[redacted]

PROTEIN STRUCTURE AND FUNCTION

Proteins play crucial roles in virtually all biological processes.

For example

(1) <u>Enzymatic catalysis</u>: Nearly all chemical reactions in biological systems are catalyzed by enzymes

- **Enzymes exhibit enormous catalytic power and usually increase reaction rate by at least a million fold**

- **Nearly all known enzymes are proteins**

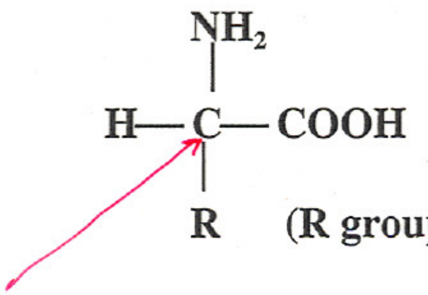
(2) <u>Transport and Storage</u>: Many small molecules and ions are transported by specific proteins (hemoglobin and myoglobin for oxygen, transferrin and ferritin for iron)

(3) <u>Coordinated Motion</u>: Proteins are the major component of structures involved in motion (e.g. muscle, flagella)

<u>**PROTEINS ARE BUILT FROM 20 AMINO ACIDS**</u>

Amino acids are the basic structural units of proteins.

Structure of an amino acid:



(R group or side chain)

a carbon

- **Twenty kinds of side chains are commonly found in proteins.**

  - **Side Chains vary in:**

    1. **Size**
    2. **Shape**
    3. **Charge**
    4. **Hydrogen-bonding capacity**
    5. **Chemical reactivity**

- **All proteins in all species, from bacteria to human, are constructed from the same set of ~~proteins.~~** amino acids.

(4) **Mechanical Support**: Skin and bone are made of proteins

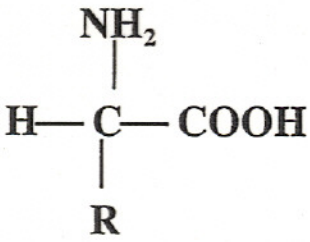
(5) **Immune Protection**: Antibodies and other components of the immune system are made of proteins

(6) **Generation and Transmission of Nerve Impulses**: The response of nerve cells to specific stimuli is mediated by receptor proteins

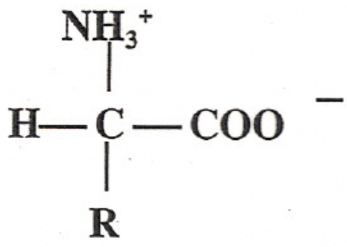
(7) **Control of Growth and Differentiation**:

- controlled expression of genes is essential for the orderly growth and differentiation of cells
- many growth factors, hormones, and cell sensors, are proteins

- **Amino acids in solutions at neutral pH (7.0) are predominately dipolar ions rather than un-ionized molecules:**



Un-ionized form



Dipolar Ion form

- **The ionization state of an amino acid varies with pH**
  - **In acid solution (e.g. pH= 1): $-NH_3^+$, $-COOH$**
  - **In alkaline solution (e.g. pH= 11): $-NH_2$, $-COO^-$**

