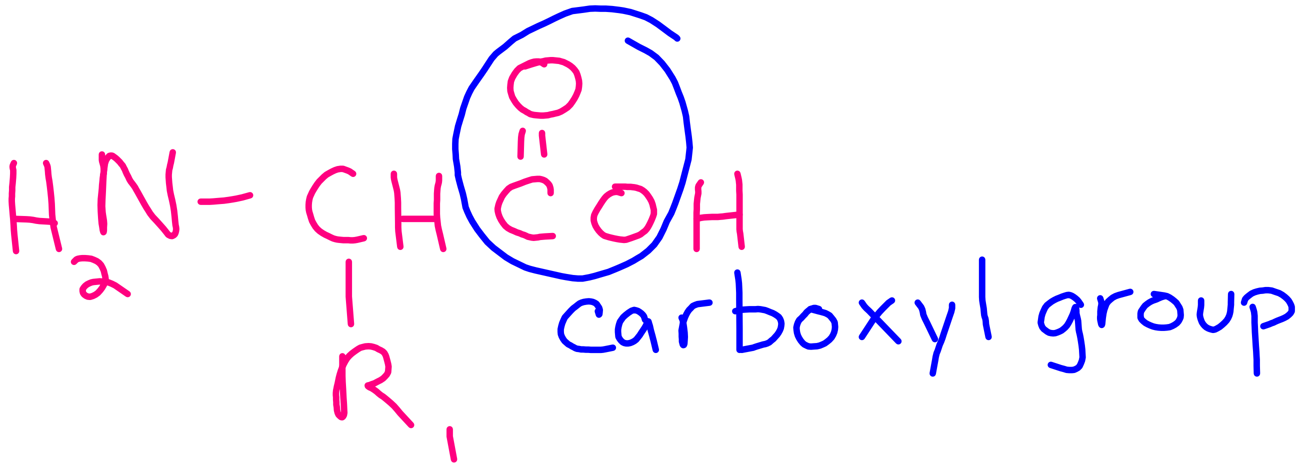
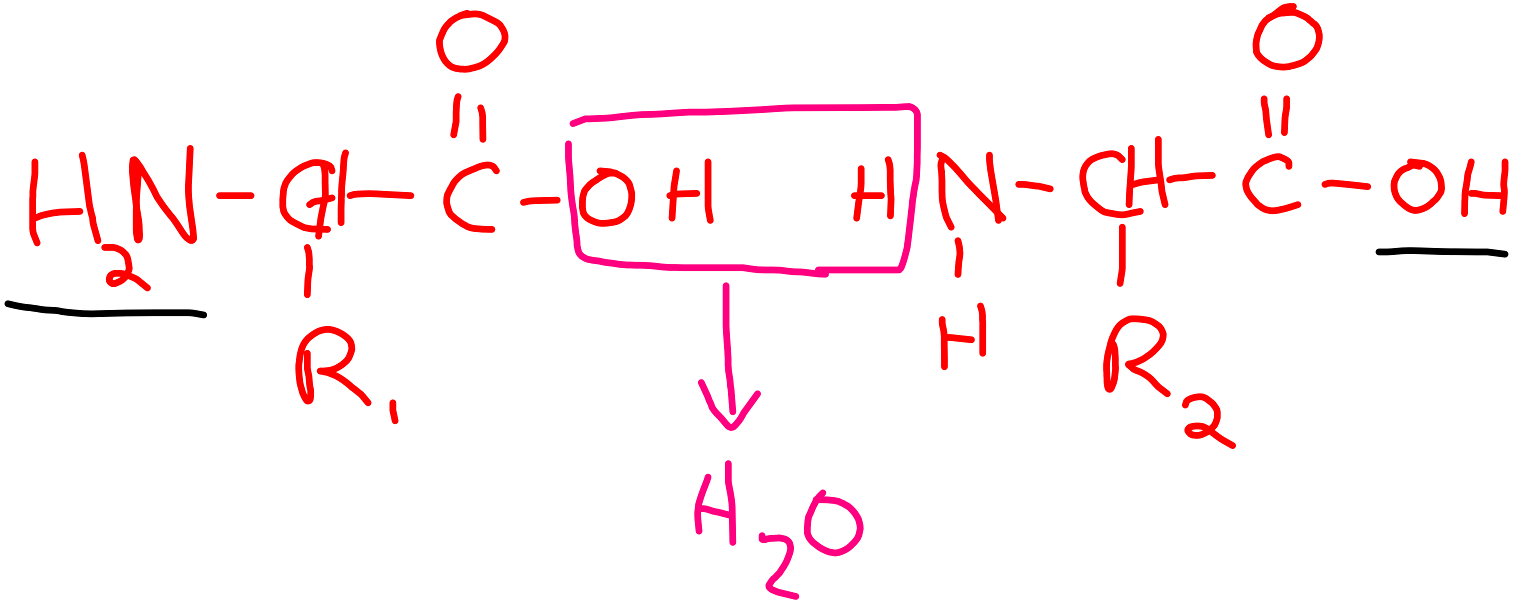


