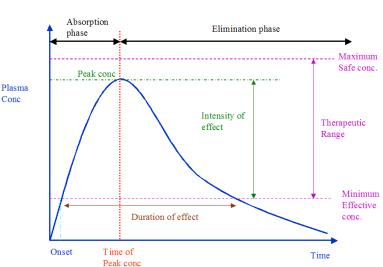
Drug Design

- **ADME** is an acronym used in pharmacokinetics and pharmacology for absorption, distribution, metabolism an excretion.
  - Ensemble of processes involved in the becoming of a drug after being administered.
    - Pharmacokinetics (PK) "what the body does to the drug"
  - Non accounting for ADME properties has led to problems when drug candidates were tested in clinical phase.

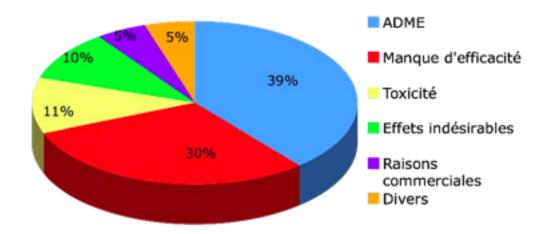
#### **Pharmacokinetics**

- How do you get it into the body?
- How long does it take to exert its action?
  - How long does it stay in the body?
    - Where does it go to in the body?
  - Is it metabolised to another form?
  - How do we analyze and detect it?

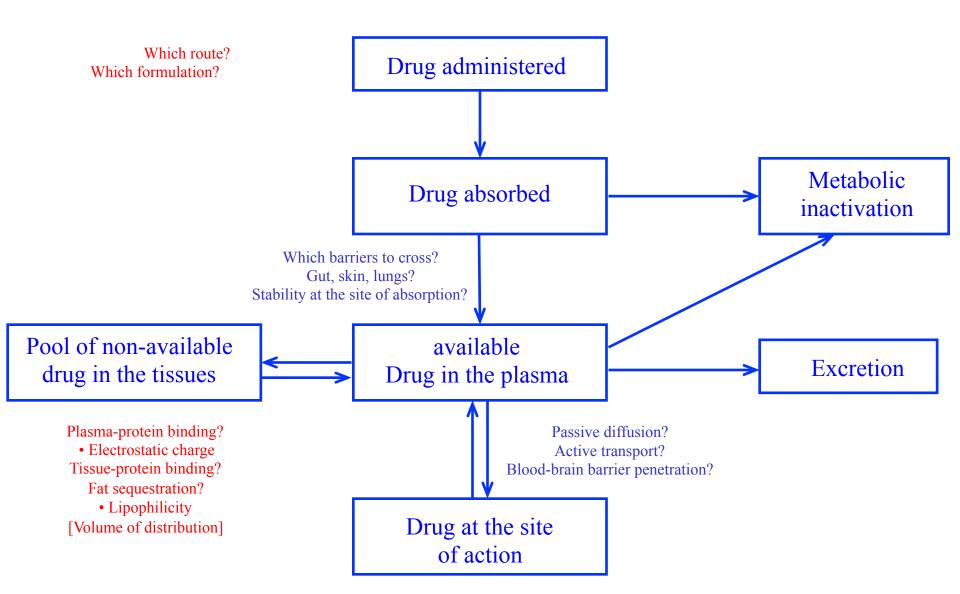
The [plasma]-time curve after drug administration



