Biomolecules: amino acids

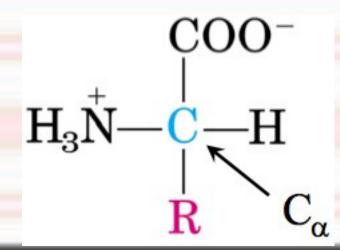
# Amino acids

- Amino acids are the building blocks of proteins
   They are also part of hormones, neurotransmitters and metabolic intermediates
- There are 20 different amino acids in nature, but they all share a common scaffold:
  - One central carbon atom hybrydized sp3
  - One amino group
  - One carboxylic group
  - One hydrogen
  - One side chain, different per each aa

$$\begin{array}{c} \mathbf{COOH} \\ \mathbf{H}_{2}\mathbf{N} - \begin{array}{c} \mathbf{C} \\ \mathbf{C} \\ \mathbf{H} \\ \mathbf{R} \end{array}$$

## Amino acids

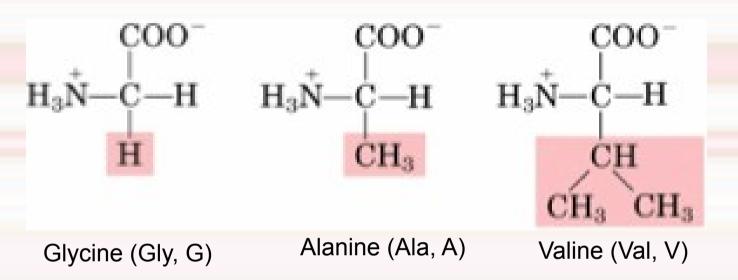
- All amino acids are non-volatile solids at RT and have very high boiling points (200-300°C)
- They are very soluble in water, but not in apolar solvents
- They have acid constants higher than general carboxylic acids (Ka=10<sup>-2</sup> 10<sup>-3</sup> M)
- They have basic constants lower than those of generic amines (Kb= 10<sup>-4</sup> M)
- All these characteristics can be explained assuming that the aa in solution has a dipolar structure, called zwitterion

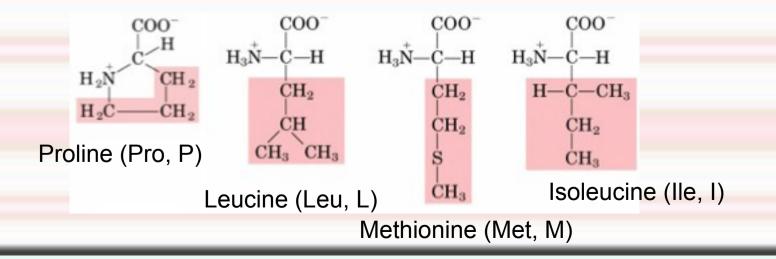


# Amino acids

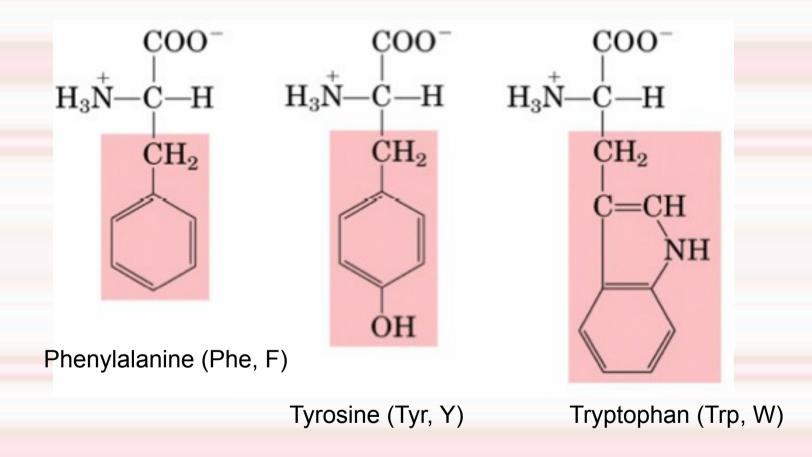
- Mammals need to assume with the diet 10 out of 20 aa, since they are not able to synthesize them:
- Cysteine, Phenylalanine, Histidine, Isoleucine, Lysine, Leucine, Methionine, Threonine, Valine and Tryptophan
- Depending on side chains characteristics, we can classify:
  - Apolar side chains (Gly, Ala, Val, Pro, Leu, Met, Ile)
  - Aromatic side chains (Phe, Tyr, Trp)
  - Uncharged polar side chains (Ser, Thr, Cys, Ans, Gln)
  - Positively charged side chains (His, Lys, Arg)
  - Negatively charged side chains (Glu, Asp)
- Their names can be shortened in a 3-letters code and in a 1-letter code

