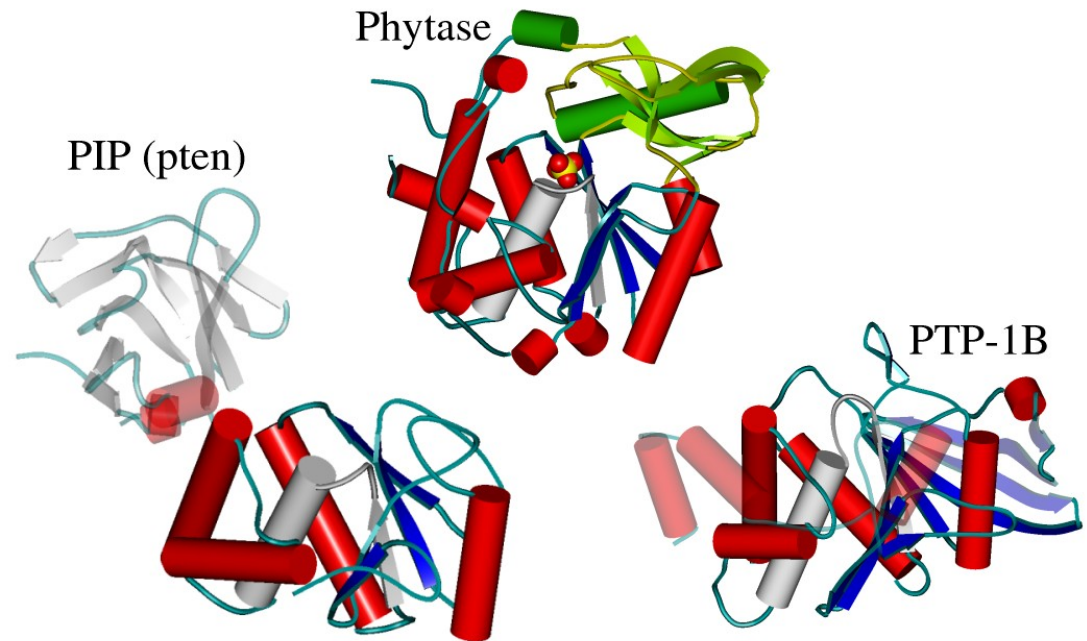
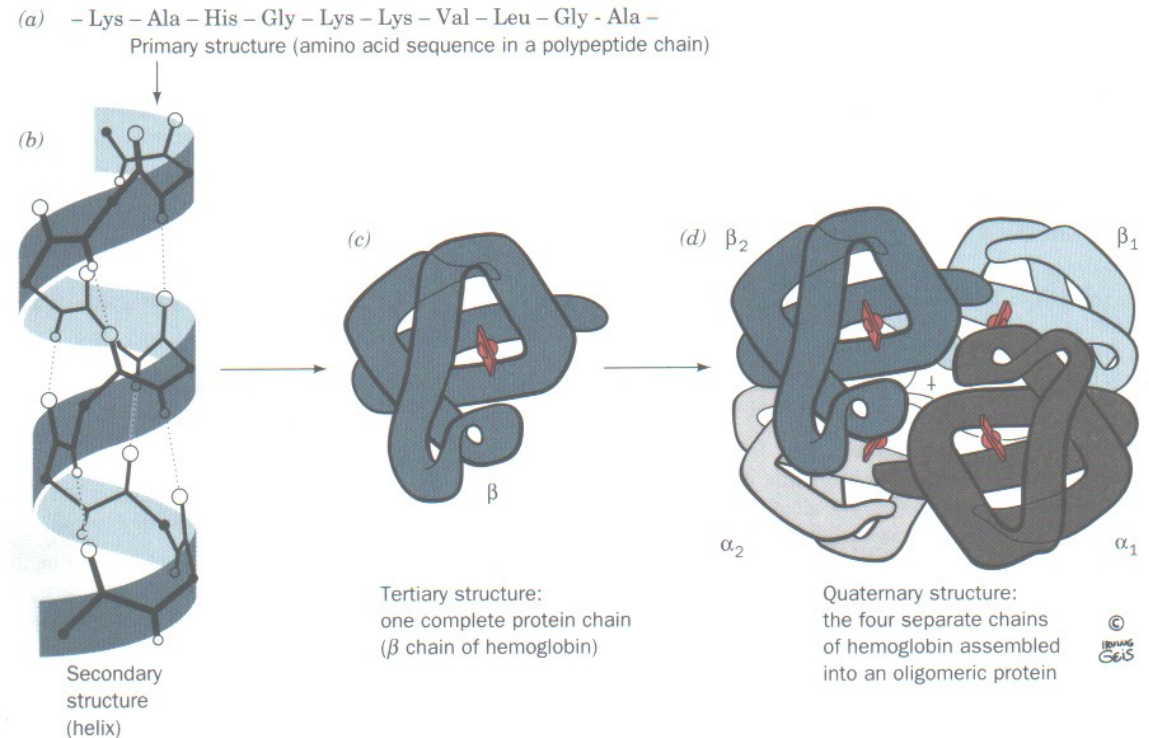


