

Biochemistry

Pavel Pestryakov

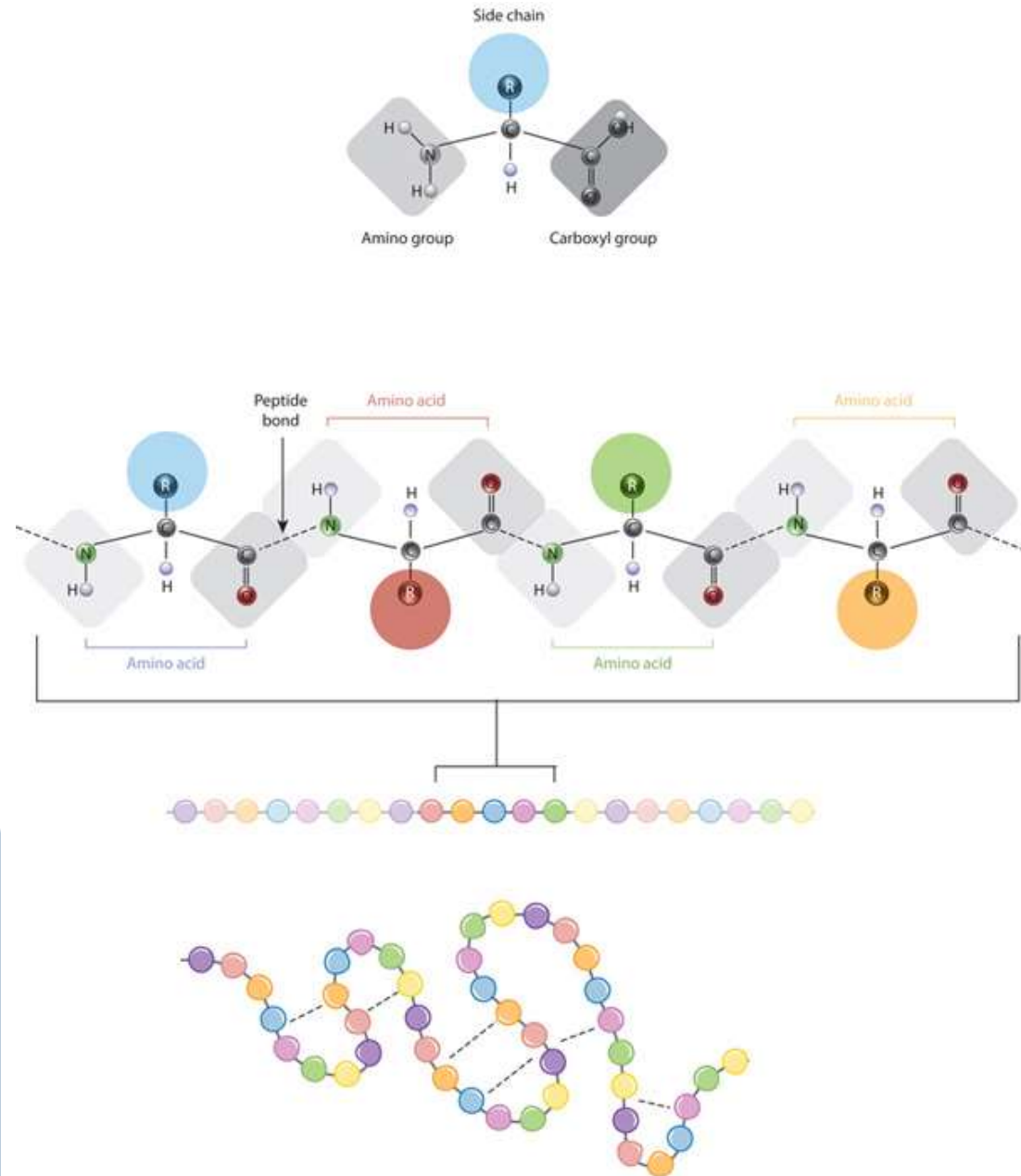
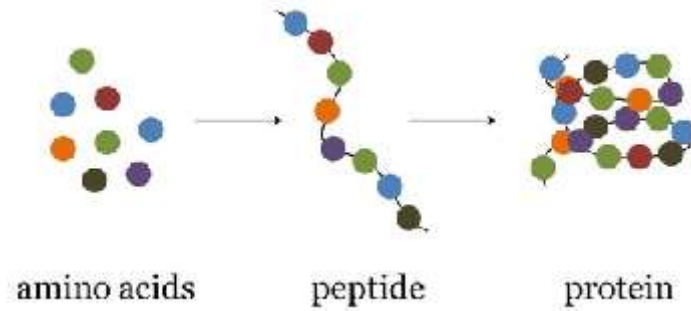
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PROTEINS



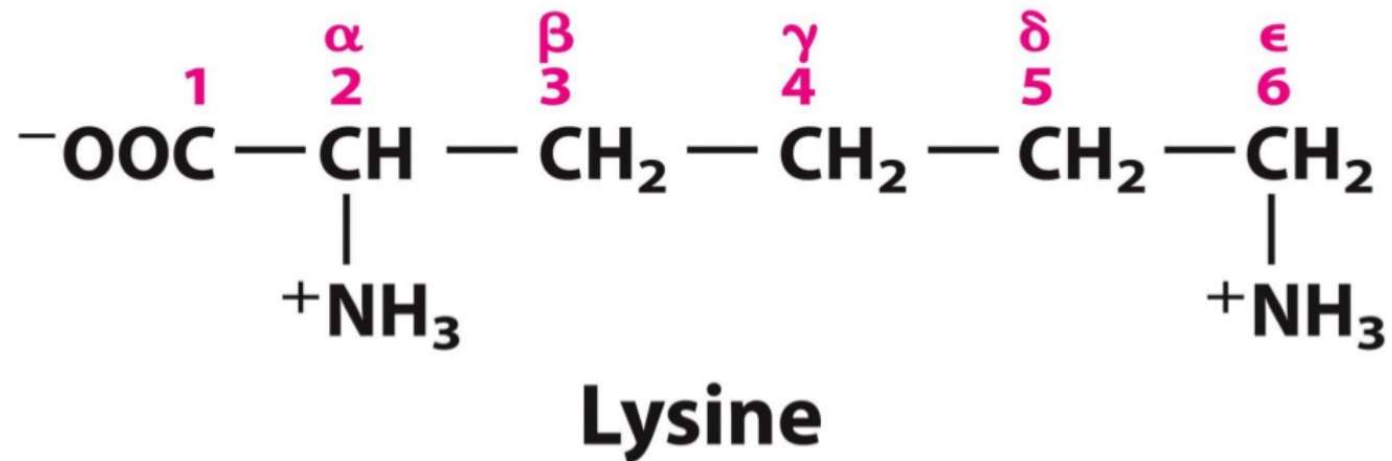
Polypeptides - polymers of amino acids covalently linked through peptide bonds