Main causes for rejecting drugs



# Pharmacokinetics



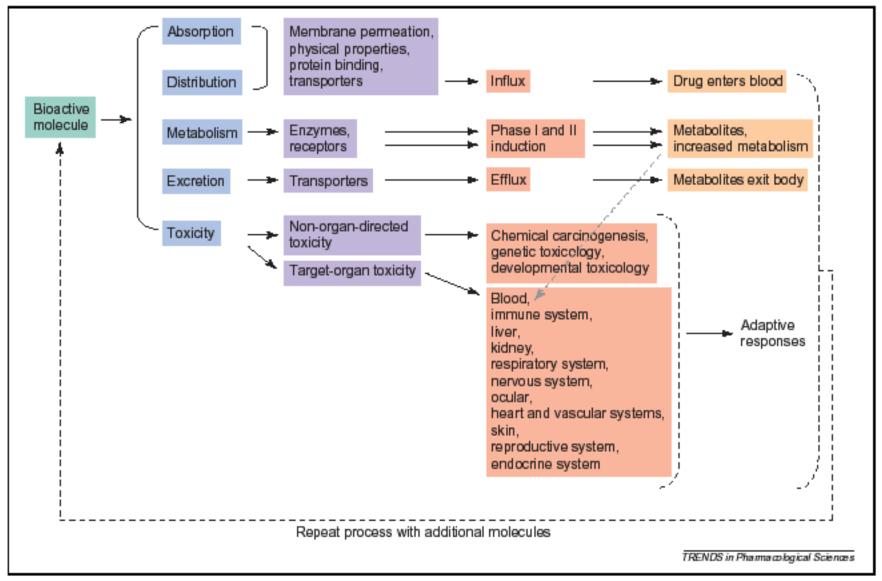


Figure 1. The iterative ADME/Tox optimization process. This figure demonstrates that a bioactive molecule is required to possess many favorable ADME/Tox properties before it can become a drug, and indicates the multidimensional nature of drug discovery. The proteins and endpoint associated with each ADME/Tox function are outlined. Adaptive responses represent the transcriptional and post-transcriptional effects following a toxic insult. Solid arrows represent the links between ADME/Tox properties, functions and endpoints. The grey dashed line represents reactive metabolites that can cause toxicity.

- **Drug molecules are processed by enzymes** evolved to cope with natural compounds
  - May be several routes of metabolism
  - May not be what terminates drug action
  - May take place anywhere BUT liver is prime site
- Not constant can be changed by other drugs; basic of many drug-drug interactions

Modify the chemical nature of the molecule to facilitate its elimination

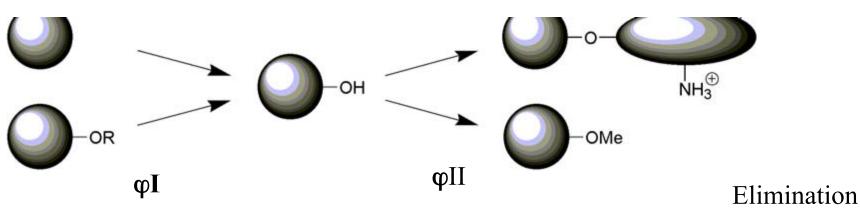
(metabolism ---> excretion)

## Transformations in phase I

• introduce functional groups

# **Transformations in phase II**

• produce polar derivatives or block functional groups by coupling (conjugaison).



kidneys

gall-bladder

# Transformations in phase I Oxydation reactions

Cytochrome P450 is a superfamily of heme proteins which use a large number of exogenous and endogenous compounds as substrates in enzymatic reactions.

Cytochrome P450 catalyses oxydations that introduce a new chemical function (-OH, -NH2, -COOH) in xenobiotic molecules making the molecules more polar.

## Molecular modelling of drug metabolizing enzymes

To understand the interaction of drugs with drug metabolizing enzymes, their 3D structures have been determined by comparative modelling using the Xray structures of bacterial **P450**s as templates.

Fifty specific and nonspecific substrates were docked into the active site of their metabolizing enzyme by automatic **rigid body docking program** DOCK.

It was found that substrate binding was favoured mainly by hydrogen bonding and electrostatic interactions between the substrates and protein residues.

More recently the crystal structure of a human P450 cytochrome in the absence and presence of warfarin was determined.

# **Drug Distribution**

# Pharmacophore models for analysis of substrate specificity

The first step in oral absorption of medically important **peptide-based drugs** is mediated by an intestinal proton-dependent peptide transporter.

This transporter facilitates the oral absorption of di- and tri-peptides resulting from the digestion of dietary proteins.

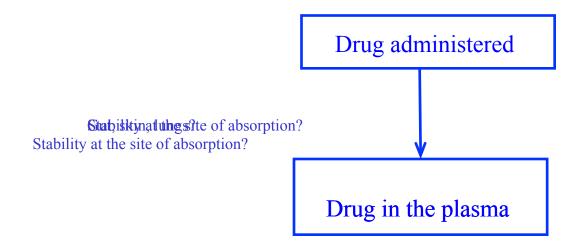
Peptidomimetics: Penicillins, cephalosporins, ACE inhibitors and other drugs are substrates of the intestinal peptide transporter.

