



# Hemoglobin

## An overview and more

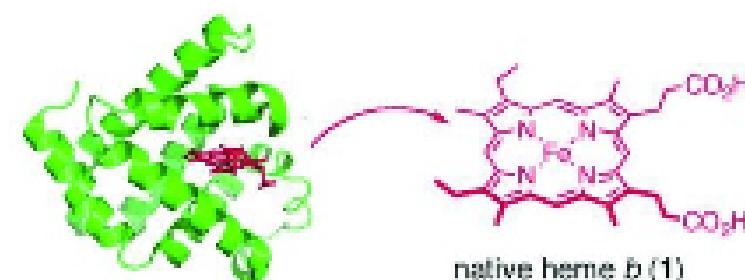
Prof. Mamoun Ahram  
Hematopoietic-lymphatic system  
2020





# Hemoproteins

- Many proteins have heme as a prosthetic group called hemoproteins.



*A prosthetic group is a tightly bound, specific non-polypeptide unit required for the biological function of some proteins. The prosthetic group may be organic (such as a vitamin, sugar, or lipid) or inorganic (such as a metal ion), but is not composed of amino acids.*

Mb, Hb

Transfer and storage  
 $O_2$

NOS, P450

Oxygenation reaction  
 $O_2 + e^-$

Cyt c, Cyt b<sub>5</sub>

Electron transfer  
 $e^-$

heme-containing  
sensor proteins

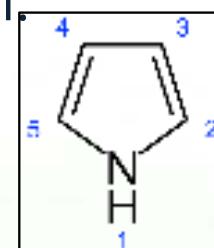
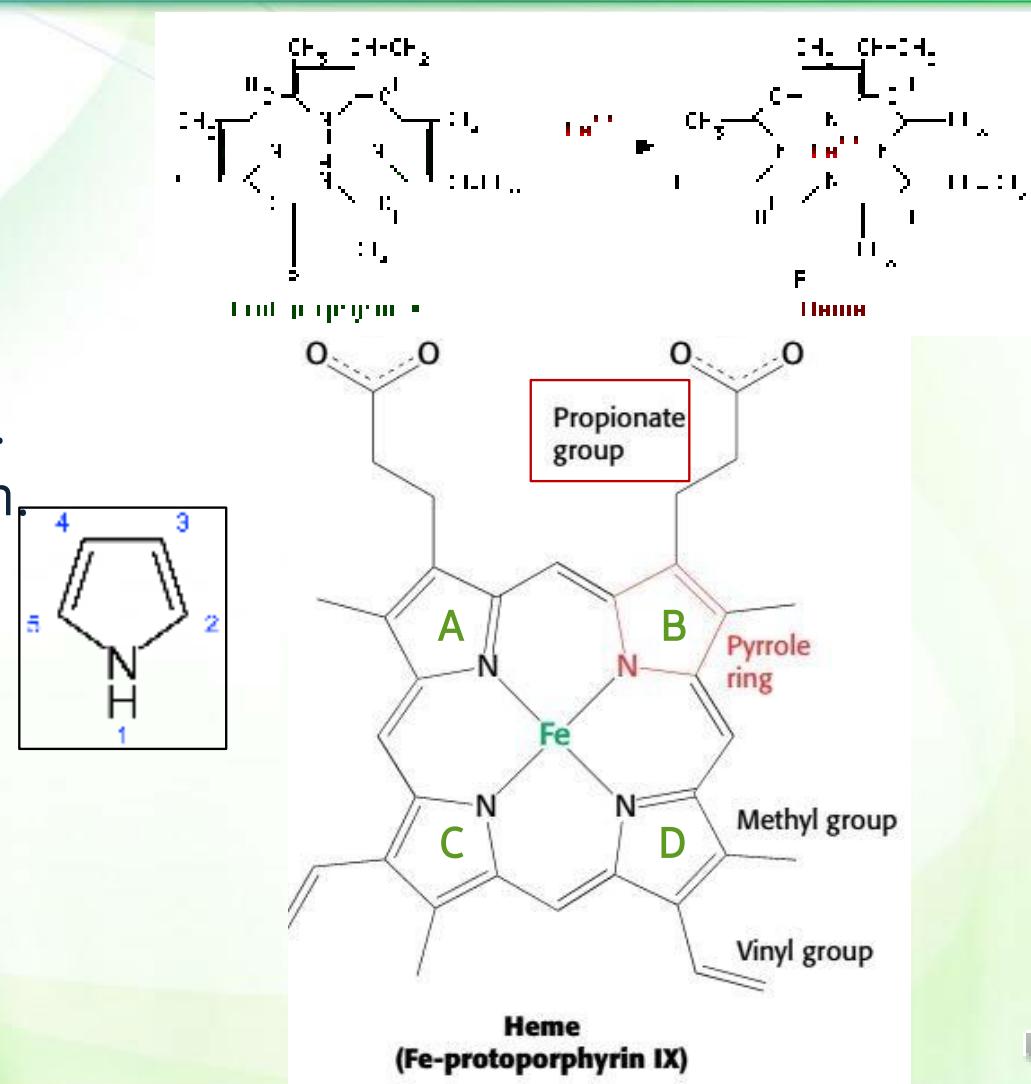
I. Heme sensors  
II. Gas sensors ( $O_2$ , CO, NO)





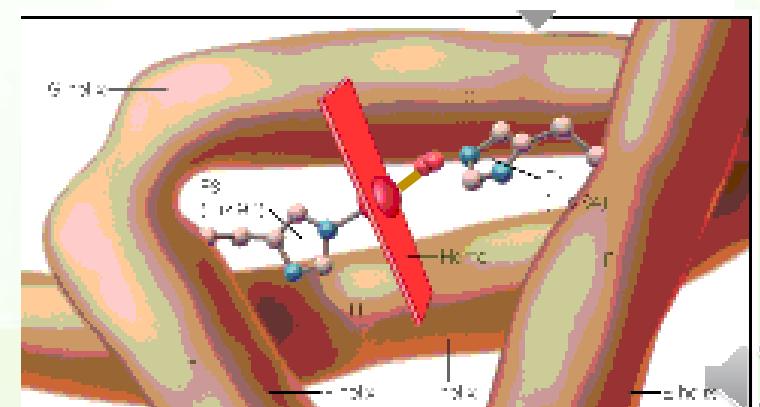
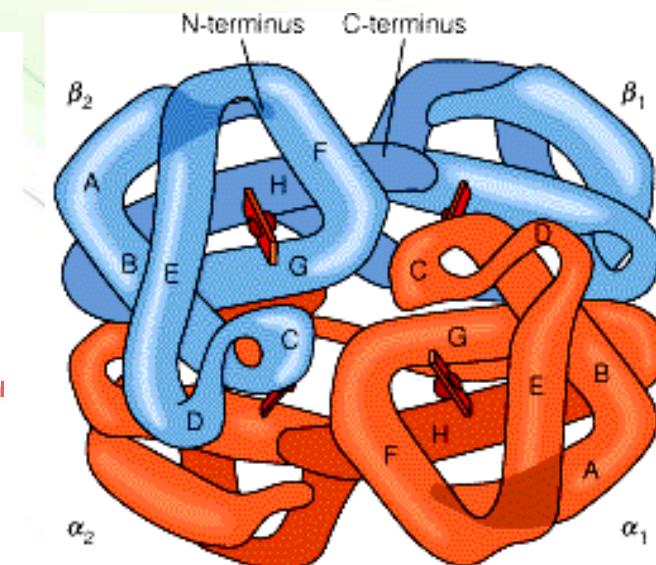
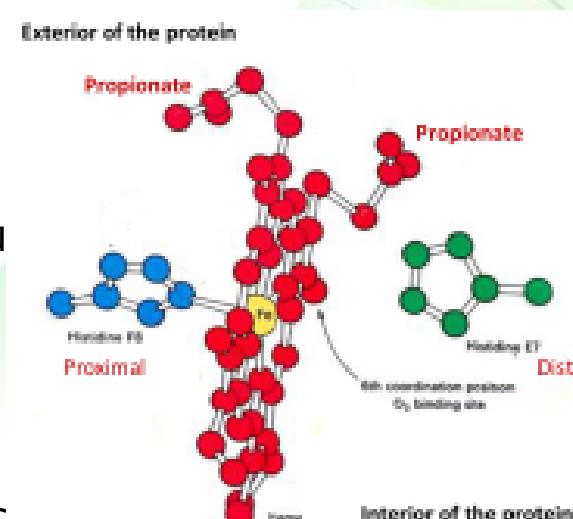
# Heme structure

- It is a complex of protoporphyrin IX + Iron ( $\text{Fe}^{2+}$ ).
- The porphyrin is planar and consists of four rings (designated A-D) called pyrrole rings.
- Each pyrrole can bind two substituents.
- Two rings have a propionate group each.
- Note: the molecule is hydrophobic.*
- Fe has six coordinates of binding.



