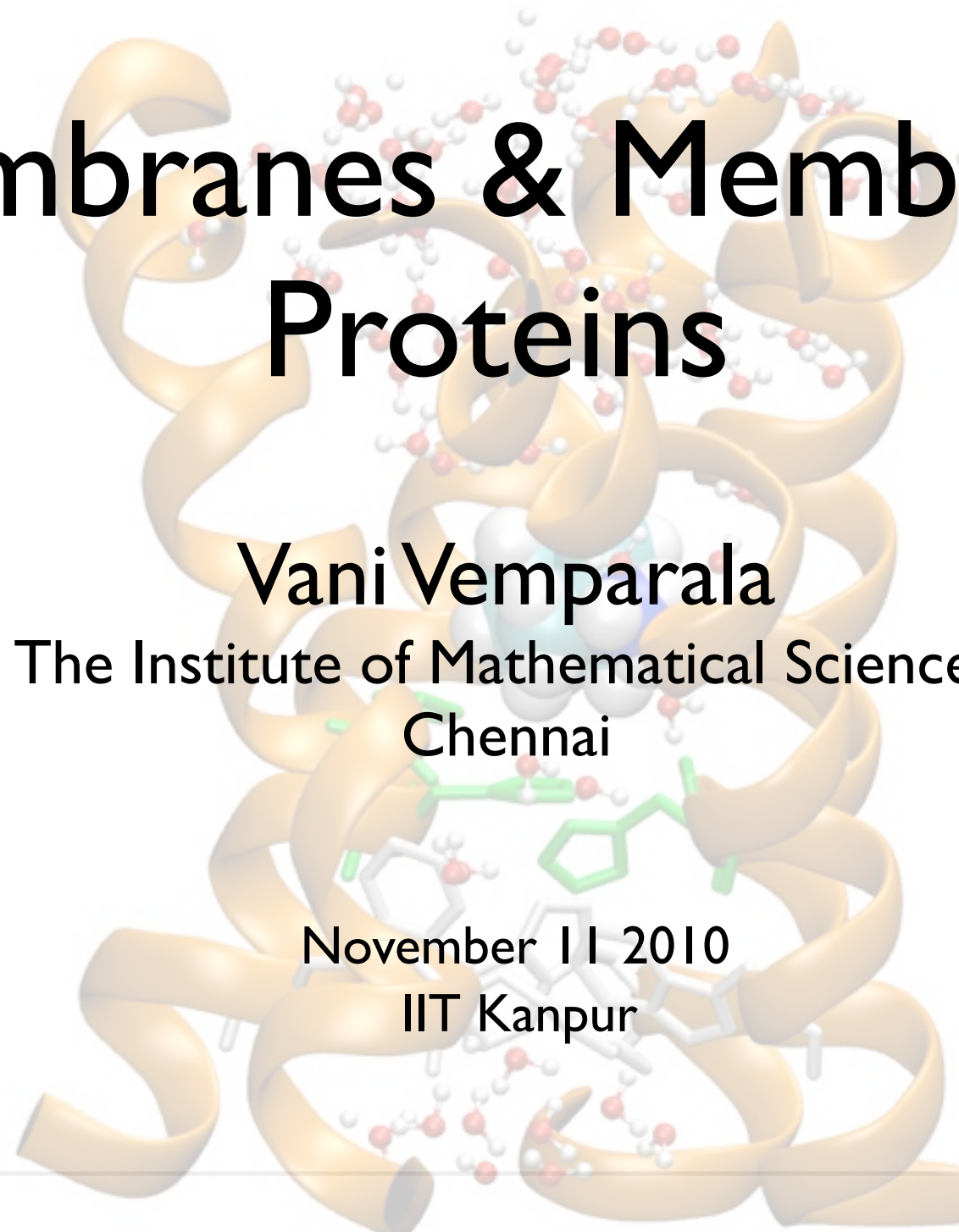


Membranes & Membrane Proteins

Vani Vemparala

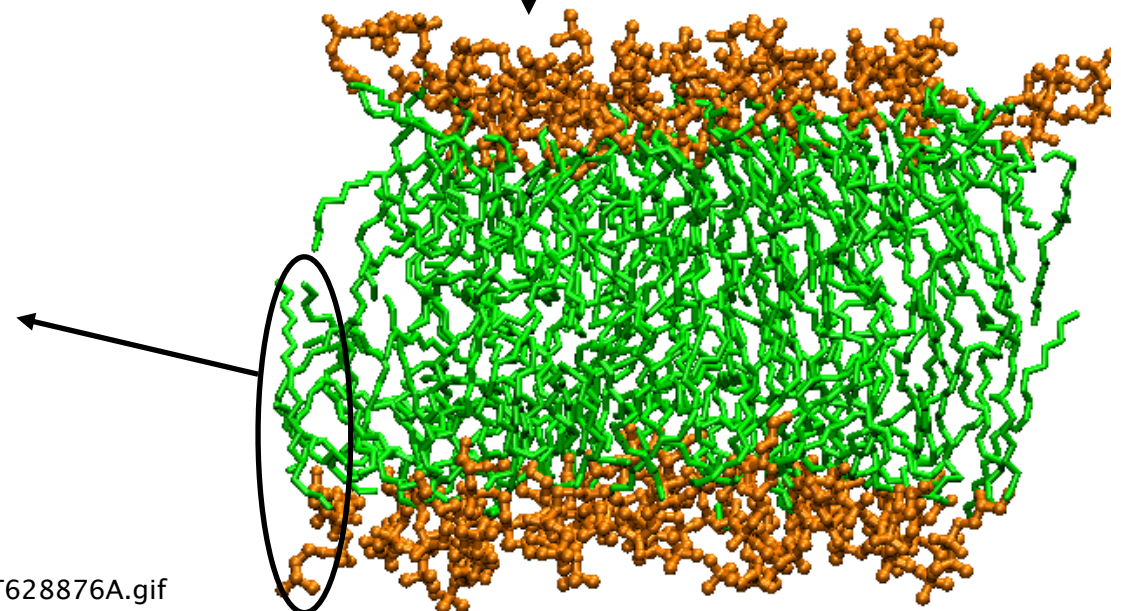
