Topic 3 Proteins as Drug Targets

Enzymes-Chapter 3, 4 Patrick and Part I Corey

Enzymes as Targets

Structure and function of enzymes The active site Substrate binding Induced fit Bonding forces

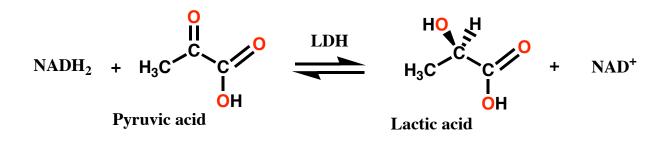
Catalysis mechanisms Acid/base catalysis Nucleophilic residues Overall process of enzyme catalysis Competitive (reversible) inhibitors Non competitive (irreversible) inhibitors Non competitive (reversible) allosteric inhibitors

Example: NSAIDS for inflammation

Structure and function of enzymes

- Globular proteins acting as the body's catalysts
- Speed up time for reaction to reach equilibrium
- Lower the activation energy of a reaction

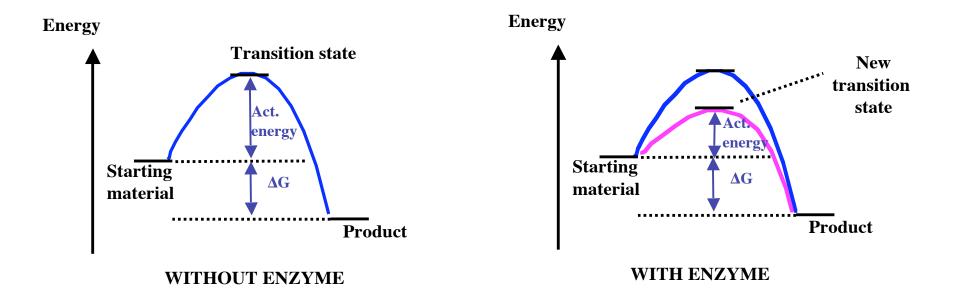
Example:



LDH = Lactate dehydrogenase (enzyme) NADH₂ = Nicotinamide adenosine dinucleotide (reducing agent & cofactor) Pyruvic acid = Substrate

1. Structure and function of enzymes

Lowering the activation energy of reaction



• Enzymes lower the activation energy of a reaction but ΔG remains the same

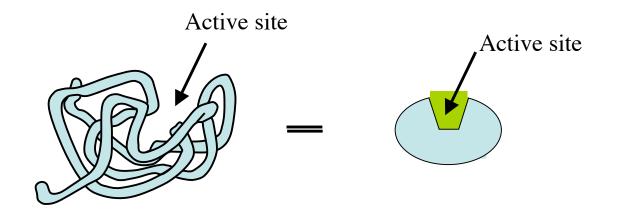
1Structure and function of enzymes

Methods of enzyme catalysis

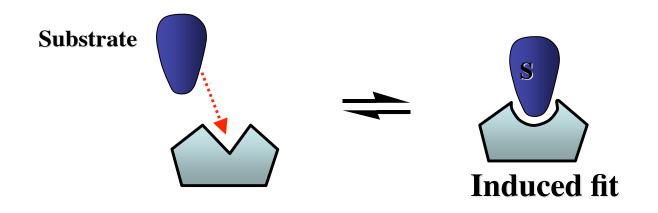
- **Provide a reaction surface (the active site)**
- Provide a suitable environment (hydrophobic)
- Bring reactants together
- Position reactants correctly for reaction
- Weaken bonds in the reactants (transition state)
- Provide acid / base catalysis
- Provide nucleophiles

The active site

- Hydrophobic hollow or cleft on the enzyme surface
- Accepts reactants (substrates and cofactors)
- Contains amino acids which
 - bind reactants (substrates and cofactors)
 - catalyse the reaction



