Protein Structure-function

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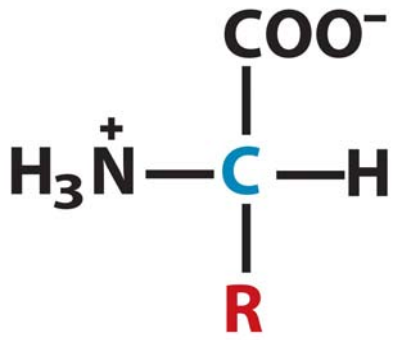
Amino acid



- Chiral center
- Optically active: rotate plane-polarized light
- Amino acid in protein: L stereoisomer

TABLE 3–1 Properties and Conventions Associated with the Common Amino Acids Found in Proteins

Amino acid	Abbreviation/ symbol	M_r	pK_a values: pK_1 (—COOH)	pK_2 ($—NH_3^+$)	pK_R (R group)	pI	Hydropathy index*	Occurrence in proteins (%)†
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

*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 11. From Kyte, J. & Doolittle, R.F. (1982) A simple method for displaying the hydropathic character of a protein. *J. Mol. Biol.* **157,** 105–132.

†Average occurrence in more than 1,150 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.), pp. 599–623, Plenum Press, New York.

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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

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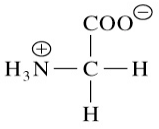
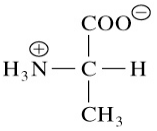
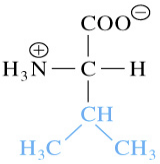
aliphatic amino acid structures



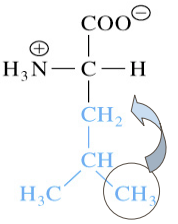
Glycine [G]
(Gly)



Alanine [A]
(Ala)

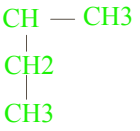


Valine [V]
(Val)



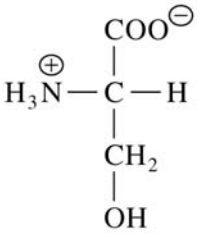
Leucine [L]
(Leu)

Isoleucine (I)
(Ile)

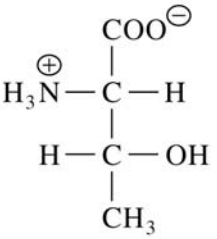


Side Chains with Alcohol Groups

- **Serine** (**Ser**, **S**) and **Threonine** (**Thr**, **T**) have uncharged polar side chains



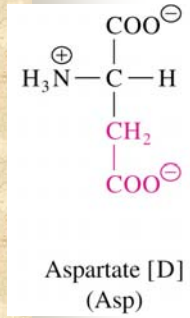
Serine [S]
(Ser)



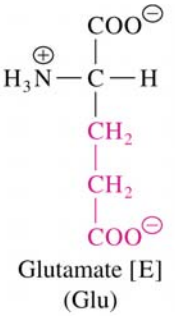
Threonine [T]
(Thr)

Catalytic role, phosphorylation, O-linked glycosylation, hydrogen bond

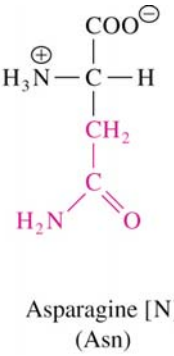
Structures of aspartate, glutamate, asparagine and glutamine



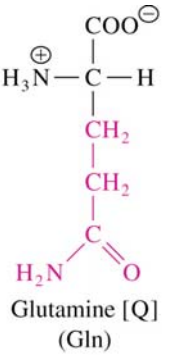
Aspartate [D]
(Asp)



Glutamate [E]
(Glu)



Asparagine [N]
(Asn)



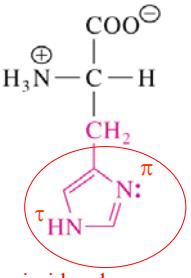
Glutamine [Q]
(Gln)