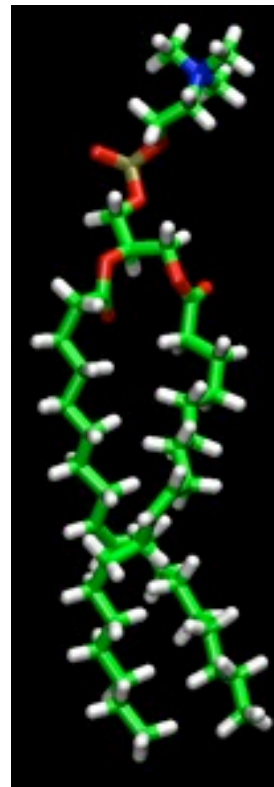
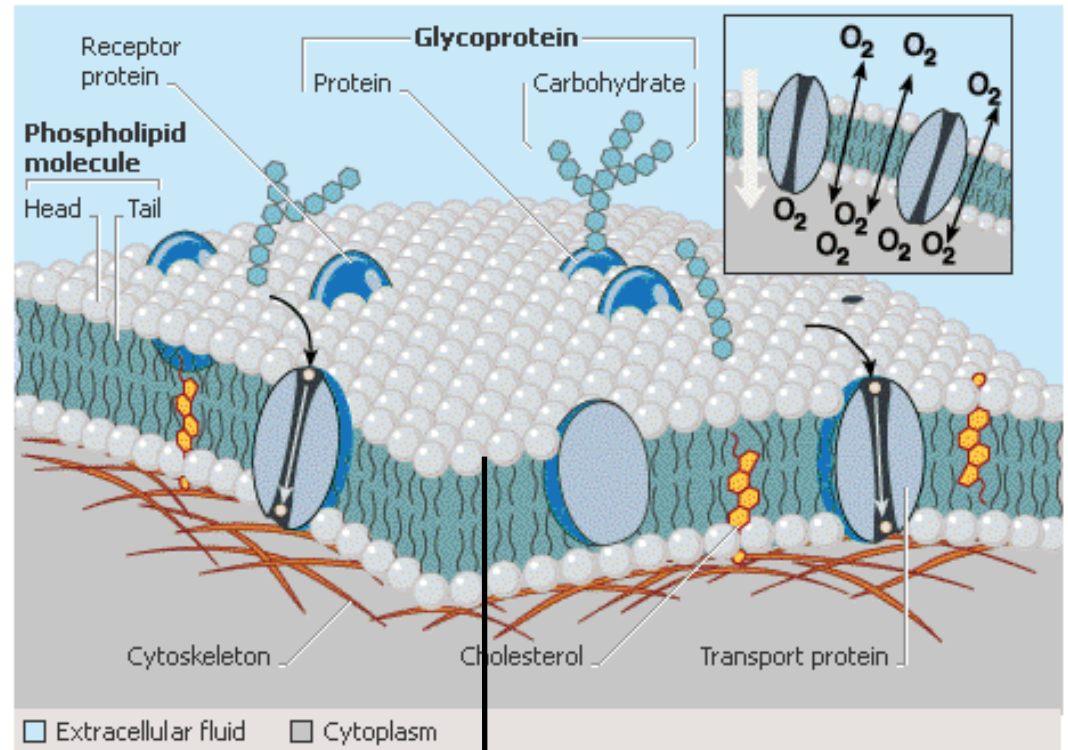
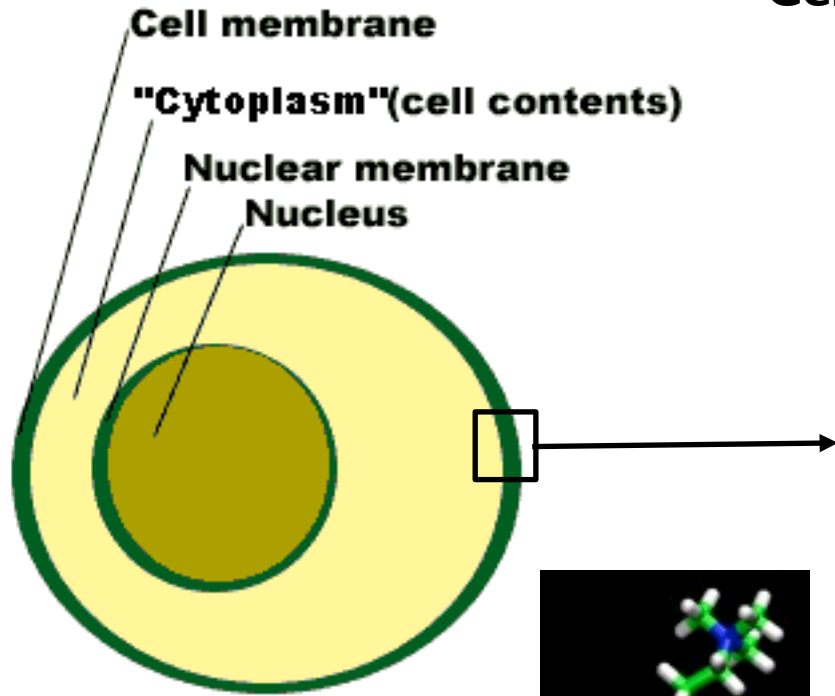
The Institute of Mathematical Sciences
Chennai

