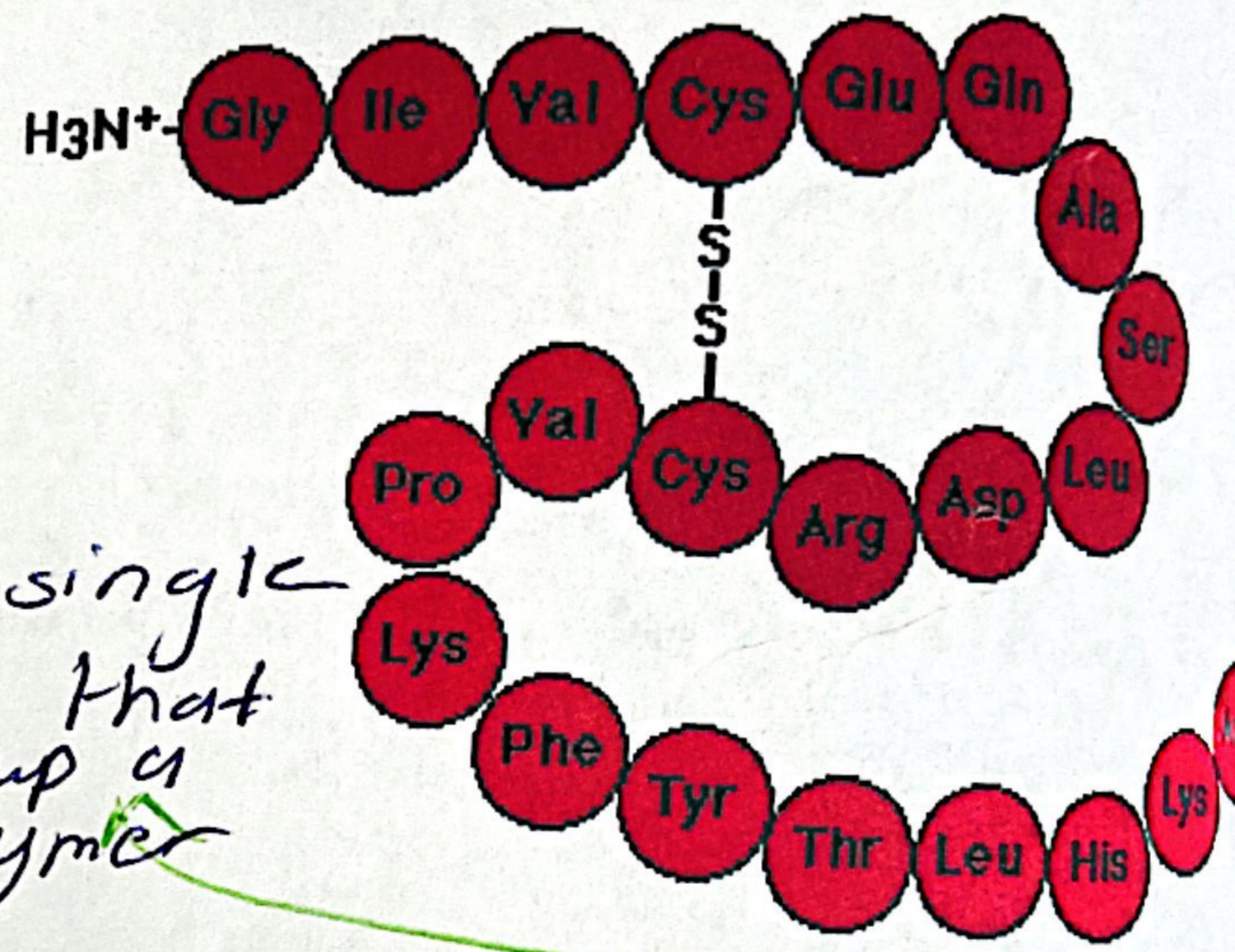


units are multiple polypeptides.

Structure (one dimensional)

ar sequence (order) of
ds from the amino to
end of protein and the
of disulfide (-S-S-)
bonds.

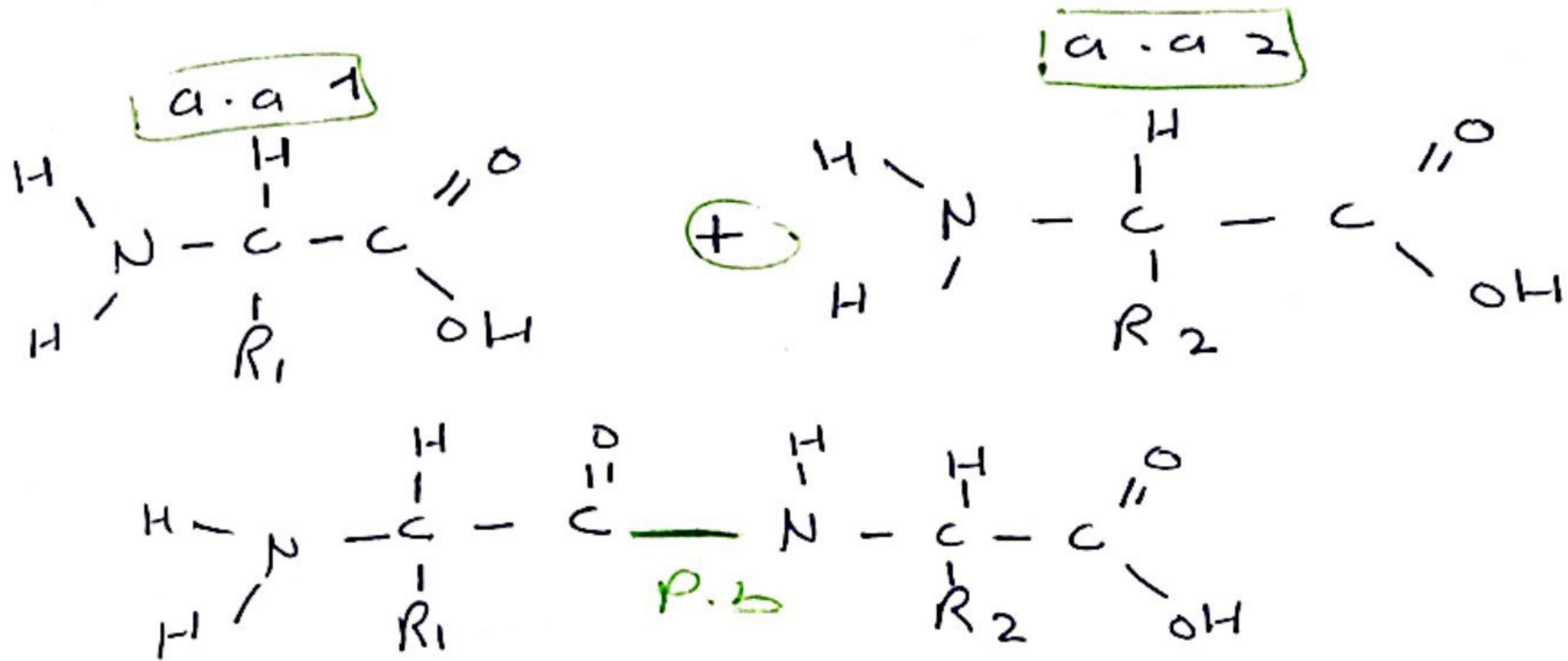
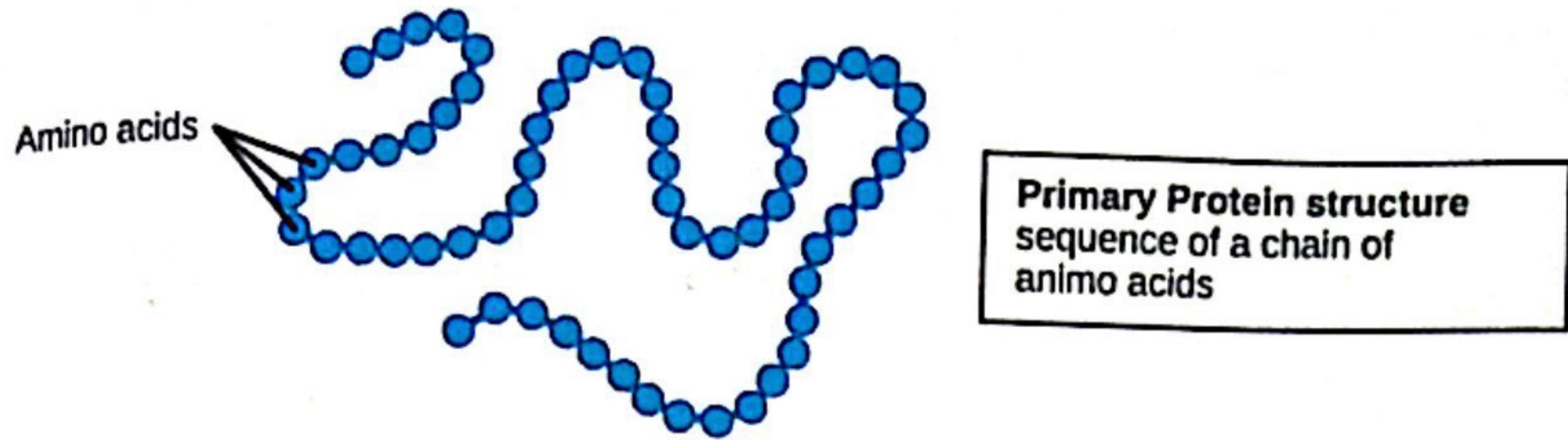
a single
unit that
makes up a
polymer



