Amino acids and peptides

proteins have only L-α amino acids

peptides in micro-organisation can contain both L
D amino acids, which can also # have theraputic valu

Amino Acids (20 of 300 constitute proteins)

1. Glycine (G)
2. Alanine (A)
3. Valine (V)
4. Leucine (L)
5. Isoleucine (I)

→ neutral aliphatic side chain

6. Serine (S)
7. Threonine (T)

→ -OH grouped

8. Tyrosine (Y)
9. Phenyl Alanine (F)
10. Tryptophan (W)

→ Aromatic

11. Cysteine (C)
12. Methionine (M)

→ S containing

13. Aspargic acid (D)
14. Aspargine (N)
15. Glutamic acid (E)
16. Glutamine (Q)

→ Acidic

17. Arginine (R)
18. Lysine (K)
19. Histidine (H)

→ Basic

20. Proline (P) → Imino acid

★ 21. Selenocysteine → Structural analog of cystein
(Se in place of S). found in han
Proteins (peroxidases, reductase
Inserted during translation and t
called '21st amino acid'.

produced by Co-translational
derived from Methionine.
synthesis of T_3, T_4.

it is not specified by specific

codon unlike other amino acid

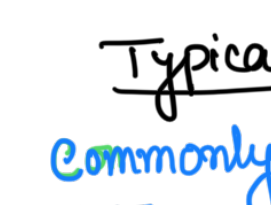
synthesised in terms of stop codon.

22. pyrrolysine → not found in human → bacterial amino acid
"22nd amino acid"

⇒ proteins can be Levo as well Dextro. rotetary.

⇒ Amino acids can function alone also

↳ Ex: . Ornithine, citrulene → Urea synthesis
. Tyrosine → thyroid H, melanin, catechola
. Glutamate → neurotransmitter biosynthesis.
. Tryptophan → niacin, serotonin, melaton
. Arginine → NO
Creatine → glycine, arginine, methionine



⇒ D-serine, D-aspartate is found in brain tissue.
D-alanine, D-glutamate in gram+ bact. cell wall.
↳ antibiotics.

- pI or Isoelectric point: the ptt where biomolecule has amount of +ve and -ve charge making it uncharged is isoelectric point.

$$R\text{-}COOH \rightleftharpoons RCOO^- + H^+ \quad PK_1 = x$$

$$R\text{-}NH_3^+ \rightleftharpoons R\text{-}NH_2 + H^+ \quad PK_2 = y$$

$$pI = \frac{x+y}{2}$$

pI is useful in electrophoresis separation.

Typical values of PK_a for ionizable groups in prote

Commonly, (±3) in these values can be found at active site enzyme! [Exception buried aspartate thioredoxin shift

α-COOH ⇒ 3.2 – 4.1

non α-COOH ⇒ 4.0 – 4.8

–OH of Tyr ⇒ 9.5 – 10.5

–SH of Cys ⇒ 8.5 – 9.5

Imidazole of Hys ⇒ 6.5 – 7.4

α-NH_2 ⇒ 8.0 – 9.0

non α-NH_2 ⇒ 9.8 – 10.4

Properties of Amino acid

* Solubility : Soluble in polar solvent (H_2O, R-OH) and not non-polar solvent (⬡, –O– etc)

* Light absorption: mostly amino acid lack the property absorp light. So, they're colourless. But, Trp F, Y can absorp UV light.

- –R, –⬡ attached amino acids are present in cytos
- –OH of serine and –SH of cystein – excellent nu: are involved in catalysis.
- Imidazole of hystedin makes it active in neutral as w both basic and acidic pH. thus have a major role in
- charged amino acids are involved in salt bridges a in 'charge relay' catalysis in mitochondria.
- Ala, Gly, Val → sweet taste
  Arg, Ile → tasteless

Class-I amino acid : animal protein (essential amino acid

Class-II amino acid : vegetable protein (↓↓ EAA)

Semi-essential amino acid : synthesized by adults but growing children : Ex: Histidine, Arginine.

Purely Ketogenic → leucine

Glucogenic + Ketogenic → Isoleucine, Tyrosine, phenyl alanine, Tr

Glycogenic →

Non-standard Amino acid

4-hydroxylproline
5-hydroxylysine
6-N-Methylysine

→ In addition to 20 common amino acids may contain residues created by modif of the common residues already incorpo in polypeptide chain

#modified by vitamin C
Post-translational modification

→ used in collagen

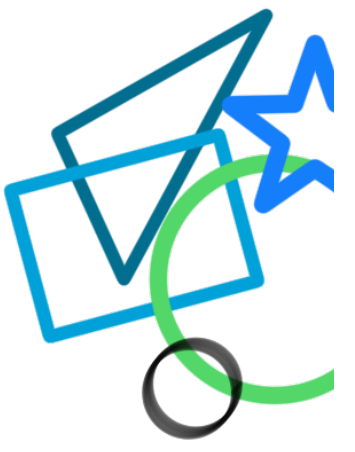
Desmosine → 4 lysine residues.