# Structure of hemoglobin

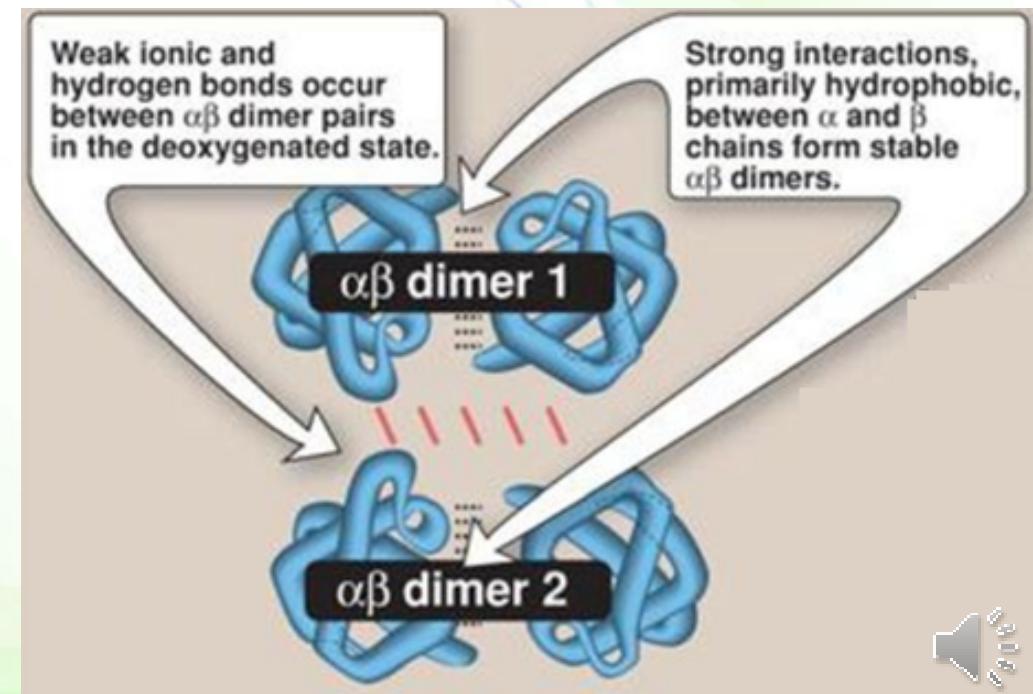
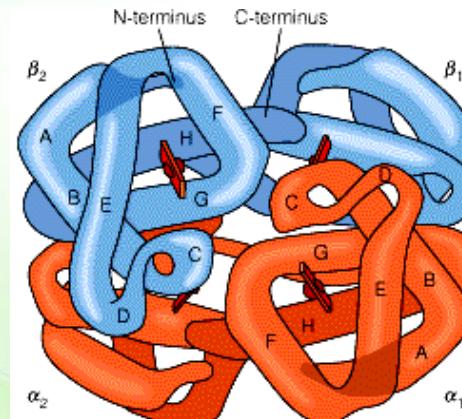
- Hb is a globular protein.
  - Amino acid distribution
    - Positions of two histidine residues
    - Proximal and distal
- It is an allosteric protein.
  - Multiple subunits ( $2\alpha + 2\beta$ )
    - $\alpha$  polypeptide = 141 amino acids
    - $\beta$  polypeptide = 146 amino acids
  - Altered structure depending on bound molecules
  - Positive cooperativity towards oxygen
  - Regulated by allosteric effectors



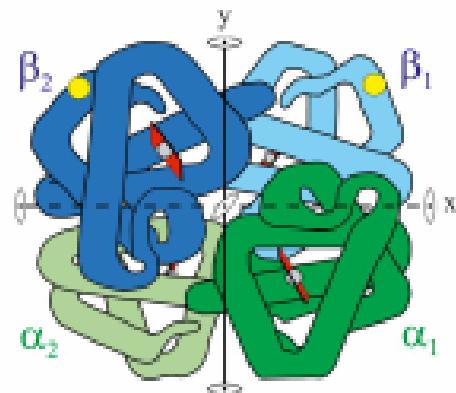


# How are the subunits bound?

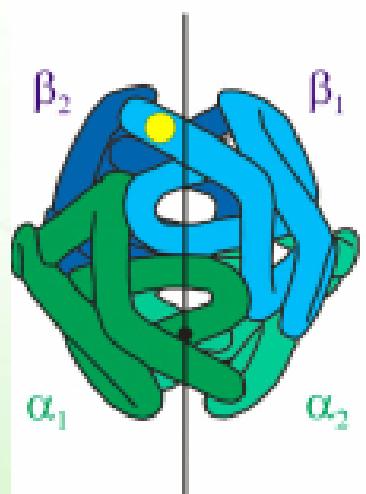
- A dimer of dimers (I made up this term)
  - $(\alpha\text{-}\beta)^2$
  - Note how they interact with each other.



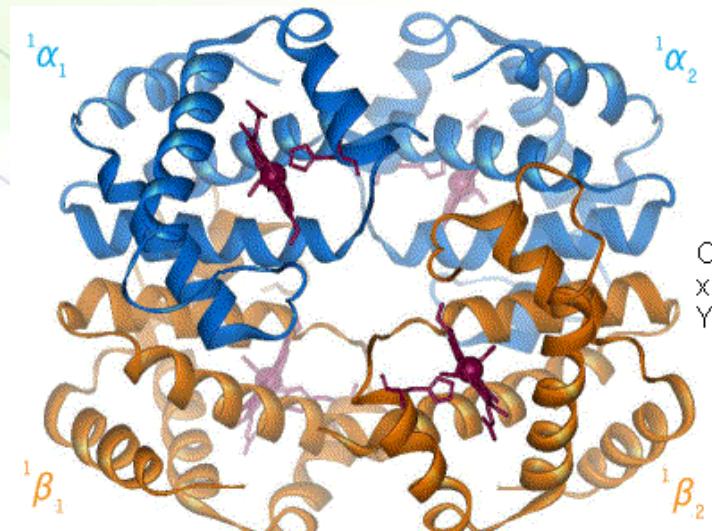
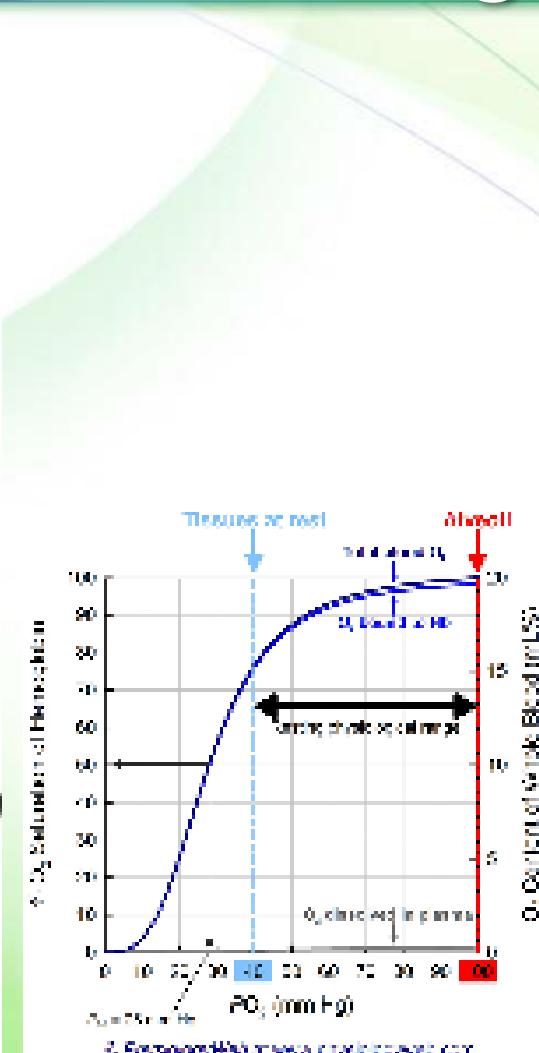
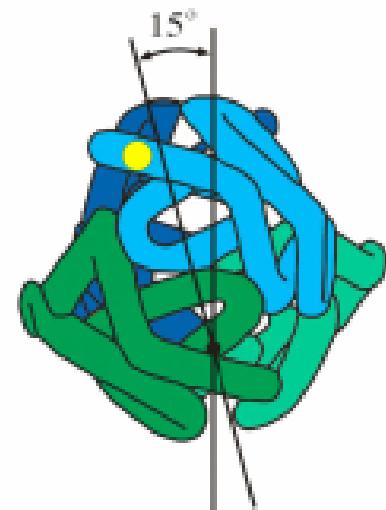
# Structural change of hemoglobin