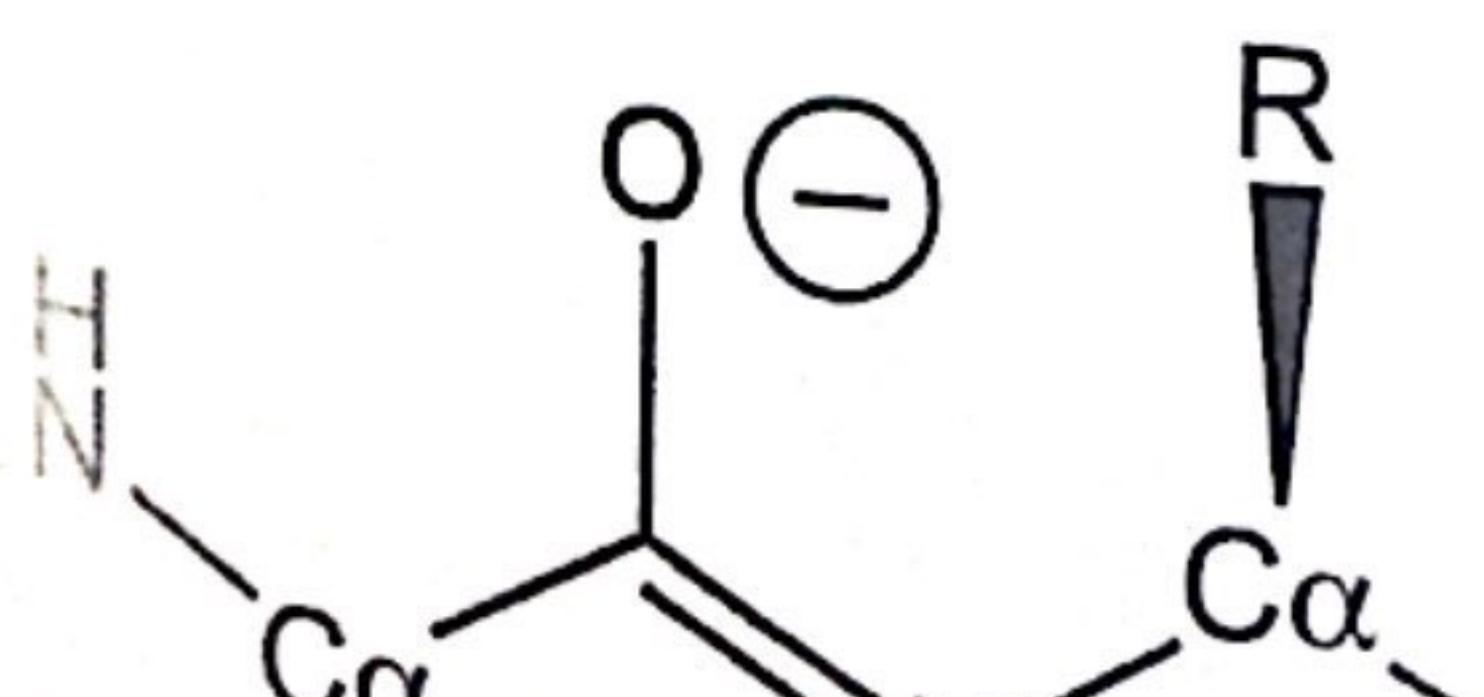
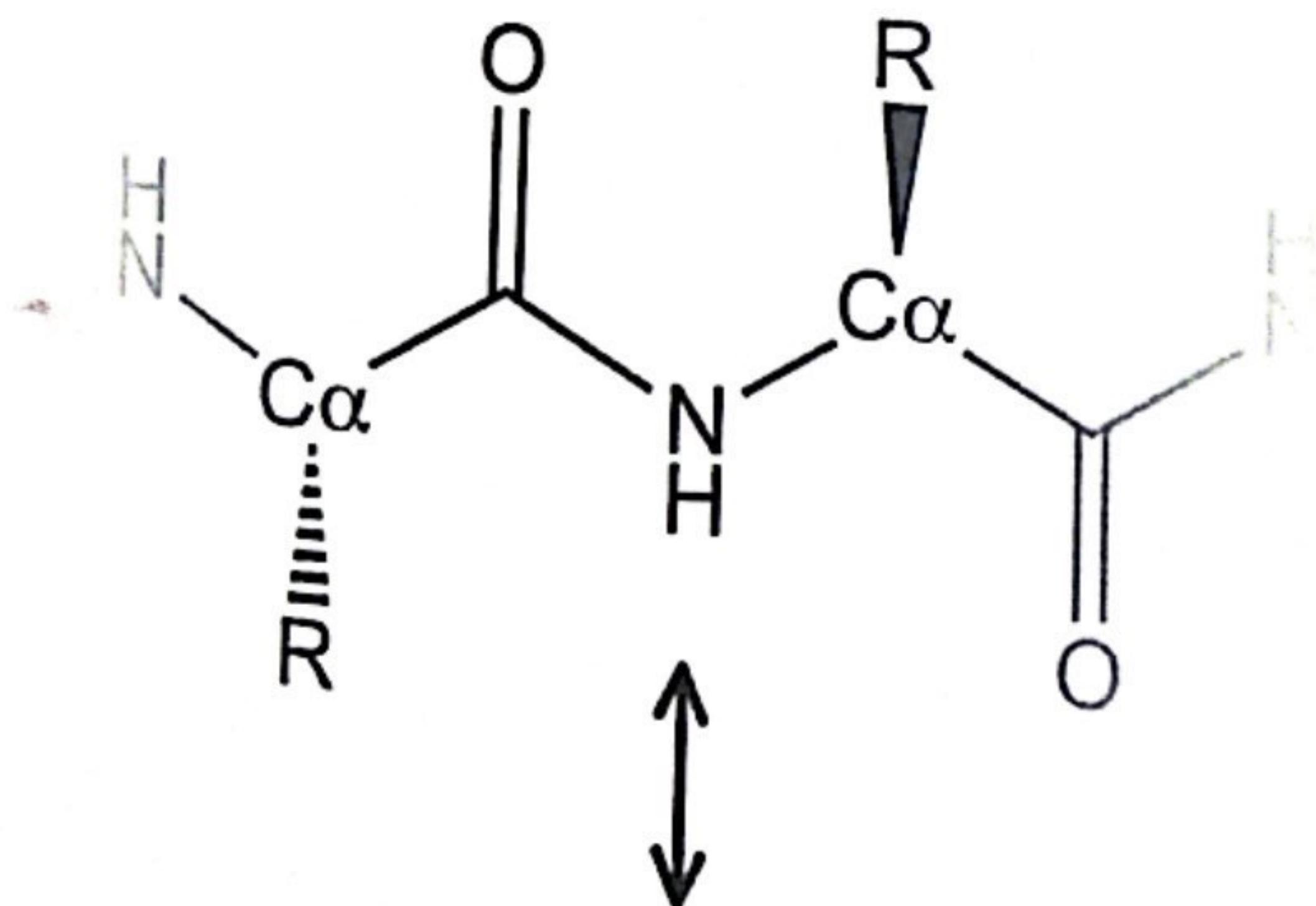
Sequence of proteins determines its 3-D conformation