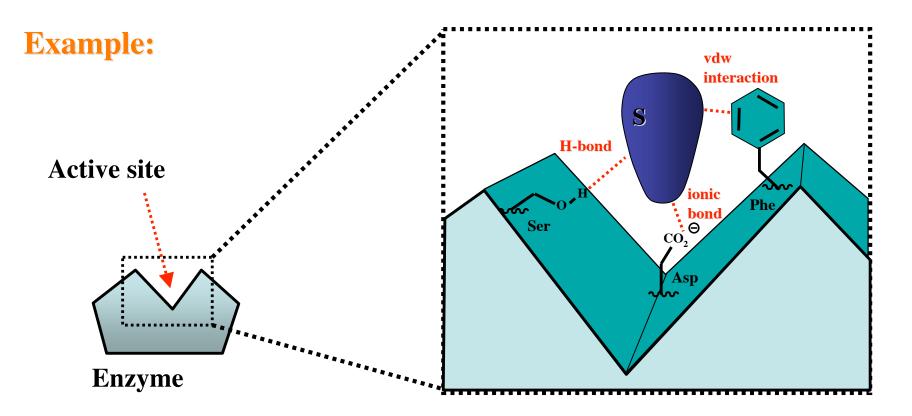
Induced fit



- Active site is nearly the correct shape for the substrate
- Binding alters the shape of the enzyme (induced fit)
- Binding will strain bonds in the substrate
- Binding involves intermolecular bonds between functional groups in the substrate and functional groups in the active site

Bonding forces

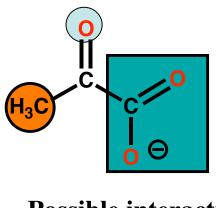
- Ionic
- H-bonding
- van der Waals



Bonding forces

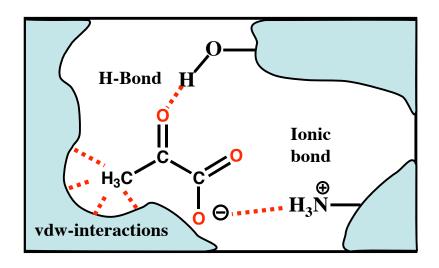
- Ionic
- H-bonding
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Example: Binding of pyruvic acid in LDH