deoxy T



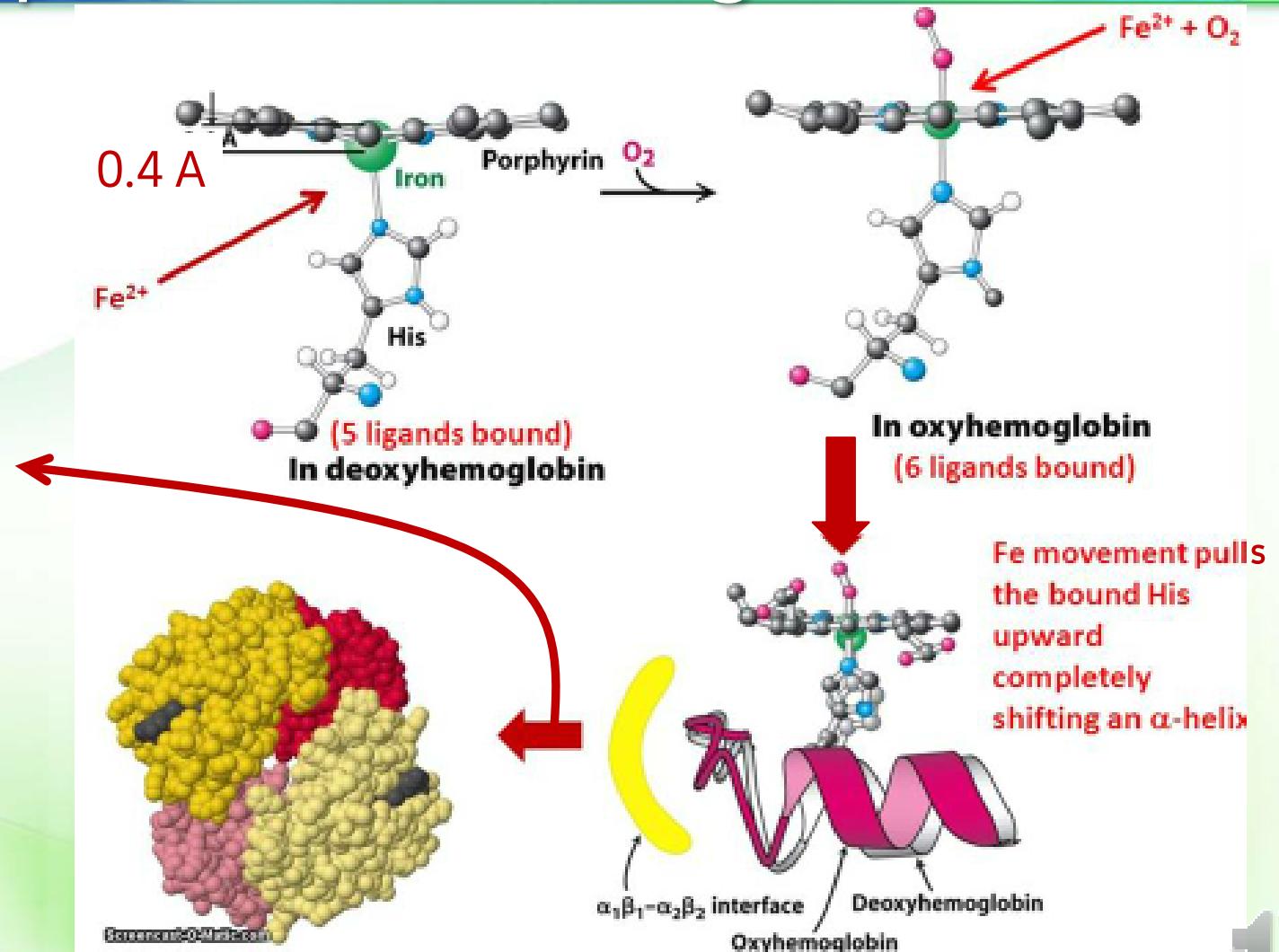
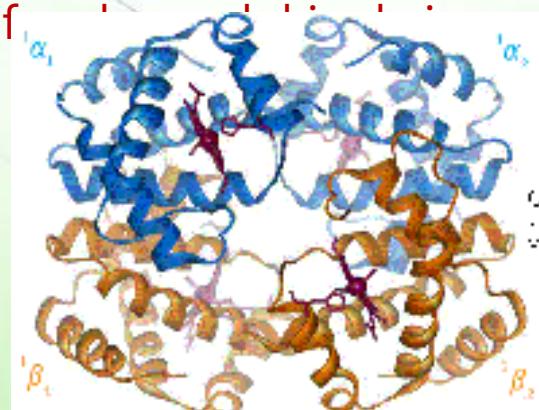
oxy R



# Structural amplification change



- Changes in tertiary structure of individual hemoglobin subunits
- Breakage of the electrostatic bonds at the other oxygen-binding sites

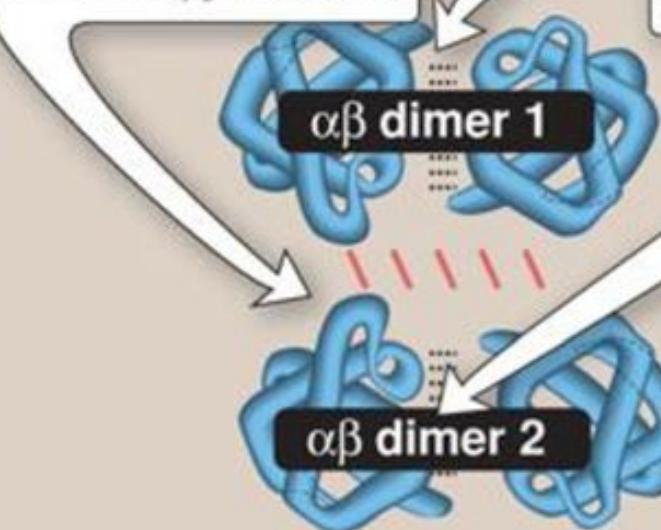


# Electrostatic interactions are broken



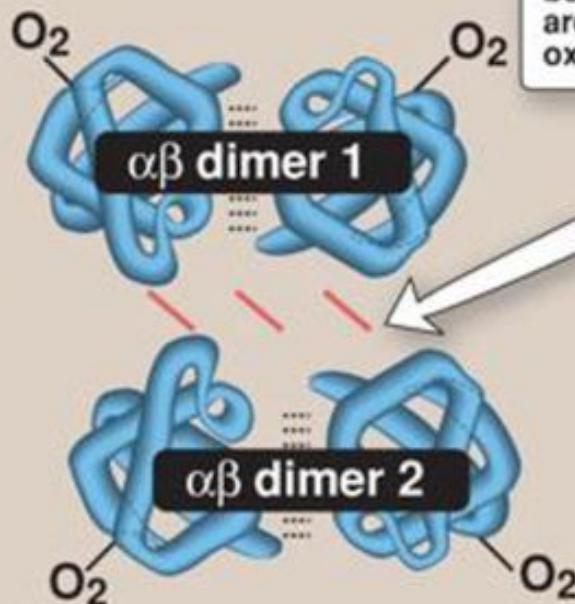
Weak ionic and hydrogen bonds occur between  $\alpha\beta$  dimer pairs in the deoxygenated state.

Strong interactions, primarily hydrophobic, between  $\alpha$  and  $\beta$  chains form stable  $\alpha\beta$  dimers.



"T," or taut, structure of deoxyhemoglobin

Some ionic and hydrogen bonds between  $\alpha\beta$  dimers are broken in the oxygenated state.