November 11 2010
IIT Kanpur



Perspective

Cell membrane

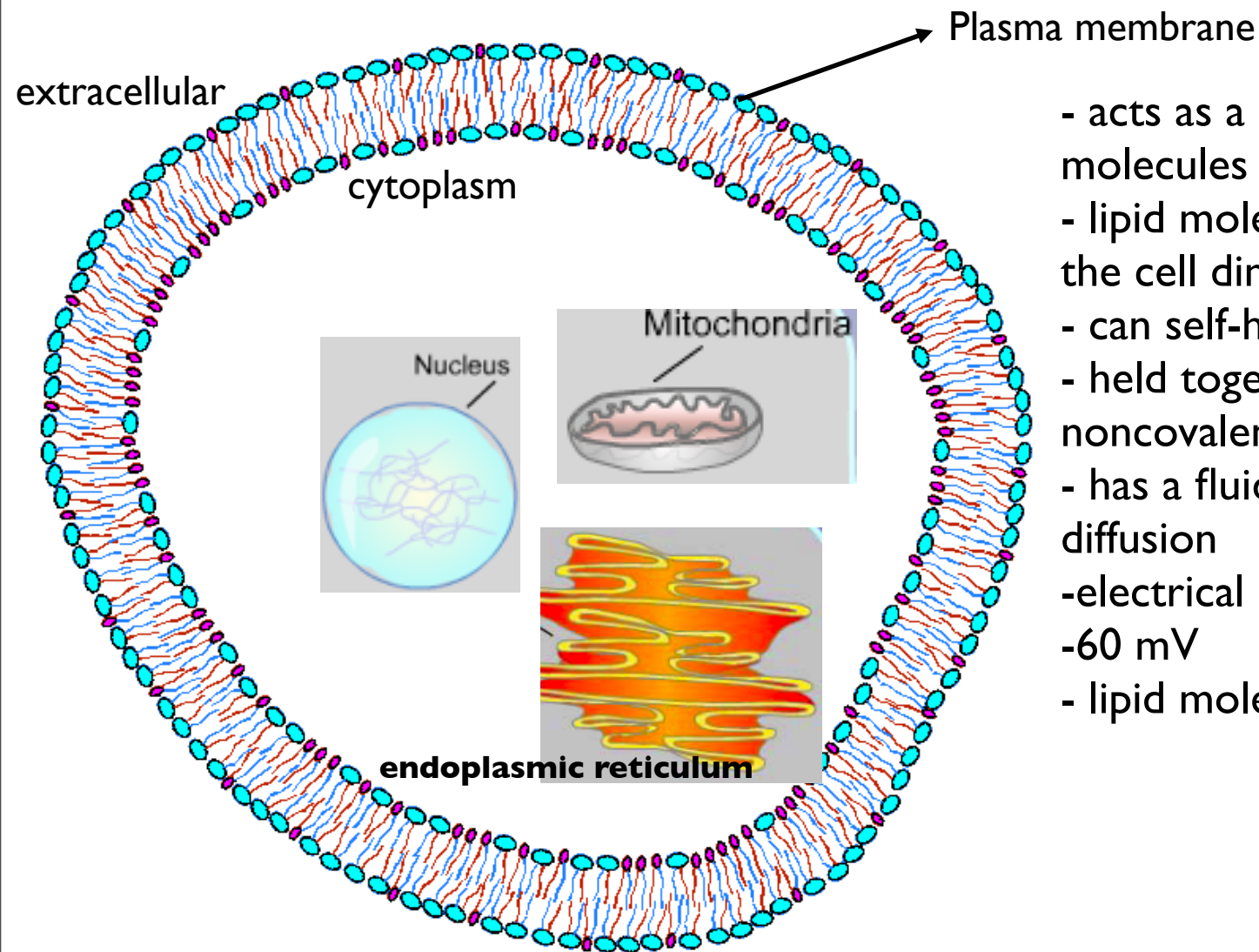


<http://www.mcl.d.co.uk/hiv/images/aEukaryoticCell.gif>

<http://images.encarta.msn.com/xrefmedia/aencmed/targets/illus/ilt/T628876A.gif>

Thursday 11 November 2010

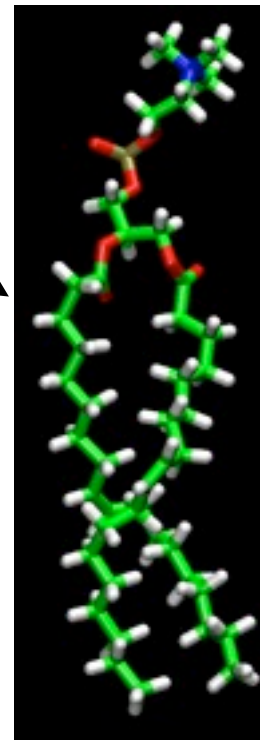
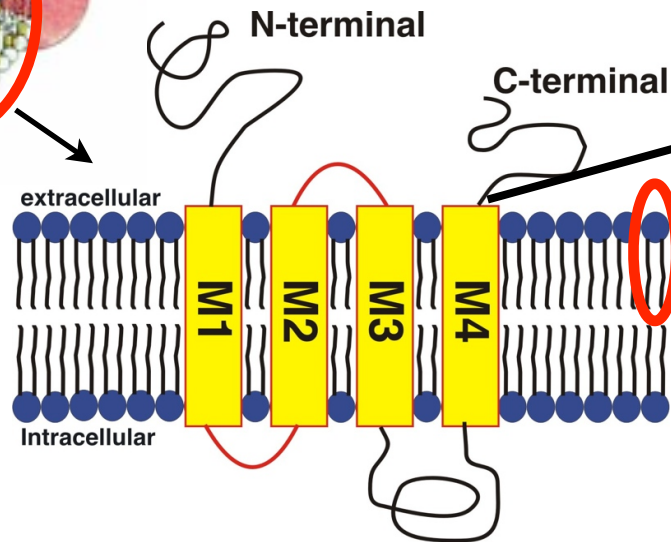
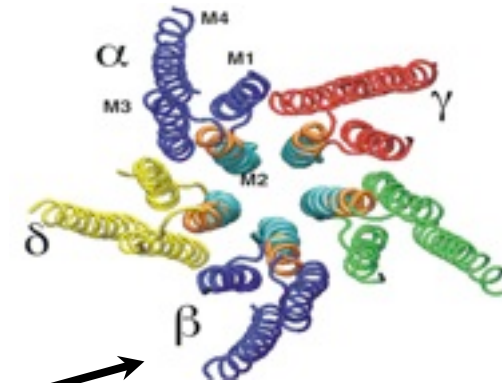
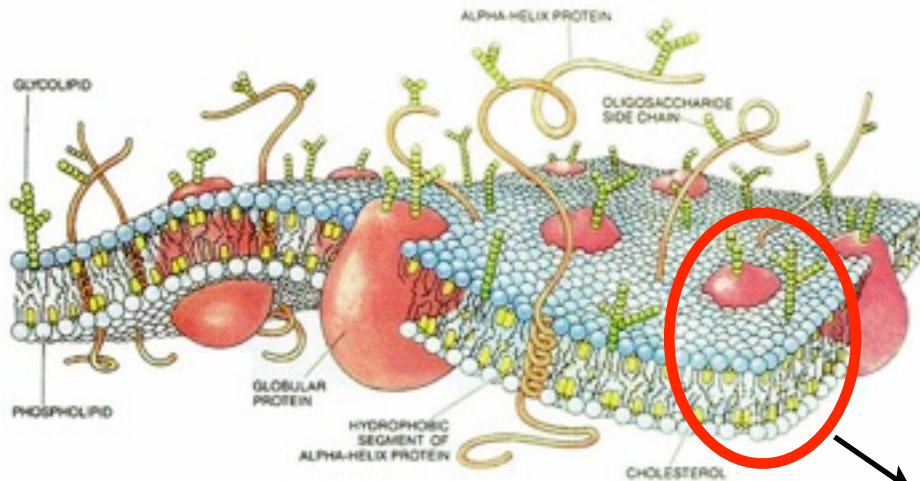
Cellular Environment