Monosodium glutamate (MSG) → Ajinamoto
↳ flavouring agent → carcin

Aspartame → Aspartic acid + phenyl alanine
↳ artificial sweetner
↳ not healthy

absorption spectra peak

Porphyrine/ heme → 400 nm
amino acid → 280 nm
nucleic acid → 260 nm.



Protein

- Titin is the largest protein.
- TRH is the smallest protein

- Insulin is polypeptide f

albumin, ← simple protein
conjoint protein
↓
Protein + non-protein

Derived protein
- derived from simple a conjugated protein
- through digestion

- peptones, proteoses

- Albumin is precipitated by full saturation with $(NH_4)_2SO_4$ solution
- Globulin is precipitated by half saturated with $(NH_4)_2SO_4$ solution

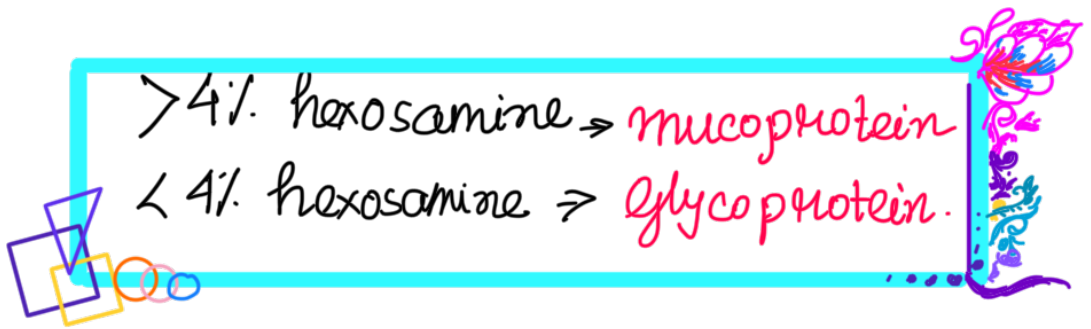
* Glutelins → wheat. Glutenin
  Rice - Oryzenin
  - insoluble in water and dilute salt solution
  - soluble in dilute acid.

- Histone: soluble in dilute acid, salt solution

Scleroprotein → insoluble in all solvents.
resistant to digestion

Mucoprotein → protein + sugar acid
amino sugar
SO_4^{2-}

↳ saliva (mucin)
egg white (ovomucoid)



- milk has phosphoprotein.

1° structure → highest energy, least stable.
2° structure → insulin.
3° structure → myoglobin
4° structure → haemoglobin.

✓ most stable confirmational exists.

Peptide bond → ϕ & ψ bond → in between single-bo

Protein starts from amino (N) terminal and ends
carboxy (C) terminal

each component amino acid in polypeptide → moiety / r

2° structure → α-Helix (Right handed) → intrachannel H-b

n → n+4th H-bond.

pitch = 5.4 Å

1 helical turns ≈ 3.6 resid

Φ = 60°, ψ = −45°

found in myoglobin, troponin C,
hair, nail, ho

glycine & polar aa destabilise α-helix

↓

found in β turn

β-pleated sheet → interchannel H-bond.

(in b/w sheets)

Parallel Anti-parallel.

» Silk,

» In Alzhimer, ↑ β pleated sheet

Left-handed α-helix → most ϕ & ψ bond

3° structure » based on various type of interactions b
– R groups.

※ No salt bridge, No polar bond.

visualised by NMR Spectroscopy
(nuclear magnetic resonance)

※ 3D-shape, stable.