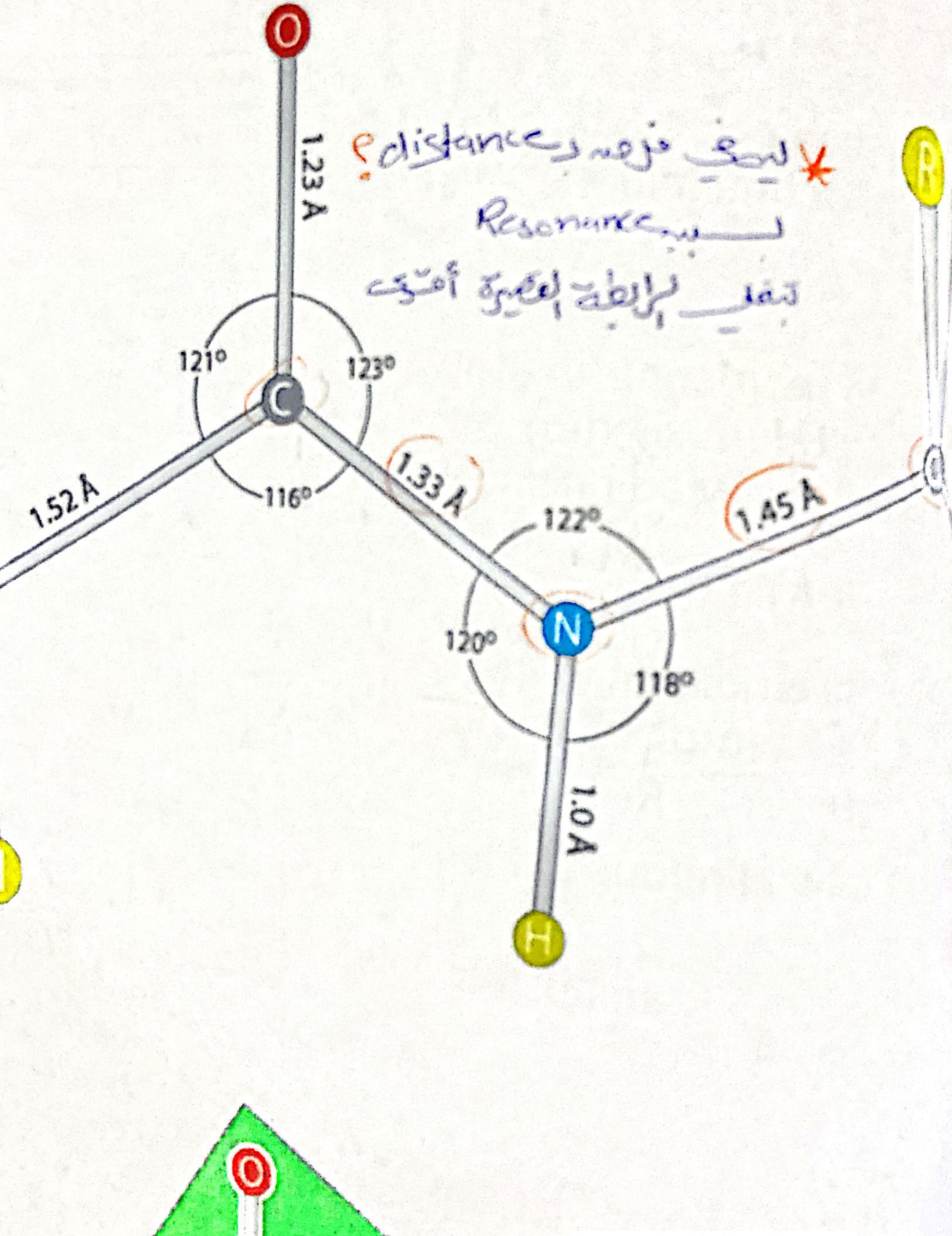
acid substitution ranges from negligible effect to a complete
and it depends on the nature of altered residue.