Natural molecules....C, H, O, N **organic**

Monomers.....**amino acids**

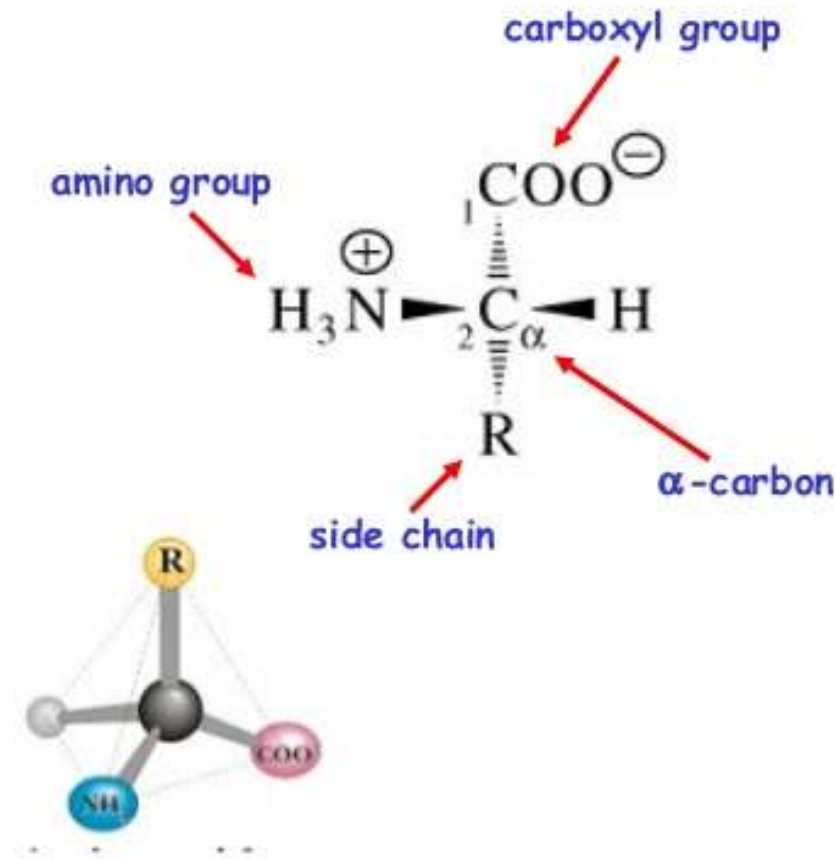
Aminoacid – monomer of protein (polypeptide)

- Organic nomenclature: start from one end
- Biochemical designation:
 - start from α -carbon and go down the R-group



Basic Amino Acid Structure

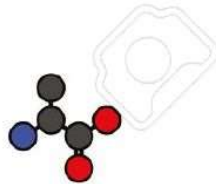
- α -carbon is chiral (except for glycine)
- at pH 7.0 uncharged amino acids are zwitterions
- amino acids have a tetrahedral structure



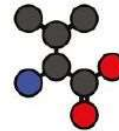
Visual representation of Aminoacids



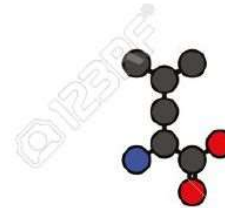
glycine (Gly, G)



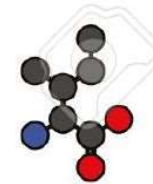
L-alanine (Ala, A)



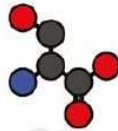
L-valine (Val, V)



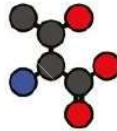
L-leucine (Leu, L)



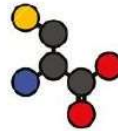
L-isoleucine (Ile, I)



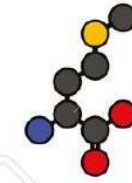
L-serine (Ser, S)



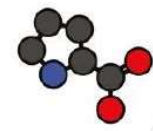
L-threonine (Thr, T)



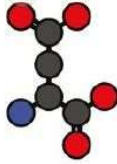
L-cysteine (Cys, C)



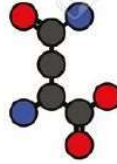
L-methionine (Met, M)



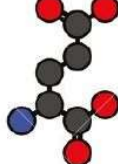
L-proline (Pro, P)



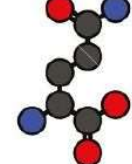
L-aspartic acid (Asp, D)



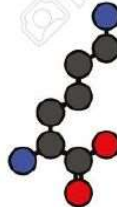
L-asparagine (Asn, N)



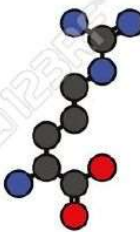
L-glutamic acid (Glu, E)



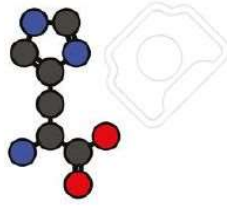
L-glutamine (Gln, Q)



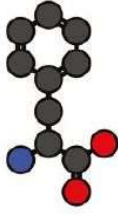
L-lysine (Lys, K)



L-arginine (Arg, R)



L-histidine (His, H)



L-phenylalanine (Phe, F)