- acts as a compartment, only few molecules thick (60-100 Å)
- lipid molecules are added/removed, as the cell dimension changes
- can self-heal
- held together by hydrophobic/noncovalent interactions
- has a fluid-like structure with rapid lipid diffusion
- electrical potential across membranes :
-60 mV
- lipid molecules are synthesized in ER

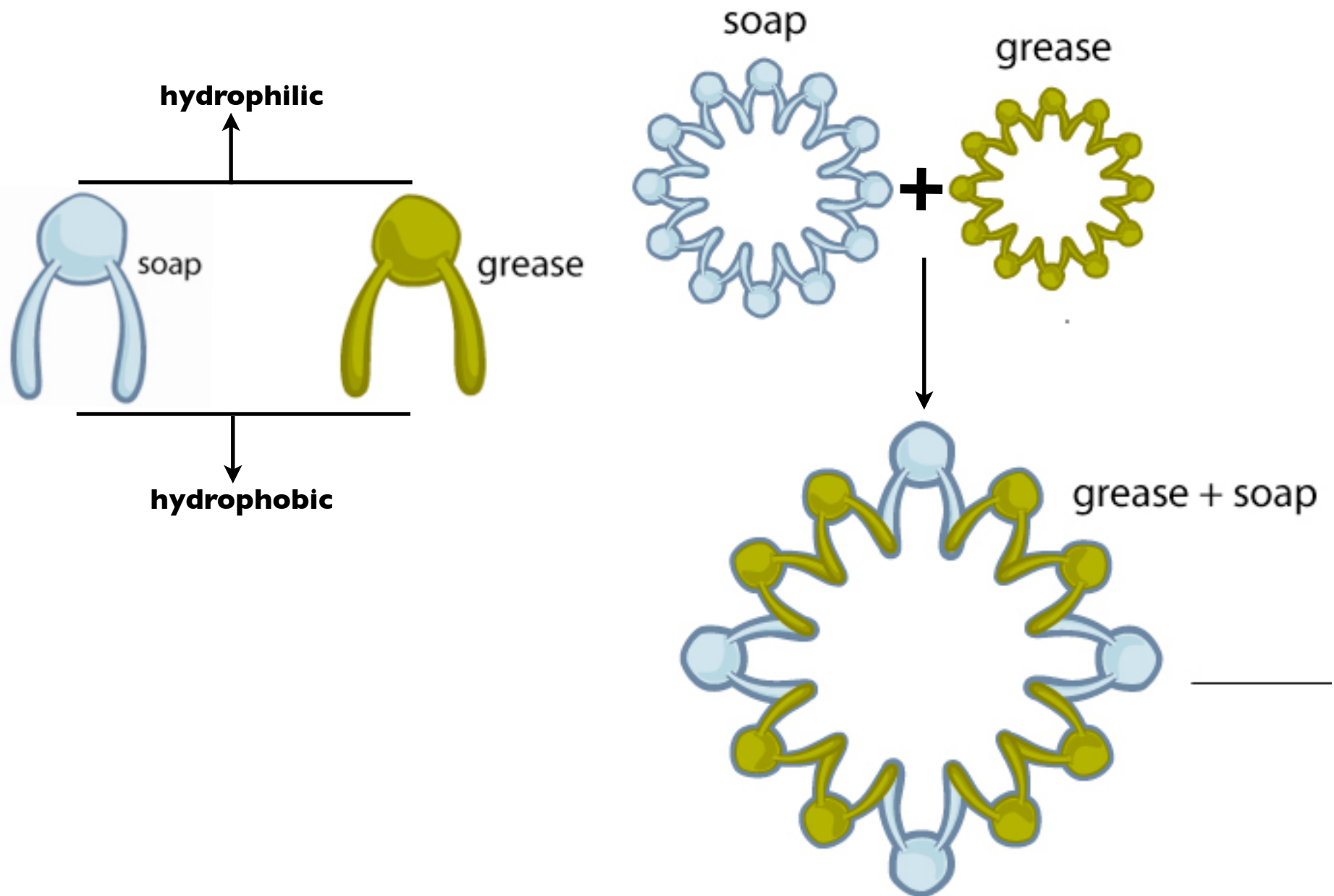
no membrane → no cell → no life

Membranes - Components



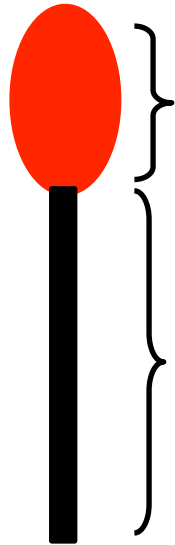
- membranes mostly contain lipids and proteins
- membrane lipids contain *hydrophobic* and *hydrophilic* moieties
- form barriers to free flow of charged species
- ~30% of proteins are membrane proteins
- ~50% of current drug targets are membrane proteins

What is a lipid?