– S–S– bond
Hydrophobic bond
H-bond
Vander walls interaction

super 2° structure → Zinc-fingers & leucine zipper
modifies DNA

Haemoglobin

succinyl co-A + glycine → porphyrene

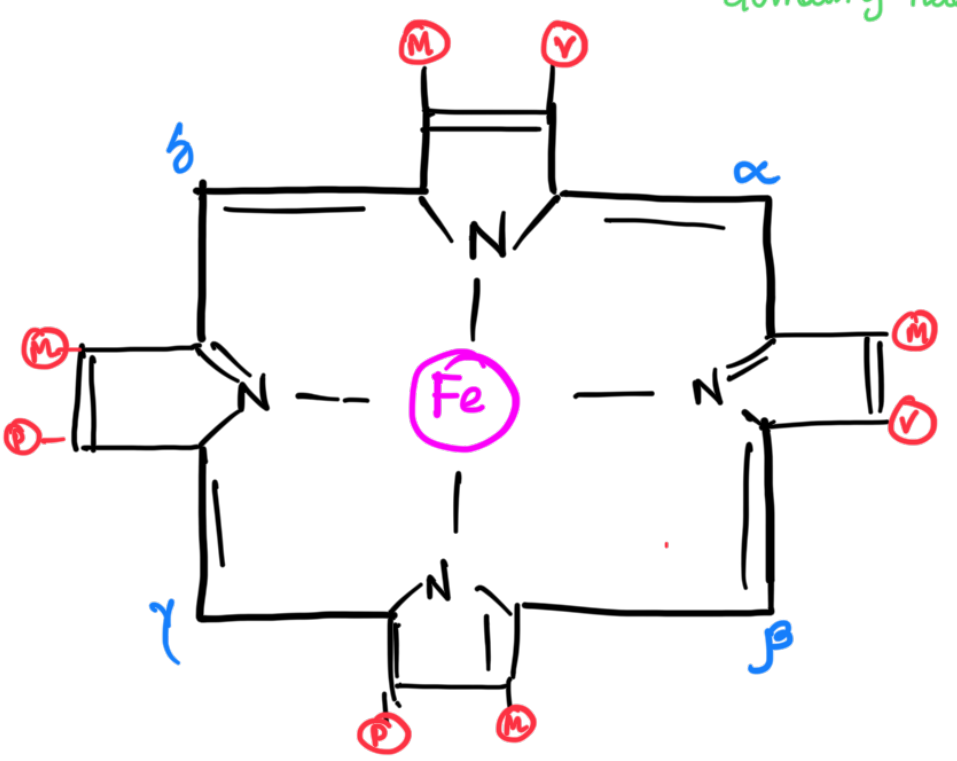
Vit B_{12} » • part of 1-C moeity of purine and pyrimidine.
• TTP (thymidylene triphosphate) synthesis

※ Haemoglobin → chromoprotein. conjugated protein with 4° structure

sickle cell anaemia → point mutation

thalassemia → deletion

2,3- bisphosphoglyceric acid (2,3- DGP) → fits to domain of haemoglobin → helps in quick delivery from haemoglobin.



M- Methyl
V- Venyl
P- Propionyl.

Porphyrenes are link
methynyl (=CH-) brid

Co-A is a part of pento
a

ALA → ß-amino levulinic acid

type III porphyrin is biologically most dominant porphyrin.

※ Biosynthesis of heme occurs in almost all tissues of body.

Heme synthesis

Step1: Succinyl co-A + glycine —(ALA synthase; PLP (pyrodoxyl phosphate) ← vit B_6; → CoA-SH)→ α-amino, β-keto adipi —(CO_2; ALA-syn + PLP)→ ß-amino levulinic a (1st stable produ

- ALA synthase is found in mitochond
- rate-limiting enzype

Step2: 2 ALA —(ALA dehydratase; sensitive to Pb; Zn; → $2H_2O$)→ porphabilinogen (PBG) [monopyrole] #not photosensitiv

ALA dehydratase is found in cyt

Step3 / **Step6** ↓ PBG —(UPG I synthase, UPG III cosynthase; → NH_3)→ Uroporphyrinogen (UPG

UPG decarboxylase

Coproporphyrinogen (CP

CPG oxidase

Protoporphyrinogen IX

PPG oxidase

Protoporphyrin IX

※ Cytoplasm

※ Mitochondria

Step 8: protoporphyrin —(Ferochelatase, Fe^{2+})→ heme.

$Fe^{2+} \longrightarrow Fe^{3+}$ (hematin)

↳ inhibits 1st stage

Fe has 6 co-ordi
bond. 4 with N.
1 with O_2
1 with h
β-globin.

※heme allosterically inhibits ALA synthase activity.

- Barbiturates induce heme synthesis.
  - 2/3 of heme is used in cytochrome P450 synthesis
- INH (Isonicotinic acid hydrazide) ↓ availability pyridoxal phosp
  may also affect heme synthesis.
- ↑↑ glucose concentration prevents induction of ALA synthase
  ↳ glucose is used to relieve the acute attack of

Porphyrias: inborn errors of metabolism associated with biosynt
heme
↑↑ porphyrins / their precursors (ALA + PBG)
- erythropoietic porphyrias
- hepatic porphyrias.