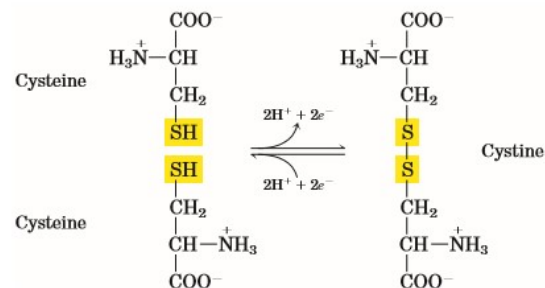
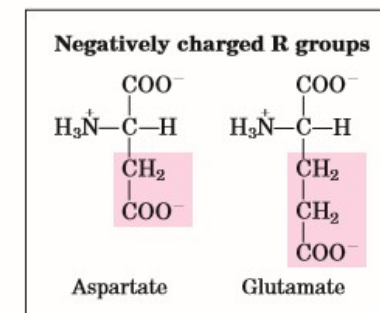
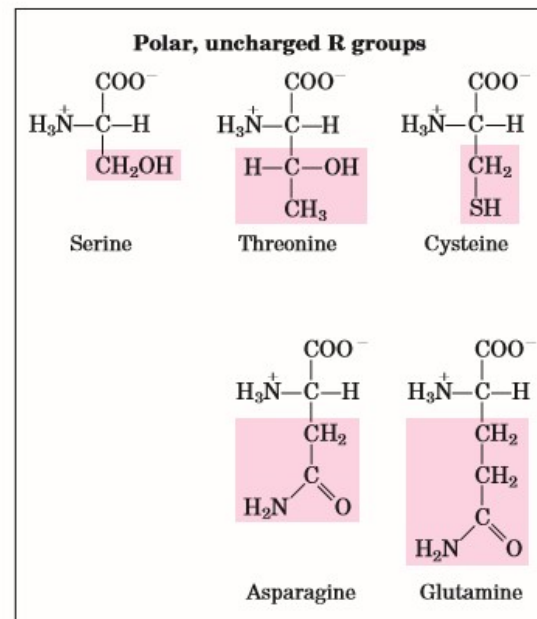
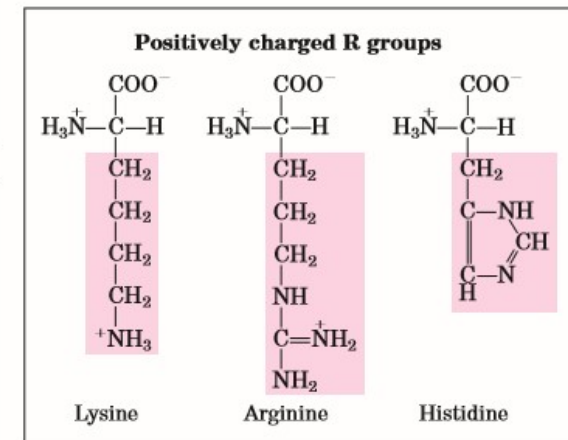
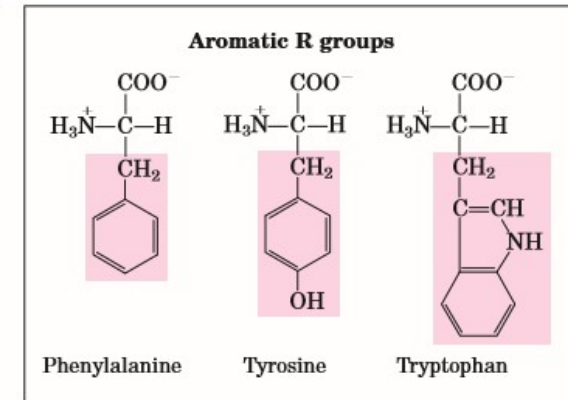
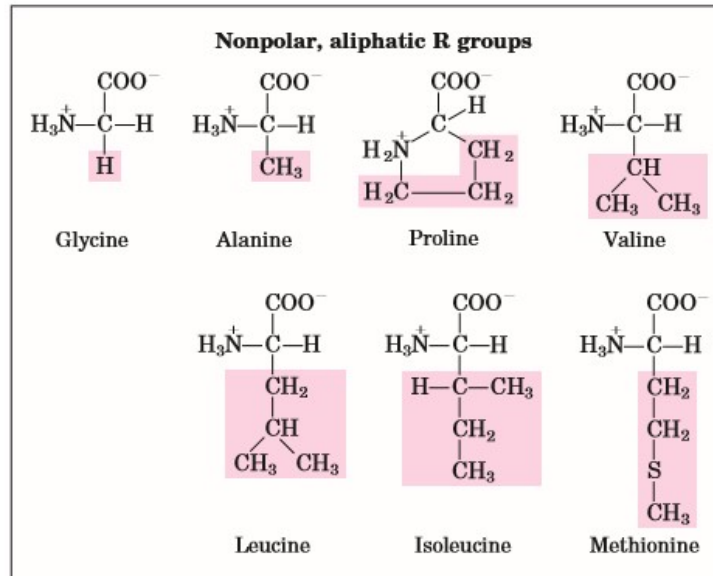
L-tyrosine (Tyr, Y)



L-tryptophan (Trp, W)

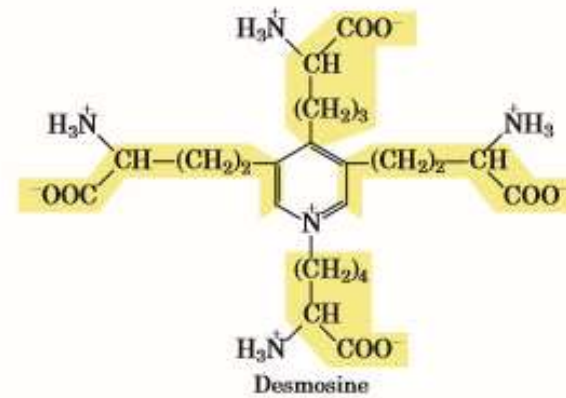
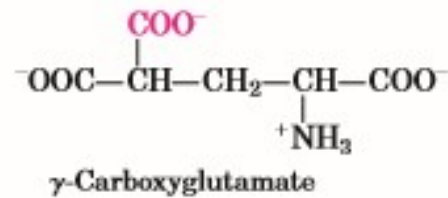
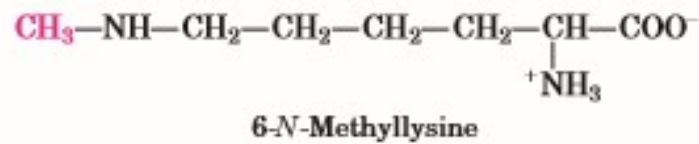
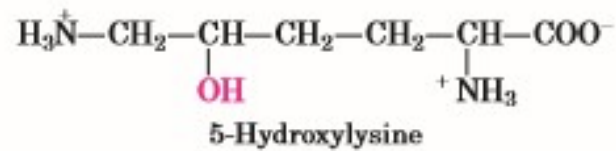
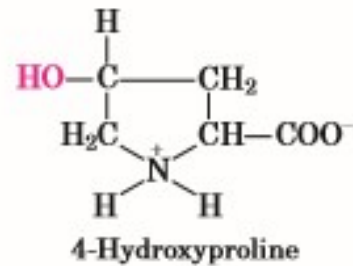
AA differ in:

1. Charge/polarity
2. Shape
3. Volume
4. Aromacy
5. Specific chemistry

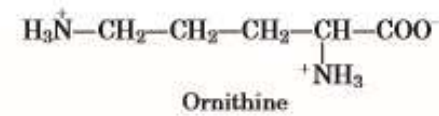
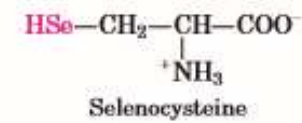


Amino acid	Abbreviation/ symbol	M _r	pK _a values			pI	Hydropathy index*	Occurrence in proteins (%) [†]
			pK ₁ (—COOH)	pK ₂ (—NH ₃ ⁺)	pK _R (R group)			
Nonpolar, aliphatic								
R groups								
Glycine	Gly G	75	2.34	9.60		5.97	−0.4	7.2
Alanine	Ala A	89	2.34	9.69		6.01	1.8	7.8
Proline	Pro P	115	1.99	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