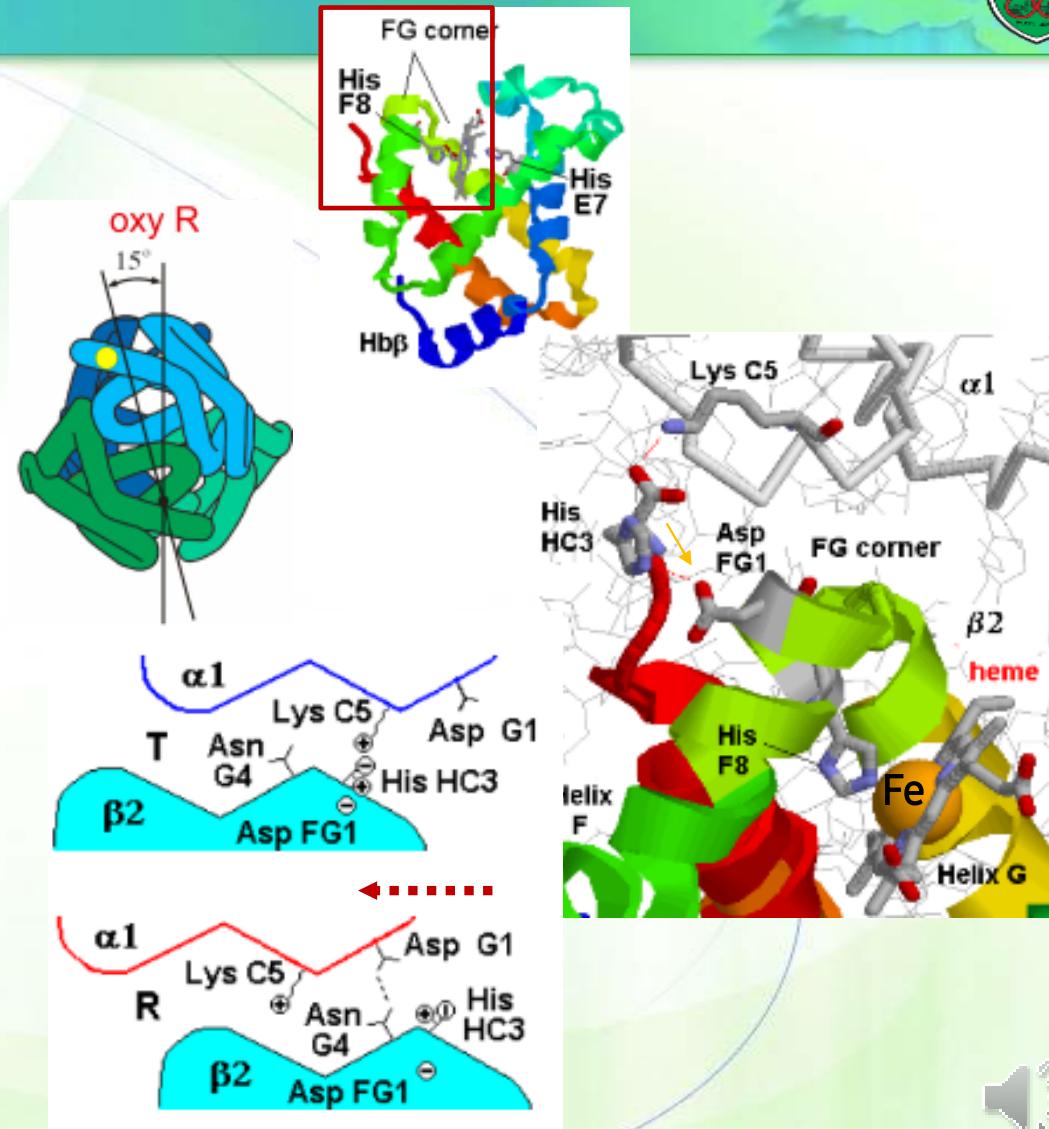


"R," or relaxed, structure of oxyhemoglobin



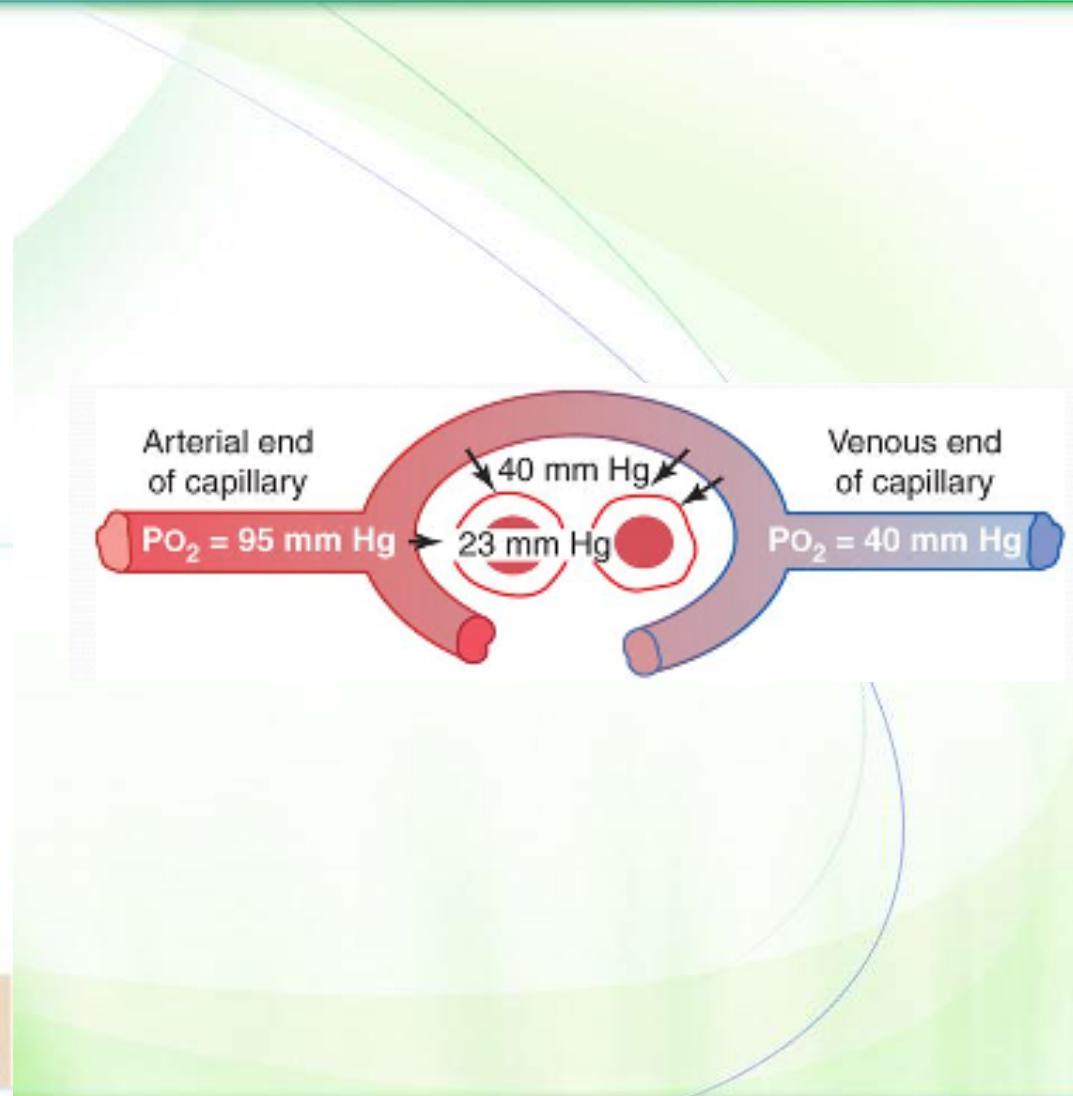
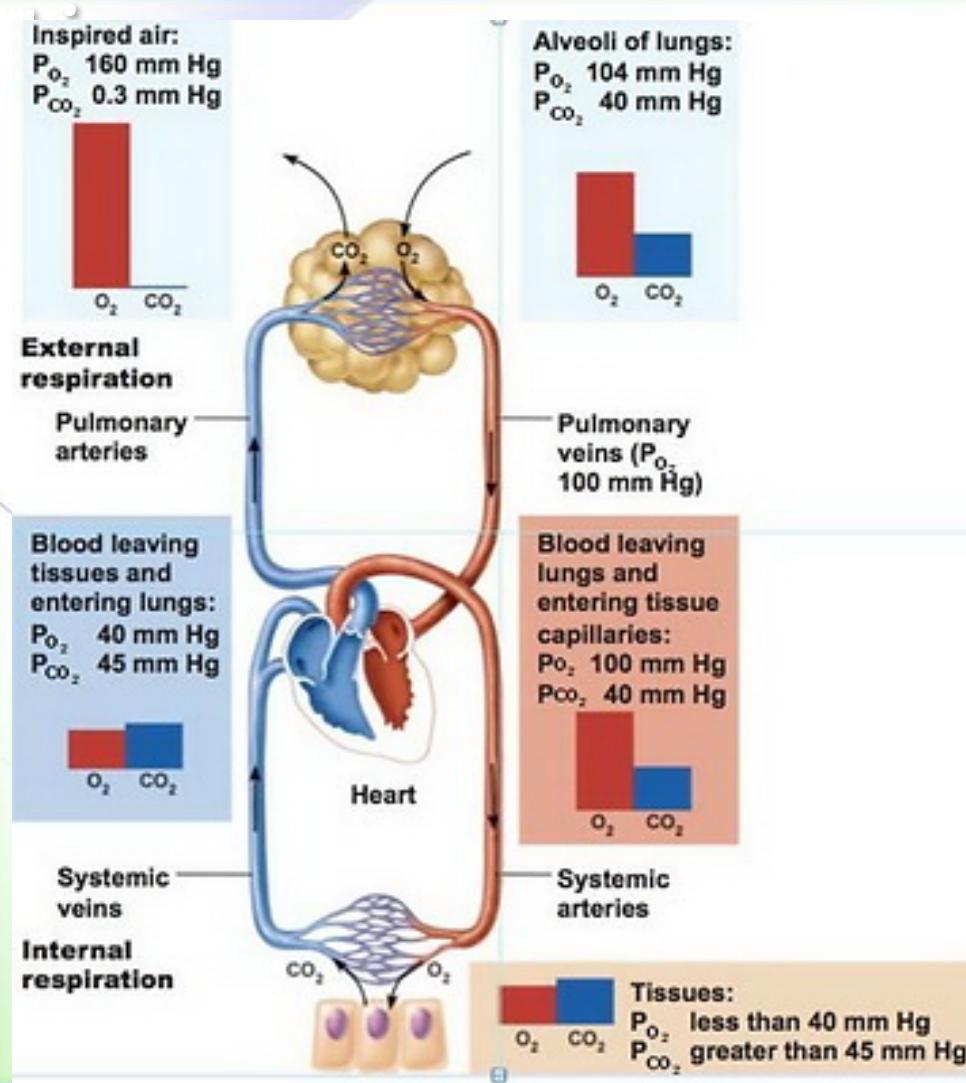
# Let's zoom in...