### Apolar amino acids

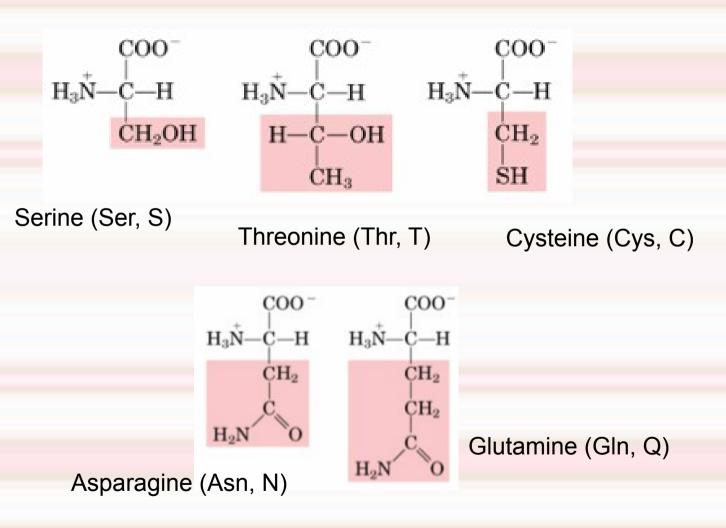




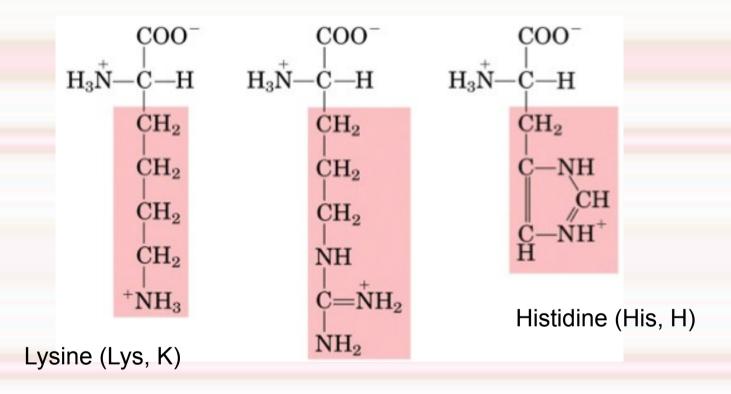
## Aromatic amino acids



#### Polar amino acids

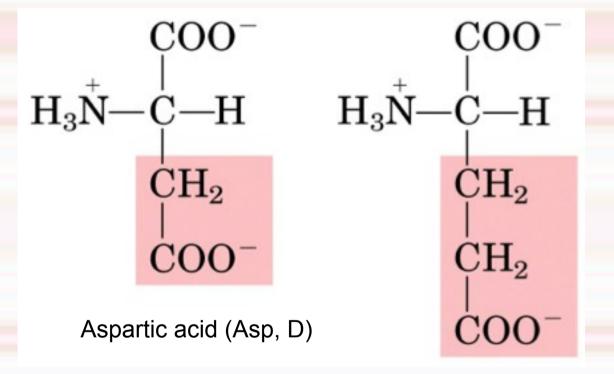


## **Basic amino acids**



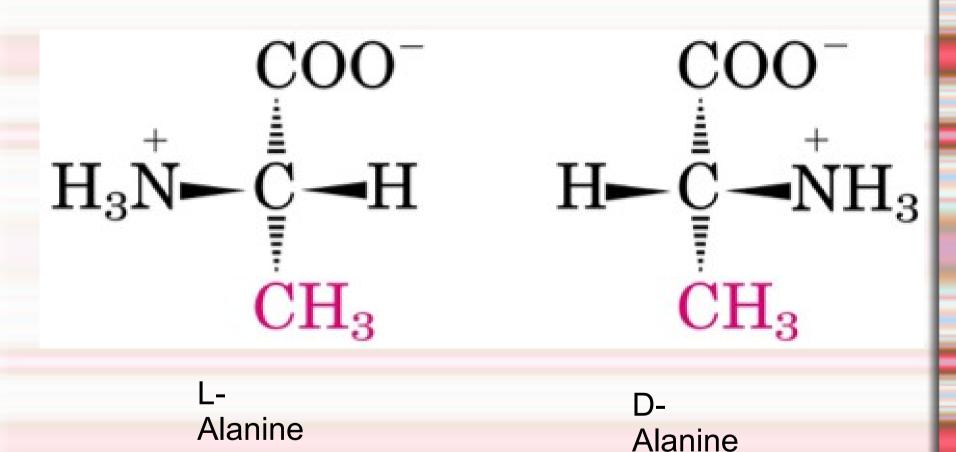
Arginine (Arg, R)

### Acidic amino acids



Glutamic acid (Glu, E)





In living organism there will only be L-amino acids incorporated into proteins

A few bacteria can synthesize D-aa, but they need a special enzyme