Chapter 7: Covalent Structure of Proteins

**Voet & Voet:
Pages 163-164,
185-194**



Structure & Function



Function is best understood in terms of structure

Four levels of structure that apply to proteins

Primary – sequence of residues

Secondary – local spatial conformation of backbone

Tertiary – overall fold or 3D arrangement of polypeptide

Quaternary – spatial arrangement of subunits in a multisubunit protein

Primary Structure Significance

Primary Structure is central to the formulation of modern concepts of Biochemistry

- (1) ***Structure Determination*** – primary sequence information is a prerequisite for structure determination and understanding molecular function
- (2) ***Evolutionary Relationships*** – sequence comparisons of related proteins in different organisms shed light upon protein function and relationships between organisms
- (3) ***Clinical Applications*** – many inherited diseases are caused by mutations that lead to amino acid changes in proteins; recognition of this fact has led to the development of therapies in many cases

Chemical Evolution

Voet & Voet calls the evolution of amino acid primary sequences

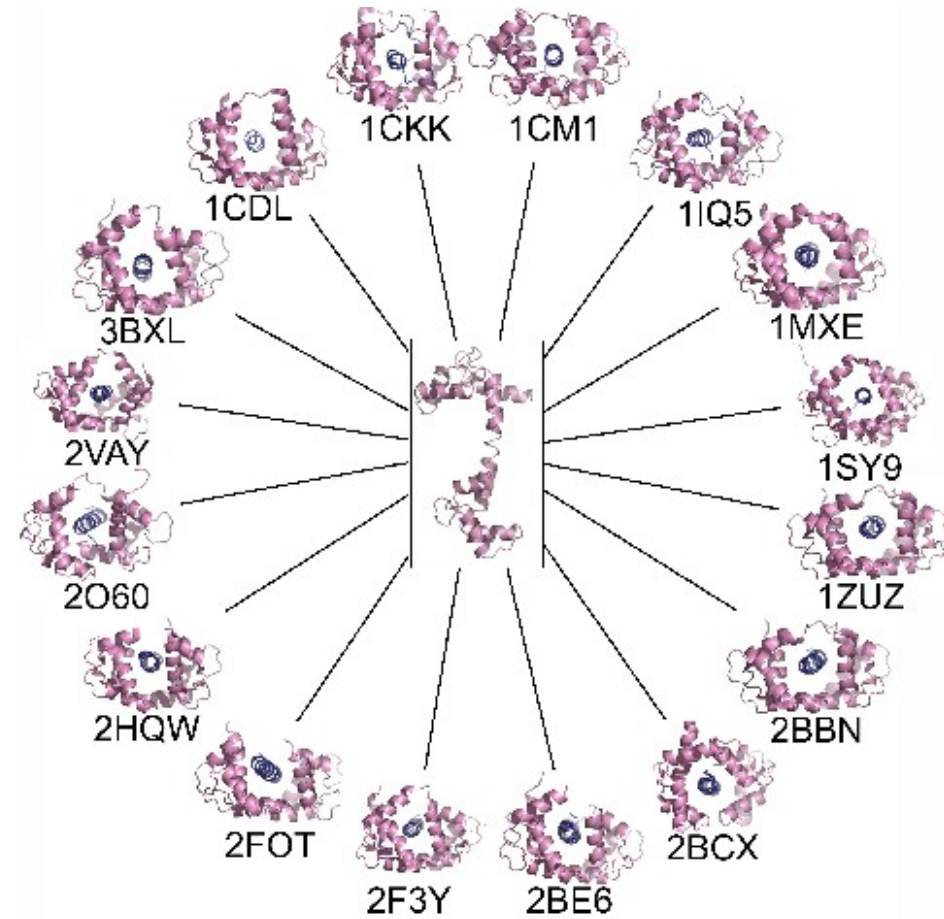
Chemical Evolution

Individuals/organisms are characterized by their genetic compositions

- *Specifies proteins that can be expressed, their quantities and schedule of appearance*

Evolutionary changes (random mutations) often alter protein structure

- *Mutations that are propagated somehow increase (or not decrease) the probability their owner will survive to reproduce*
- *Mutations that are deleterious or lethal in their effect rapidly die out*



Sickle Cell Anemia: An example of Chemical Evolution

Normal individuals

Red blood cells normally adopt a flexible, biconcave disk shape

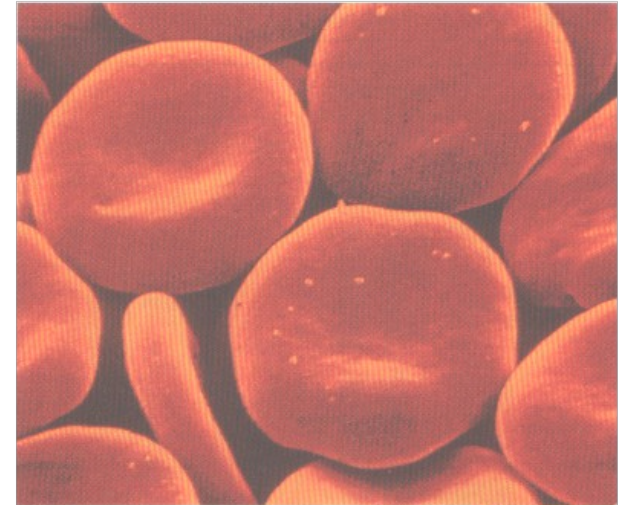
- Allows cells to pass through very small capillaries

Sickle Cell Anemia individual

Red blood cells form irregular, crescent-like shape under the low oxygen conditions typical in capillaries

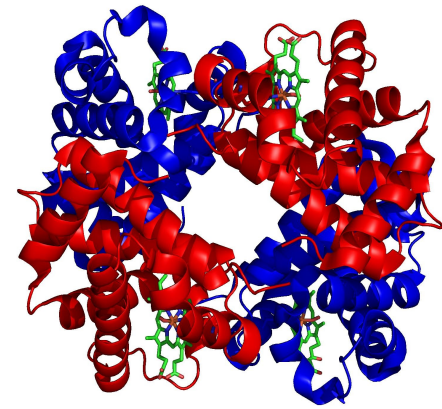
- Increased red blood cell rigidity and impedes blood flow through capillaries
- Tissue damage, pain, hemolytic anemia, early death