- In the T-state, The C-terminal His146 amino acid of the  $\beta$ -globin forms two ion pairs :
  - Its C-terminal carboxylate group ion-pairs to Lys C5 of the opposite  $\alpha$ -globin,  $\beta$ 2 to  $\alpha$ 1 or  $\beta$ 1 to  $\alpha$ 2
  - its side chain ion pairs to the Asp FG1 of the same  $\beta$ -globin.
- When  $O_2$  binds, the  $\alpha 1\beta 1$  globin rotates  $15^\circ$  relative to axis of deoxy  $\alpha 2\beta 2$ , the  $\alpha 1$  surface slides and His146 relocates and loses contact with Lys C5 and Asp FG1.
- A hydrogen bond is formed between Asp of  $\alpha$  chin with Asn of  $\beta$  chain stabilizing the R form of hemoglobin.





# Oxygen distribution in blood versus





# Oxygen saturation curve

- The saturation curve of hemoglobin binding to  $O_2$  has a sigmoidal shape.
- It is allosteric.
- At 100 mm Hg, hemoglobin is 95-98% saturated (oxyhemoglobin).
- As the oxygen pressure falls, oxygen is released to the cells.
- Note: at high altitude (~5000 m), alveolar  $pO_2 = 75 \text{ mmHg}$ .*

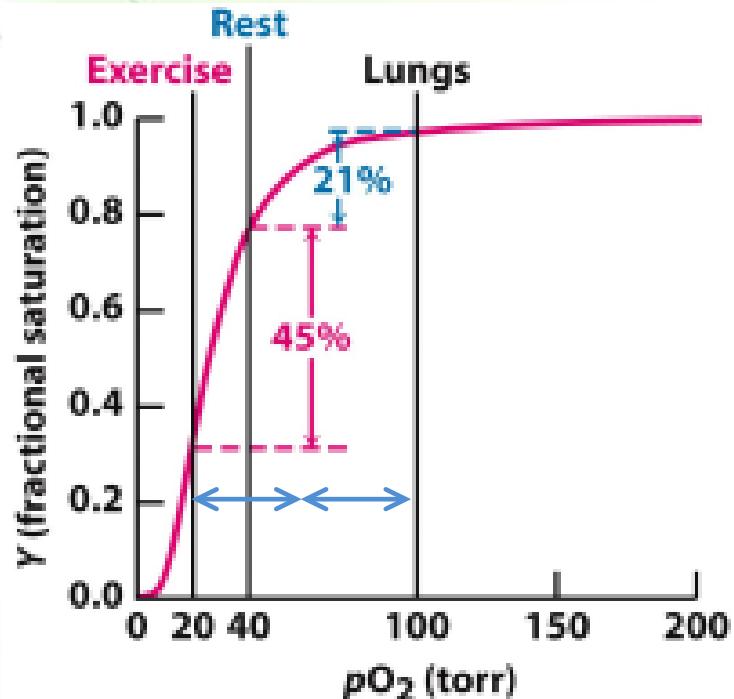


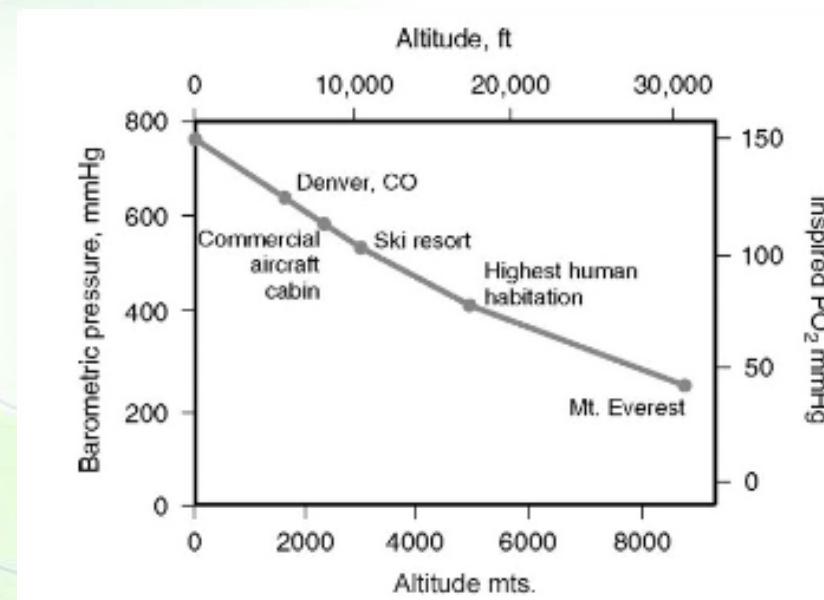
Figure 7.12  
Biochemistry, Tenth Edition  
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# pO<sub>2</sub> at different altitudes

| Altitude (feet) | Atmospheric Pressure (mm/Hg) | PAO <sub>2</sub> (mm/Hg) | PVO <sub>2</sub> (mm/Hg) | Pressure Differential (mm/Hg) | Blood Saturation (%) |
|-----------------|------------------------------|--------------------------|--------------------------|-------------------------------|----------------------|
| Sea Level       | 760                          | 100                      | 40                       | 60                            | 98                   |
| 10,000          | 523                          | 60                       | 31                       | 29                            | 87                   |
| 18,000          | 380                          | 38                       | 26                       | 12                            | 72                   |
| 22,000          | 321                          | 30                       | 22                       | 8                             | 60                   |
| 25,000          | 282                          | 7                        | 4                        | 3                             | 9                    |
| 35,000          | 179                          | 0                        | 0                        | 0                             | 0                    |





