

①

(b)

three letter code

Non polar, Hydrophobic

Polar unchanged

Polar, uncharged

Positively charged



2

Ser-Ala-Val-Glu-Met-Glu-Gly-Ala-Met-Thr-Arg-Pro-Pro-Glu-Asp-Gly-Asn-Ala-Gly-Glu-Asn-Glu

2

3

PN - HS - HM - PM - HL - PM - HM - HS - HL - PN - PP -
_S _A _V _E _M _E _I _A _M _T _R

HS - HS - HS - PM - PM - HM - PN - HS - ~~HS~~ - HS - PM - PN - PM
A P P E D I N A G E N E

③ Helical Parameter for different types of helices.

compact

Parameters are -

n = no. of residue per turn

p = rise in angstrom per turn

$d = p/n$ = rise in angstrom per residue.

Type of Helix	n	p	d	ϕ	ψ	H-bond
2.2						
3_{10} helix	3	6.0	2 \AA	-49	-26	$n+3$
3.6_{13} helix (α -helix)	3.6	5.4	1.5 \AA	-57	-47	$n+4$
4.4_{16} helix π helix	4.4	5.2	1.18 \AA	-57	-70	$n+5$

n = no. of amino acid

Stability of helices in terms of H-bond :-

3_{10} helix $>$ α helix (3.6_{13}) $>$ π helix (4.4_{16})

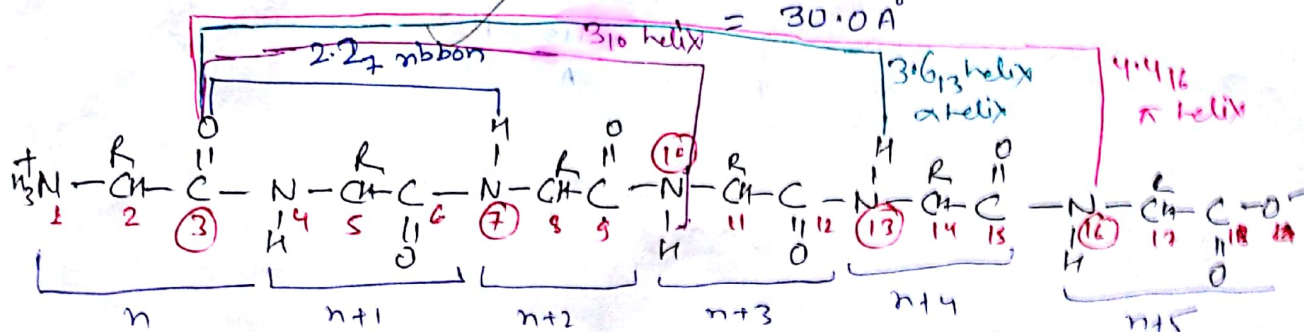
(b)

\Rightarrow length of 20 residue long polypeptide chain, if it is an alpha helical conformation.