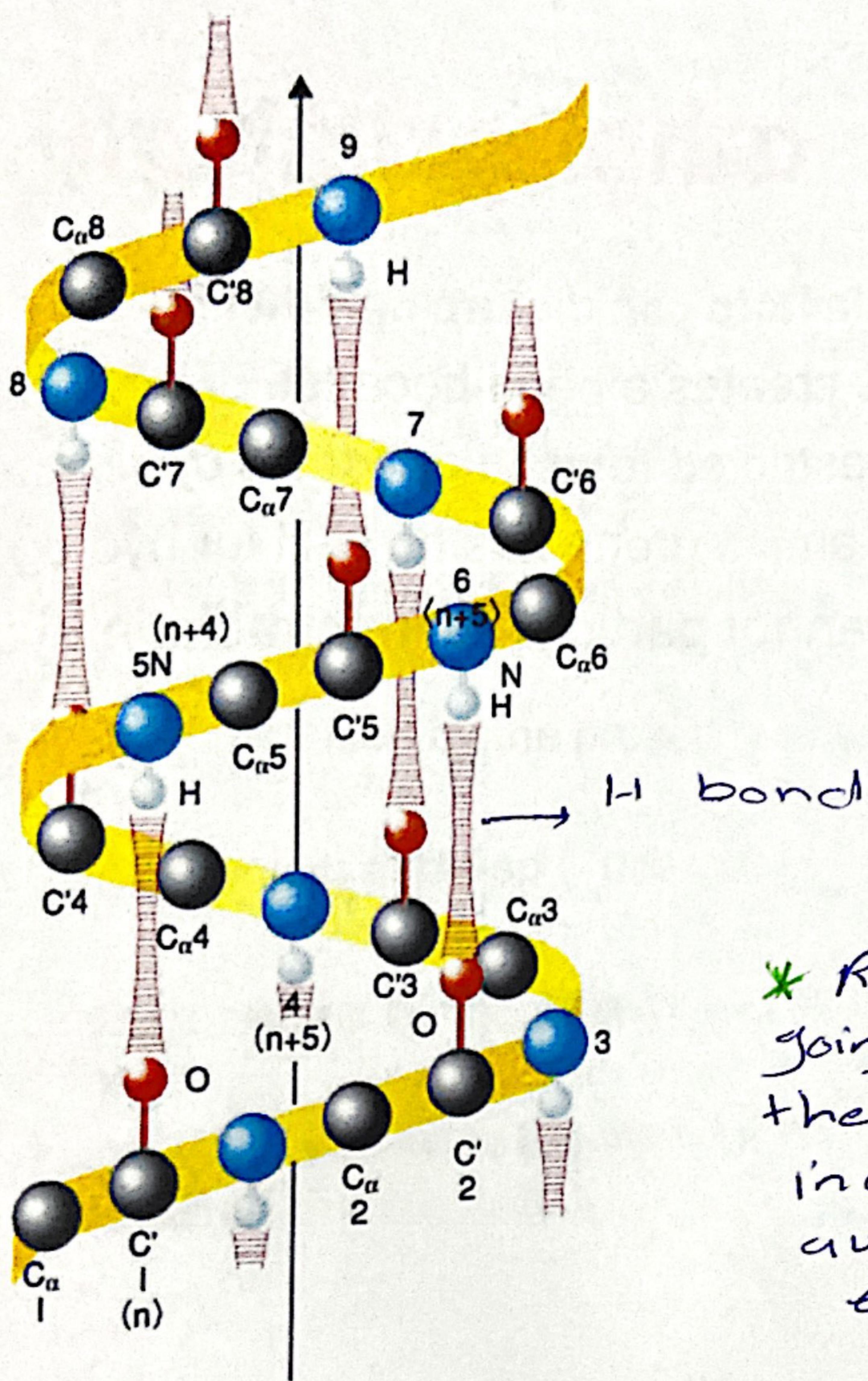
in just one amino acid in a sequence of protein can alter
function, e.g. hemoglobin associated with sickle-cell anemia
ation of 1° sequence is ...



Chemical bond
formed between
2 molecules when the
carboxyl group of one
molecule reacts with the
amino group of
the other molecule
releasing a
molecule of
water