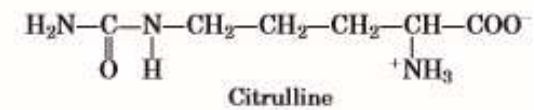
UNCOMMON RESIDUES



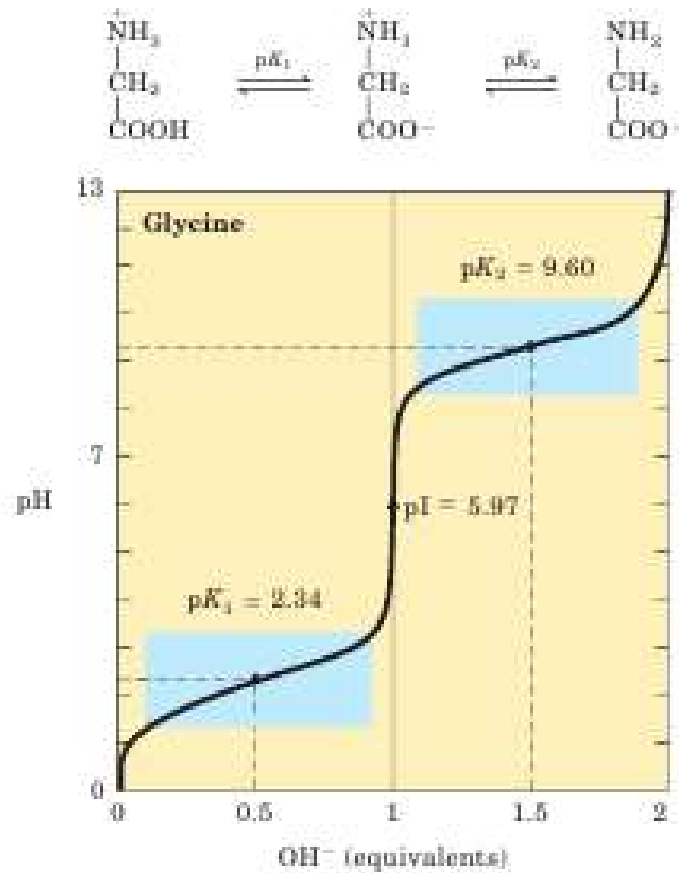
(a)



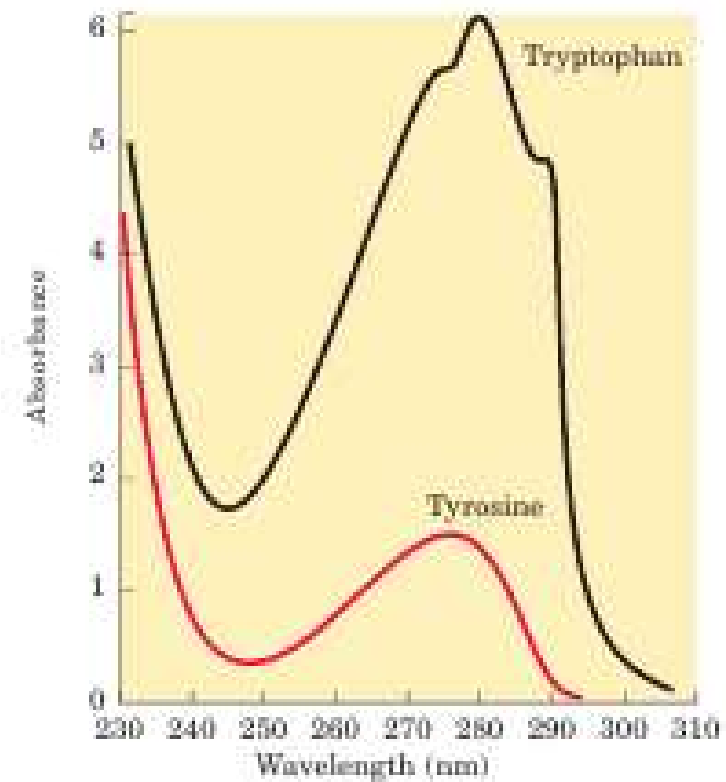
(b)