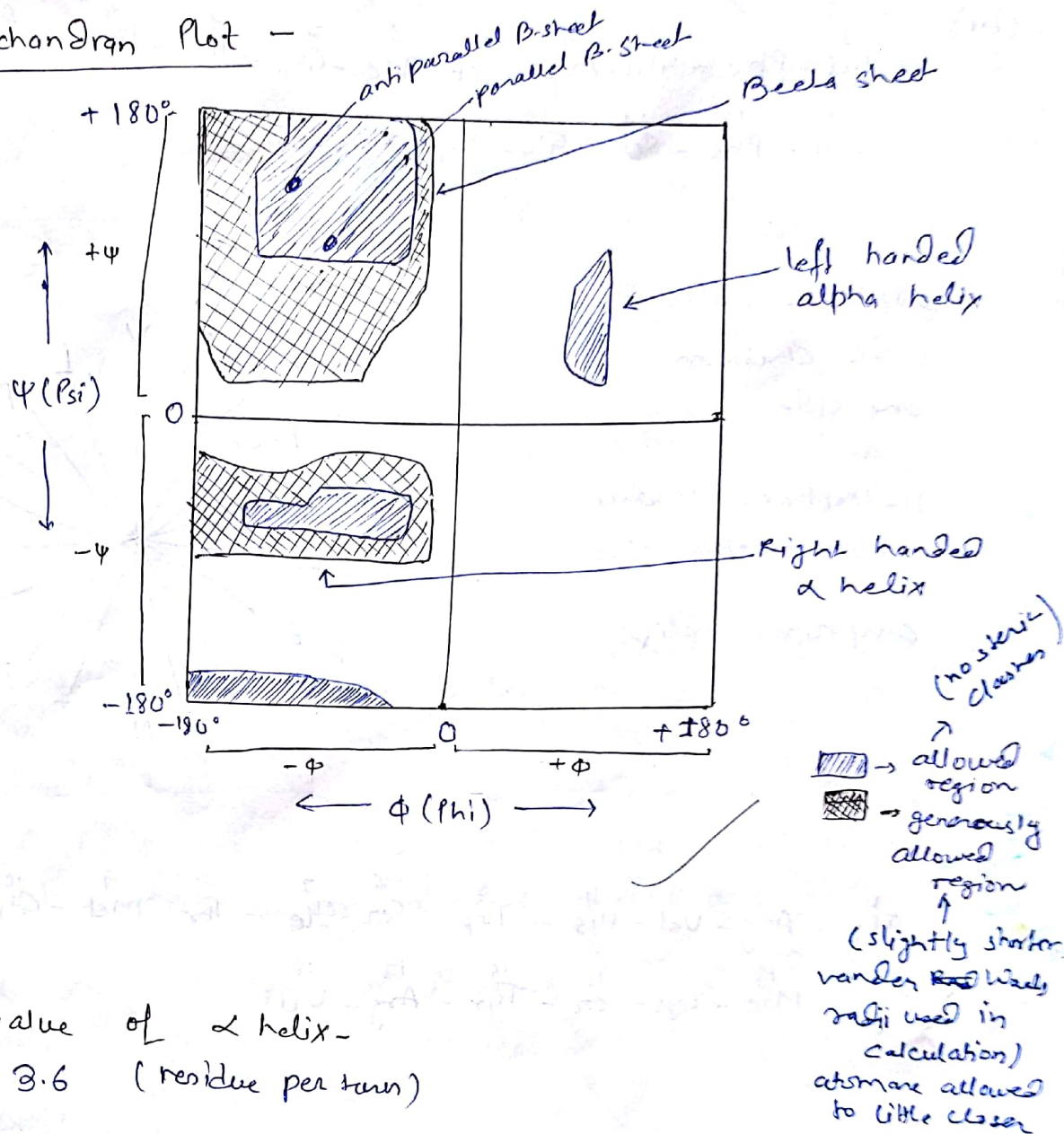
length of one residue in α -helix conformation = 1.5 \AA
(or rise in \AA / residue)

\therefore 20 residue, length is = $20 \times 1.5 \text{ \AA}$

= 30.0 \AA



Ramachandran Plot -



(c)

(i) n value of α helix -
3.6 (residue per turn)

(ii) angle b/w two 'spokes' corresponding to the consecutive residue

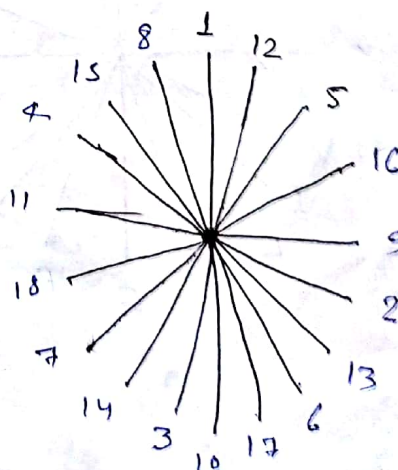
no of residue per turn = 3.6

for 3.6 residue $\rightarrow 360^\circ$

$$L \rightarrow \frac{360}{3.6} = 100^\circ$$

angle b/w ~~base~~ residue = 180°
total residue = 18, 360°

$$\text{angle b/w two spoke} = \frac{360}{18} = 20^\circ$$



H → Hydrophobic
P → Polar

Val¹ - Phe² - Glu³ - Arg⁴ - Met⁵ - Ile⁶ - Glu⁷ - Thr⁸ - Leu⁹ - Asn¹⁰ - Arg¹¹ -
Leu¹² - Phe¹³ - Ser¹⁴ - Glu¹⁵ - Trp¹⁶ - Ile¹⁷ - Ser¹⁸