$$H_2N-\underset{\displaystyle R_1}{\underset{|}{C}}H-\overset{\displaystyle O}{\overset{\|}{C}}OH$$

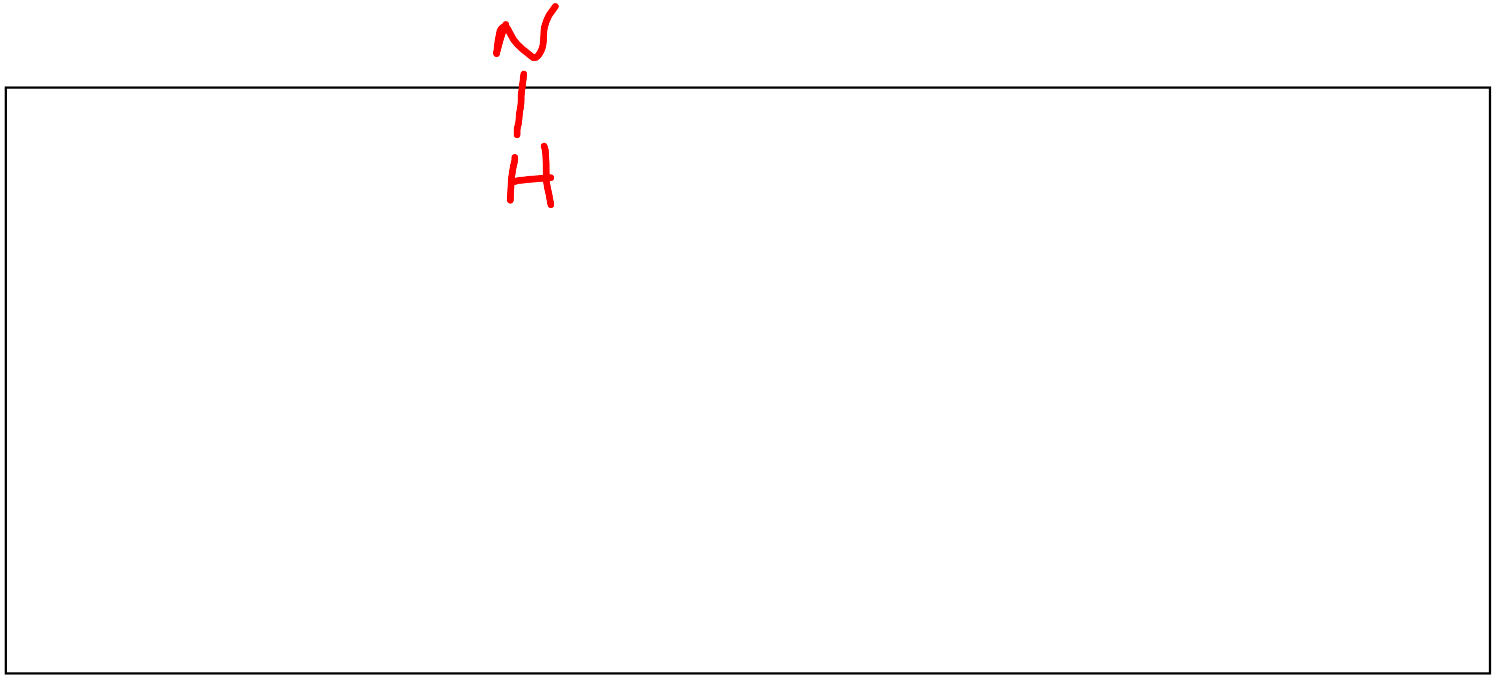
amino acid

R_1 = alkyl chain
or a hydrogen

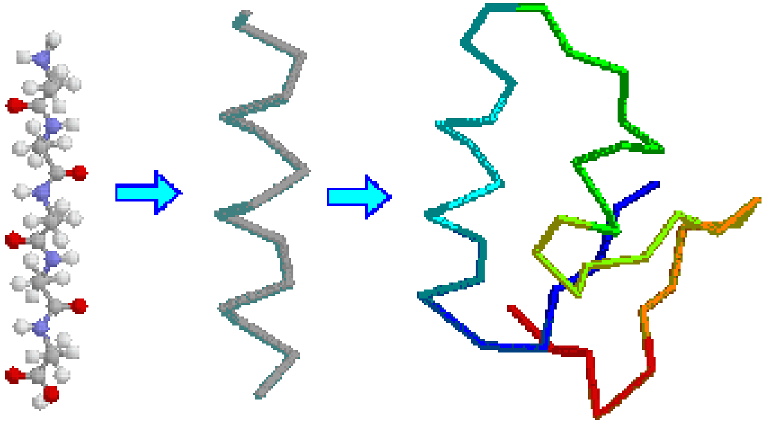
A peptide bond is formed via covalent binding of the carbon atom of the Carboxy group of one amino acid to the nitrogen atom of the amino group of another amino acid by dehydration.


O
O
H2N – CH – C – OH
H
HN – CH – C – OH
H
R1
R2
H2O

Secondary Structure is a local regulary occuring structure in proteins and is mainly formed through hydrogen bonds between backbone atoms. So-called random coils, loops or turns don't have a stable secondary structure. There are two types of stable secondary structures:**Alpha-helices and beta-sheets**. Alpha-helices and beta-sheets are preferably located at the core of the protein wereas loops prefer to reside in outer regions


N
H

Tertiary structure describes the packing of the alpha-helices, beta-sheets and random coils with respect to each other on the level of one whole polypeptide chain.