### **Properties of amino acids: acid-base reaactions**

	pK <sub>COOH</sub>	pK <sub>NH3+</sub>	pK <sub>R</sub>	pI
GLY	2.3	9.6	-	6.0
ALA	2.3	9.7	-	6.0
VAL	2.3	9.6	-	6.0
PRO	2.0	10.6	-	6.3
LEU	2.4	9.7	-	6.0
MET	2.3	9.2	-	5.8
ILE	2.4	9.7	-	6.1
PHE	1.8	9.1	-	5.5
TYR	2.2	9.1	10.1	5.7
TRP	2.4	9.4	-	5.9
SER	2.2	9.2	-	5.7
THR	2.6	10.4	-	6.5
CYS	1.8	10.8	8.3	5.0
ASN	2.0	8.8	-	5.4
GLN	2.2	9.1	-	5.7
LYS	2.2	9.0	10.5	9.8
ARG	2.2	9.0	12.5	10.8
HIS	1.8	9.2	6.0	7.6
ASP	2.1	9.8	3.9	3.0
GLU	2.2	9.7	4.3	3.2

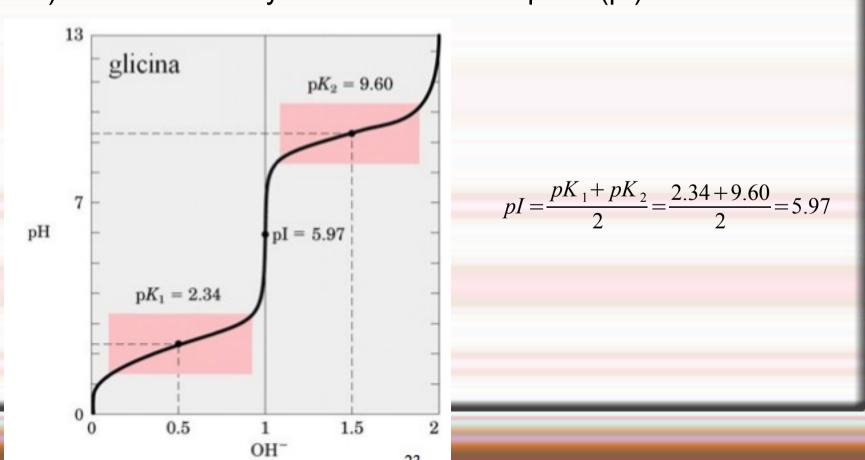
pKa ranges from 1.8 and 2.4 pKb ranges from 9.0 and 10.8