Polar

Hydrophobic

H

H

L

H

W

L

F

L

I

H

I

H

P

P

H

P

E

S

P

E

P

S

R

R

P

E

P

T

V

1-12, 8, 16, 9, 2, 13,
6, 17, 10, 3, 14, 7, 18,
11, 4, 15, 5

[illegible]

(a)

Proline 1 - Cis

Proline 2 - Trans

Proline 3 - Trans

Proline 4 - Cis γ trans

Proline 5 - Cis γ trans

(0.5)

- (b) β -sheets are the secondary structure of protein. In sheet (β) strand of protein lie adjacent to one another, interacting via H-bond between backbone carbonyl oxygen and amino hydrogen atom. It is short (5-8 residue) and side chains point in alternate opposite directions for adjacent residue in chain.

There are two types of β sheets:-

Parallel and Anti parallel β sheets.

(2)

→ Parallel β -sheet -

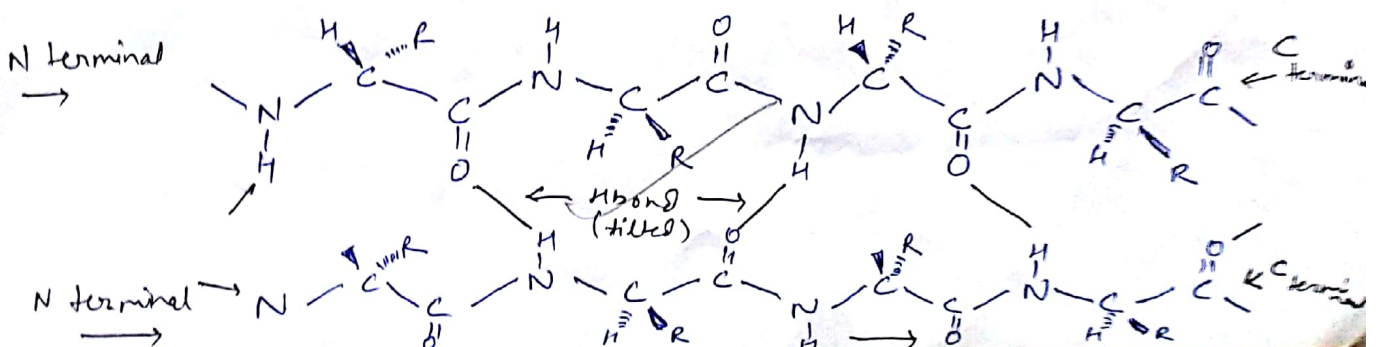
→ N terminus of both strand are same in direction

→ $\phi = 119^\circ$, $\psi = +113^\circ$

→ Slightly bent H bond

→ Repetitive period for parallel β sheet is 6.5 \AA

→ large str, composed of 10-15 strands are rare



→ In parallel β -sheet the strands consist of hydrophobic residues on both sides of the sheet (from Biochemistry by G. F. Minns)