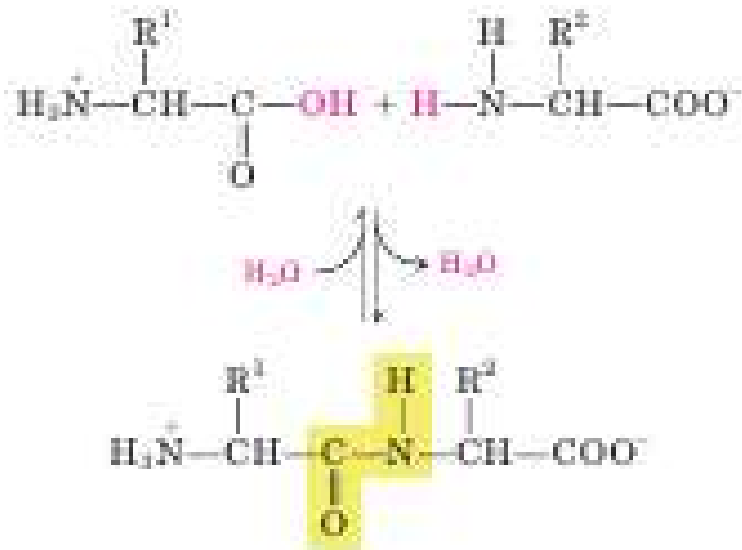
Important physical properties of AA



Titration Curves Predict the Electric Charge of Amino Acids



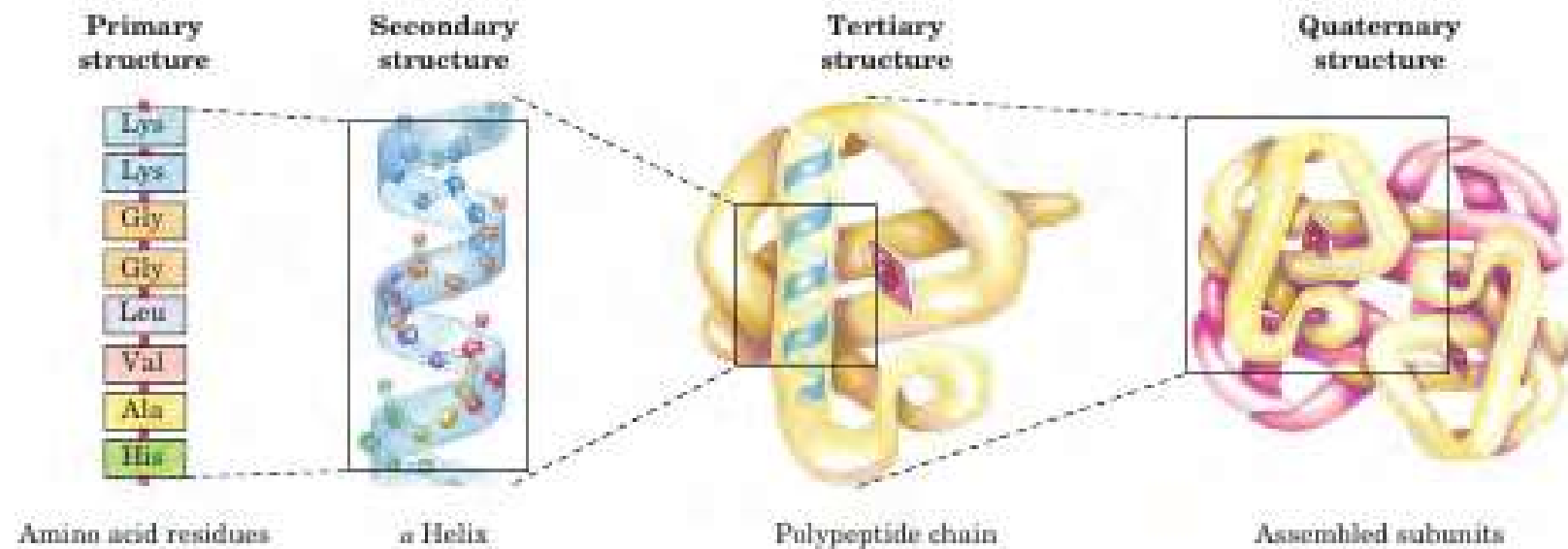
UV absorbance



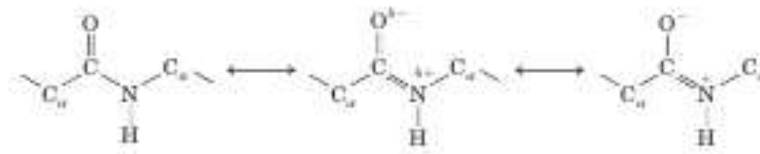
Peptide bond formation, size of the protein

	Molecular weight	Number of residues	Number of polypeptide chains
Cytochrome c (human)	13,000	104	1
Ribonuclease A (bovine pancreas)	13,700	124	1
Lysozyme (chicken egg white)	13,930	129	1
Myoglobin (equine heart)	16,890	153	1
Chymotrypsin (bovine pancreas)	21,600	241	3
Chymotrypsinogen (bovine)	22,000	245	1
Hemoglobin (human)	64,500	574	4
Serum albumin (human)	68,500	609	1
Hexokinase (yeast)	102,000	972	2
RNA polymerase (<i>E. coli</i>)	450,000	4,158	5
Apolipoprotein B (human)	513,000	4,536	1
Glutamine synthetase (<i>E. coli</i>)	619,000	5,628	12
Titin (human)	2,993,000	26,926	1