Charge
Hydrogen bond

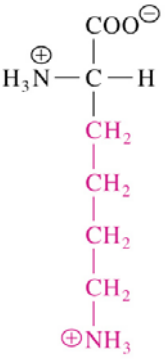
N-linked glycosylation

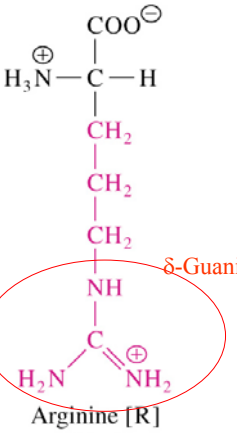
Structures of histidine, lysine and arginine

Charge, H bond



imidazole group





δ-Guanido group

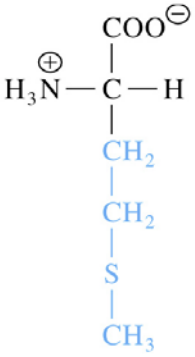
Metal chelating

Histidine [H]
(His)

Lysine [K]
(Lys)

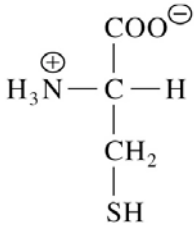
Arginine [R]
(Arg)

Methionine and cysteine



Methionine [M]
(Met)

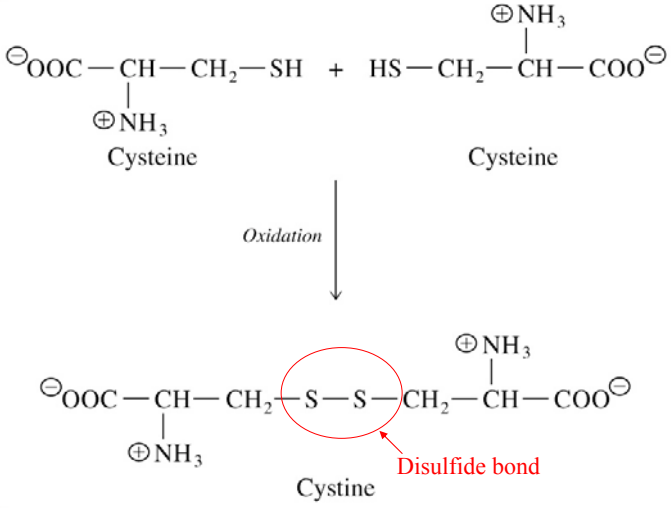
First a.a.



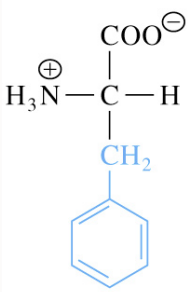
Cysteine [C]
(Cys)

Catalytic role, disulfide bond

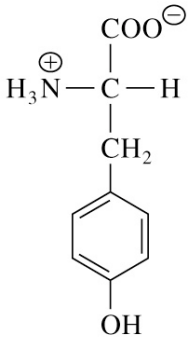
Fig 3.4 Formation of cystine



Aromatic amino acid structures

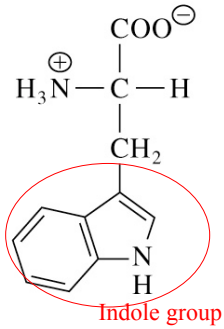


Phenylalanine [F]
(Phe)



Tyrosine [Y]
(Tyr)

phosphorylation



Tryptophan [W]
(Trp)