They were subjected to a **pharmacophore** analysis.

It was found that the affinity for the peptide transporter could be diminished either by:

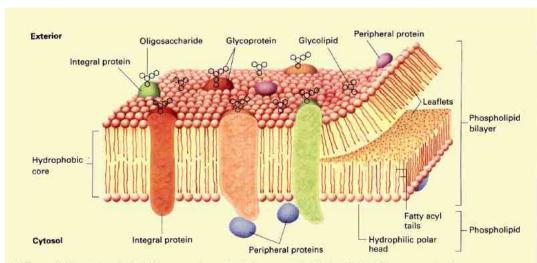
Esterification of the free carboxylic moiety Introduction of a second negative group

This is an essential tool in pharmacokinetics as bioavailability must be accounted for calculating doses.



- Biological membrane is essential to the separation of the inside and outside of the cell.
- It is composed of a phospholipid bilayer in which proteins are associated.

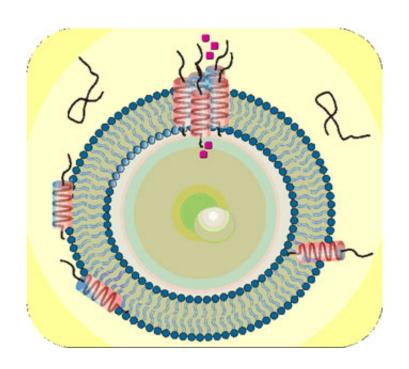
 Biological membranes are made of two main parts with different physicochemical properties:
One is hydrophobic and the other hydrophilic.



▲ Figure 13-1 A phospholipid bilayer constitutes the basic structure of biological membranes. The hydrophobic fatty acyl tails of the phospholipids form the middle of the bilayer; the polar, hydrophilic heads of the phospholipids line both surfaces. Integral proteins have one or more regions

embedded in the lipid bilayer. Peripheral proteins are primarily associated with the membrane by specific protein-protein interactions. Oligosaccharides bind mainly to membrane proteins; however, some bind to lipids, forming glycolipids.

• The role of the biological membrane is to define the extent of the cell and to settle a boarder preventing the permeation of undesired compounds to the interior of the cell.



- Absorption of a drug in the body is determined by its capacity to cross the lipid bilayer of cells.
- This phenomenon of diffusion is named permeation and permeability is the associated physical quantity.

- Two types of processes characterise the
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# trapasseivthaoudgaetheendessione:

- Passive diffusion does not need energy
- Rapplycadiffusione dogradientes ducheagy conceptly tional or electrical gradients through concentration or electrical gradients through

the membrane.

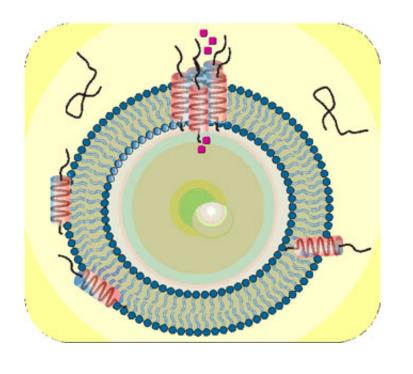
• Active diffusion requires the presence of a

protein or an energy supply.

• Drugs mainly use the passive diffusion

process to cross the membrane.

• Their absorption is influenced by their



- A system of biopharmaceutical classification separates drugs into 4
- Adiffstrent of roups depending on their solubility and permeability:

Class I: High solubility and permeability

Class I: High solubility and permeability



Class II: Weak solubility and high permeability

- Compounds which belong to class I are the most searched for
  - **High solubility** leads to a complete dissolution of the drug
- **High permeability** is the guarantee that the drug is fully absorbed during its passage in the intestine.

Experimental and in silico methods

3 approaches:

3 approaches:

- Partition coefficient octanol/water (log P)
- Partition coefficient octanol/water (log P)
  - Diffusion through a layer of cells

Experimental methods

Partition coefficient (log P)

- It is the most often used descriptor to characterise the lipophilic character of a drug.
- It is obtained using a two-phase solution octanol/water shaken with the solute and by measuring the concentration of solute in both phases.
- The correlation between the partition coefficient octanol/water and the permeability value is rather weak.
- It is however used together with an ensemble of other descriptors.