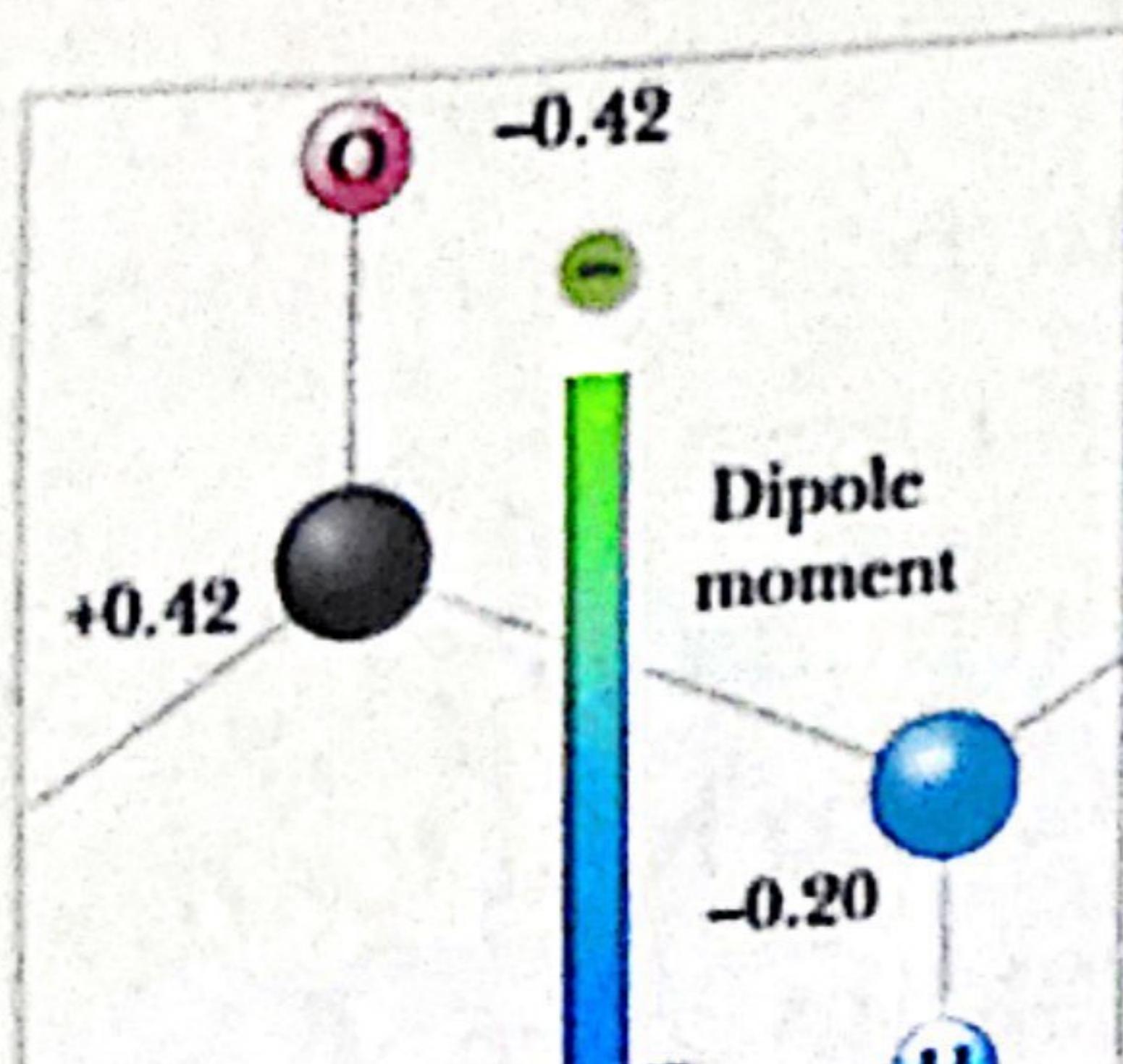






* Rgroups
going out of
the α helix
in all directions
away from
each other

α -helix dipole moment



Antiparallel sheets often use β turns