Levels of protein structure

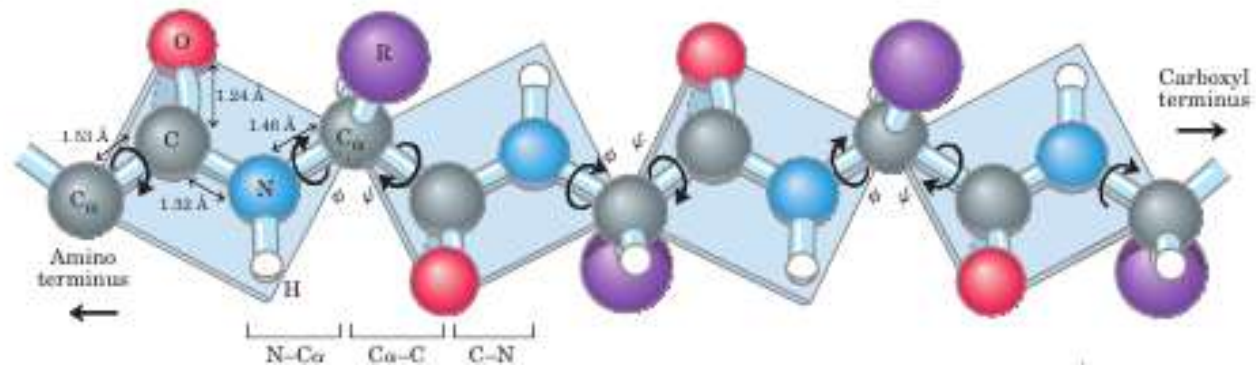


Primary - sequence

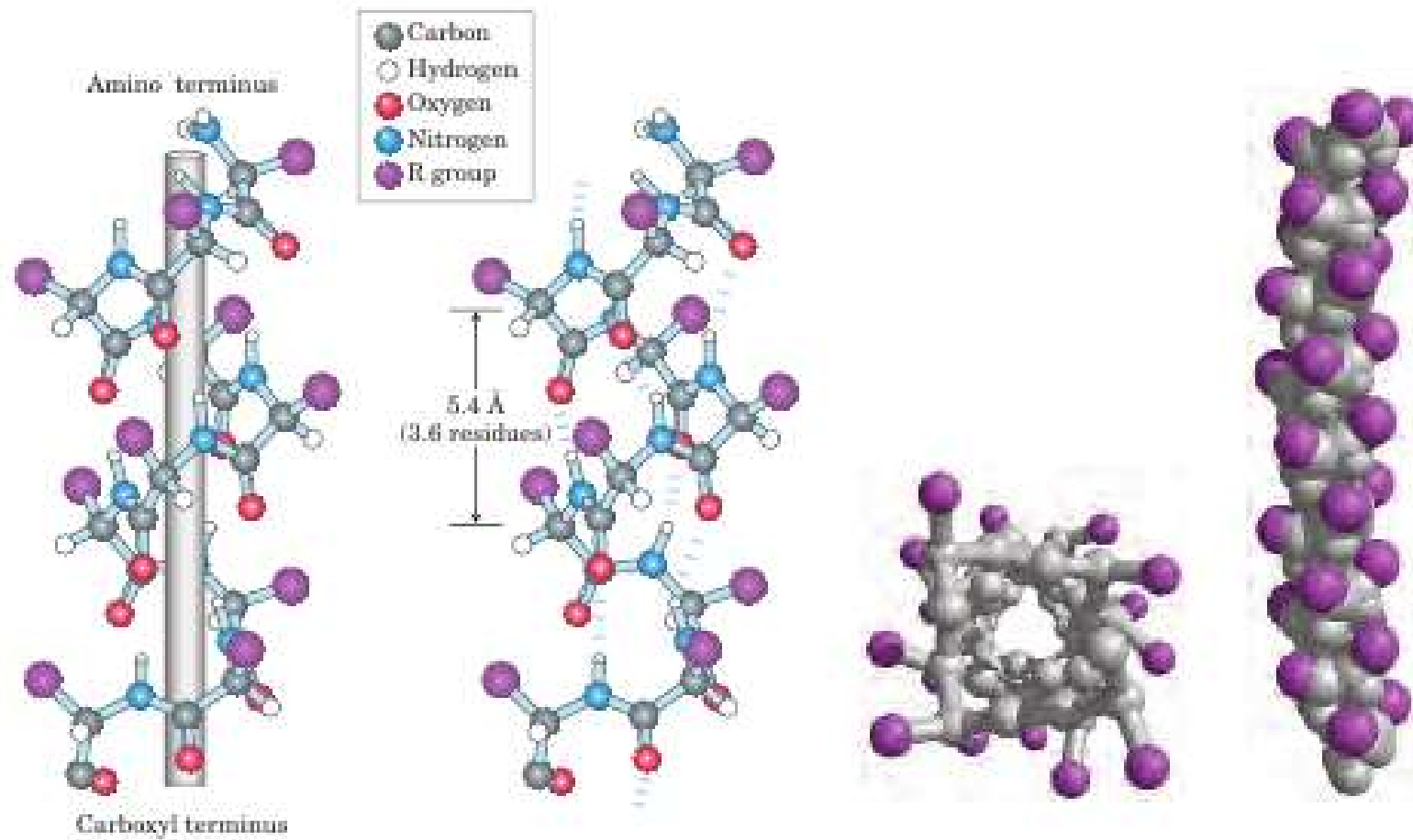


The carbonyl oxygen has a partial negative charge and the amide nitrogen a partial positive charge, setting up a small electric dipole. Virtually all peptide bonds in proteins occur in this trans configuration; an exception is noted in Figure 4-8b.

(a)

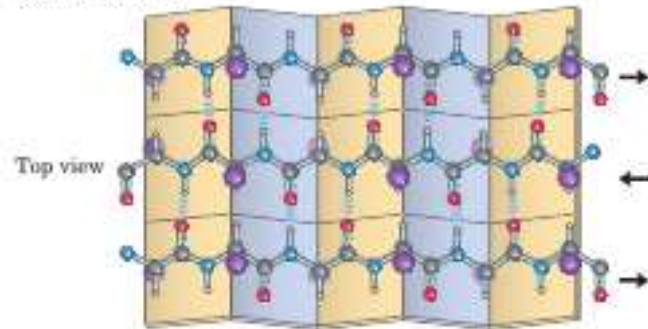


Secondary – a) alpha spiral

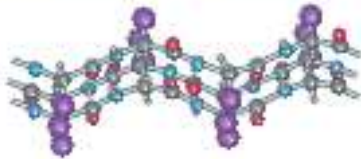


Secondary – b) beta sheets

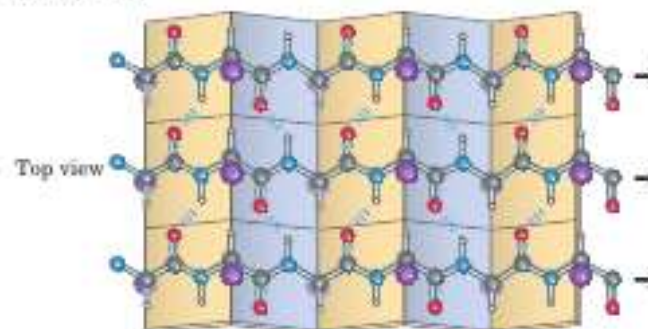
(a) Antiparallel



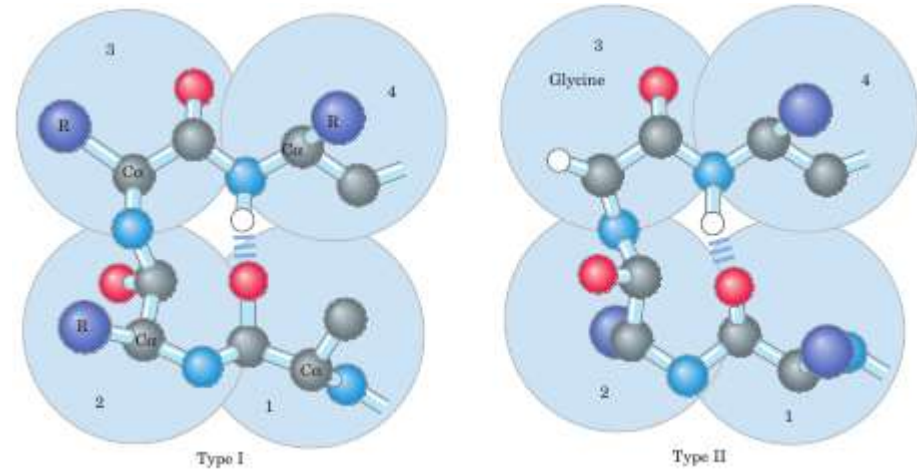
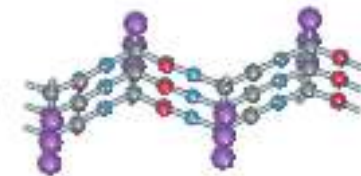
Side view



(b) Parallel

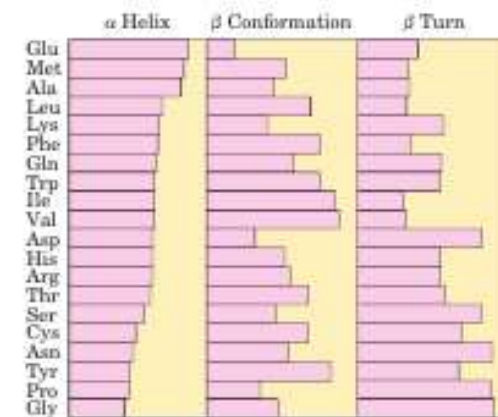
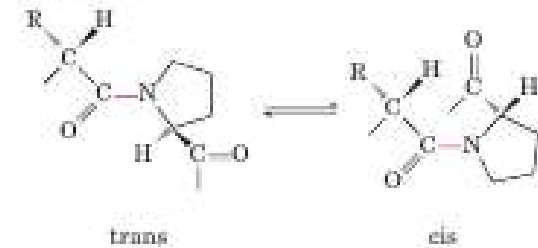