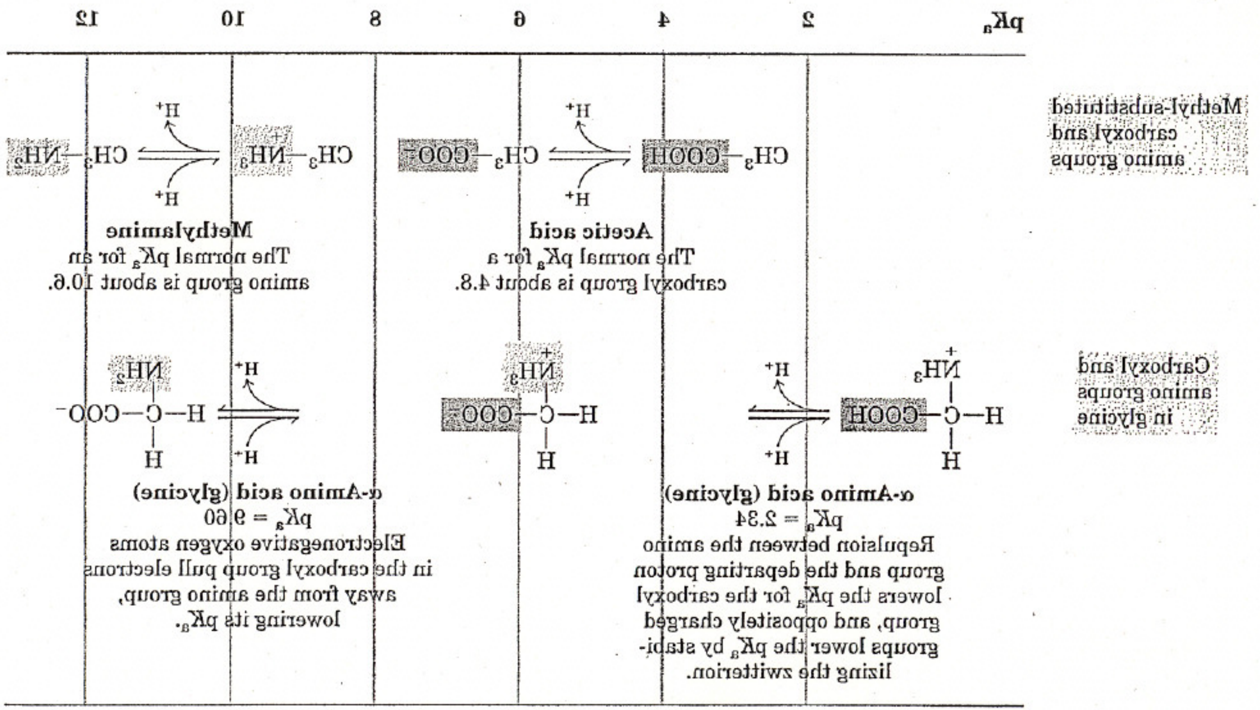
For glycine: $pK_{COOH} = 2.3$ $pK_{NH2} = 9.6$

pH : a quantity used to express the acidity of a solution, equivalent to $-\log[H^+]$

pk : a quantity used to express the tentancy for an acid to donate a proton, equivalent to $-\log k$, where k is the acid's dissociation constant.

figure 5–11

Effect of the chemical environment on pK_a. The pK_a values for the ionizable groups in glycine are lower than those for simple, methyl-substituted amino and carboxyl groups. These downward perturbations of pK_a are due to intramolecular interactions. Similar effects can be caused by chemical groups that happen to be positioned nearby—for example, in the active site of an enzyme.