Lipid Structure

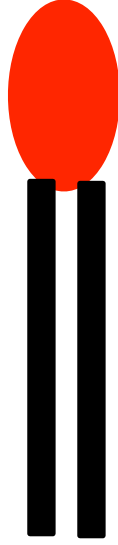
cholesterol



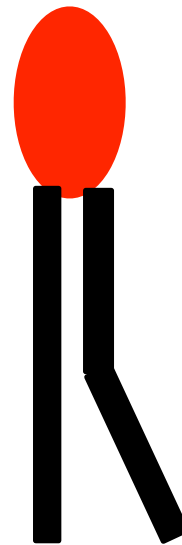
Hydrophilic head
polar

Hydrophobic tail
nonpolar

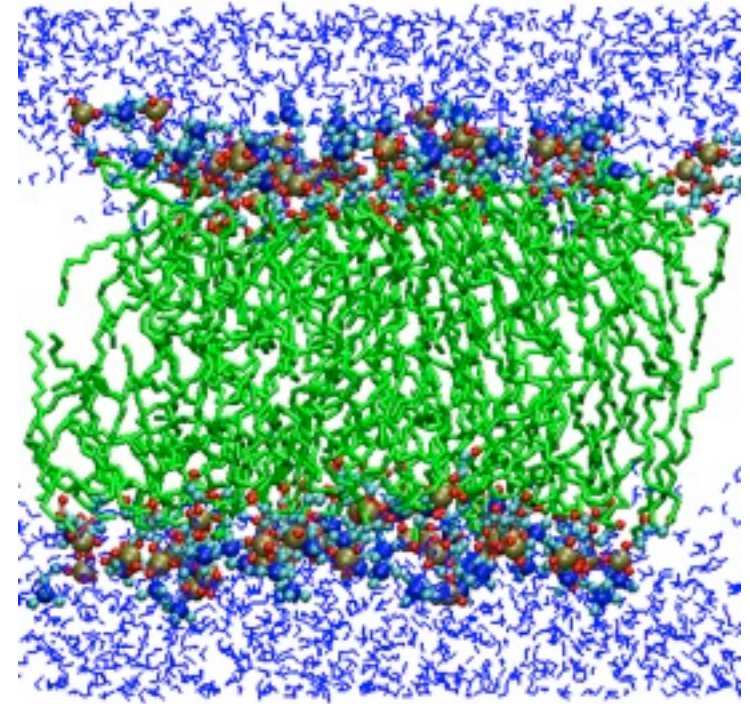
phospholipids



saturated



unsaturated



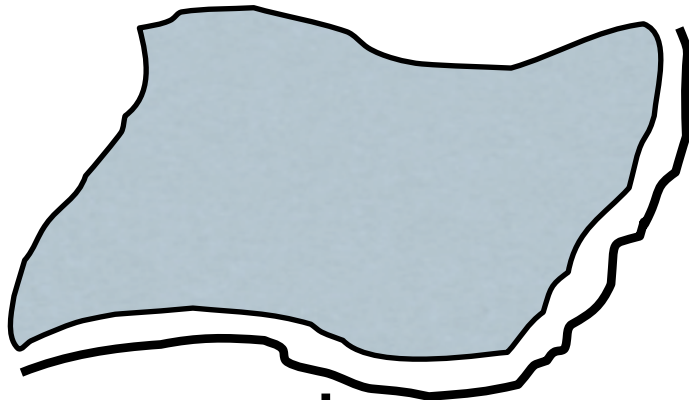
Lipid molecules are amphipathic

Hydrophilic molecules readily dissolve in water (forming favourable electrostatic / hydrogen bond interactions)

Hydrophobic molecules are insoluble in water. Energetic cost minimized if hydrophobic molecules cluster (e.g., oil coalesces to form a drop when dispersed in water)