Side view



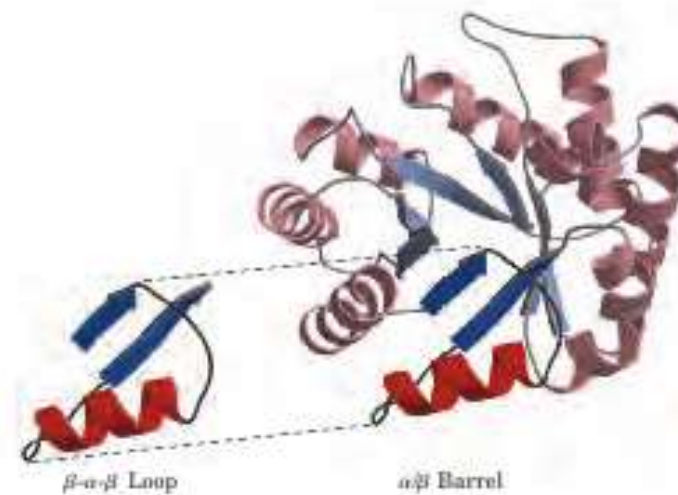
beta sheets turns

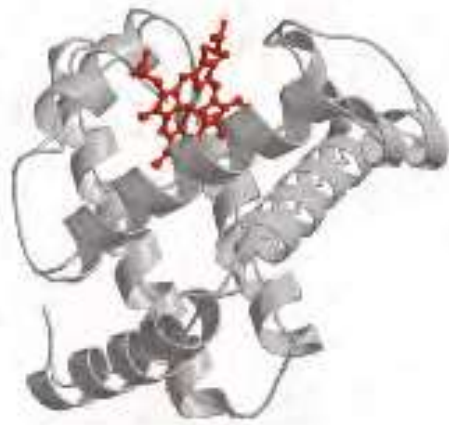
(b) Proline isomers



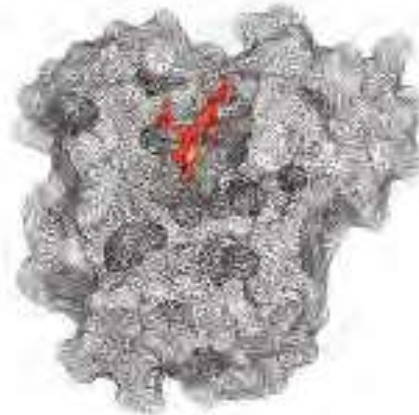
Different folds

FOLD classification

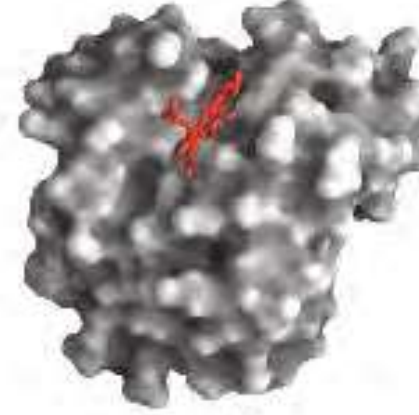




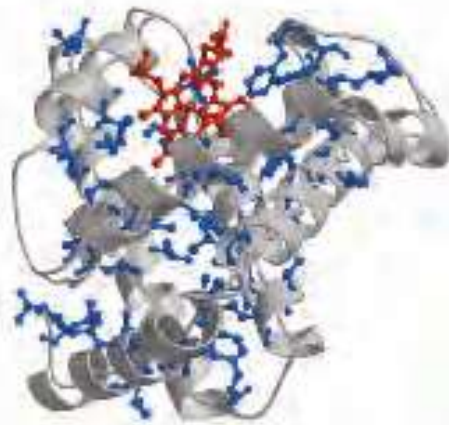
(a)



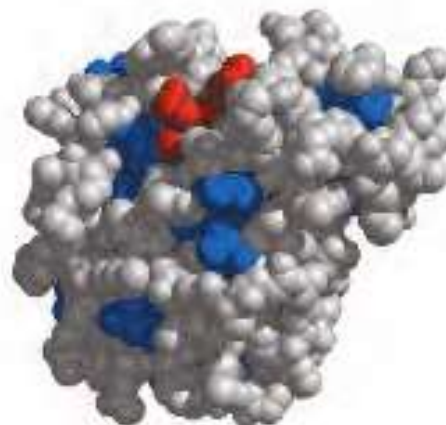
(b)



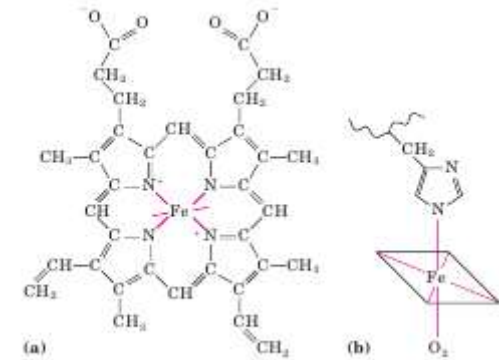
(c)



(d)



(e)