# Positive cooperativity

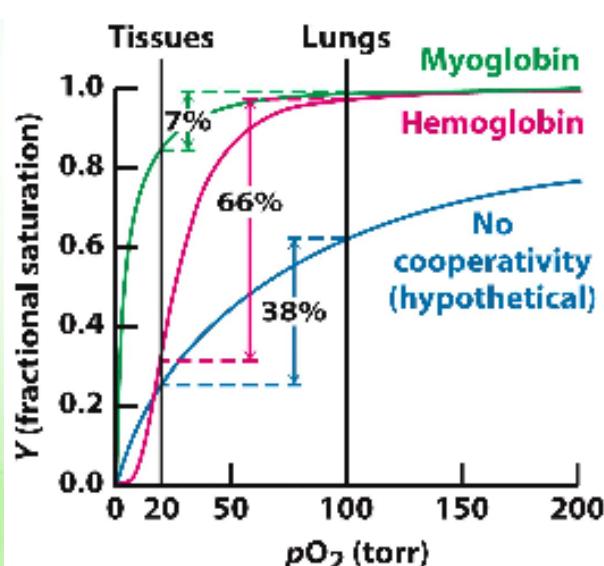
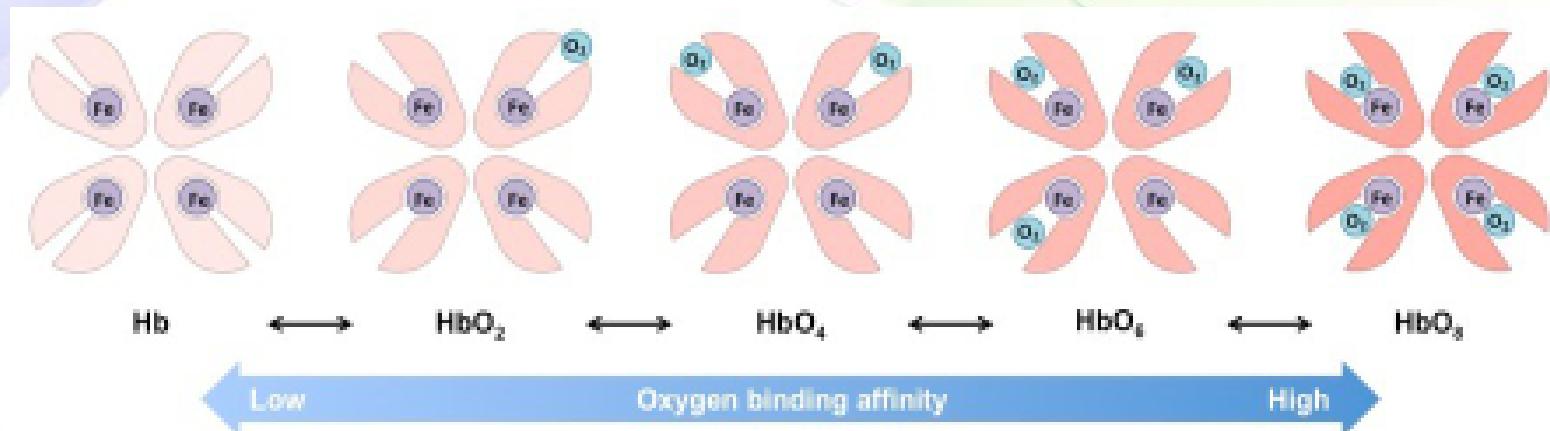


Figure 7.9  
Allosteric, Semireactive  
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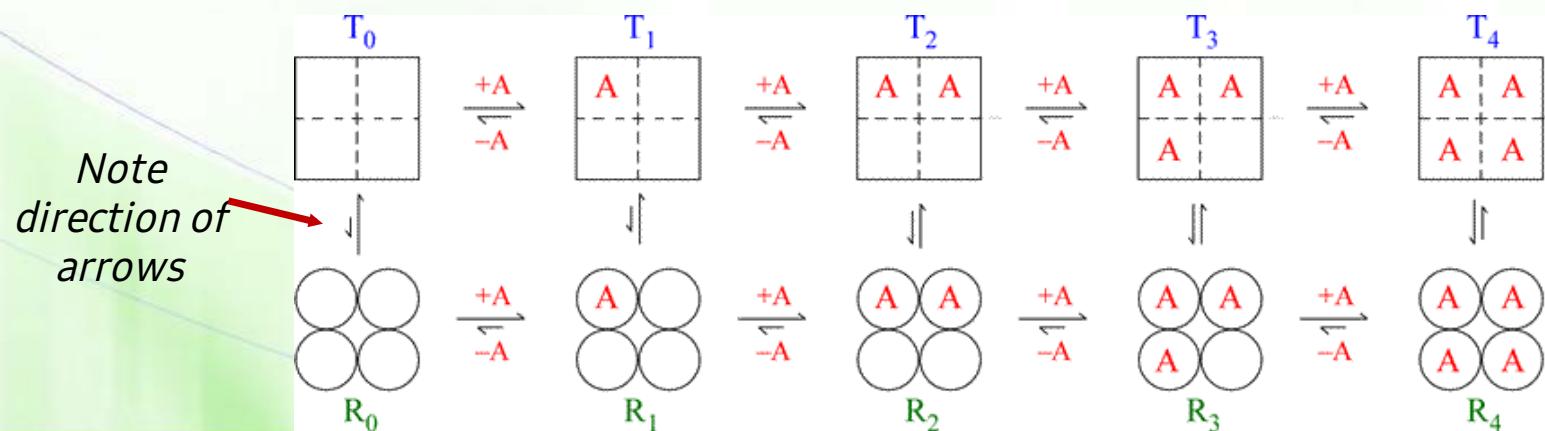


# The concerted model (MWC model)

## Most accurate

The protein exists in two states in equilibrium: T (taut, tense) state with low affinity and R (relaxed) state with high affinity.

- Increasing ligand concentration drives the equilibrium between R and T toward the R state (**positive cooperativity**) **sigmoidal curve**
  - The effect of ligand concentration on the conformational equilibrium is a **homotropic effect (oxygen)**.
  - Other effector molecules that bind at sites distinct from the ligand binding site and thereby affect the R and T equilibrium in either direction are called **heterotropic effectors (to be discussed)**.

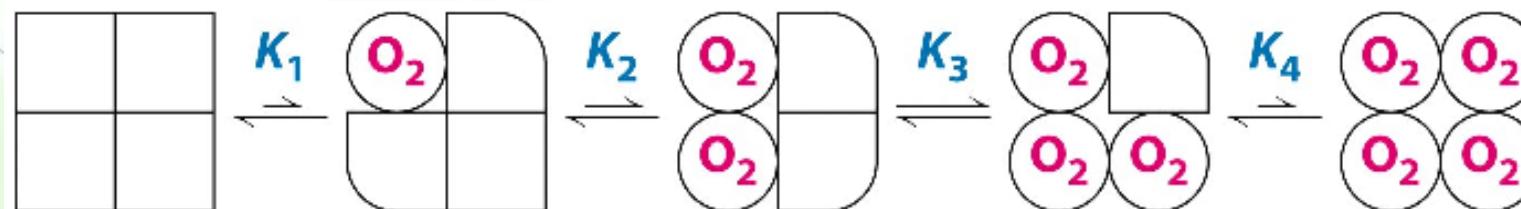




# The sequential, induced fit, or KNF model

• **Less accurate** The subunits go through conformational changes independently of each other, but they make the other subunits more likely to change, by reducing the energy needed for subsequent subunits to undergo the same conformational change.

- Ligand binding may also result in negative cooperativity.
  - The MWC model only suggests only positive cooperativity.