 $\mathsf{pK}_{_{\!\!R}}$  refers to the properties of the charged side chains

pl is the isoelectric point: the pH at which the aa has reached neutrality (no net charge)

### **Properties of amino acids: acid-base reaactions**

The previous table has been obtained by titrating each amino acid with a strong base Here is shown the titration curve for Glycine There are two areas where the curve resembles that of a buffer (pK1 and pK2) and there is only one neutralization point (pI)



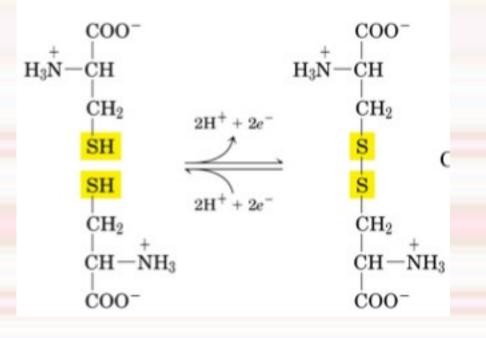
#### **Properties of the aa: acid-base reactions**

- The ionizability of an aa is pH dependent:
- At  $pH > pI \rightarrow$  the aa has a net charge of -1 (cation)
- At  $pH < pI \rightarrow$  the aa has a net charge of +1 (anion)
- At  $pH = pI \rightarrow$  there is the zwitterion, with a net charge of 0

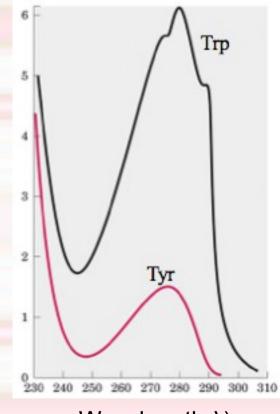
$$\stackrel{+}{\overset{}_{\operatorname{CH}_{3}}}_{\operatorname{CH}_{2}} \stackrel{pK_{1}}{\longleftarrow} \stackrel{pK_{1}}{\underset{\operatorname{CH}_{2}}{\overset{pK_{2}}{\longleftarrow}} \stackrel{pK_{2}}{\underset{\operatorname{CH}_{2}}{\overset{pK_{2}}{\longleftarrow}} \stackrel{NH_{2}}{\underset{\operatorname{CH}_{2}}{\overset{\mu}{\longleftarrow}} \stackrel{pK_{2}}{\underset{\operatorname{COO}^{-}}{\overset{\mu}{\longleftarrow}} \stackrel{NH_{2}}{\underset{\operatorname{CH}_{2}}{\overset{\mu}{\longleftarrow}} \stackrel{pK_{2}}{\underset{\operatorname{COO}^{-}}{\overset{\mu}{\longleftarrow}} \stackrel{NH_{2}}{\underset{\operatorname{CH}_{2}}{\overset{\mu}{\longleftarrow}} \stackrel{nH_{2}}{\underset{\operatorname{COO}^{-}}{\overset{\mu}{\longleftarrow}} \stackrel{nH_{2}}{\underset{\operatorname{COO}^{-}}{\underset{\operatorname{COO}^{-}}{\overset{\mu}{\longleftarrow}} \stackrel{nH_{2}}{\underset{\operatorname{COO}^{-}}{\underset{\operatorname{COO}^{-}}{\overset{\mu}{\longleftarrow}} \stackrel{nH_{2}}{\underset{\operatorname{COO}^{-}}{\underset{\operatorname{COO}^{-}}{\overset{\mu}{\longleftarrow}} \stackrel{nH_{2}}{\underset{\operatorname{COO}^{-}}{\underset{\operatorname{COO}^{-}}{\overset{\mu}{\longleftarrow}} \stackrel{nH_{2}}{\underset{\operatorname{COO}^{-}}{\underset{\operatorname{COO}^{-}}{\overset{\mu}{\longleftarrow}} \stackrel{nH_{2}}{\underset{\operatorname{COO}^{-}}{\underset{\operatorname{COO}^{-}}{\underset{\operatorname{COO}^{-}}{\underset{\operatorname{COO}^{-}}{\underset{\operatorname{COO}^{-}}{\underset{\operatorname{COO}^{-}}{\underset{\operatorname{COO}^{-}}{\underset{\operatorname{COO}^{-}}{\underset{\operatorname{COO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^{-}}}{\underset{\operatorname{CO}^{-}}{\underset{\operatorname{CO}^$$