Experimental method

# Diffusion through a layer of cells Diffusion through a layer of cells

- A layer of human colon adenocarcinoma cells (Caco-2) are used to model the transport of molecules through the intestine epithelium
- A layer of human colon adenocarcinoma cells (Caco-2) are used to

model the transport of molecules through the intestine epithelium

- A good correlation was found between the permeability through this layer and the oral absorption in humans.
- However experimental procedures are not standard and it is difficult to

compare permeability values from different labs.

Experimental methods

- Good reproductibility of the results
- Rapidity of the tests and possibility to work on a large number of compounds
  - Not too costly

• Several softwares have been designed to evaluate adsorption properties:
• Several softwares have been designed to evaluate adsorption properties:



Lipinski's rule of five:

Lipinski's rule of five:

- 1. Molecular weight of drug candidates < 500
- 1. Mollean her weighd rougen dichates < 500
- 3.2NiNubeberfdfyldydgegehdrohdodoptorss < 510
- 3. Number of hydrbænPbonfd acceptors < 10

4. Log P < 5

Advantages: easy to implement

Drawbacks: Problem A dwfabitages ilabisity to amplement ven for the molecules

Drawbacks: Problems of bihav pilability heans occur even for the molecules

In silico methods: qualitative methods derived from the analysis of data bases of drugs

Model used to evaluate the blood-brain barrier (Norinder and Haeberlein) (The ability of a molecule to enter the nervous central system may also be desirable depending on the therapeutic target)

A high permeability for penetrating the brain is predicted if

- 1. The sum of the number of nitrogen (N) and oxygen (O) atoms in a molecule is  $\leq 5$
- 2. If  $\log P (N+O)$  is > 0 (N+O is the sum of the number of atoms of nitrogen and oxygen in a molecule)

*In silico* methods: quantitative methods

- Computer predictions of permeability are based on quantitative structure-property relationships (QSPR).
- This method describes the chemical structure of a molecule into a series of descriptors of properties which can be related to the permeability of this molecule
- A mathematical relation is then elaborated to quantitatively associate the values of the descriptors with the value of the permeability.

P = f(chemical descriptors)

• With this relation one can screen other chemical compounds to predict their permeability

*In silico* methods : quantitative methods

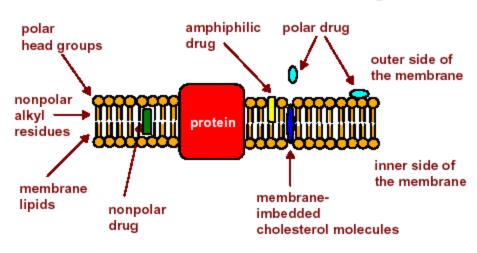
These approaches have been designed to correlate the experimental measurements of permeability to one or more descriptors.

# Descriptors used are:

- Lipophilic character of the molecules
- Properties related to the hydrogen bonds (number of donors and acceptors)
  - Molecular weight

These descriptors can be obtained with the knowledge of the 2D structure of the compounds

#### Membranes and the Action of Drugs



In silico methods: quantitative method

#### Drawbacks:

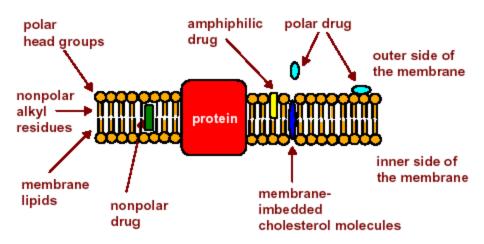
If the mathematical relation is obtained with

- A size of the data too small
- Data on compounds transported actively instead of passively

## *In silico* methods : quantitative methods

- Interactions between the drug and the biological membrane depend on the interactions between the 3D structures of the drug compound and the phospholipids of the membrane.
- Van der Waals, electrostatic, hydrogen bonds, hydrophobic interactions at the surface influence the passive permeability of the drugs across the biological membranes