Parallel sheets use $\beta\alpha\beta$

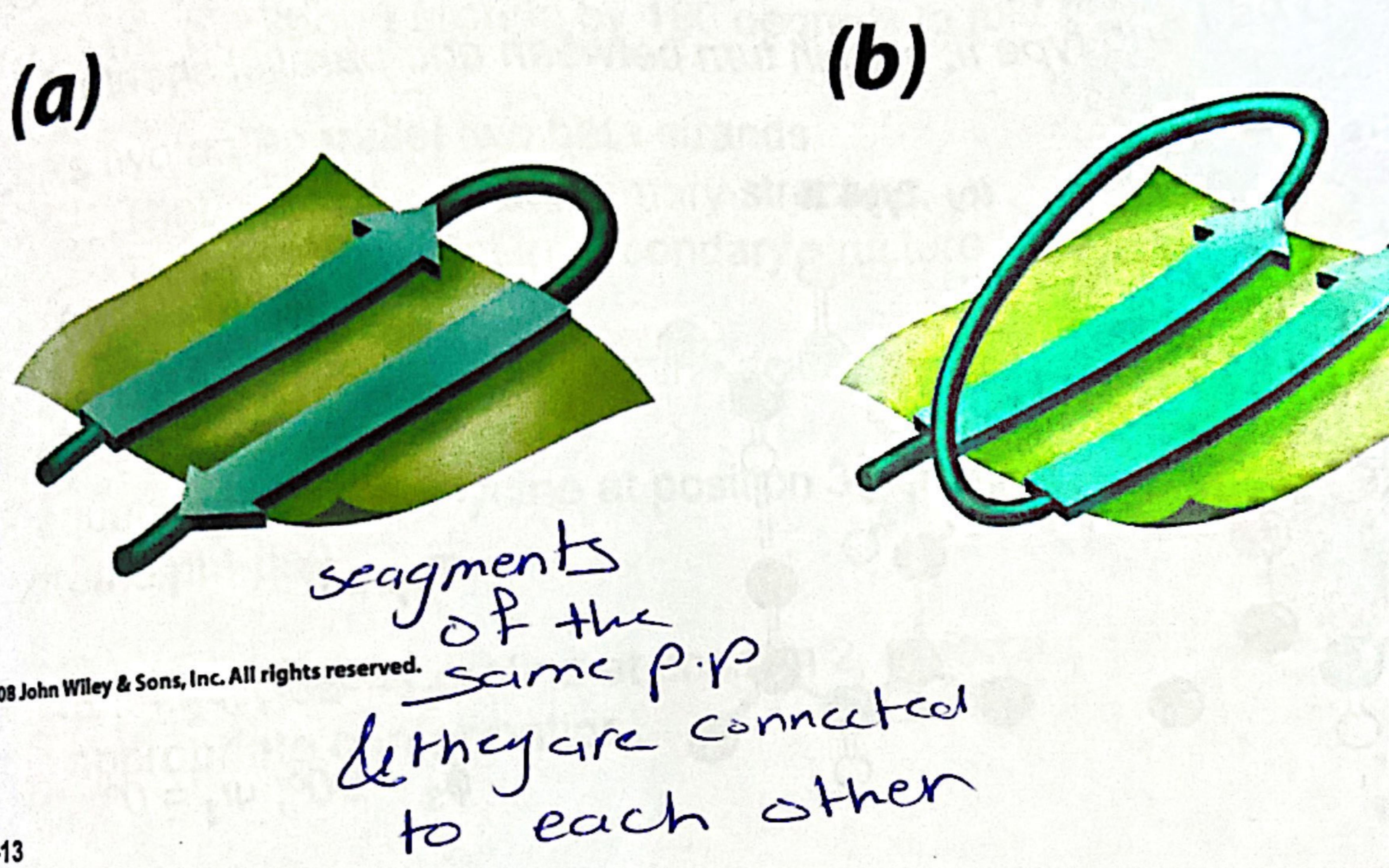
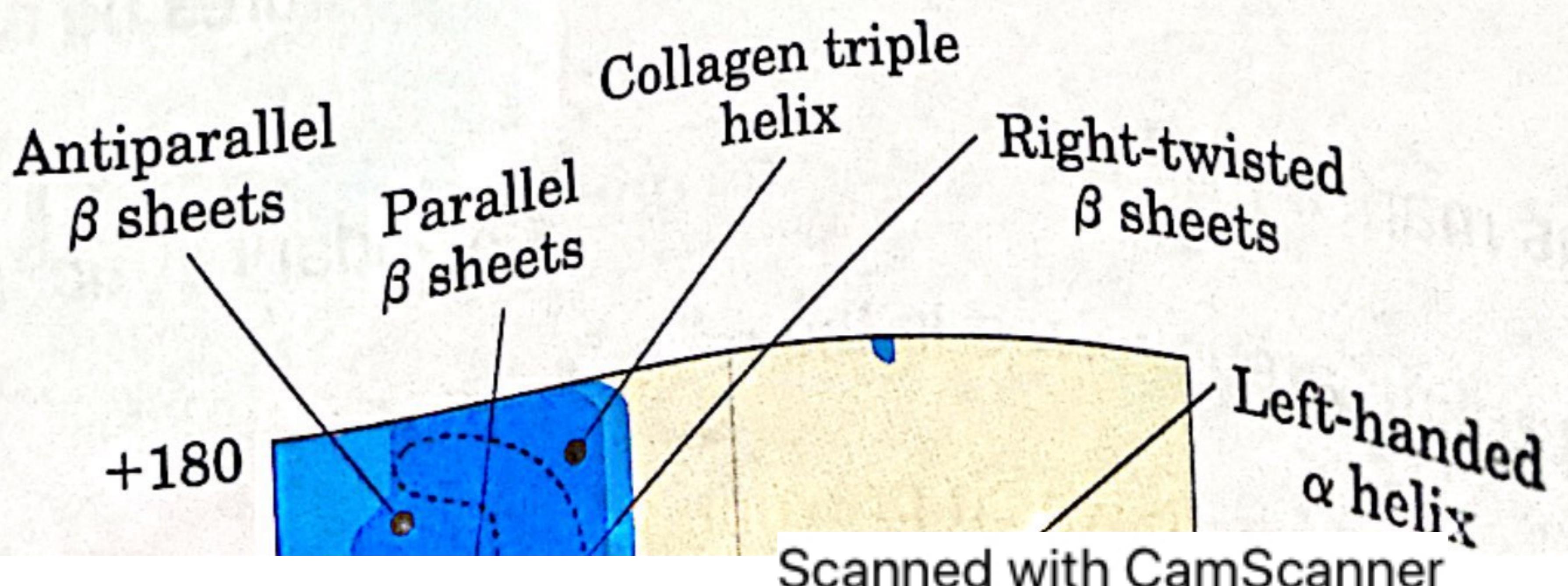
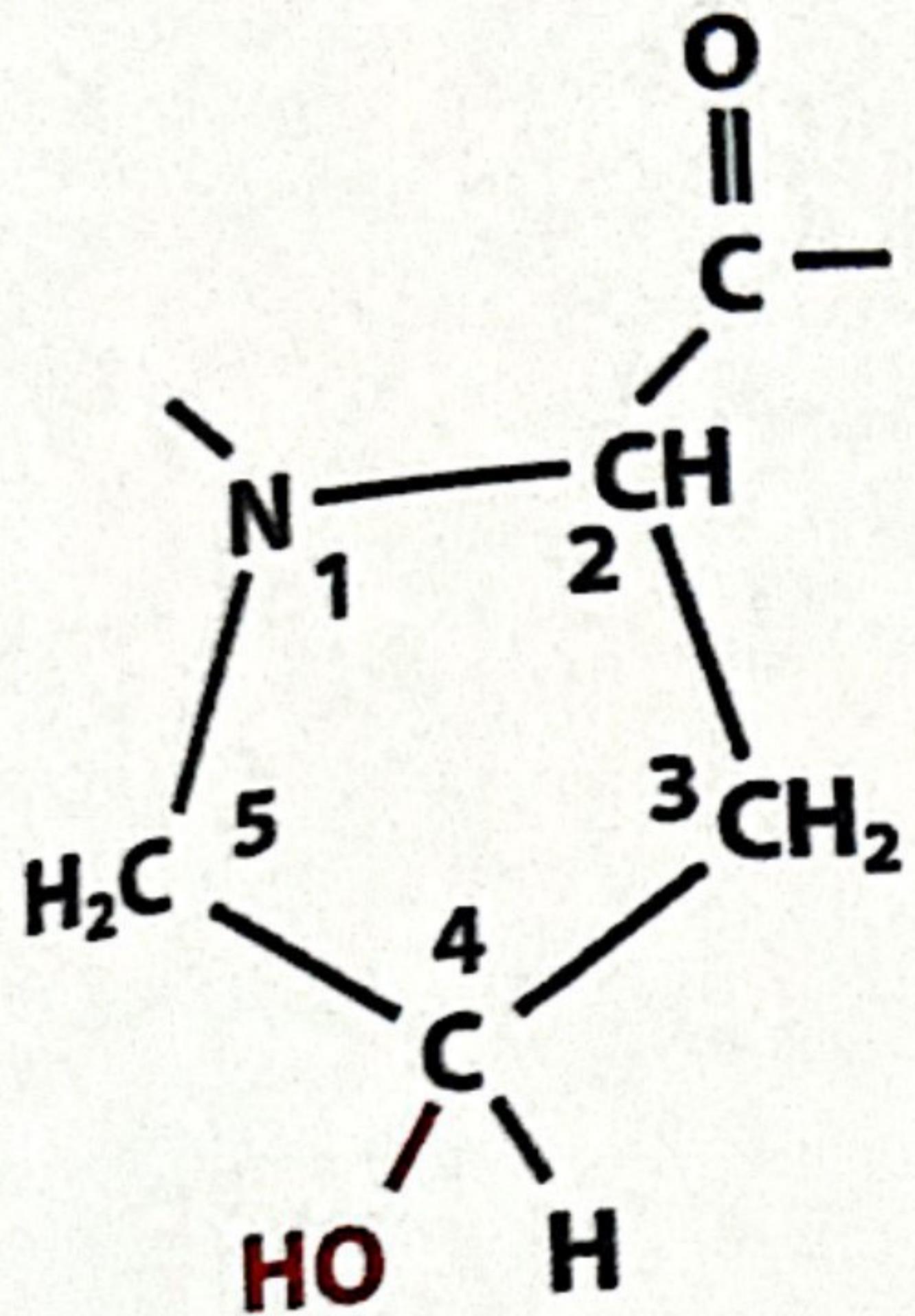