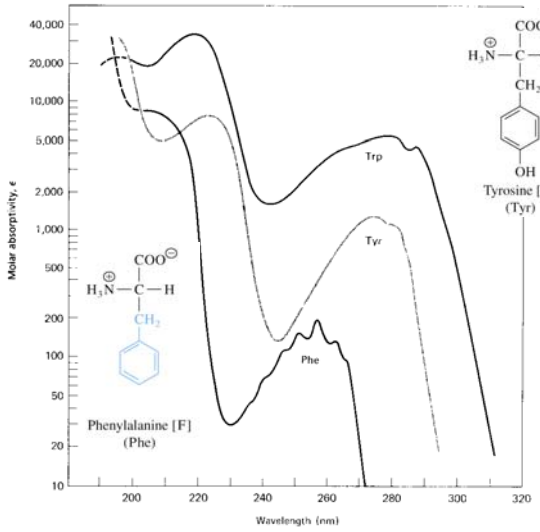
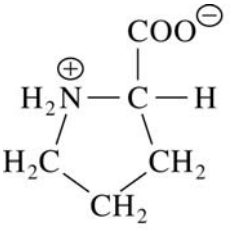


FIGURE 1.4
Ultraviolet absorbance spectra of the aromatic amino acids at pH 6. Incorporation of these amino acids into peptides has little direct effect on the absorbance properties of their side chains, unless they are placed into different environments. (From D. B. Wetlaufer, *Adv. Protein Chem.* 17:303–390, 1962.)

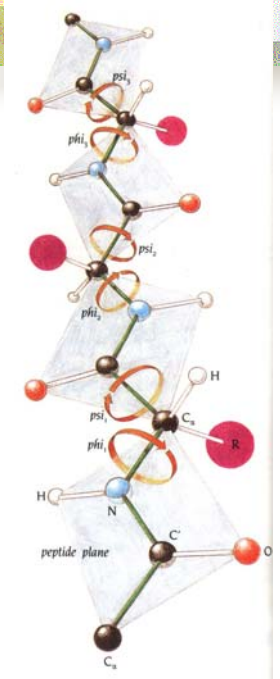
Proline has a nitrogen in the aliphatic ring system

- **Proline** (**Pro**, **P**) - has a three carbon side chain bonded to the α-amino nitrogen
- The heterocyclic pyrrolidine ring restricts the geometry of polypeptides

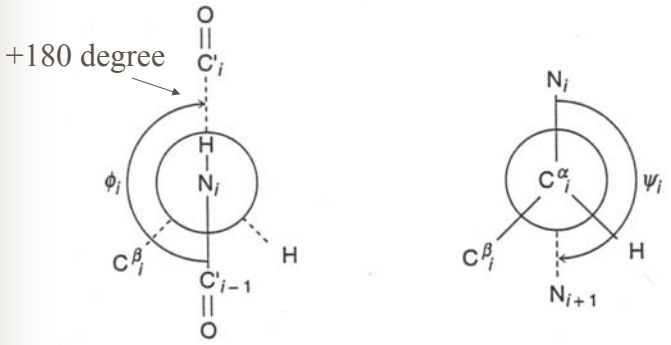
$\phi = -60$



Proline [P]
(Pro)