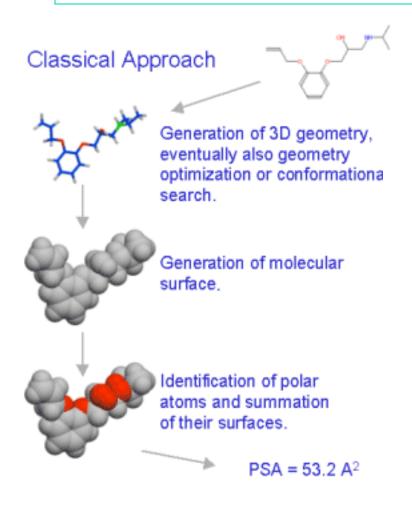
#### Membranes and the Action of Drugs



*In silico* methods : quantitative methods

- The surface properties of the drug candidates, in particular the Polar Surface Area (PSA), have been frequently used as a descriptor to predict the permeability of compounds across the membranes.
- PSA is defined as the sum of the partial surfaces associated with oxygen, nitrogen and polar hydrogen atoms which contribute to the total surface of the drug candidate.

## *In silico* methods : quantitative methods



- To compute the PSA one uses the van der Waals radius of each atom and the molecular 3D conformation of the molecules.
- This polar area or PSA accounts for the capability of a molecule to form hydrogen bonds.
- The PSA descriptor does not of course discriminate between molecules having a similar PSA value but with different sizes and lipophilic character.

*In silico* methods : quantitative methods

Another method (VolSurf) proposes another approach relating the physicochemical properties essential for the permeation and the 3D structure of the drug candidates.

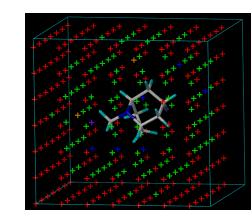
VolSurf is a computational procedure to produce 2D molecular descriptors from 3D molecular interaction energy grid maps.

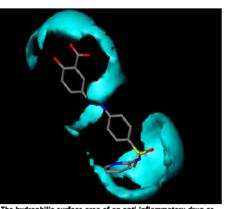
The basic idea of VolSurf is to compress the information present in 3D maps into a few 2D numerical descriptors which are very simple to understand and to interpret.

The most important descriptors are

The properties of hydrogen bonds (number of hydrogen bond acceptors and donors)

The lipophilic character

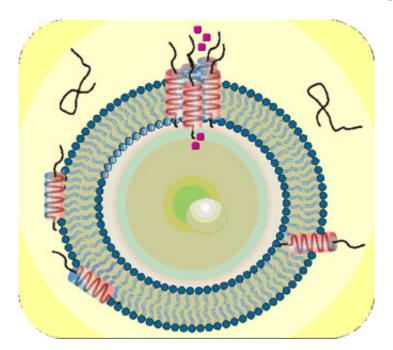




The hydrophilic surface area of an anti-inflammatory drug as determined by VolSurf.

*In silico* methods : quantitative methods

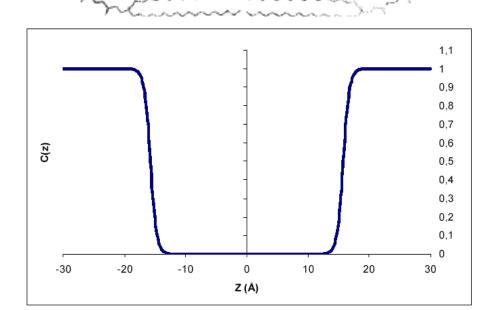
Models of membranes are essential for a better understanding of the general principles controlling the membrane organisation and to better apprehend the interaction between biological membranes and other chemical entities such as drugs



*In silico* methods : quantitative methods

- Membrane can be considered as a continuum medium characterised by macroscopic properties.
  - In IMPALA (Brasseur et al.) lipid/water interfaces are described by a function which varies along a Zaxis perpendicular to the membrane.

$$C_{(z)} = 1 - \frac{1}{1 + e^{\alpha(|Z| - Z_0)}}$$



hydrophobic core

*In silico* methods : quantitative methods

Two different types of interactions are considered

One simulates the hydrophobic interaction which depends on the accessible surface S(i) of the different atoms i, of the transfer energy  $E_{tr}(i)$  of the corresponding atom

The values of  $E_{tr}(i)$  are calculated from experimental free energies of transfer of amino acids

$$E_{\text{int}} = \sum_{i=1}^{N} S_{(i)} E_{tr(i)} \left( 1 - C_{(z_i)} \right)$$

The general behaviour is that E is unfavourable when hydrophilic atoms penetrate the membrane ( $E_{tr}>0$ ) and favourable (<0) when hydrophobic atoms do

*In silico* methods : quantitative methods

The perturbation in the organisation of the phospholipids caused by the penetration of the molecule into the membrane.