Figure 6-13

Ramachandran plot

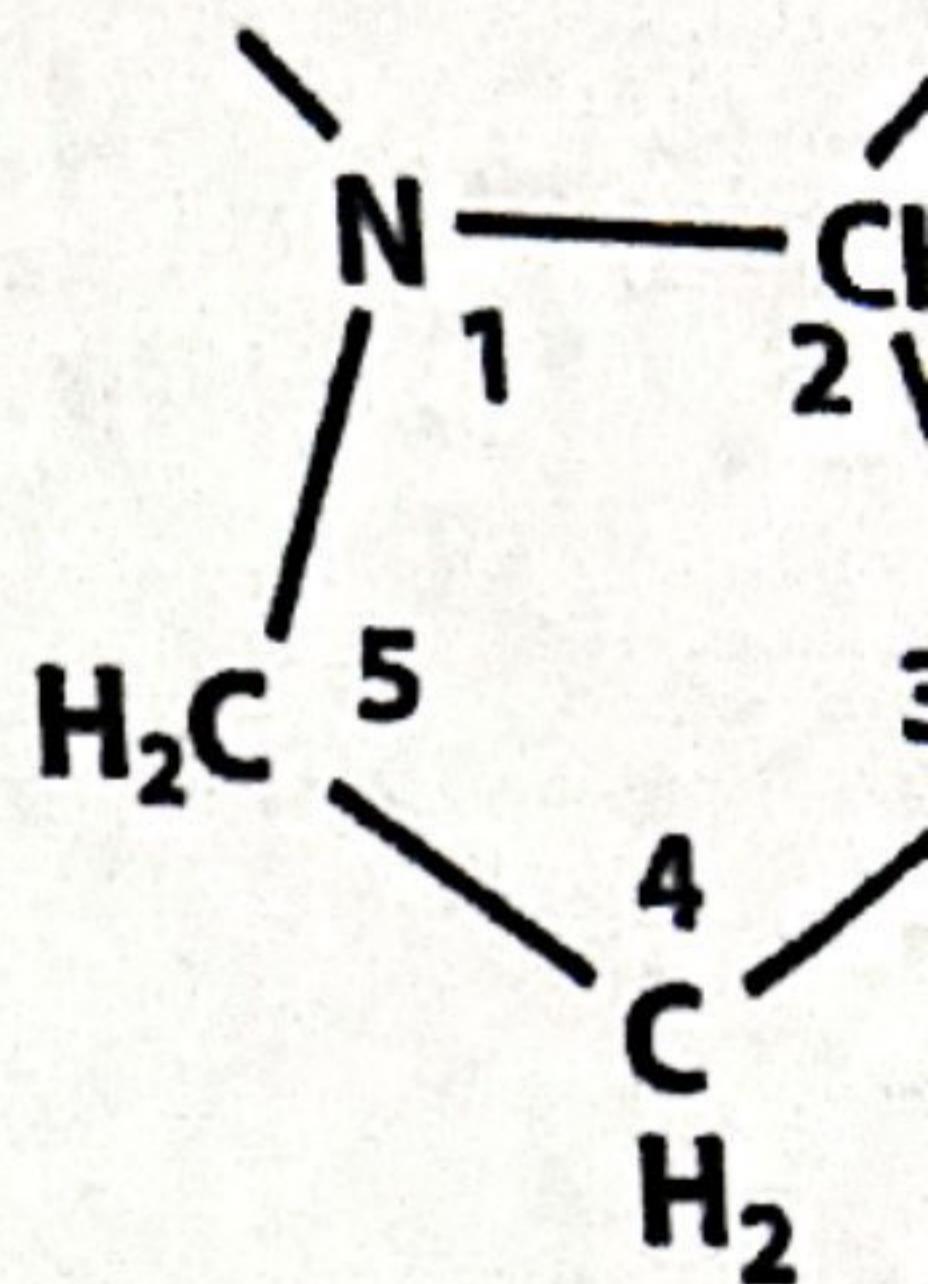




4-Hydroxyprolyl residue (Hyp)

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added
to carbon
number



3-Hydroxy residu

Collagen is also covalent

* Structure of proteins

- proteins consist of a-a

protein → 1 p.p or more

single p.p already adapted 3D struc.
& now have function & even if p.p

3D → p.p

e.g. active sites! ~~by "j"~~

Because some peptide they require
post translational modifications

Typically protein adapt certain 3D stru.
- because they have specific sequence
of a-a

so order of a-a in p.p will
dictate the structure

For most proteins (Eukaryotes etc)
there will be only 1 major
structure or what we call
native conformation
with limited flexibility

* Structure of protein isn't rigid it's dynamic

- Function of many protein depend on Flexibility

even few protein they can change their structure dramatically when they are in active compair when they aren't active

bond
distance
 \angle , torsion
atoms
 abj°

- Resonance of peptide bond have 2 sequences

1) Make pep bond stronger
2) Make atoms surrounding peptide bond co planar

3) make p.bond highly polar

* Rotation of atoms around P.b is restricted

Free rotation 360°

- P.b
 ↓
 cis
 Trans

* Residuo \rightarrow a.a within a protein

Primary struc → order of aa

↳ rely on formation of p.b
between a.a.

p.b ↗ unique type of bond

The shorter the distance between
2 atoms participating, the c. bond
will be stronger

cis
Lys

C. bond between N & C

Cis → Make R Groups close together

gives steric hindrance

trans is more common

90% p.b trans / 10% cis specially
if there is a proline
q.a Why?

free R Group Lys is less

M1 planes → connected to each other by α
Carbon

rotate with respect to each other
but the rotation in plane itself
is very respective

* Angle of rotation is called Psi & Phi

Measure the rotation
of a group with respect
to other group

Dihedral angles of psi

→ 2, 3 & phi

location of the 6 coplanar
atoms with respect to the 6
coplanar atoms

* phi → cov. bond between
N & α carbon

دیجیتال فایل میں اسکے ψ , ϕ کے ممکنے والے
psi → phi →

that are allowed in proteins,

Some other values aren't allowed

2 struc → Depend on having certain
angles rotation of phi & psi

2° struc. signs 20 میں کا راہ لی -

* Different types of helix & β -sheet

پی
different type of psi & phi

* After pp syn. by ribosome, certain regions from pp will start adapting a 2 level of structure called 2° structure

The 2 Major types of 2° structure

↳ α helix, B-sheets

Form because H-bonding between backbone atom, between hydrogen of α -group & oxygen of carbon group

369

Interactions between R Group atoms

~~It's 2° structure no repeating struc -~~

α helix

B-sheets

Form because of H-bonding between backbone atoms of very close by aa typically between carbonyl Group of 1 aa & H of an aa

Right handed helix, amid planes must be twisted with the respect of each other

* A full turn of helix called pitch requires 3.6 a.a & the vertical length of full turn is 5.4 n°

α helix slope - Always H bond is between the C's O₂ of 1 a.a & H of a.a 4 residues after

* Each a.a in the middle of p.p can form 2 H bond Why?

Because each a.a in the middle will have H of amino Group & O of the carbon Group

* It turns out that the 4 atoms (O, C, N, H) this O can form H bond & H can also form H bond, but because of resonance & the high polarity we have Dipole moment

which means on p.bond one side (which is the side of O) will be more negative & the side of H will be more positive

This means these 2 parts can form stronger H bonds because we have more separation of charges

~~Q31~~
Dipole moment

C terminalis more -
P " " +

* Some a-a can form α helixs. Some
considered disrupters of α helixs

g-a don't allow the formation of α helix because it will restrict rotation around psi & phi angles

نکی بلودین

cause bind in α helix which prevent formation of α helix

Introducing to it)

By site directed mutagenies

العنوان

Dura levi

* All a.a in the middle of α helix can participate in 2 H bond

~~Side chain only.~~

? \rightarrow

One water molecule

H on amino Group

is?

R Group connected to P

* having a.a with charged ($+/-$) R Group very close together

~~in~~ α helix \leftarrow $\text{Asp} \text{ & Lys}$

~~Asp & Lys~~

repulse to each other

- hemoglobin : 8 α helix

- Myohemocytin : 5 α helix

* Each type of α helix have certain values of psi & phi

~~gives~~ gives strong

α helix

2 kinds of 2^o struc.