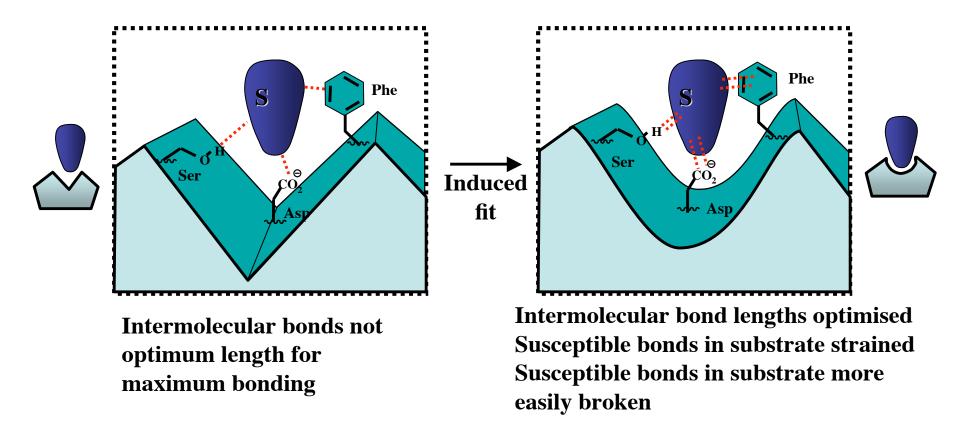
Possible interactions



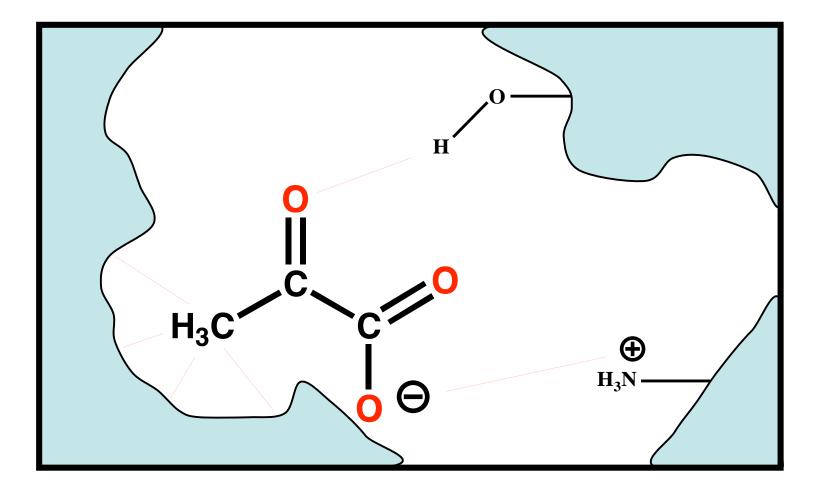


Bonding forces

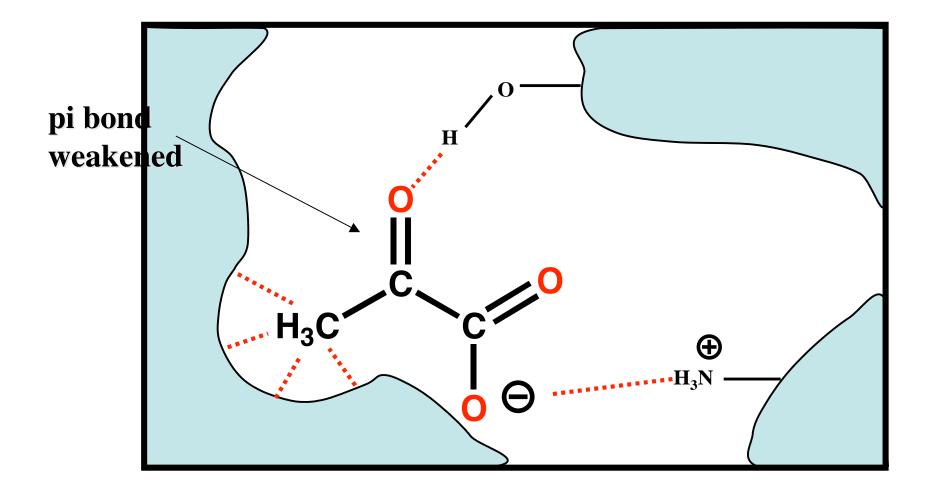
• Induced fit - Active site alters shape to maximise intermolecular bonding



Example: Binding of pyruvic acid in LDH



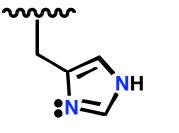
Example: Binding of pyruvic acid in LDH



Catalysis mechanisms

4.1 Acid/base catalysis

• Histidine



⊕N H

+H

-H⊕

Non-ionised Acts as a basic catalyst (proton 'sink') Ionised Acts as an acid catalyst (proton source)

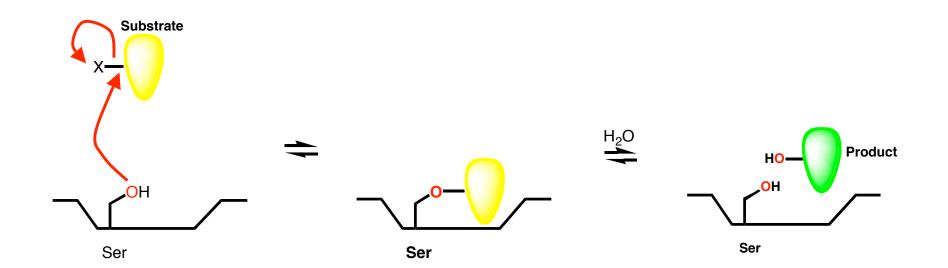
NH

4.2 Nucleophilic residues

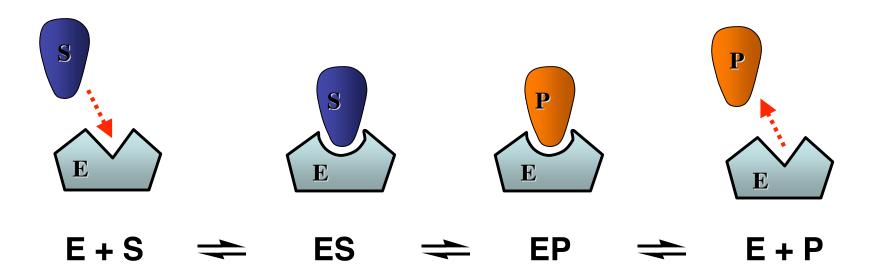


Catalysis mechanisms

Serine acting as a nucleophile



Overall process of enzyme catalysis

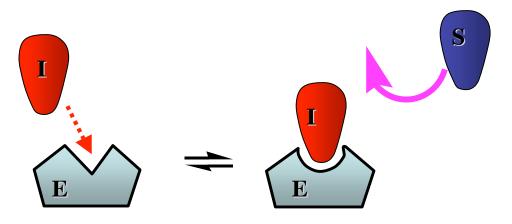


• Binding interactions must be;

- strong enough to hold the substrate sufficiently long for the reaction to occur