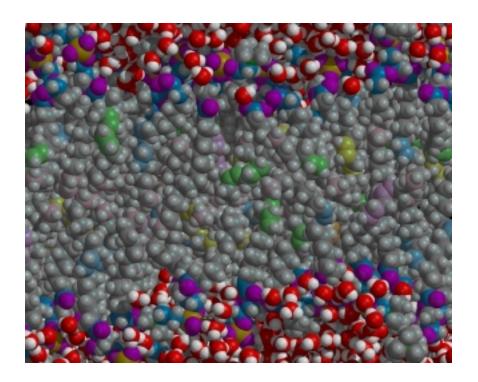
This function minimises the interaction of the molecule with lipids relative to that between the phospholipids themselves.

$$E_{lip} = a_{lip} \sum_{i=1}^{N} S_{(i)} (1 - C_{(z_i)})$$

A<sub>lip</sub> is an empirical factor

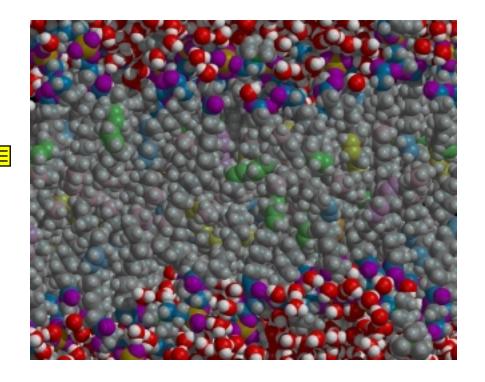
*In silico* methods : quantitative methods

• Statistical simulations (Molecular dynamics or Monte Carlo) to the estimation of transfer free energies of pharmacologically relevant organic molecules are used.



# *In silico* methods : quantitative methods

- Large-scale molecular dynamics simulations were carried out on a series of four solutes, viz. antipyrine, caffeine, ganciclovir, and alpha-D-glucose, at the water-dodecane interface as a model of a biological water-membrane interfacial system.
- Agreement with experimentally determined partition coefficients is remarkable, demonstrating that free energy calculations, when executed with appropriate protocols, have reached the maturity to predict thermodynamic quantities of interest to the pharmaceutical world.



# *In silico* methods : quantitative methods

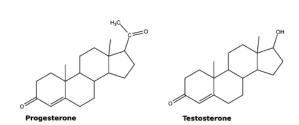


Fig. 2 Steroid hormone structures.

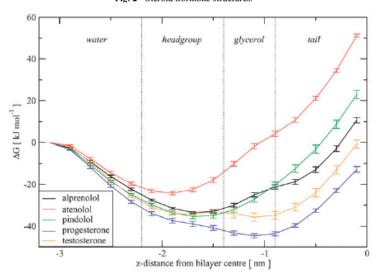


Fig. 3 Free energies of transfer from water to selected z-distances along the bilayer normal. To facilitate interpretation, different regions across the system are marked in italics, namely, the bulk water region, the lipid headgroup region, the lipid glycerol region and the hydrocarbon tail core. Approximate boundaries between these regions are defined by the vertical dotted lines.

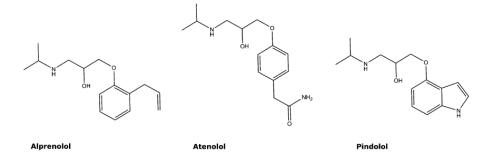


Fig. 1  $\beta$ -blocker structures.

Orsi and Essex, Soft Matter, 2010

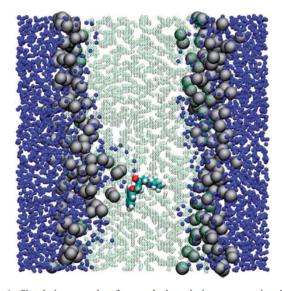


Fig. 6 Simulation snapshot from a dual-resolution z-constraint simulation. The permeant alprenolol is located at a distance of 0.1 nm from the bilayer centre towards the left monolayer. CG colour code: water molecules are blue, lipid headgroups are grey, lipid tails are transparent green. AL permeant colour code: carbon atoms are cyan, hydrogen atoms are white, oxygen atoms are red, nitrogen atoms are blue.