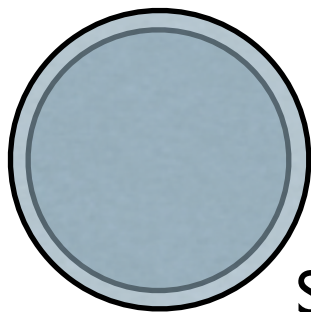
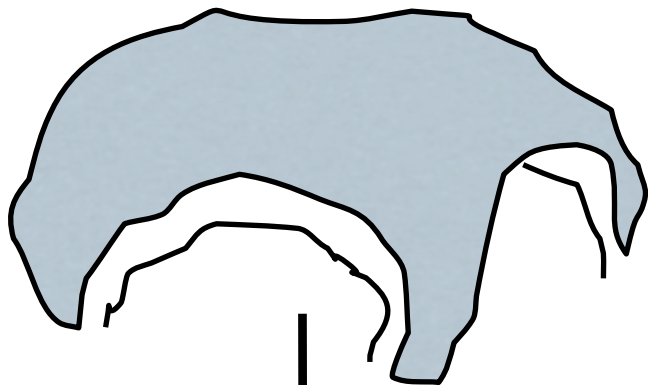
Conflicting forces experienced by amphipathic molecules resolved in the formation of bilayer - energetically most favourable

Lipids to Cells



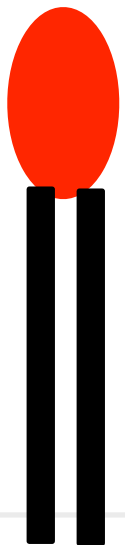
Free edges with exposed hydrophobic tails

- Self-healing property of lipids
- Free edges are energetically expensive
- overriding principle: free edges should be eliminated
- profound effect: formation of closed compartmental structures