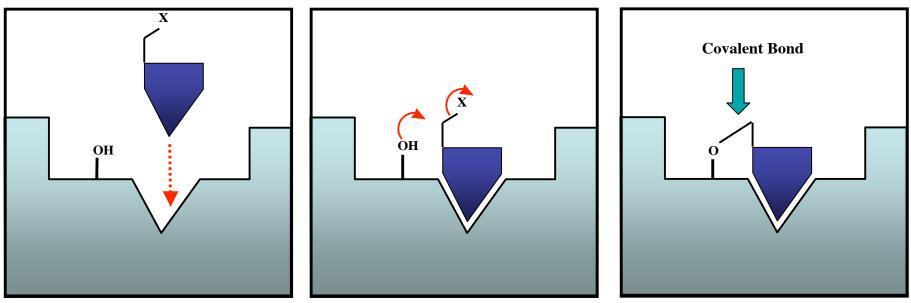
- weak enough to allow the product to depart
- Implies a fine balance
- Drug design designing molecules with stronger binding interactions results in enzyme inhibitors which block the active site

Competitive (reversible) inhibitors



- Inhibitor binds reversibly to the active site
- Intermolecular bonds are involved in binding
- No reaction takes place on the inhibitor
- Inhibition depends on the strength of inhibitor binding and inhibitor concentration
- Substrate is blocked from the active site
- Increasing substrate concentration reverses inhibition
- Inhibitor likely to be similar in structure to the substrate

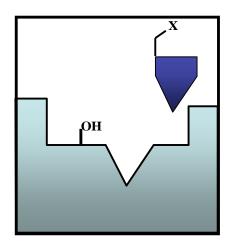
Non competitive (irreversible) inhibitors

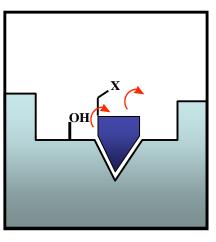


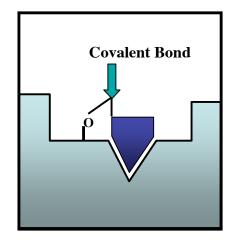
Irreversible inhibition

- Inhibitor binds irreversibly to the active site
- Covalent bond formed between the drug and the enzyme
- Substrate is blocked from the active site
- Increasing substrate concentration does not reverse inhibition
- Inhibitor likely to be similar in structure to the substrate

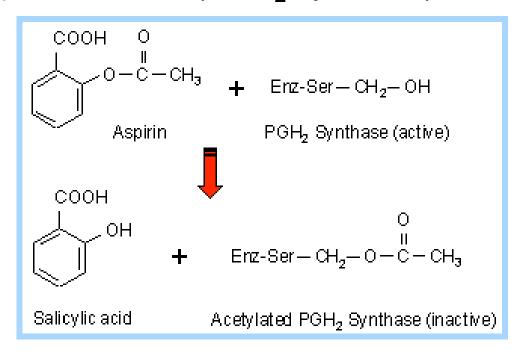
Non competitive (irreversible) inhibitors