### **Properties of aa: redox reactions**

- Cysteine has a reactive -SH group which can shuttle electrons and protons to acceptor proteins
- It can also react with a second Cys to form a covalent bond: the disulfide bond
  - Disulfide bonds usually occurs in extracellular proteins, given that the extracellular environment is highly oxidative



#### **Properties of aa: spectroscopic behaviour**

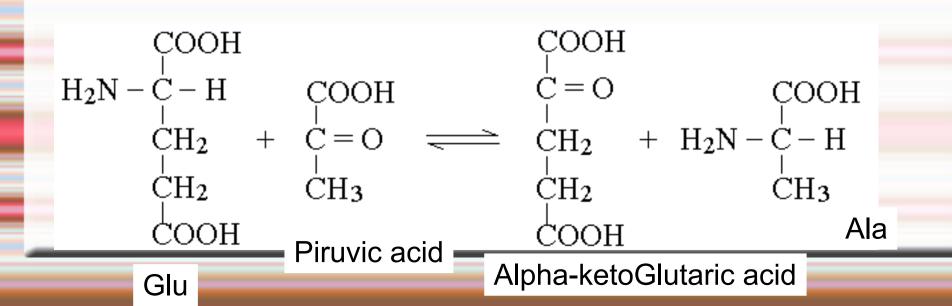


Wavelength  $\lambda$ )

 Aromatic side chains can absorb UV light and can be used to calculate protein quantity in solution
 The total absorbance of a sample is directly proportional to the number of Trp and/or Tyr and hence to the concentration of a given protein

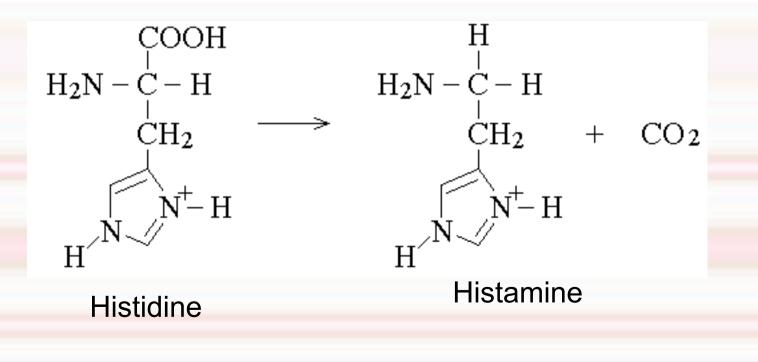
#### Reaction of aa: transamination

Aa can exchange amino and ketonic groups: this reaction is reversible and called transamination
it is usually performed inside the cytoplasm
One aa can react with an alpha-ketoacid to give an alpha-ketoacid and an amino acid
Many of those enzymes work in the liver and the level of transaminase in the blood will reveal a pathological state of this organ