Primary Structure

Secondary Structure

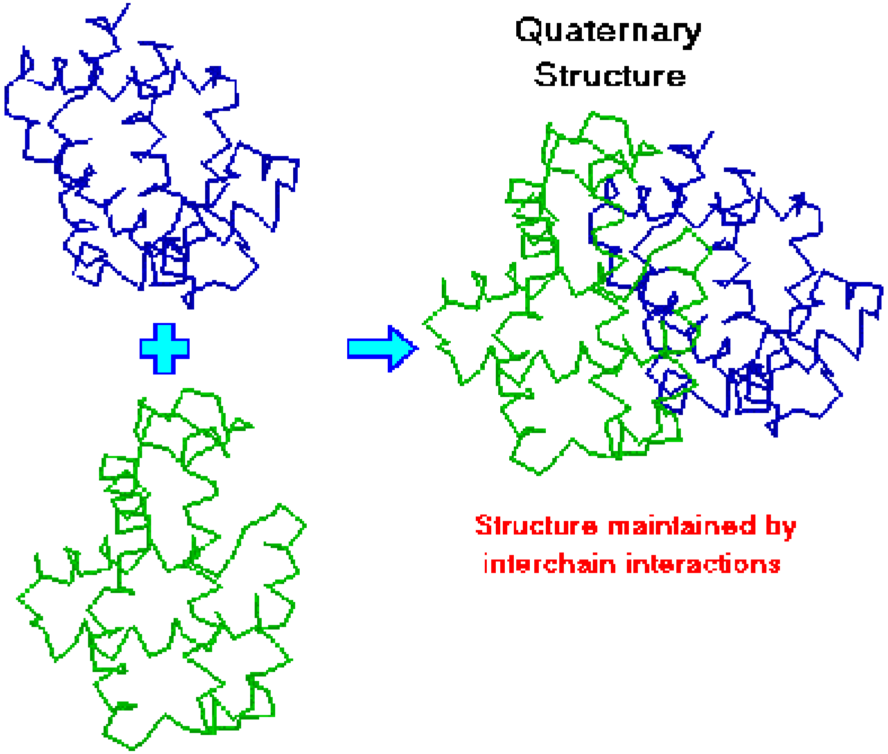
Tertiary Structure

The sequence of amino acids

Local folding maintained by short distance interactions

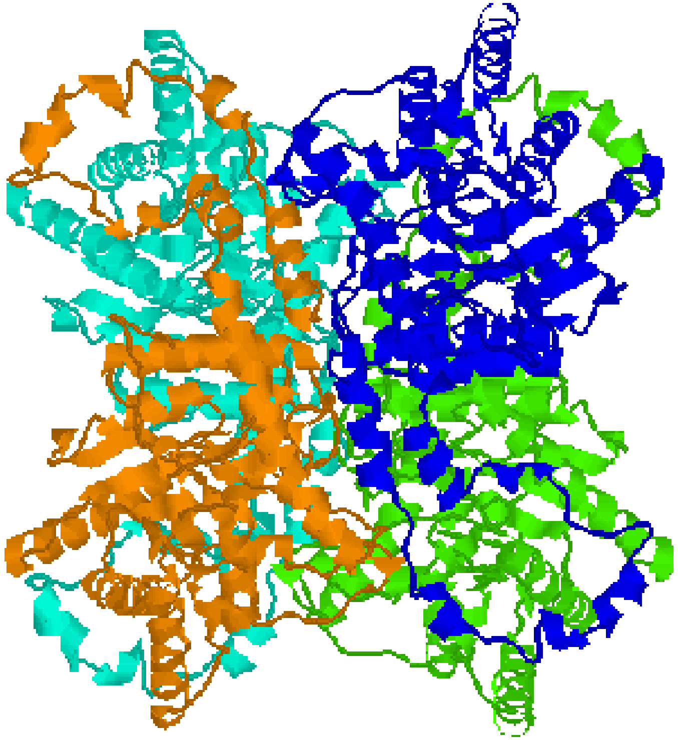
Additional folding maintained by more distant interactions

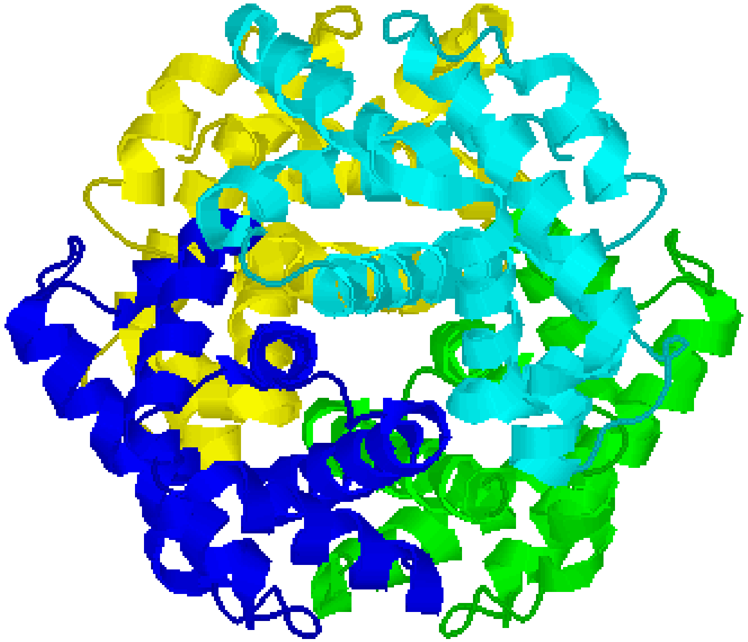
Quaternary Structure - the combination of two or more chains, to form a complete unit. The ineractions between chains are not different from those in tertiary structures, but ar distinquished only by being interchain rather than intrachain.



Quaternary Structure

Structure maintained by interchain interactions





Title: Apr 5 - 12:57 PM (14 of 21)

Radiation Lab	10th
Distillation Lab	17th
Test III	24th
Lab-Lab	May 1st

May 8th

1:30 - 4:00

Tues.