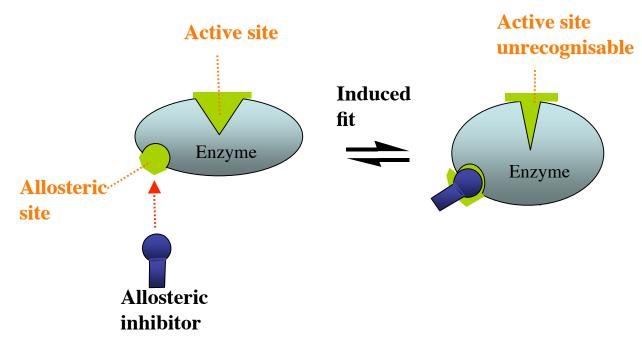




Example: aspirin for COX (PGH₂ synthase) Irreversible inhibition

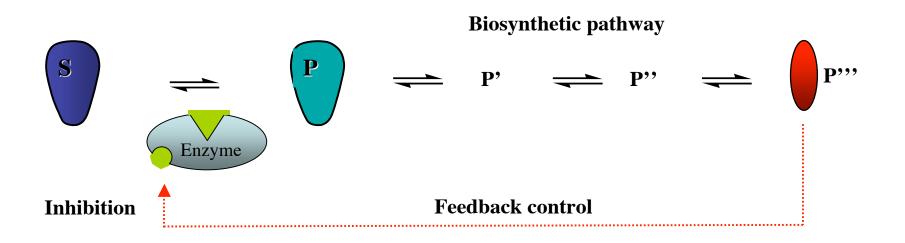


Non competitive (reversible) allosteric inhibitors



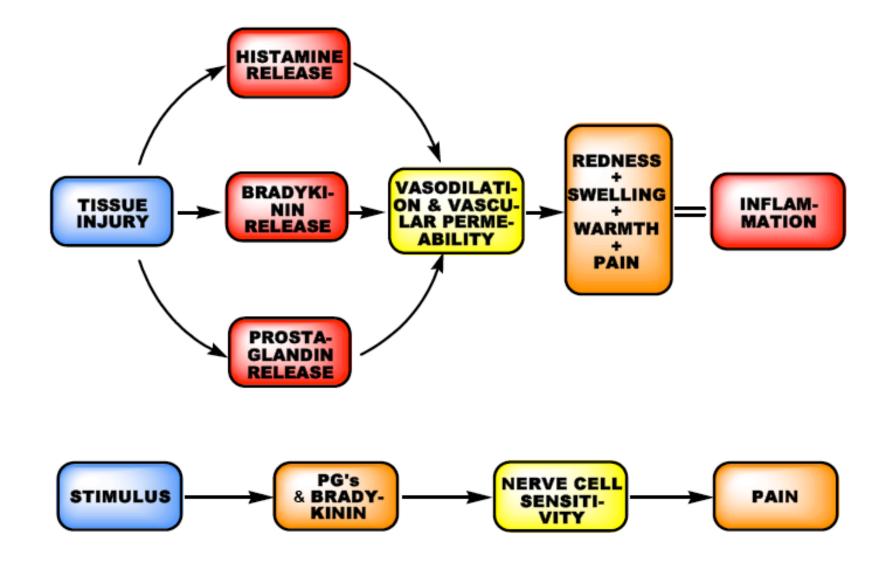
- Inhibitor binds reversibly to the allosteric site
- Intermolecular bonds are formed
- Induced fit alters the shape of the enzyme
- Active site is distorted and is not recognised by the substrate
- Increasing substrate concentration does not reverse inhibition
- Inhibitor is not similar in structure to the substrate

Non competitive (reversible) allosteric inhibitors

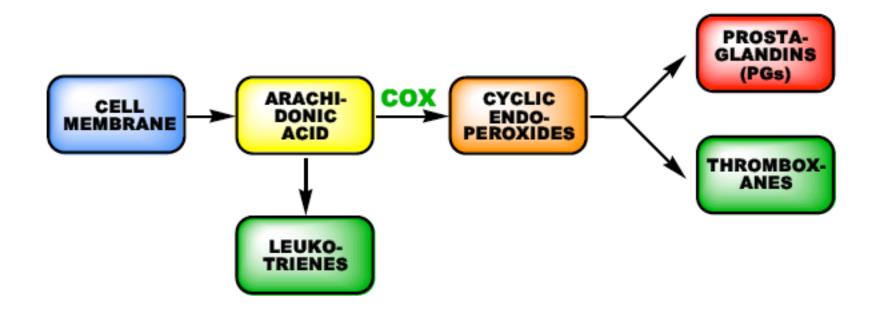


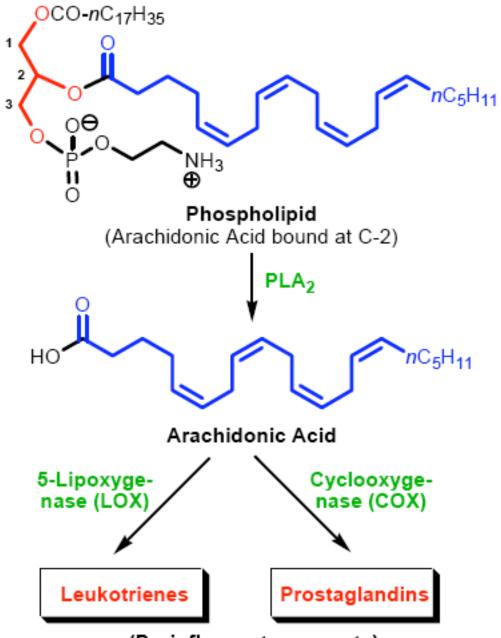
- Enzymes with allosteric sites often at start of biosynthetic pathways
- Enzyme is controlled by the final product of the pathway
- Final product binds to the allosteric site and switches off enzyme
- Inhibitor may have a similar structure to the final product

EXAMPLE: NSAIDS for inflammation Inflammatory, Cardiovascular and Metabolic Diseases An Overview of Inflammation II.