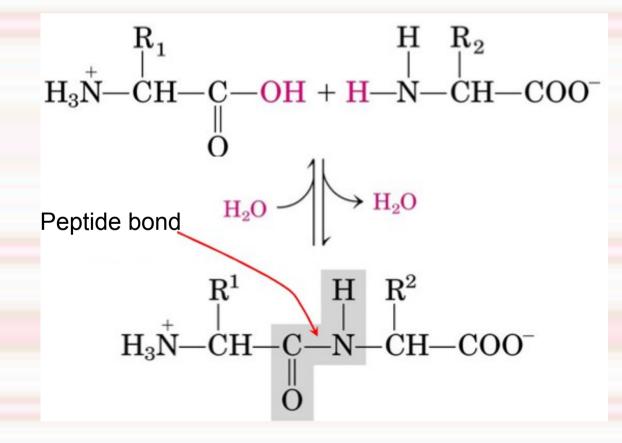


### Reaction of aa: decarboxylation

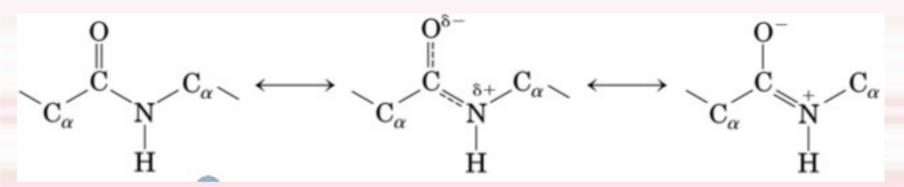
- This reaction will lead to the formation of CO<sub>2</sub> and the amine
- It is catalysed by amine decarboxylases
   some of the amines produced could be hormones or active metabolites



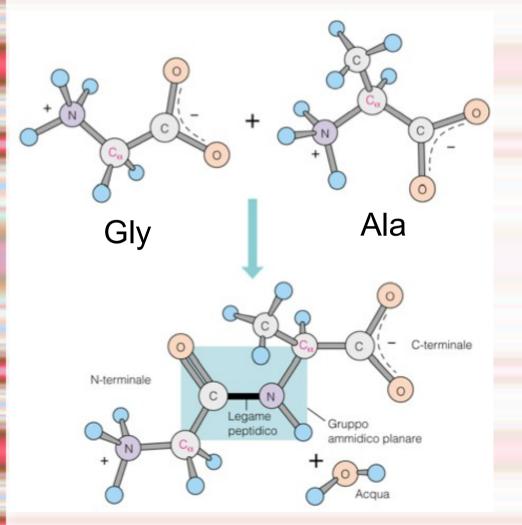
 The acid group of one aa will react with the amino group of the following residue in a condensation reaction leading to a dipeptide



- This reaction, which would normally give rise to an amide bond, lead to the formation of a special bond: the peptide bond
- Its length is shorter than a single bond and longer than a double bond
- its energy is in between that of a single and of a double bond



There is resonance due to the particular electronic configuration of the bond  $\rightarrow$  rigidity of the molecule and *trans* configuration of the bond



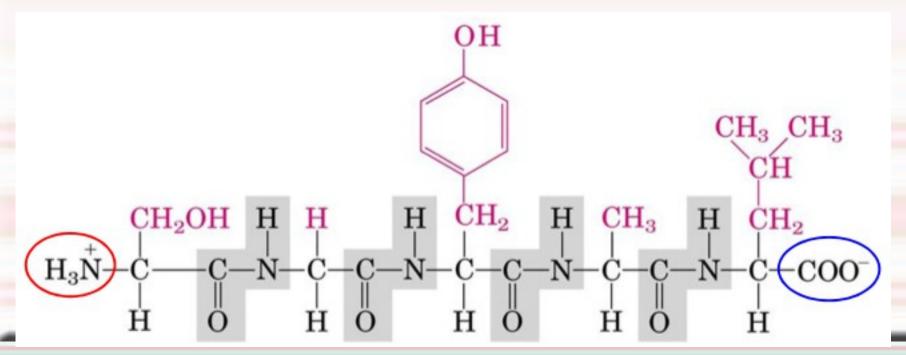
 The peptide bond has 40% character of double bond