Normal Red Blood Cells



Sickle Red Blood Cells

Sickle Cell Anemia: A Molecular Disease

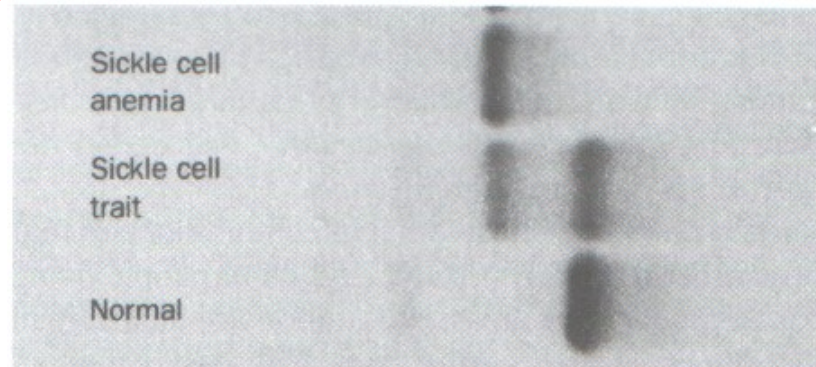


Single (point) mutation in hemoglobin (Hb) β subunit

- Pauling: HbS (sickle cell Hb) has ~2 fewer negative charges than Hb
- Trypsin (an enzyme) digests shows mutation is associated with β subunit
 - Trypsin specifically cuts polypeptides into smaller fragments
 - sequencing reveals nature of mutation; Glu 6 mutated to Val 6
- Deoxygenated HbS aggregates into filaments that deform red blood cells

Negative

Positive



Non-denaturing
Gel Electrophoresis

Sickle Cell Anemia: Why has mutation propagated?

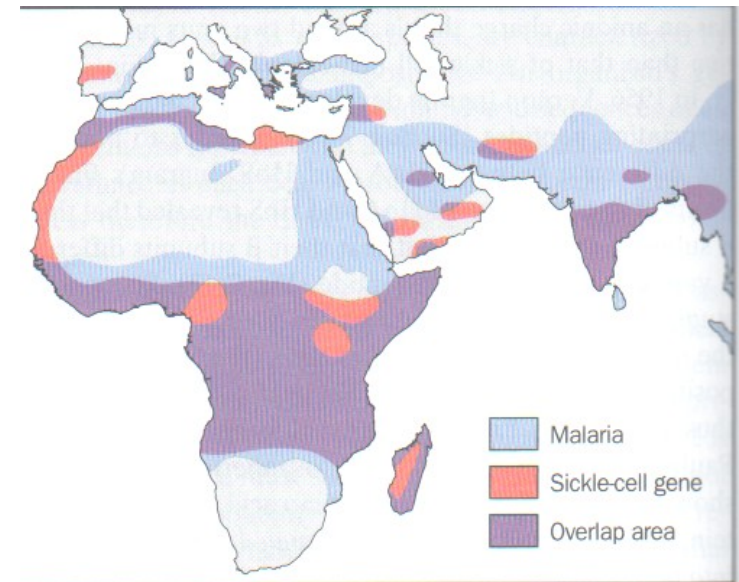
Sickle Cell Anemia is a deadly disease
(both chromosomes encode HbS)

All red blood cells sickle

Sickle Cell Trait confers resistance to
malaria (one chromosome encodes HbS)

Some red blood cells sickle

- Malaria kills ~ 1 million people per year (usually the very young)
- Individuals with Sickle Cell Trait have normal lifespans (though red blood cells have shorter lifespan)



Sickle cell trait occurs in the same areas of world as malaria



Sickle Cell Anemia: How does it confer resistance?

Malaria is caused by protozoan, *Plasmodium falciparum*

In Normal Red Blood Cells

- (1) Enters cell; reduces the pH
- (2) Cells stick to 'walls' of blood vessels and avoid removal by the spleen
- (3) Too many cells stick, blood flow is impeded and organs may fail

In [Sickle cell trait](#) Red Blood Cells

- (1) Enters cell; reduces the pH
Increases tendency to sickle
- (2) Sickle cells do not stick to walls of blood vessels and infected cells are removed by spleen
- (3) Blood flow remains adequate
- (4) Sickling also impairs *Plasmodium falciparum* replication

Neutral Drift: Species Variation

According to **evolutionary theory**, related species evolved from a common ancestor

- It follows that proteins in related species must also have evolved from a common ancestral protein
- **Homologous** – evolved or derived from a common ancestor

eg. Homologous primary sequences evolved from a common ancestor sequence.