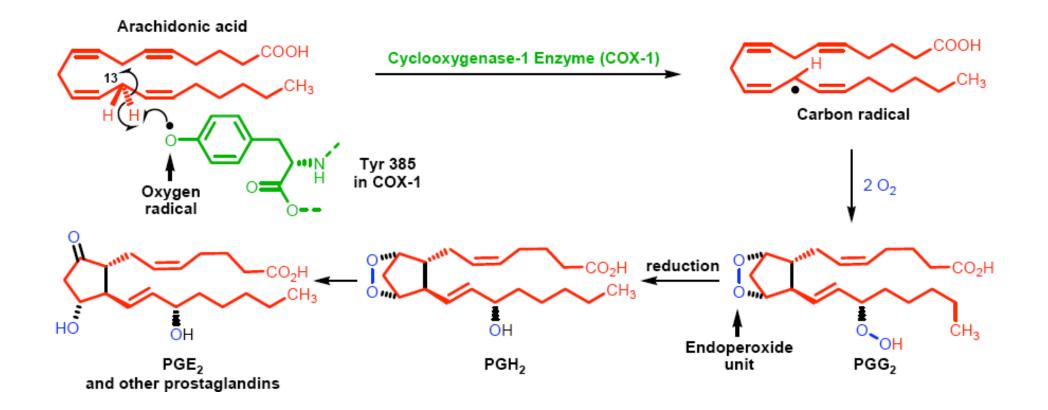
Inflammatory, Cardiovascular and Metabolic Diseases An Overview of Inflammation I.



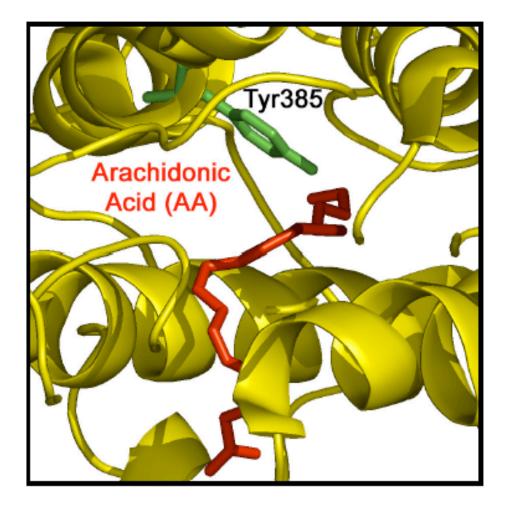


(Proinflammatory agents)

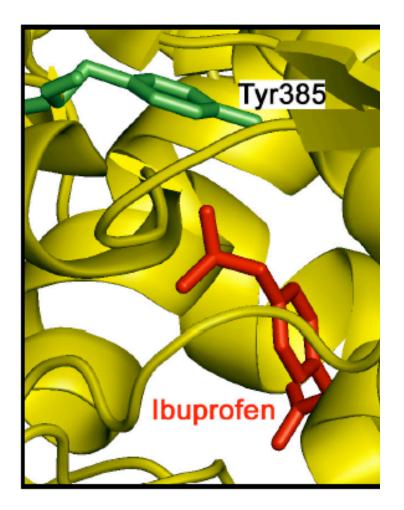
Inflammatory, Cardiovascular and Metabolic Diseases How Do Anti-Inflammatory Drugs Work? I.



Inflammatory, Cardiovascular and Metabolic Diseases How Do Anti-Inflammatory Drugs Work? II.