1 repetitive

(up/down helix), so it has

α helix, β sheet

2 non repetitive

β turns
loops

p.p start running
up & down

- At least 2 β strand form β -sheet

(interact with each other H bond)

* parallel β -sheets \rightarrow 2 β strand run
on the same way

Hydrogen bond

* Antiparallel \rightarrow β strands

β -strand \downarrow some extention

this doesn't mean

long!

couple of a-a that will adapt
 β -strands & become a part of β -sheets

* Antiparallel H bond they are shorter
& the H & H acceptor are in the same
line
stronger ~~weak~~

* parallel \rightarrow H donor & acceptor not on
the same line

is it (as in net) if we join β -sheets lie of *
R Groups & they alternate in their
Position (pointing up or down)

will

insure that there will not
be steric clashes between
R Groups

* Ramachandran plot

↳ lists all possible Psi & Phi degrees
of p-p chain
2 regions case no 2

- color indicates that will be no
2° struc. formed with Psi & phi corresponding
to this place area

- only limited number of Psi & phi
will result in the formation of 2° struc.

* Blue regions represent the pos of Phe that will result in the formation of 2° structure

* It's estimated that 50% of Gobular protein will have repeated structure

* Some regions just connect elements of 2° structure or they will form loops

- β -turns form β hairpin between antiparallel sheets

β -turns rich in proline & glycine

- & they are stabilized by H bond between the carbonyl group (O) of residue number 1 of β -turn & H of residue of number 3

* Commonly proline is found at position number 2

Glycine n. 3

L > L > O

* pro. at pos. 2 will allow P.P to change it's direction by 100 degree

- Glyc. it has RGroups (H) which allows it to fit nicely in β -turns
Crowdy β -turns
it will not cause clashing

β -turns \rightarrow type 1
1, 2

? β -turns

Mainly in phi & psi angles of residue number 2

* Mainly β -turns connect β -strands

typically β -turns are found in protein surfaces & typically connects to antiparallel β -strands

- Some β -turns might consist up to 5 a.a but it's typically 4

* When scientist analyzed thousands of proteins & their structure & the composition of each 2° structure in terms of α - α , they found that some α - α they are commonly found in α helix, some in β -sheets

loops → have flexible, they don't adapt repetitive 2° struct.

found on surface of protein & connect the 2° structure element w/e in

connect α helix with α helix or 2 β -sheets with 2 β -sheets

Vary in their location on surface, length, shape

found rich in polar charged α - α g surface (is S_{polar}) \rightarrow like contact with water & make bonds

c. α helix, β sheet in α helix loop ~~loop~~ ~~to~~ *

ND

Note → Majority of α - α contribute to the structure, some might contribute to the function of protein

* Some loops imp. for activation of proteins

ex) Tyrosine kinase enzyme

- The movement of the loops activates the enzymes.

Tyrosine enzyme has an active site in middle, this loop serves as a gate it opens & closes

active site \downarrow if substrate is open closed

* loops \rightarrow in enzymatic

↳ p.p of antibody have loops

* Each antibody can bind a specific antigen because the shape of antibody is complementary to antigen

* Antibody consist of a lot of β -sheet & β -strands but actual side of binding of antigen is loop

* Different antibodies recognize different antigens because their loops make different binding shape

- some loops bind metal ions

like zinc ions

- some loops in protein allow protein bind to DNA

- some loops are imp. for the formation of active site of certain enzymes

* In certain cases, certain compensation of β & α helix they come together to form what we call super second structure motifs



- stabilized by weak interactions H-bond

- $\beta\text{-}\beta$, 2 parallel β strand connected by a loop that have an α helix

* Sometimes we find proteins consist of more than 1 type of these 2 structures.

- * ~~smaller proteins can't form enough electrostatic interaction (interaction that result in 3D structure) need help from metal ions~~

1 ex³ of protein that have
a ter- struc. but if you
think about it, it's just a protein
that consist of 3 helix interact
with each other → collagen

α helix \rightarrow سلسلة مثلثية β helix \rightarrow جدول *

α helix \rightarrow collagen \rightarrow helix \rightarrow سلسلة CDP

α helix \rightarrow زوجي ψ و ϕ

* Each helix might consist of 100 a-a
every second a-a will be prolines

Bundling the regions where 3 helixes
touch each other because it's small

وَجْهٌ مُرْتَبَكٌ -
staggered way

* Collagen fibers could be cross linked by cov. bonding between a-a

* To make the collagen tougher, the collagen might form a network of fibers. It this require the collagen fibers to be cross linked by the cov. bond between a-a within the collagen helix

For ex → an enzyme will convert the lysine into N¹lysine

3° Structure results from global interaction

compact 3D structure where the p.p formed coiled & become twisted itself

H bonding one of the interactions that plays role in 3 str.

~ 200 a.a could form polypeptide with 3D str., some a.a could fold more than region called Domains

units of structure & functions, it could form an function independently from each other

* Disulfide bond → only type of cov. bond in 3° str.

& it add stability to protein outside the cell, observed more in extracellular proteins

* domains connected with each other through flexible linker (coupe of a-a)

don't adapt any
2° or 3° structure

* Nonpolar a-a they are more likely to be found inside core of protein away from water

- polar can interact with water, so it's more usually on the surface

they might be found on the surface of protein clustered together forming hydrophobic patches

↳ usually used to bind to their ligands or to other protein p+p interaction / P-L binding

* Polar in core must have another polar a-a in the core to interact with each other

* The higher structure determinations used for 3° & 4°

* Software used to predict how the 3D stru. formed by knowing the 1 input a-a sequence

↳ which regions will form α or β which will interact with each other

Note → NMR analysis is based on the fact that a # of atomic nuclei display a magnetic moment (H^1 , C^{13} , N^{15} , P^{31})

* Myoglobin → consist only of α helix, 3 levels of protein stores O_2 in muscle

Heme Group → binding O_2

* Metamorphic proteins → proteins exist in 2 or more well defined structures in the absence of ligands or co factors

- Specific characteristic protein seq - → signature sequence

Note → subunit: could adapt 2 different domains

* 1DP's → Don't adapt a defined 3D structure

↳ They might adapt 2D or 3D structure once it binds to another protein

CEM → used for viruses or large membrane proteins

4^o structure

- One or more 3D protein interact with each other
- The proteins that form a 4^o structure called subunits
- Make more protein of the Genetic Code
- allows the cell to highly control the efficiency of the protein

- Make large protein complexes
(making & removing more efficiently)

* NMR → Study the structure dynamic

frozen

* cryogenic EM → To take pictures



For very large proteins/protein complexes

- The protein must be frozen → liquid nitrogen or helium

then → thrown in the surfaces EM,
- take picture to 100-1000 of protein.
Each protein will form a different angle.

take picture to try to draw a 3D picture
for the protein