6. N, P, A, B

7. Put together an amino acid chain

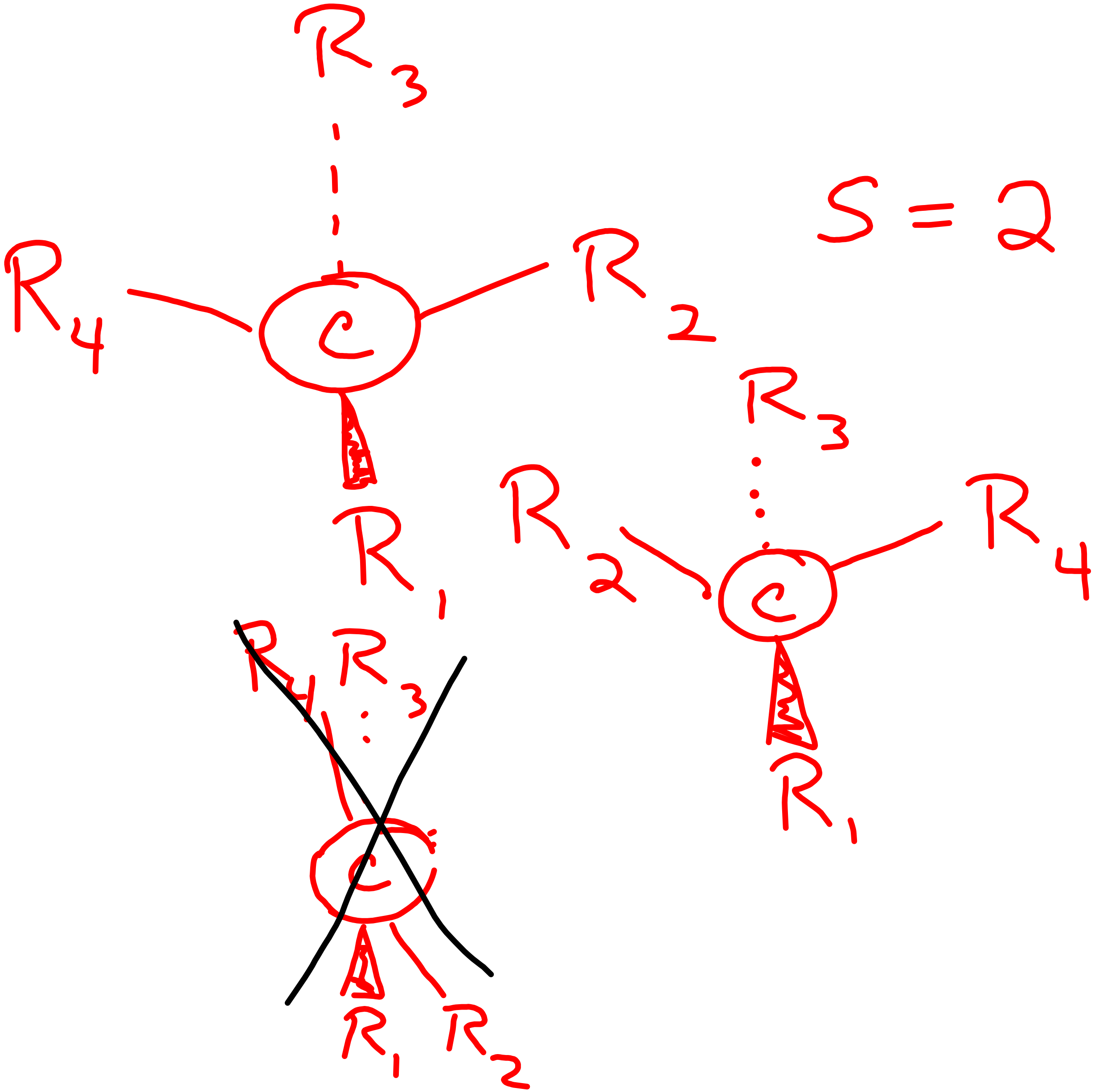
12.

Isomer - same molecular formula, but differently built.

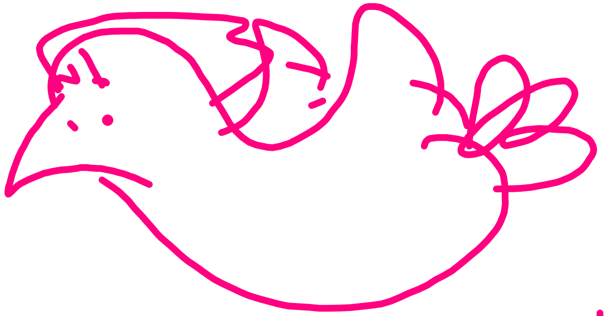
Sterioisomer-

mirror image

Carbon atom must have 4 different attachments to it.



$S = 2$



this
is
right?