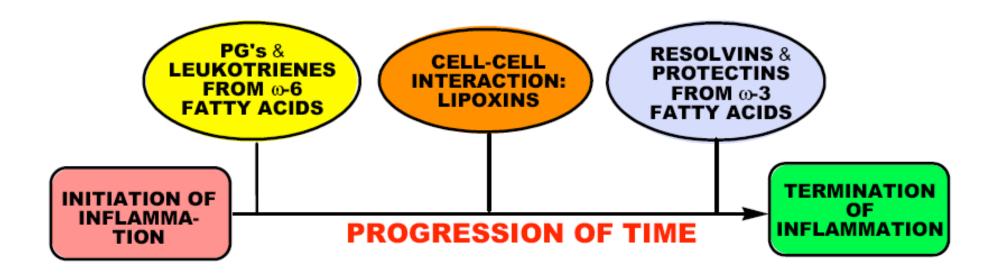


A. Arachidonic Acid in the Active



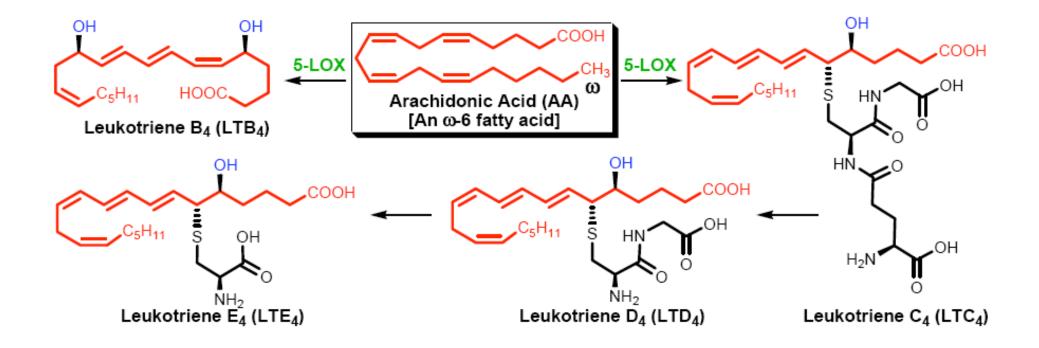
B. Ibuprofen in the Active

Inflammatory, Cardiovascular and Metabolic Diseases Other Eicosanoids in Inflammation I.



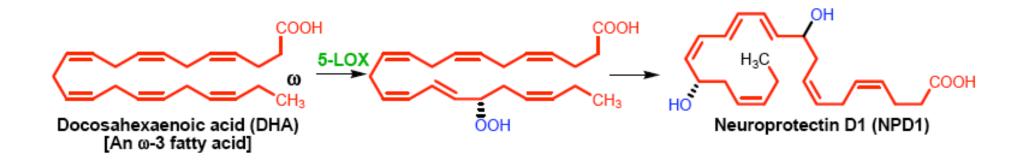
Mediators of Inflammation

Inflammatory, Cardiovascular and Metabolic Diseases Other Eicosanoids in Inflammation II.



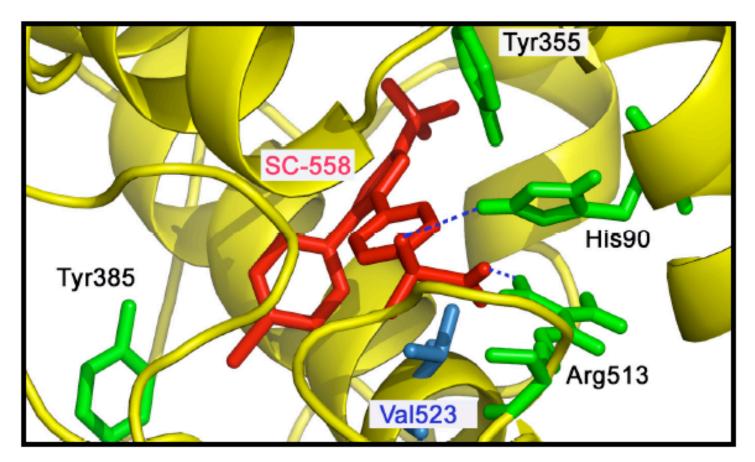
Formation of Various Leukotrienes from Arachidonic Acid via 5-Lipoxygenase

Inflammatory, Cardiovascular and Metabolic Diseases Other Eicosanoids in Inflammation III.



Formation of Neuroprotectin D1 from Docosahexaenoic Acid via 5-Lipoxygenase

Inflammatory, Cardiovascular and Metabolic Diseases Anti-Inflammatory Agents – Celecoxib (Celebrex[™]) III.



The picture above shows a close structural relative of celecoxib, SC-558, bound in the active site of COX-2. The selectivity results because the phenylsulfonyl group binds in a pocket (formed from His90, Arg513 and Val523) that is not available in COX-1 since it is occupied by a bulky isoleucine side chain rather than the smaller isopropyl group of valine (Val523). The carboxyl group of rofecoxib interacts not with Arg513 but with a different residue, Arg120.