**Figure 7.14**  
*Biochemistry, Seventh Edition*  
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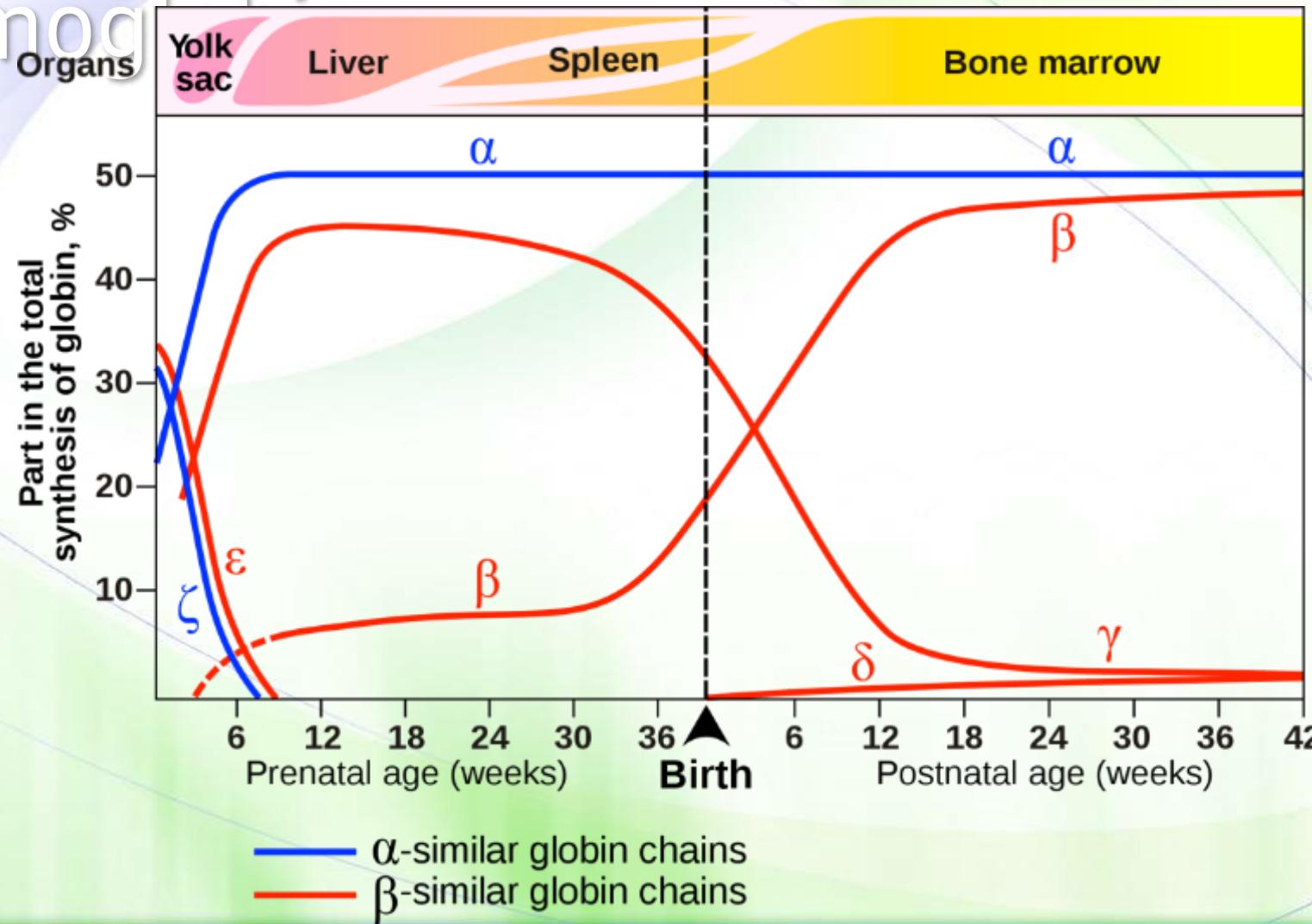


It is not only one hemoglobin





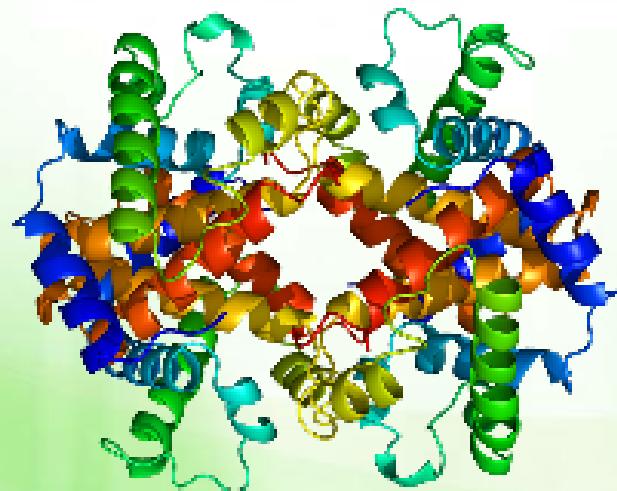
# Developmental transition of hemoglobin





# The embryonic stage

- Hemoglobin synthesis begins in the first few weeks of embryonic development within the yolk sac.
- The major hemoglobin (HbE Gower 1) is a tetramer composed of 2 zeta ( $\zeta$ ) chains and 2 epsilon ( $\epsilon$ ) chains
- Other forms exist: HbE Gower 2 ( $\alpha_2\epsilon_2$ ), HbE Portland 1 ( $\zeta_2\gamma_2$ ), HbE Portland 2 ( $\zeta_2\beta_2$ ).





# Beginning of fetal stage

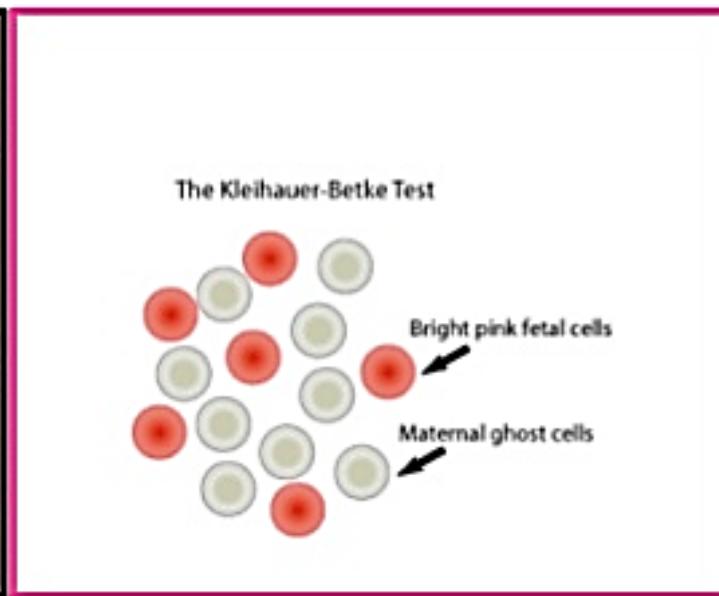
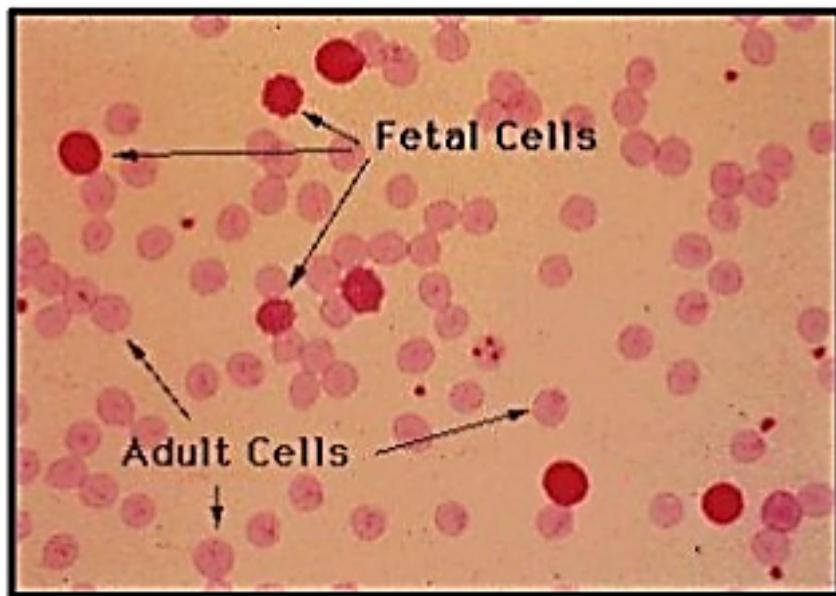
- By 6-8 weeks of gestation, the expression of embryonic hemoglobin declines dramatically and fetal hemoglobin synthesis starts from the liver.
- Fetal hemoglobin consists of two  $\alpha$  polypeptides and two gamma ( $\gamma$ ) polypeptides ( $\alpha_2\gamma_2$ )
- The  $\alpha$  polypeptides remain on throughout life.





# Beginning of adult stage

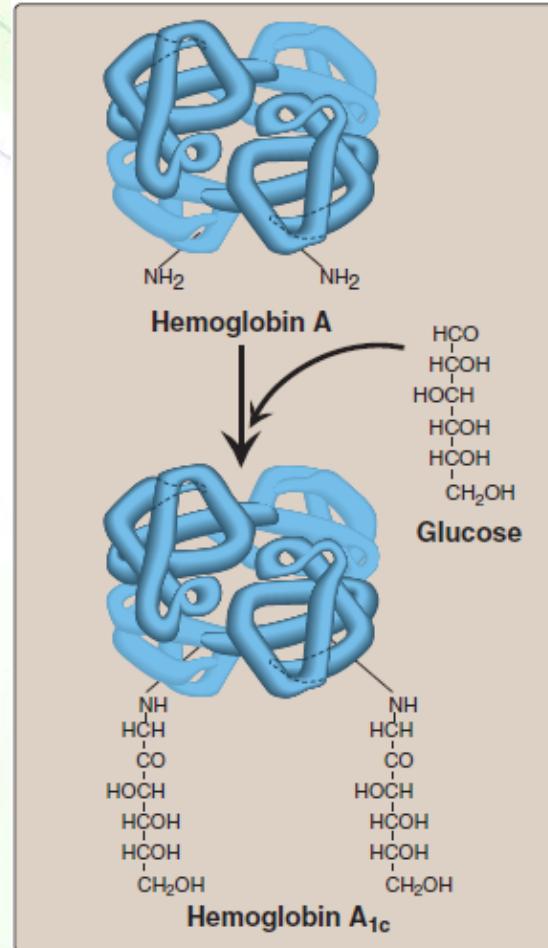
- Shortly before birth, there is a gradual switch to adult  $\beta$ -globin.
- Still, HbF makes up 60% of the hemoglobin at birth, but 1% of adults.
- At birth, synthesis of both  $\gamma$  and  $\beta$  chains occurs in the bone marrow.