Newman projections



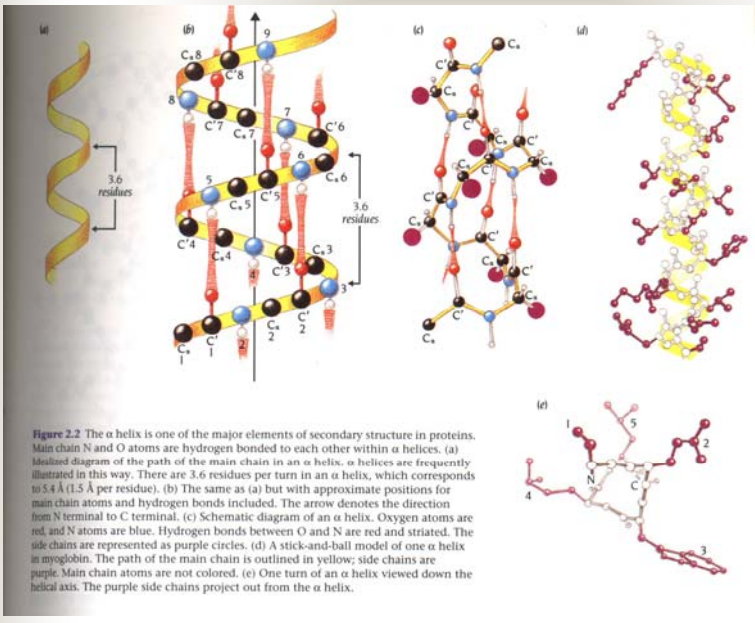
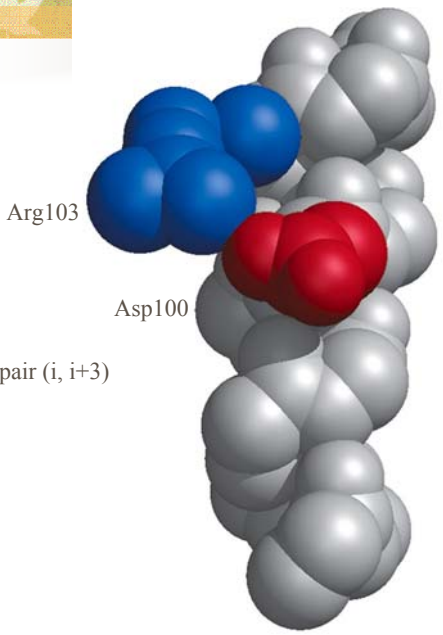
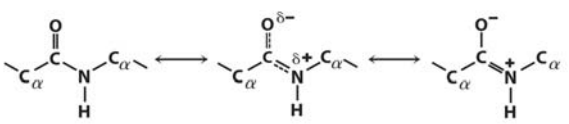
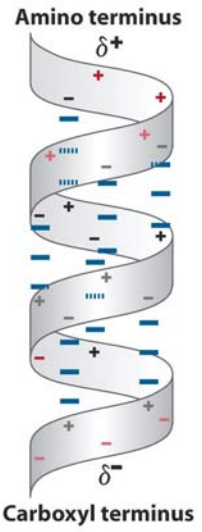


Figure 2.2 The α helix is one of the major elements of secondary structure in proteins. Main chain N and O atoms are hydrogen bonded to each other within α helices. (a) Idealized diagram of the path of the main chain in an α helix. α helices are frequently illustrated in this way. There are 3.6 residues per turn in an α helix, which corresponds to 5.4 Å (1.5 Å per residue). (b) The same as (a) but with approximate positions for main chain atoms and hydrogen bonds included. The arrow denotes the direction from N terminal to C terminal. (c) Schematic diagram of an α helix. Oxygen atoms are red, and N atoms are blue. Hydrogen bonds between O and N are red and striated. The side chains are represented as purple circles. (d) A stick-and-ball model of one α helix in myoglobin. The path of the main chain is outlined in yellow; side chains are purple. Main chain atoms are not colored. (e) One turn of an α helix viewed down the helical axis. The purple side chains project out from the α helix.



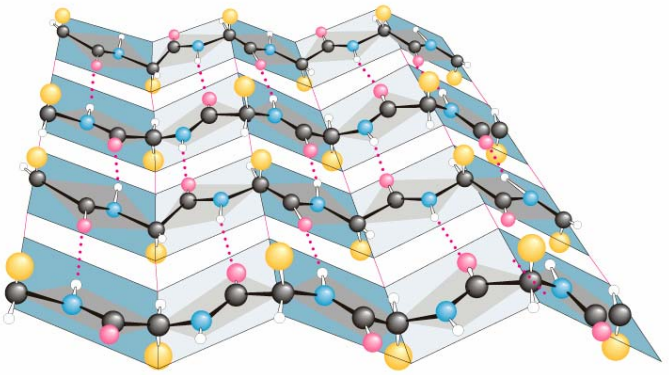


The carbonyl oxygen has a partial negative charge and the amide nitrogen a partial positive charge, setting up a small electric dipole. Virtually all peptide bonds in proteins occur in this trans configuration; an exception is noted in Figure 4–8b.