 6 atoms lie in the plane of the bond

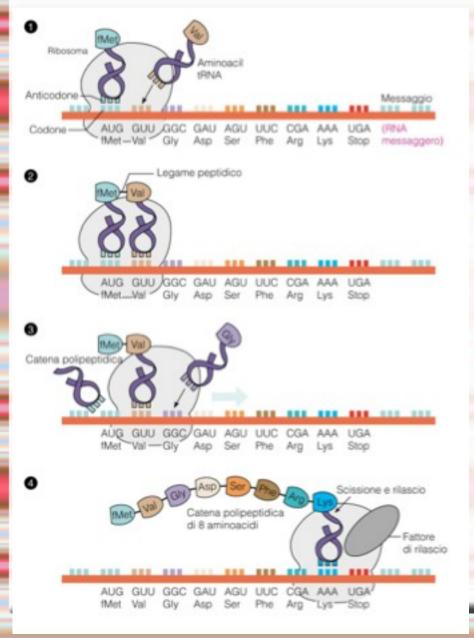
•There is a partial negative charge on the carbonyl O and a partial positive charge on the amino N

• All the peptide bonds in proteins are in the *trans* configurations

- The condensation reaction always attaches the -COOH of the  $a_{i}$  to the -NH<sub>2</sub> of  $a_{i+1}$
- The polypeptide chain has a polarity: it will start with a free amino group and it will end with a free carboxylic group
- These are called N-terminal and C-terminal ends



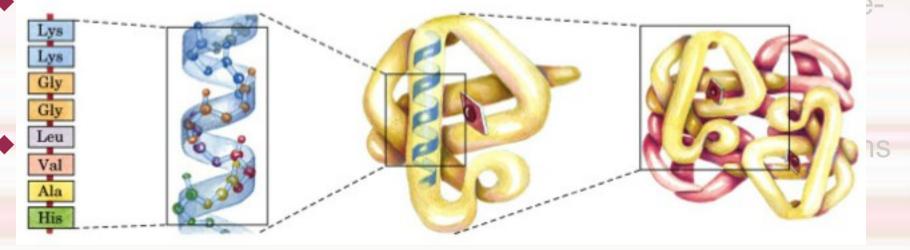
## In vivo polymerization: translation



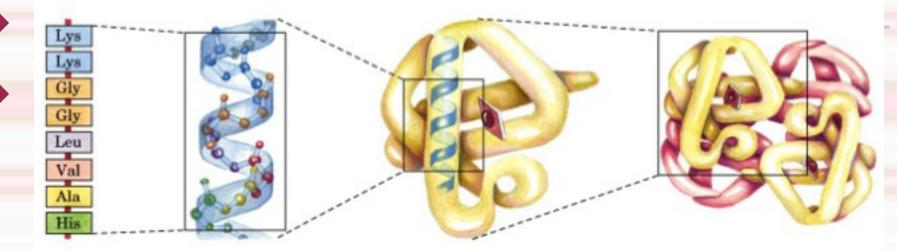
 Polypeptide chains and proteins are synthesized by the ribosomes, which read the mRNA and charge the proper aatRNA

## Hierarchical organization of proteins

- Primary structure: the linear sequence of aa bound by peptide bonds
- Secondary structures: regular organization of aa in the space, stabilized by hydrogen bonds among CO and NH of several peptide bonds. It can either be periodic (alpha-helix, beta-sheet) or random. Not all the possible fold are allowed given the restrictions dictated by the peptide bond



## Hierarchical organization of proteins



- **Tertiary structure**: real 3D structure of a folded protein, derived from the assembly of secondary structure elements. These are stabilized by polar and hydrophobic interactions among the side chains
- **Quaternary structure**: oligomeric assembly (not all proteins have this arrangement)