Enzyme (↓/x)	Disorder
ALA synthase	Sideroblastic anaemia
PBG-deaminase/UPG-I-synthase	acute intermittent porp

↳ ↑ PBG & ALA in uru
- urine gets darkened
- peak at 400nm

expressed after puberty.
↳ abdominal pain, vomi abnormality
↳ neuropsychiatric de due to ↓ tryptophan accumulation of Trp and Tryptamine

UPG decarboxylase

Porphyria cutanea tar
- most common porphy
- cutaneus photosensitivity
- ALA, PBG leads to neuro.
- visceral manifestation

meth-haemoglobin → $Fe^{2+} \rightarrow Fe^{3+}$ in haemoglobin

there is around 1-2% met-Hb in body.

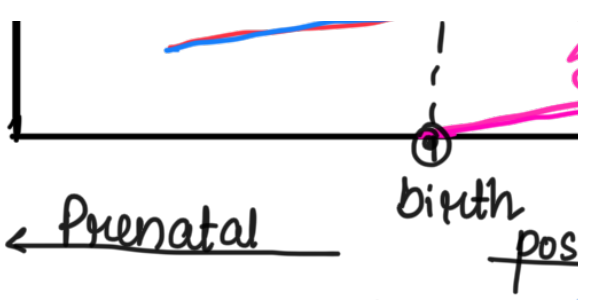
1 haemoglobin → 4 heme + 4 globin chain. (65 KDa)

※ when globin chains are taut (due 2,3-DPG), deoxyg occurs, when relaxed oxygenation occurs.

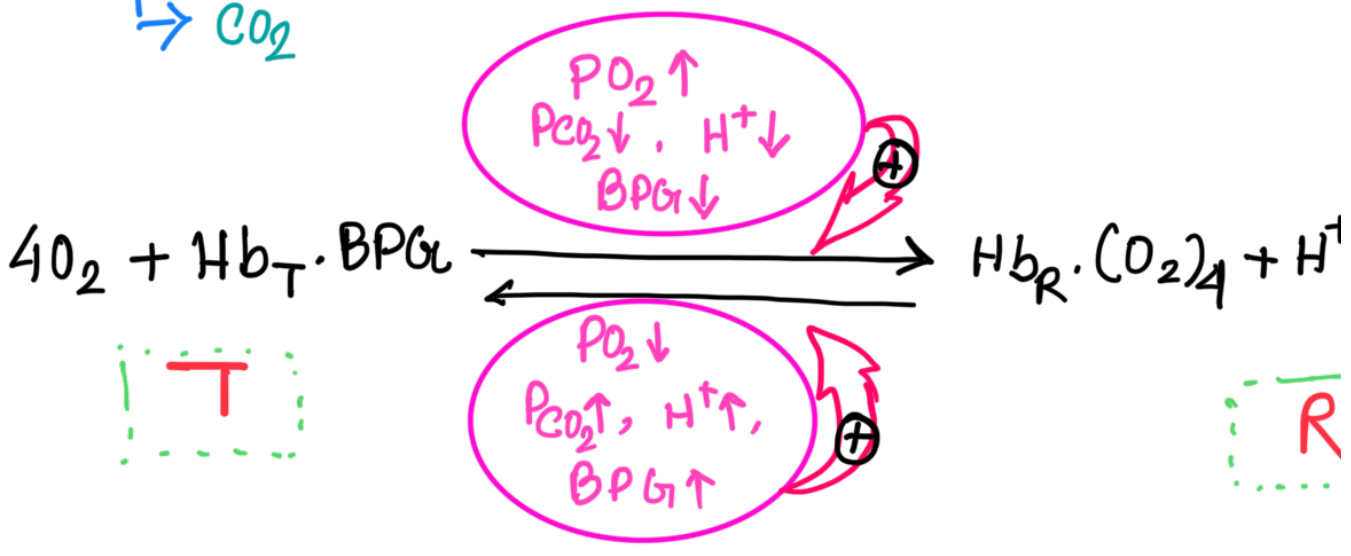
- globin is formed in RER.