Antiparallel

Garrett & Grisham: Biochemistry, 2/e
Figure 6.10



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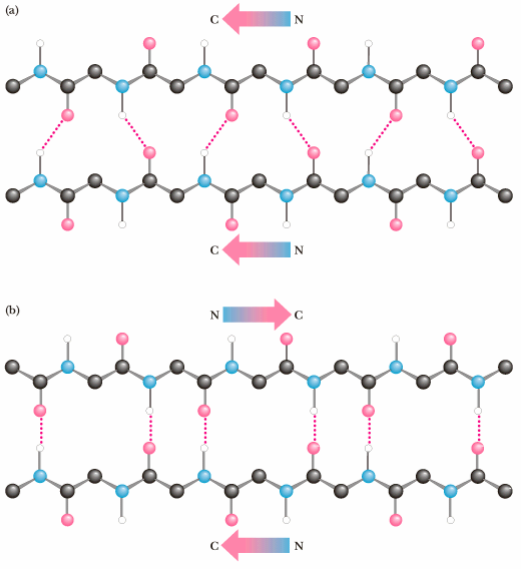
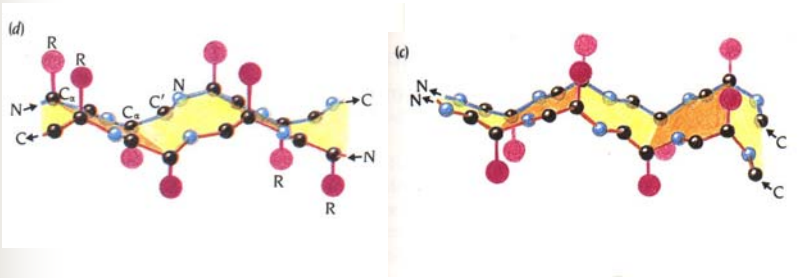


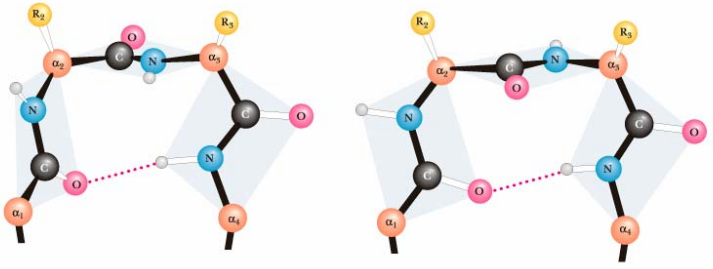
Antiparallel β-strand

Parallel β-strand



Hydrogen bond between i, i+3

Garrett & Grisham: Biochemistry, 2/e
Figure 6.12



Type I turn

Type II turn

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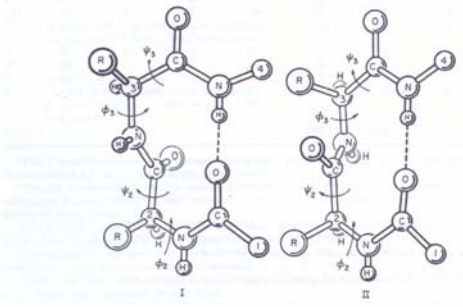
Chou and Fasman (1977)
JMB, 115, 135-175



Classification of bend types according to the dihedral angles of the two central residues[a] of β-turns and their frequency of occurrence in 26 proteins[b]