Neutral Drift - random mutations in well adapted proteins that do not affect function

- All proteins continue to evolve over time

Neutral Drift: Sequence Variation

Comparison of primary sequence of homologous proteins from different organism reveals residues that are **functionally important**

Residue types in sequence comparisons

Invariant residues have essential function

- cannot mutate without loss of function

Conservative substitutions indicate less stringent functional role

- can only mutate to residues with similar physiochemical properties (eg. polar uncharged to polar uncharged)

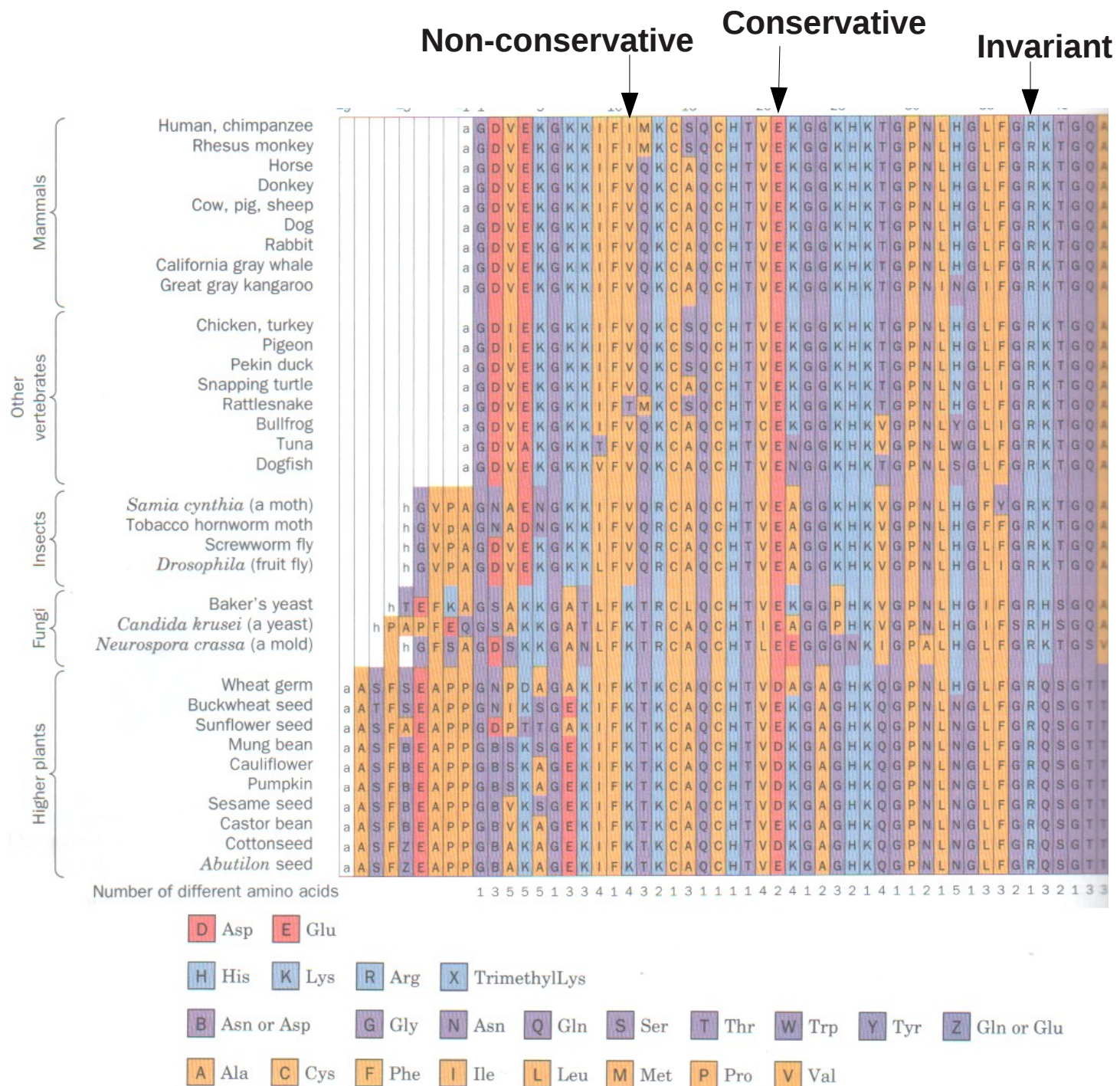
Non-conservative substitutions and hypervariable regions indicate non-specific functional role

