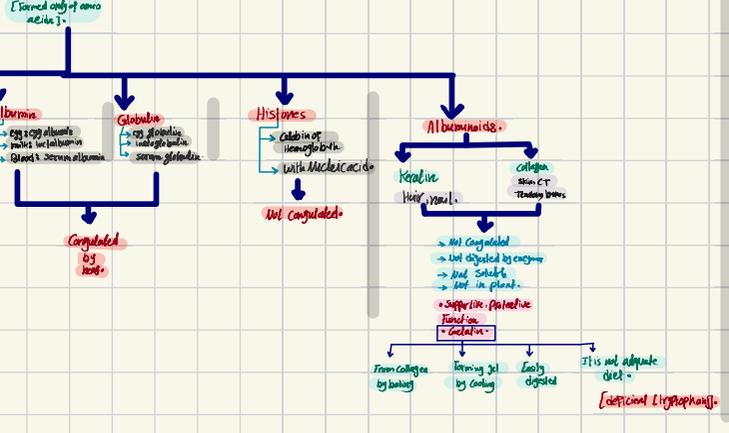


Protein

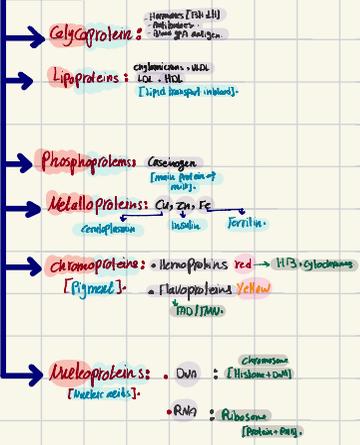
Nitrogenous Compounds
 C, O, H, N (+S)
 Forming polymers [Polypeptides]
 Connected together by Peptide Link
 Carboxyl group: C-terminal at one end.
 Amino group: N-terminal at the other end.

Formation of a
 - Enzyme - hormones
 - Hemoglobin - Plasma protein [Haptoglobin]
 - Immunoglobulins [antibodies]
 - Supporting structure [cartilage, skin, nail, hair, etc...].

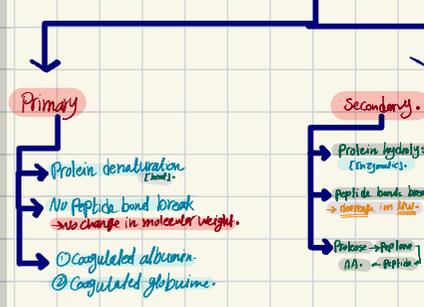
Simple



Conjugated



Derived protein



Protein Folding: Process by which a polypeptide chain

folds to become a biologically active protein in its native 3D structure.

→ Protein's 1° is crucial to its function

⊗ The wide variation in AA sequences → different shape of proteins

1 Primary + S: Polypeptide chain

Main bond: peptide + B

⊗ Any change in AA → physiological defect

We count the AAs from the N terminal

2 Secondary + S:

α-Helix (coil)
 → stab. by H-bonds
 → hydrogen bond between peptides by in the same chain
 → between AA in the same or adjacent segment of the same chain

β-sheets
 → strands
 → arranged side by side
 → hydrogen's between adjacent polypeptide chain
 or adjacent segment of the same chain

3 Tertiary:

It is 3D shape of protein
 → Formed of 2nd + S [α, β]
 Final functional 3D structure of protein called domain

⊗ Bonds: between side chains [C]

- ① Hydrogen: B: between polar side
- ② Hydrophobic: B: between non-polar B
- ③ Ionic: bonds [electrostatic]: between oppositely charged AA
- ④ Disulfide (covalent bond): between sulfur [Cysteine]

4 Quaternary + S: B: is the association arrangement of several polypeptide chains

or subunits into a 3D spatial arrangement. Each of subunits has its own primary, 2nd, tertiary + S

⊗ Bonds:

- ① Disulfide
- ② Ionic and hydrophobic between separate polypeptide chains

 [eg] ① Hemoglobin and lactate dehydrogenase [LDH] enzymes are tetramers [4]

⊗ Creative Kinase [CK] enzymes is dimer [2]