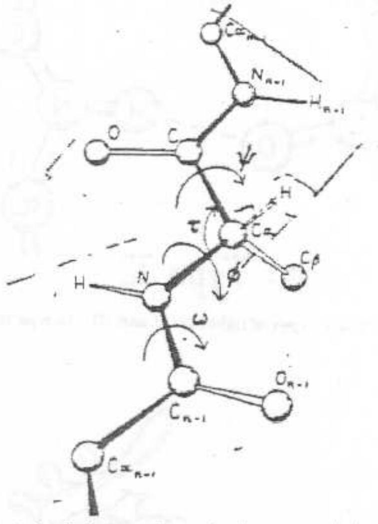


FIG 5 A key to standard nomenclature for the atoms and the more important bond angles and dihedral angles along the polypeptide backbone. Atoms of the central residue are without subscripts.

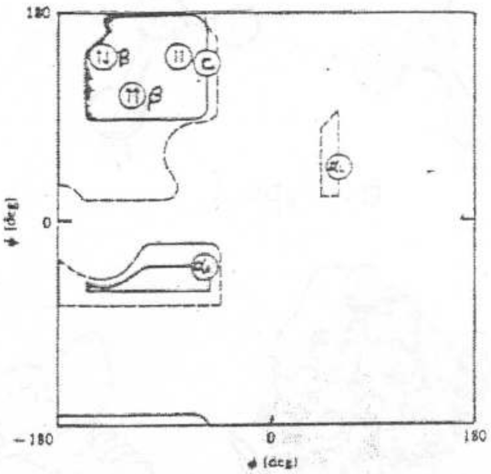


Figure 5-4

Steric contour diagram for an L-alanyl residue in a polypeptide chain. Dark zones show "normal" and light zones show "outer-limit" contours. Coordinates of right- and left-handed α helices (α), parallel (↑↑) and antiparallel (↑↓) pleated sheets, polyglycine II (II), and collagen (C) are denoted (see also Table 5-2). [After P. J. Flory, *Statistical Mechanics of Chain Molecules* (New York: Interscience, 1969); and G. N. Ramachandran et al., *J. Mol. Biol.* 7 95 (1963).]

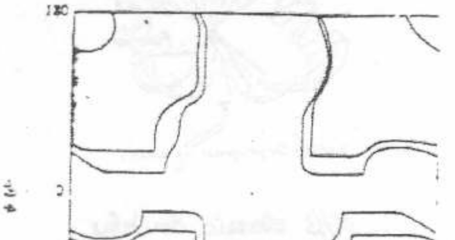
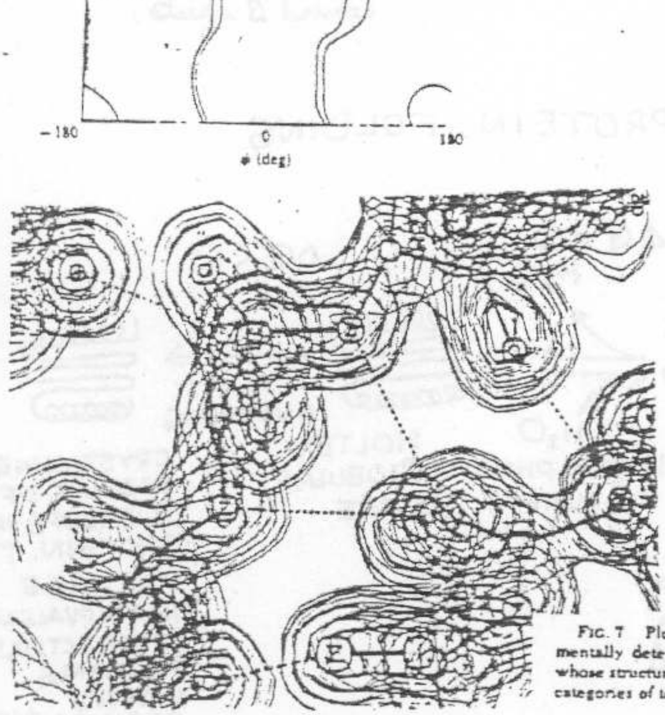


Figure 5-3

Steric contour diagram for a glycyl residue in a polypeptide chain. Dark zones show "normal" and light zones show "outer-limit" contours. [After G. N. Ramachandran et al., *Biophys. J.* 6 849 (1966).]