- can mutate to residues with different physiochemical properties (eg. non-polar to polar charged)



Neutral Drift: Species Variation

Cytochrome C primary sequences (38 organisms) aligned to each other



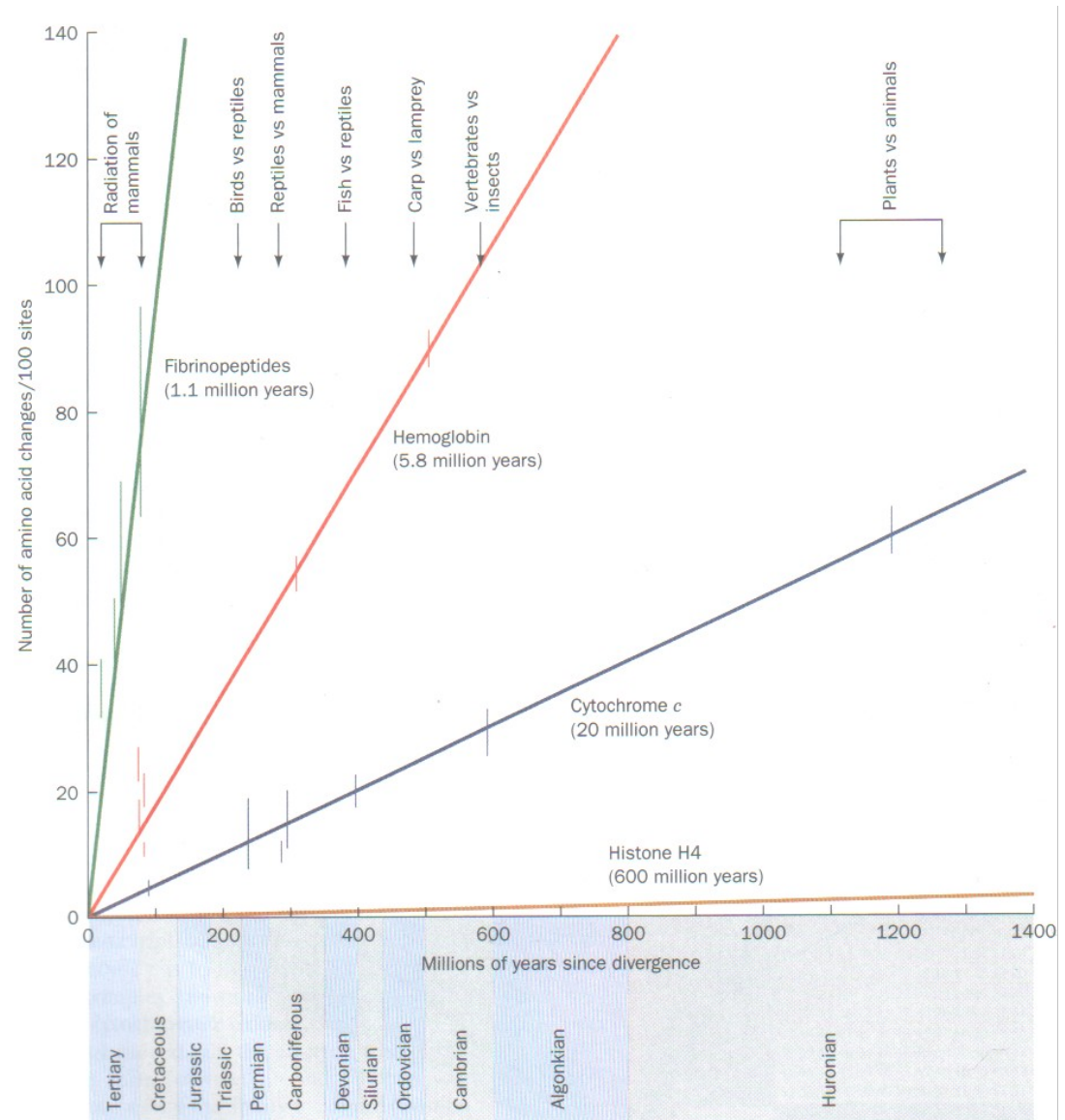
Evolutionary Rates

Evolution distance (accumulated changes) can be plotted vs time since divergence to yield an evolutionary rate (slope of line)

- Rate expressed as the time req'd to accumulate 1% change since divergence

Rate of accumulation < rate of random mutation

- Random mutations can be reversed
- Rate of accumulation limited by invariant and conservative residues



Mutational Rates

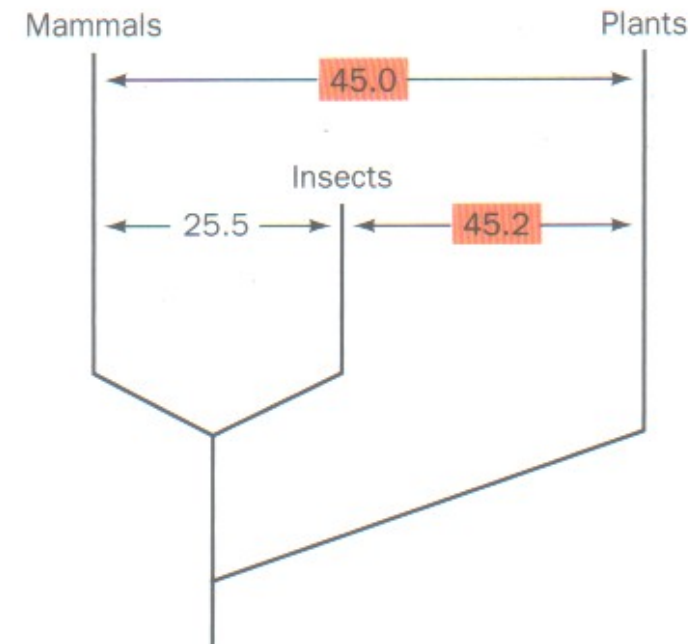
What mechanism accounts for observed mutations?

Model 1 - Mutations primarily arise from **replication errors** and the rate of mutation depends upon the number of organism generations

Model 2 – Mutations primarily arise from **chemical modification** and the rate of mutation depends upon the absolute time

Comparing the rate of mutation of insects (short generations) and mammals (long generations) for cytochrome C (figure)

- Each is an equal evolutionary distance from plants suggesting mutations primarily arise from random **CHEMICAL MODIFICATION** of DNA



Insects and mammals diverge from plants at same point yet are same evolutionary distance from plants.



Organismal Evolution

- **Protein evolution and taxonomical analysis generate very similar phylogenetic trees**
- **Protein evolution is not sufficient to explain all differences in organismal evolution**

eg. Small evolutionary distances between Human and Chimpanzee (>99% sequence identity among proteins) suggest a closer relationship than anatomical and behavioral studies

Mutations affecting regulation and scheduling of protein production affect the evolution of organisms more strongly than the average rate of mutation of proteins