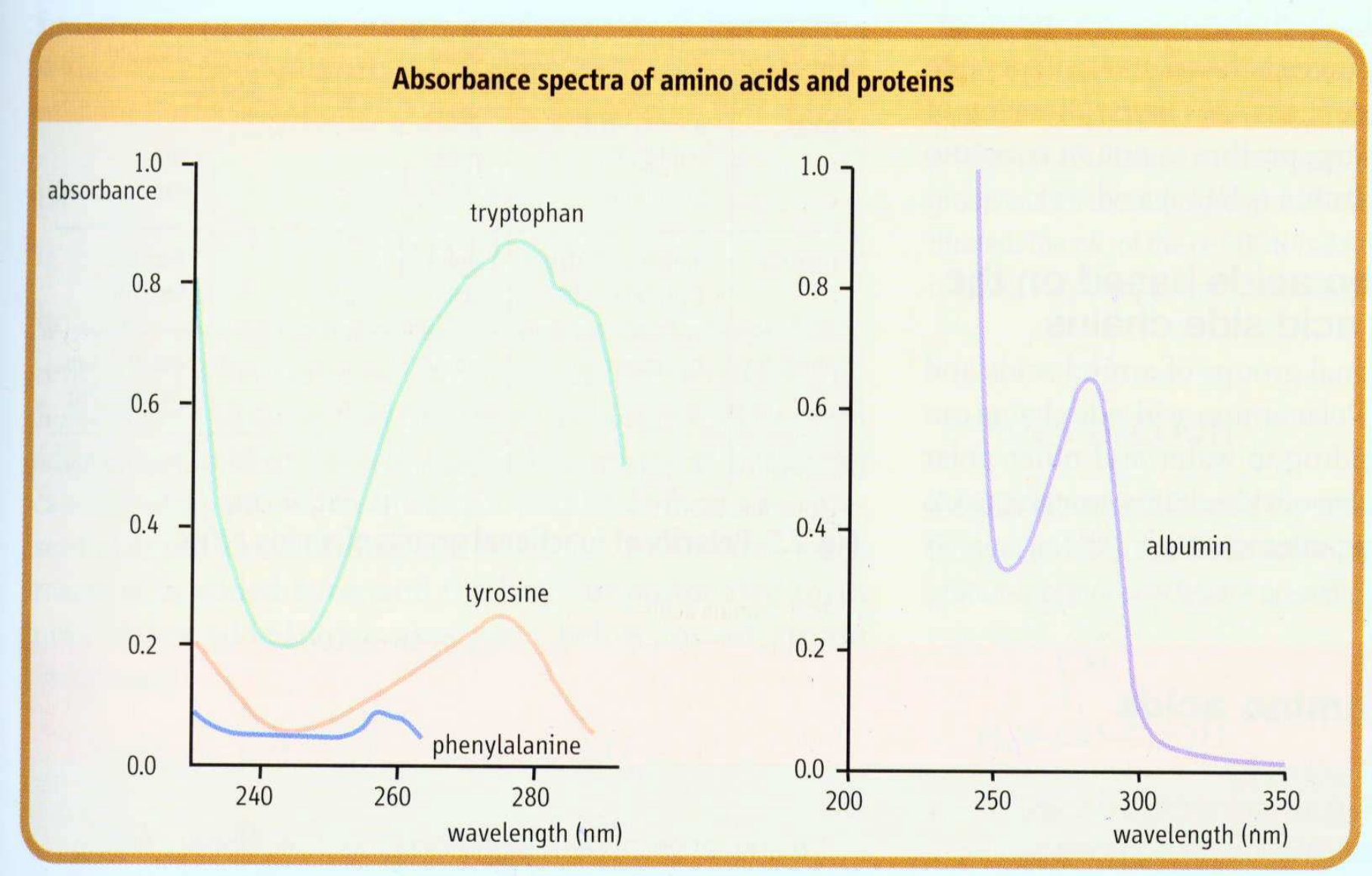
colloidal-osmotic pressure = onkotic pressure

- proteins can be salting-out of the solution
  (~ water sheet removing)

- proteins can be **denaturated**
  - heat, whipping, shaking, radiation
  - strong pH changes, salt of heavy metals, organic solvents, detergents



- proteins strongly **absorb UV radiation**



- proteins are **ampholytes**

$$-COOH \rightleftharpoons -COO^- + H^+$$

$$-NH_2 + H^+ \rightleftharpoons -NH_3^+$$

under physiological pH
proteins are negatively charged