HbA → $\alpha_2\beta_2$
HbA_2 → $\alpha_2\delta_2$
HbF → $\alpha_2\gamma_2$
↳ more affinity for O_2

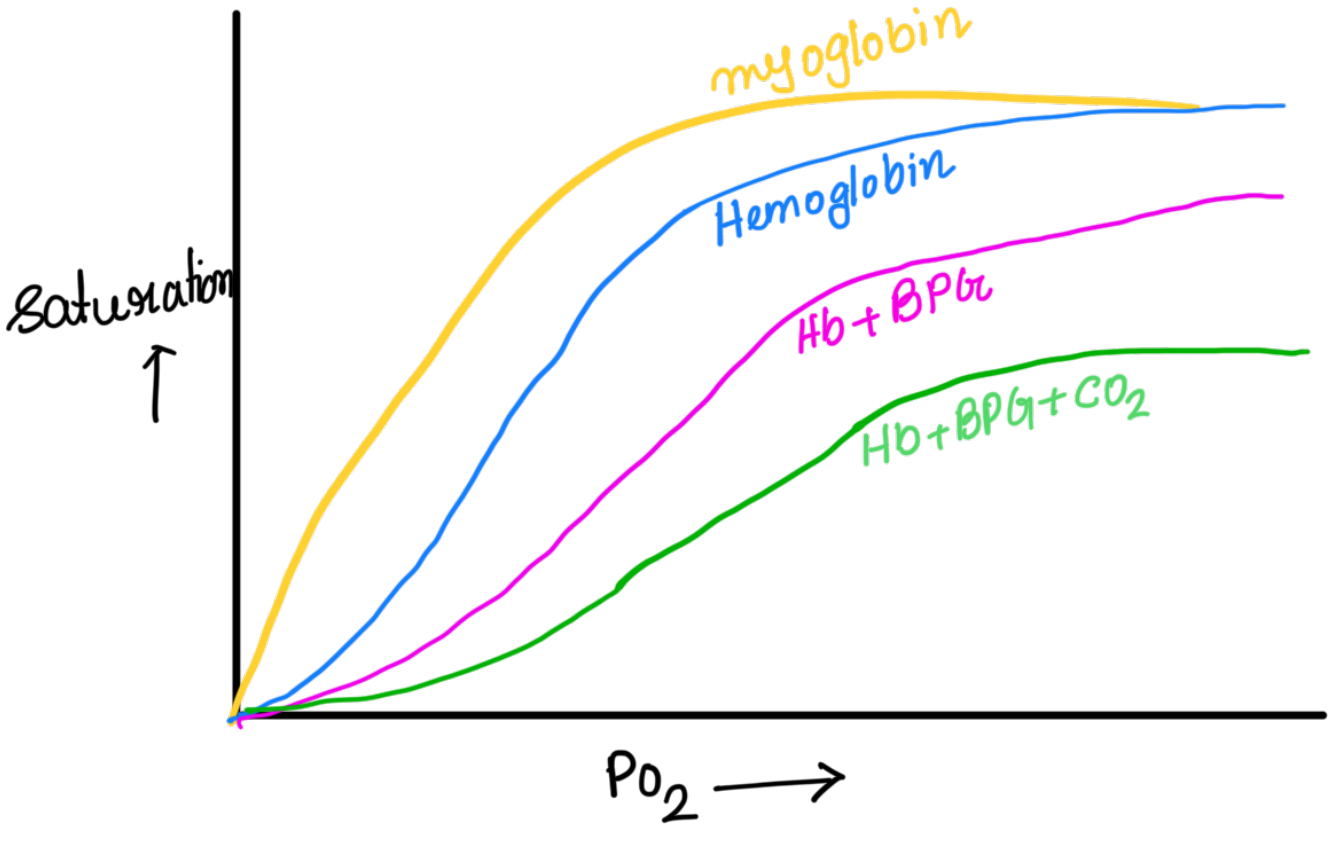
yolk sac → liver → spleen
6 w
3 bw
α
γ



- many substances act on Hb as an allosteric sub though Hb isn't an enzyme. allosteric behaviou shown.
  - → 2,3-DGP
  - → H^+
  - → CO_2



- in blood banking, 2,3-DPG is an limitation, becau it being a glycolysis product, we can not maint it.



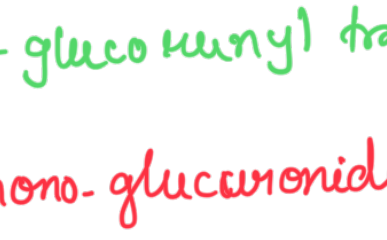
Hemoglobinopathies

Type	α-chain	β-chain	γ-chain	Disease	Fea
Hb bart	×	- - - -	↑↑	α-thalassemia (4 alleles affected)	γ-t
Hb H	↓↓	↑↑	- - - -	α-thalassemia	β-

$HbA_2 > 3.5\%$	↑↑	↓/x	↑↑	β-thalassemia (β chains affected)
HbS	=	glu → valine (6th posi)	=	
HbC	=	glu → lysine (6th posi)	=	
HbSc	=		=	

Co-operative behaviour in gas binding —

O_2 bind → salt bridge breaks → further O_2 bind



Heme catabolism