# Adult hemoglobins

- The major hemoglobin is HbA1 (a tetramer of 2  $\alpha$  and 2  $\beta$  chains).
- A minor adult hemoglobin, HbA2, is a tetramer of 2  $\alpha$  chains and 2 delta ( $\delta$ ) chains.
- HbA can be glycosylated with a hexose and is designated as HbAc.
  - The major form (HbA1c) has glucose molecules attached to valines of  $\beta$  chains.
  - HbA1c is present at higher levels in patients with diabetes mellitus.





# Advantages of HbA1c testing

- Blood **fasting** glucose level is the concentration of glucose in your blood at a single point in time, i.e. the very moment of the test.
- HbA1c provides a longer-term trend, similar to an average, of how high your blood sugar levels have been over a period of time (2-3 months).
- HbA1c can be expressed as a percentage (DCCT unit) or as a value in mmol/mol (IFCC unit). **IFCC is new.**
- Limitations of HbA1c test:
  - It does not capture short-term variations in blood glucose, exposure to hypoglycemia and hyperglycemia, or the impact of blood glucose variations on individuals' quality of life.





# Table

| BLOOD GLUCOSE |       | STATUS       | HbA1c |          |
|---------------|-------|--------------|-------|----------|
| mmol/L        | mg/dL |              | %     | mmol/mol |
| 5.4           | 97    | Normal       | 5     | 31       |
| 7.0           | 126   |              | 6     | 42       |
| 8.6           | 155   | Pre-Diabetes | 7     | 53       |
| 10.2          | 184   | Diabetes     | 8     | 64       |
| 11.8          | 212   | Diabetes     | 9     | 75       |
| 13.4          | 241   |              | 10    | 86       |
| 14.9          | 268   | Diabetes     | 11    | 97       |
| 16.5          | 297   |              | 12    | 108      |





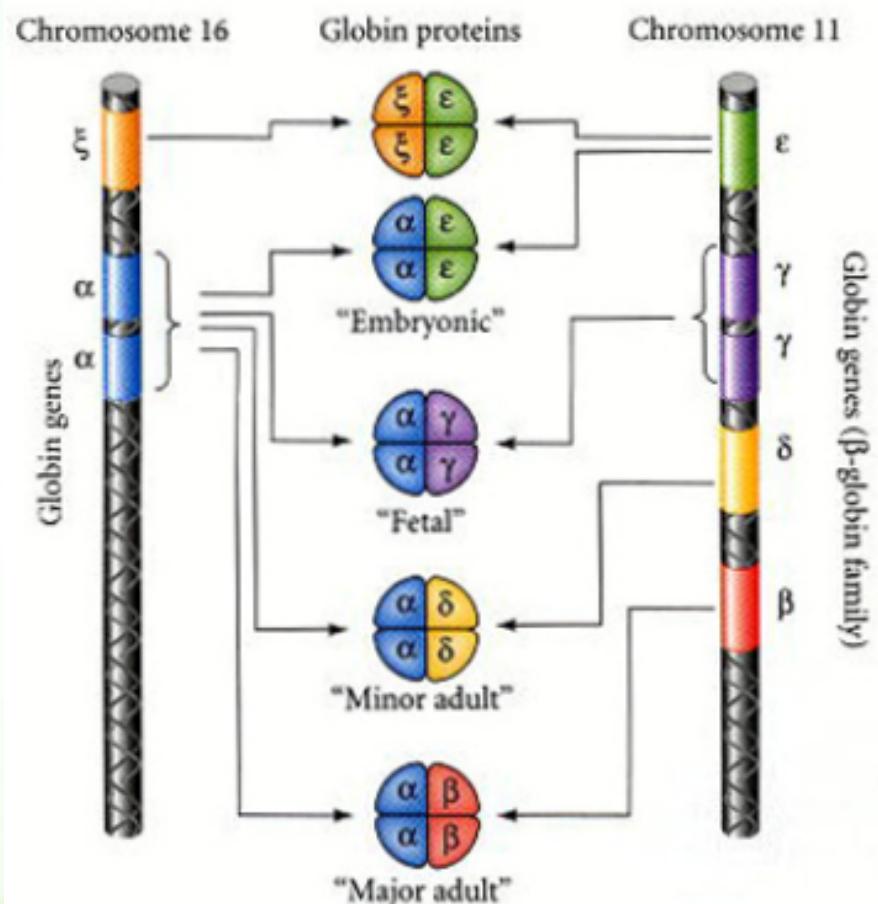
# Genetics of globin synthesis





# The genes

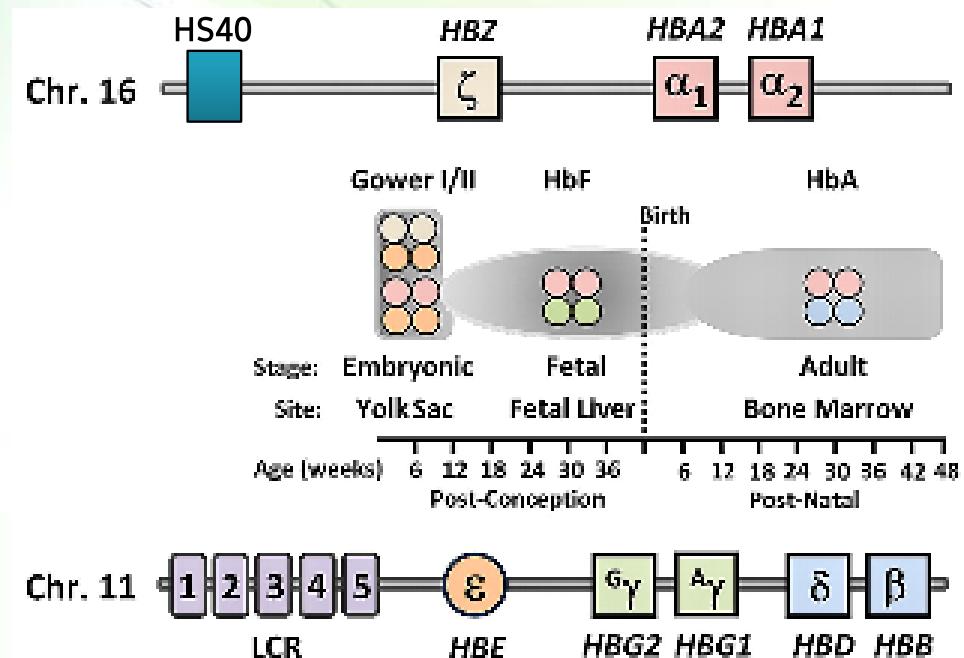
- The  $\alpha$  gene cluster contains two  $\alpha$  genes ( $\alpha_1 \alpha_2$ ) and  $\zeta$  (zeta) gene.
- The  $\beta$  gene cluster contains  $\beta$  gene in addition to  $\epsilon$  (epsilon) gene, two  $\gamma$  (gamma) genes, and  $\delta$  (delta) gene.
- The gene order parallels order of expression.
- Genetic switching is controlled by a transcription factor-dependent developmental clock, independent of the environment.
- Premature newborns follow their gestational age.





# Locus structure

- Each gene has its promoter and regulatory sequences (activators, silencers).
- The  $\alpha$  gene cluster is controlled by HS40 region.
- The  $\beta$ -globin cluster is controlled by a master enhancer called locus control region (LCR).



# The mechanism of regulation

- The mechanism requires *timed* expression of regulatory transcription factors for each gene, epigenetic regulation (e.g. acetylation, methylation), and chromatin looping.
- Note: treatment!!