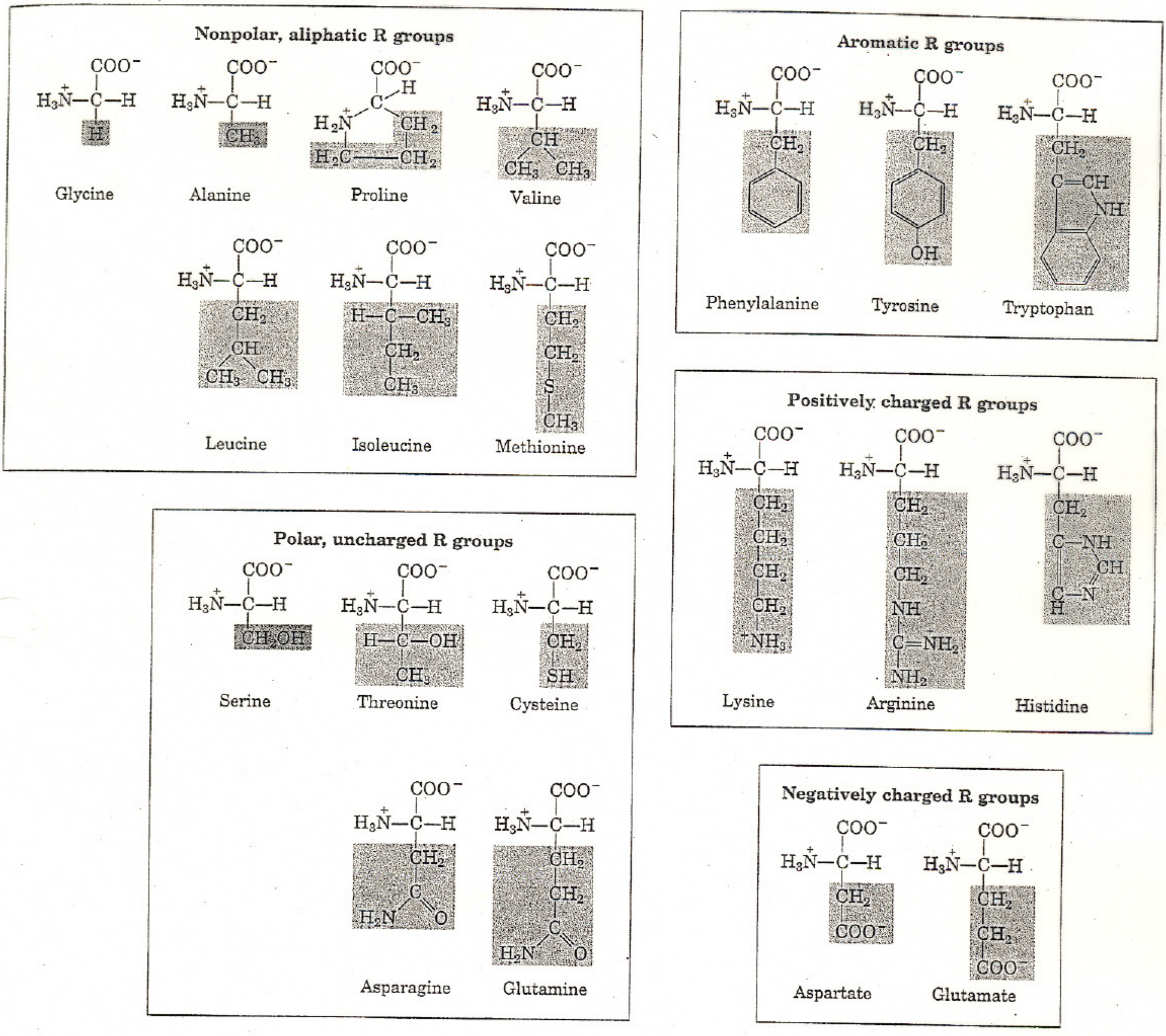


figure 5–5

The 20 standard amino acids of proteins. The structural formulas show the state of ionization that would predominate at pH 7.0. The unshaded portions are those common to all the amino acids; the portions shaded in red are the R groups. Although the R group of histidine is shown uncharged, its pK_a (see Table 5–1) is such that a small but significant fraction of these groups are positively charged at pH 7.0.

Properties and Conventions Associated with the Standard Amino Acids

Amino acid	Abbreviated names		M_r	pK_a values			pI	Hydropathy index*	Occurrence in proteins (%)†
				pK_1 (—COOH)	pK_2 ($—NH_3^+$)	pK_R (R group)			
Nonpolar, aliphatic R groups									
Glycine	Gly	G	75	2.34	9.60		5.97	−0.4	7.2
Alanine	Ala	A	89	2.34	9.69		6.01	1.8	7.8
Proline	Pro	P	115	1.99	10.96		6.48	1.6	5.2
Valine	Val	V	117	2.32	9.62		5.97	4.2	6.6
Leucine	Leu	L	131	2.36	9.60		5.98	3.8	9.1
Isoleucine	Ile	I	131	2.36	9.68		6.02	4.5	5.3
Methionine	Met	M	149	2.28	9.21		5.74	1.9	2.3
Aromatic R groups									
Phenylalanine	Phe	F	165	1.83	9.13		5.48	2.8	3.9
Tyrosine	Tyr	Y	181	2.20	9.11	10.07	5.66	−1.3	3.2
Tryptophan	Trp	W	204	2.38	9.39		5.89	−0.9	1.4
Polar, uncharged R groups									
Serine	Ser	S	105	2.21	9.15		5.68	−0.8	6.8
Threonine	Thr	T	119	2.11	9.62		5.87	−0.7	5.9
Cysteine	Cys	C	121	1.96	10.28	8.18	5.07	2.5	1.9
Asparagine	Asn	N	132	2.02	8.80		5.41	−3.5	4.3
Glutamine	Gln	Q	146	2.17	9.13		5.65	−3.5	4.2
Positively charged R groups									
Lysine	Lys	K	146	2.18	8.95	10.53	9.74	−3.9	5.9
Histidine	His	H	155	1.82	9.17	6.00	7.59	−3.2	2.3
Arginine	Arg	R	174	2.17	9.04	12.48	10.76	−4.5	5.1
Negatively charged R groups									
Aspartate	Asp	D	133	1.88	9.60	3.65	2.77	−3.5	5.3
Glutamate	Glu	E	147	2.19	9.67	4.25	3.22	−3.5	6.3

*A scale combining hydrophobicity and hydrophilicity of R groups; it can be used to measure the tendency of an amino acid to seek an aqueous environment (− values) or a hydrophobic environment (+ values). See Chapter 12. From Kyte, J. & Doolittle, R.F. (1982) *J. Mol. Biol.* **157**, 105–132.

†Average occurrence in over 1150 proteins. From Doolittle, R.F. (1989) Redundancies in protein sequences. In *Prediction of Protein Structure and the Principles of Protein Conformation* (Fasman, G.D., ed) Plenum Press, NY, pp. 599–623.