Bend type[c]	ϕ_2 (°)	ψ_2 (°)	ϕ_3 (°)	ψ_3 (°)	No. of ideal bends[d]	No. of non-ideal bends[e]	Total no. of bends	No. of H-bonded bends[f]
I	−60	−30	−90	0	130	46	176	99
I′	60	30	90	0	8	5	13	10
II	−60	120	80	0	41	23	64	43
II′	60	−120	−80	0	15	5	20	16
III	−60	−30	−60	−30	66	11	77	45
III′	60	30	60	30	11	2	13	7
IV	A bend with 2 or more angles differing by at least 40° from those given above				0	35	35	5
V	−80	80	80	−80	1	2	3	0
V′	80	−80	−80	80	0	4	4	2
VI	A *cis* Pro at position 3				8	0	8	6
VII	A kink in the protein chain created by $\phi_2 \approx 180°$ and $\lvert\phi_3\rvert < 60°$ or $\lvert\psi_2\rvert < 60°$ and $\phi_3 \approx 180°$				8	0	8	1
Total					288	133	421	234

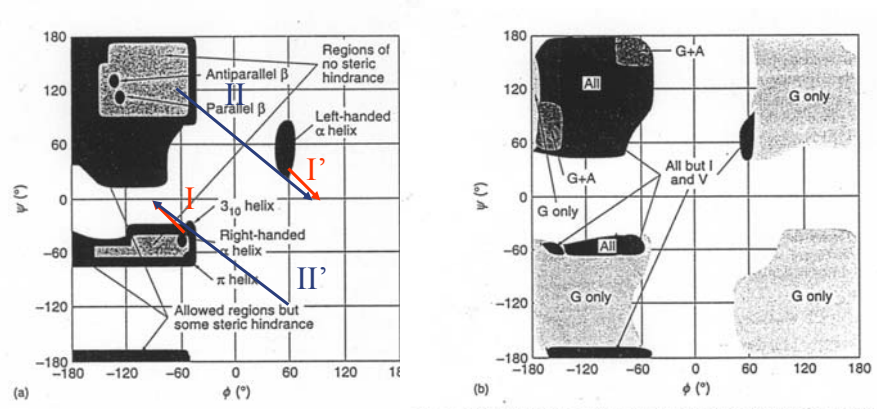
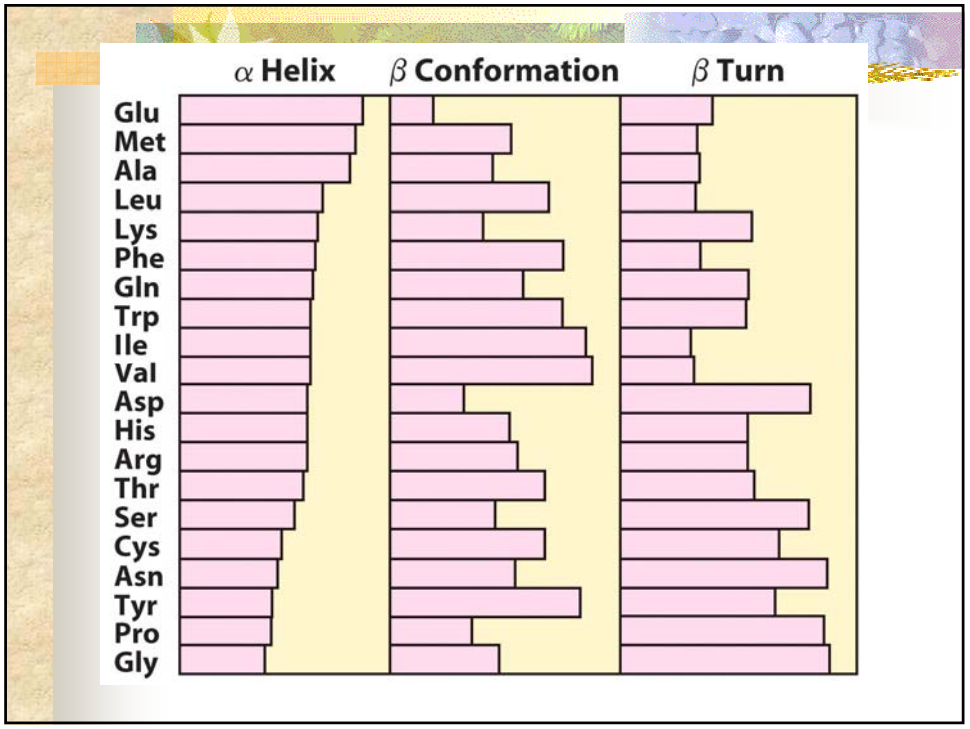
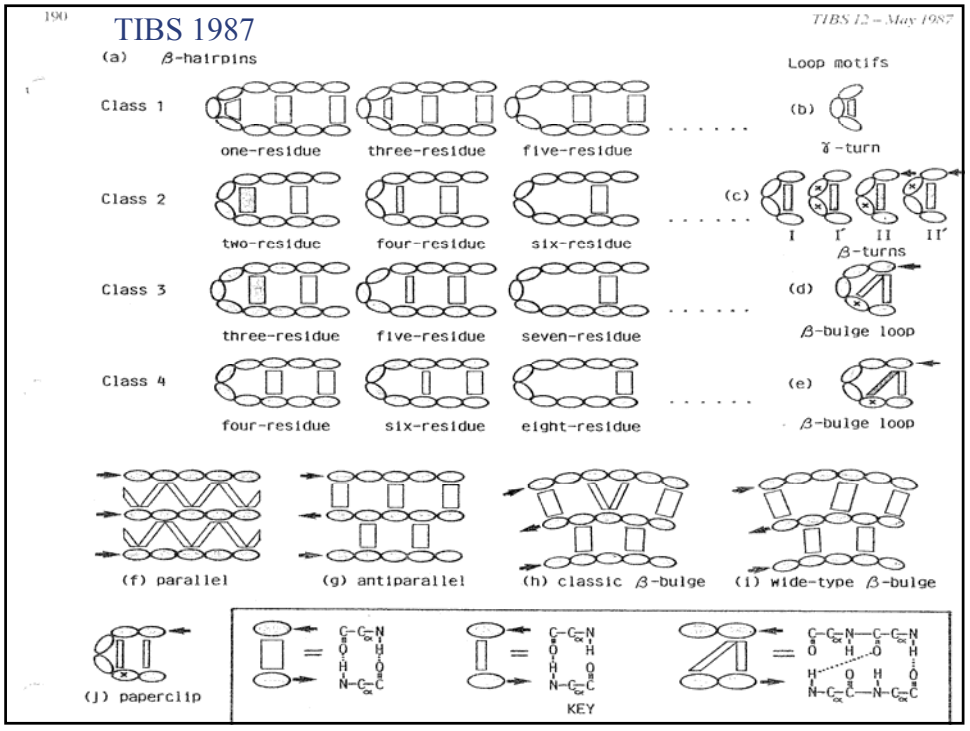


Figure 1.11 Ramachandran diagrams illustrating the preferred conformations of the polypeptide chain. (a) The allowed regions and their relationship to different types of secondary structure. (b) The different conformational restrictions for the different amino acids. Note the high conformational freedom for glycine (G) and the restrictions on isoleucine (I) and valine (V).


α Helix
β Conformation
β Turn
Glu
Met
Ala
Leu
Lys
Phe
Gln
Trp
Ile
Val
Asp
His
Arg
Thr
Ser
Cys
Asn
Tyr
Pro
Gly

TIBS 1987


190
TIBS 12 – May 1987
(a) β-hairpins
Loop motifs
Class 1
one-residue
three-residue
five-residue
(b)
γ-turn
Class 2
two-residue
four-residue
six-residue
(c)
I
I′
II
II′
β-turns
Class 3
three-residue
five-residue
seven-residue
(d)
β-bulge loop
Class 4
four-residue
six-residue
eight-residue
(e)
β-bulge loop
(f) parallel
(g) antiparallel
(h) classic β-bulge
(i) wide-type β-bulge
(j) paperclip
KEY

JMB (1989)206, 759-77

Table 1

Classification of β-hairpin structures

A. Summary of proposed classification for modelling