⇒ Antiparallel β -sheet :-

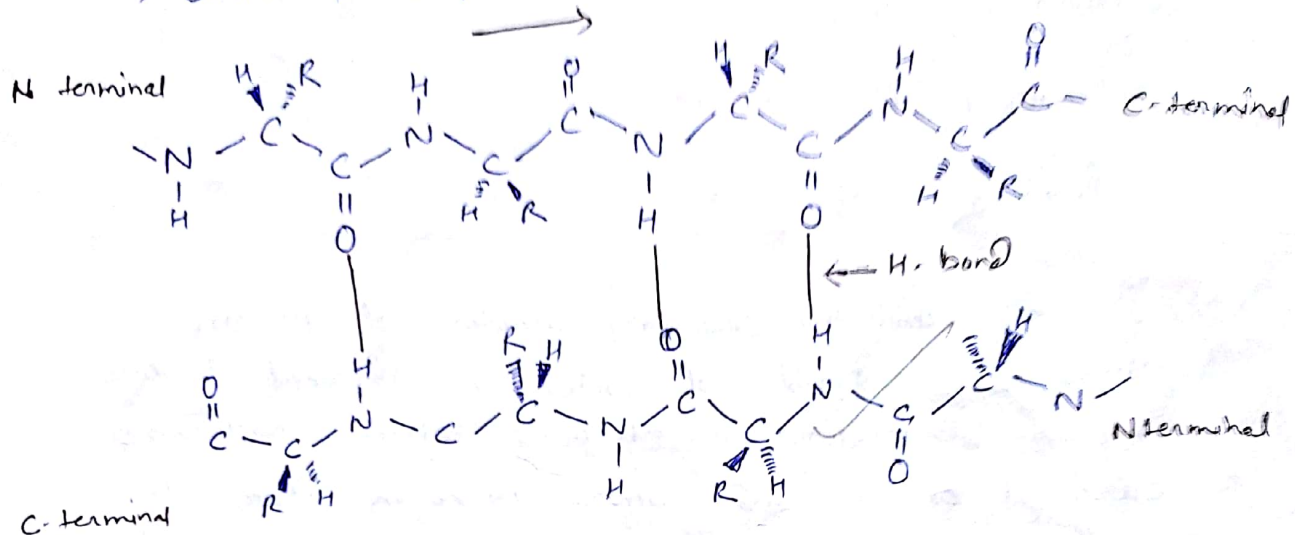
→ N terminal of both strands are opposite to each other in direction

→ $\phi = 139^\circ$, $\psi = +135^\circ$

→ Linear H-bond

→ Repetitive period 7.0 \AA .

→ Consist of as few as two strands



→ Antiparallel sheets are usually arranged with all their hydrophobic residues on one side of the sheet

⇒ Antiparallel sheets form stabler hydrogen bond.

It allows intra-hydrogen bonding b/w oxygen of carbonyl carbon and hydrogen of amines which are straight or planar.

→ H-bond is perpendicular to the strand and narrowly spaced bond pairs alternate with widely spaced pairs.

Amino acids classification — hydrophobic & or polar and surface or buried.

Correlation between these two classification.

In the aqueous environment, the hydrophobic residue (GAV L I M F W P) tend to be buried in the interior and polar side chains exposed to solvent.

This is due to hydrophobic effect which is major driving force for the folding of globular proteins. Hydrophobic side chains are located ~~are~~ predominantly in the interior of protein, they ~~are~~ buried, tend to be buried (away from the solvent, having nonpolar side chain) and polar side chains are located at the surface so that they are exposed to solvent.

②

⑥ Proline is usually classified as a 'surface' amino acid.

Proline is unique that is the only amino acid which has fused ~~ring~~ side chain. i.e., side chain of proline is connected with NH_3^+ of backbone.

Proline has imino group (NH_2 group) instead of NH_3^+ amino group. So because of its fused side chain, it is unable to occupy the many chain conformations which is easily adopted by other amino acid.

It is considered as opposite to Glycine (can adopt more main chain conformations), it is found in tight turns in protein structure.

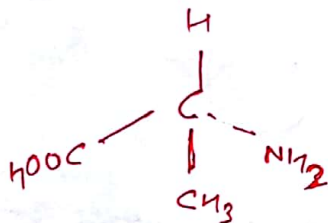
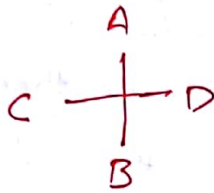
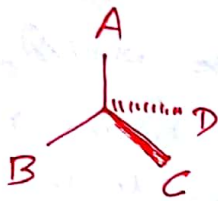
So, since proline is more preference for turn structure ~~rather~~ despite being aliphatic & hydrophobic ~~str~~, ~~more~~ this is usually found on the protein surface.

CORN Rule

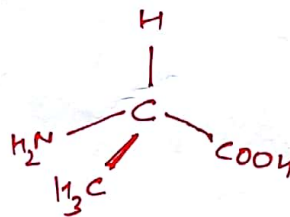
CORN anticlockwise ↺
H above
the plane

COO^- , R, N anticlockwise
 C_α behind plane

COO^- , R, NH_2 & H in clockwise
around the C_α atom.
L-aa.



D-Amino acid



L-Amino acid