1000 non-glycine residues (hi resolution struct.)

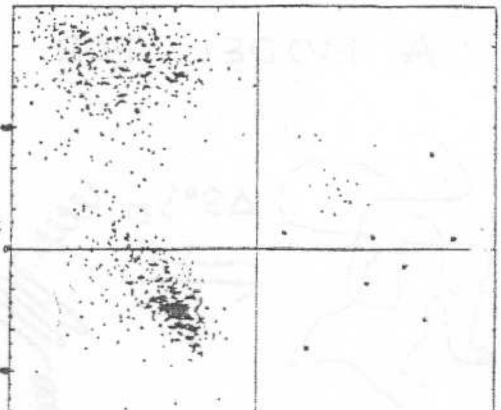
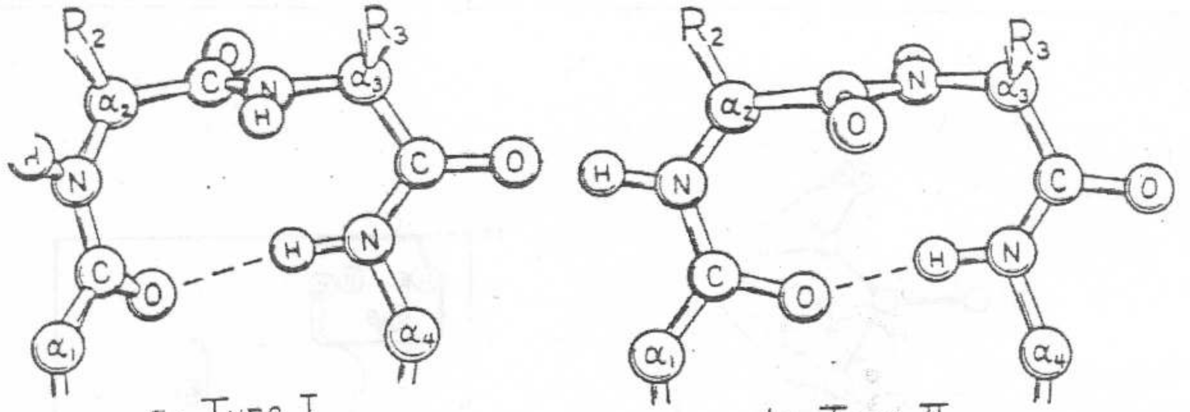


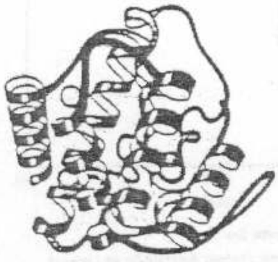
FIG. 7 Plot of main chain dihedral angles ϕ and ψ (see Fig 5 for det[illegible] mentally determined for approximately 1000 nonglycine residues in [illegible] whose structures have been refined at high resolution (chosen to be rep[illegible] categories of tertiary structure)



a: Type I

b: Type II

FIG. 30. The two major types of tight turn (I and II). In type II (bottom), R_3 is generally glycine.



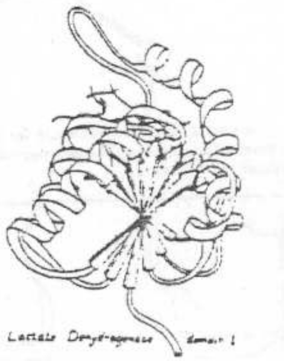
Thermolysin domain 2

ALL HELICAL

JANE RICHARDSON
ADVANCES IN PROTEIN
CHEMISTRY 34: 168-339
QD431-A1A2 1981

Triose Phosphate Isomerase

α/β Singly wound
parallel β Barrels.



Lactate Dehydrogenase domain 1

α/β classic doubly
wound β sheets

A MODEL FOR PROTEIN FOLDING