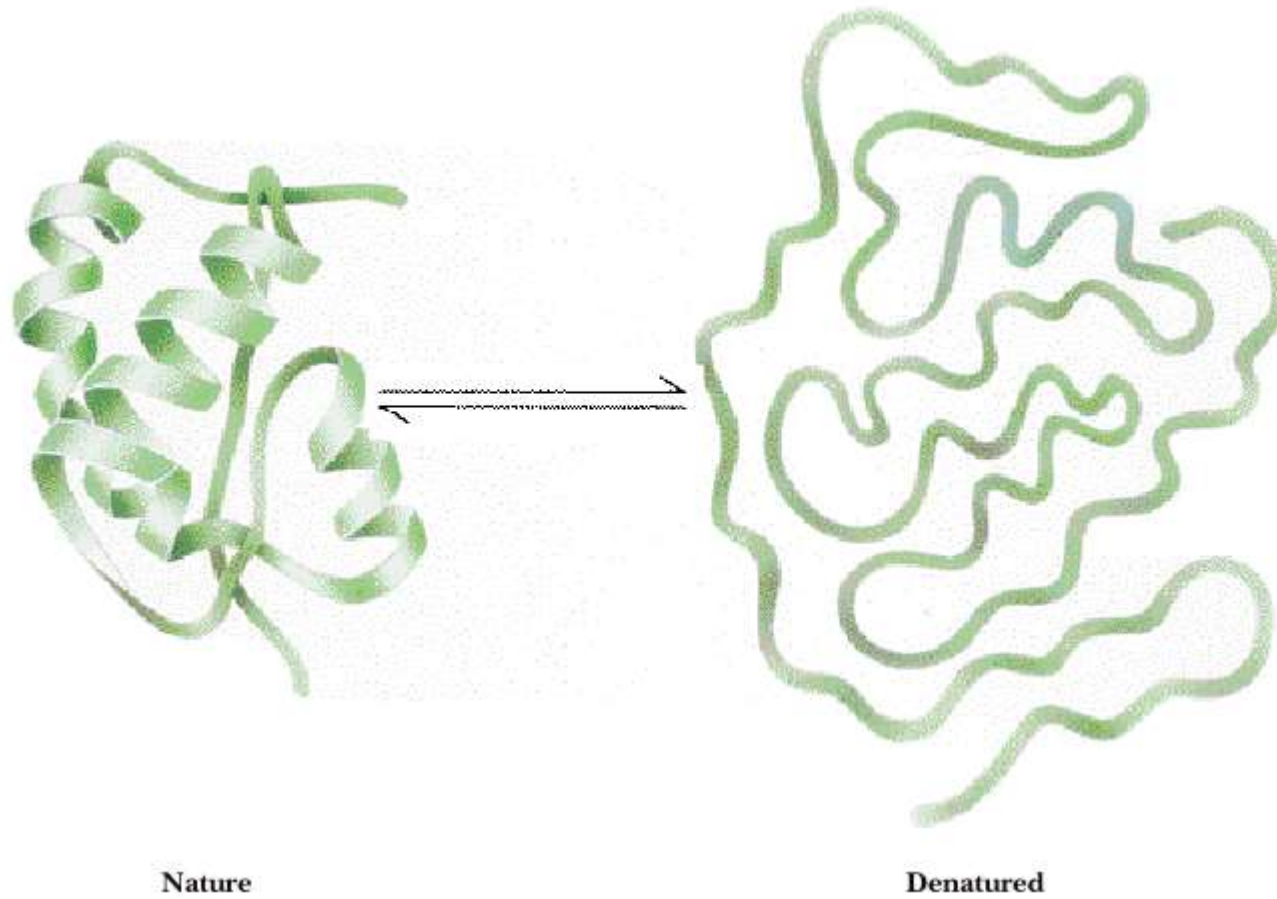
β Conformation
2,000 $\times$ 5 Å

α Helix
900 $\times$ 11 Å

Native globular form
100 $\times$ 60 Å

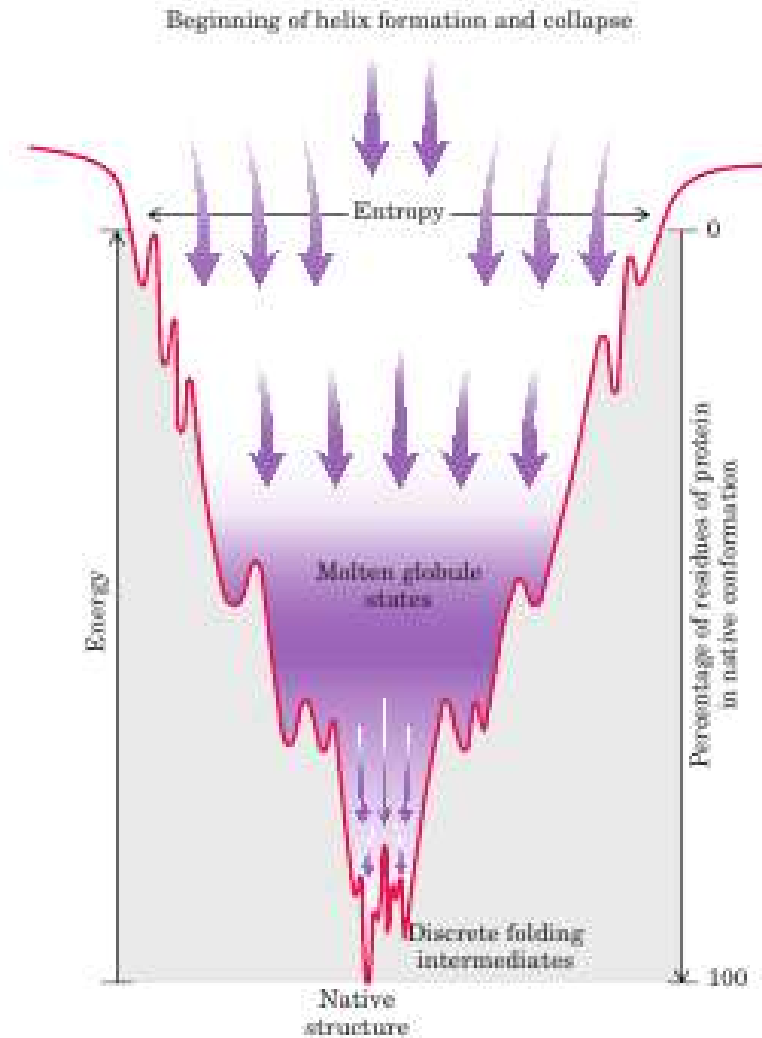
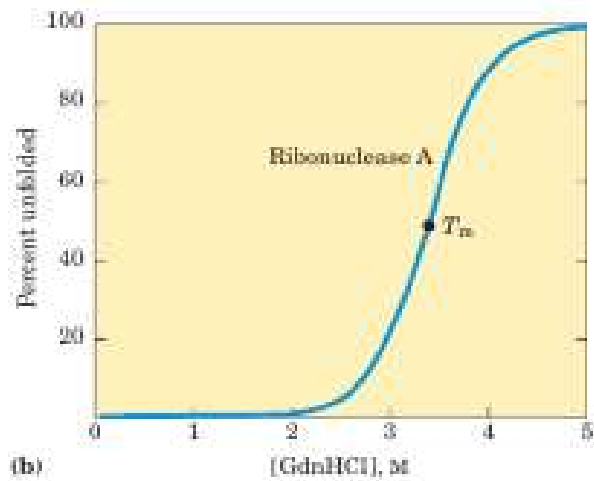
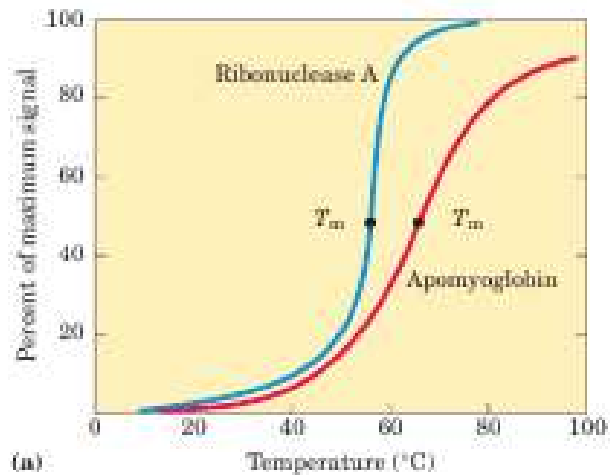
Real globular protein – alpha-beta composition

How solid is protein globule?



Heat // pH // chaotropic agents, denaturants // salt // ...

How solid is protein globule?



Energetic profile

Denaturation - renaturation

Literature biochemistry

1. Lehninger Principles of Biochemistry
(Nelson D.L., Cox M.M.)
2. Principles and Techniques of
Biochemistry and Molecular Biology
(Wilson K., Walker J.)