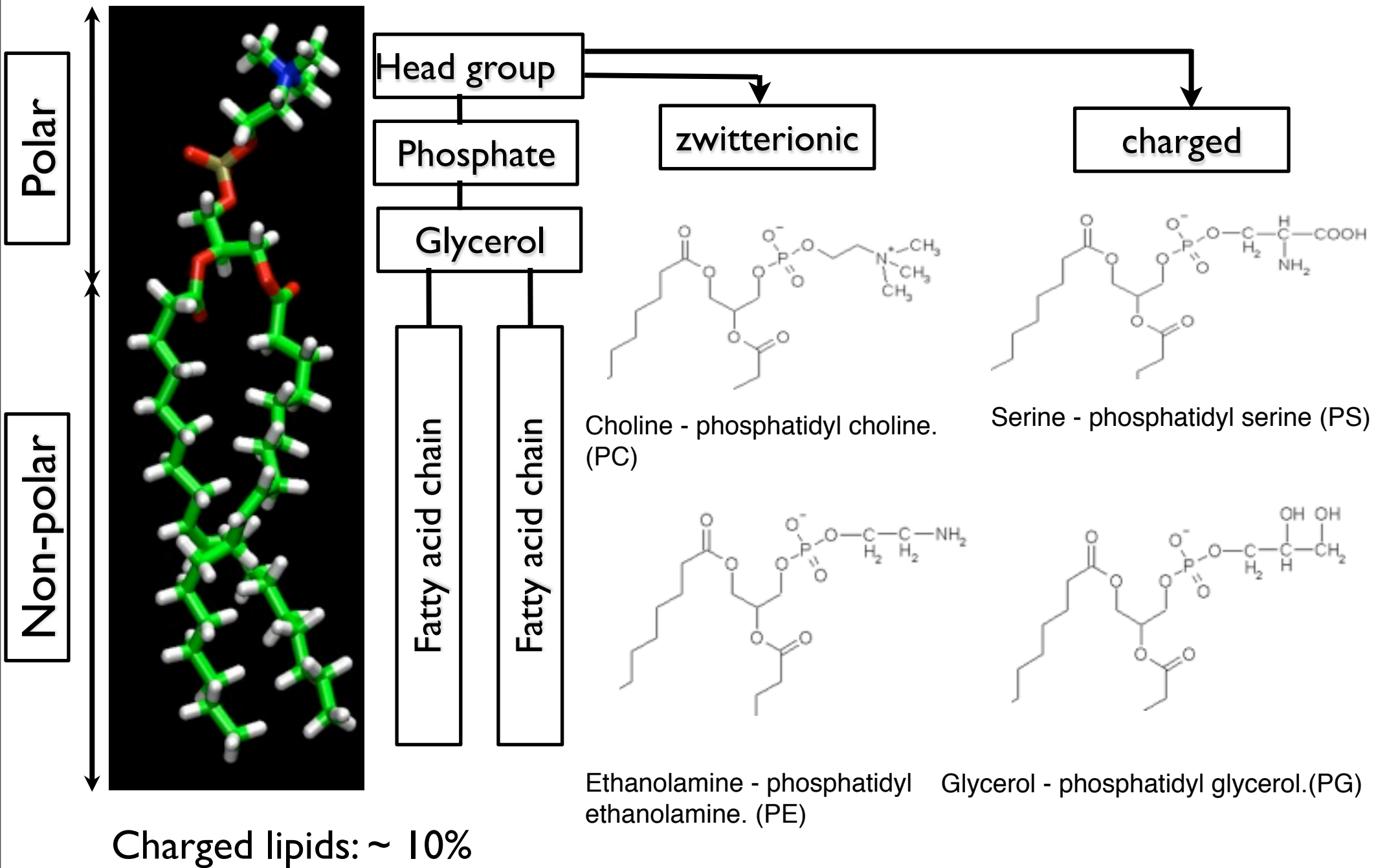


Sealed compartments

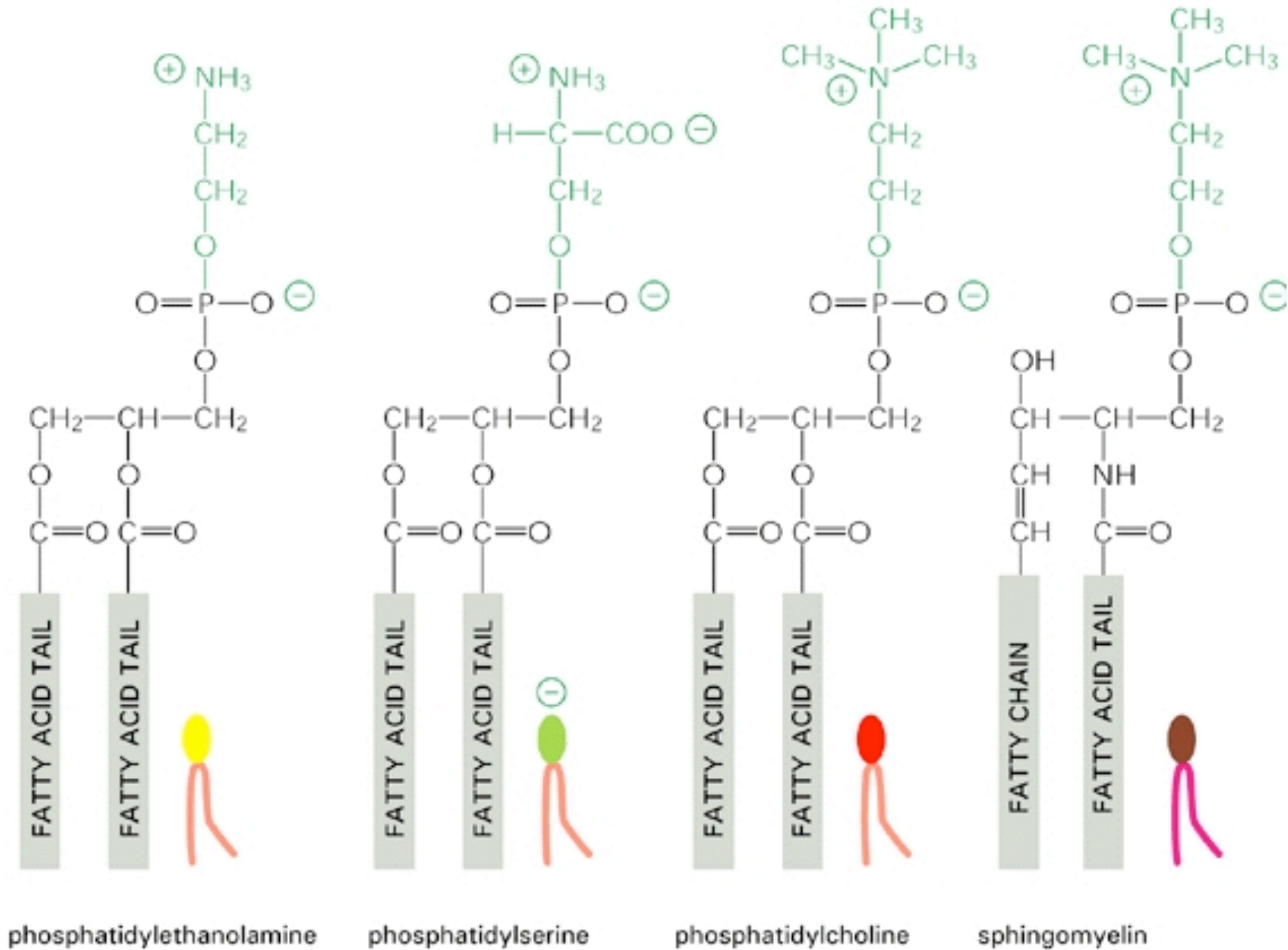
- Amphipathic nature of lipids is fundamental



Phospholipid Structure

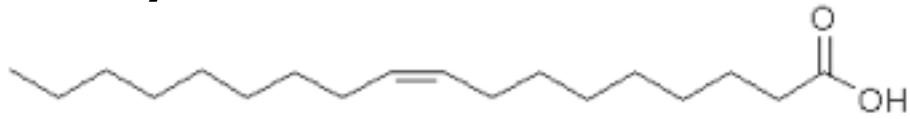


Lipid : Head groups



Lipid: Fatty Acid Chains

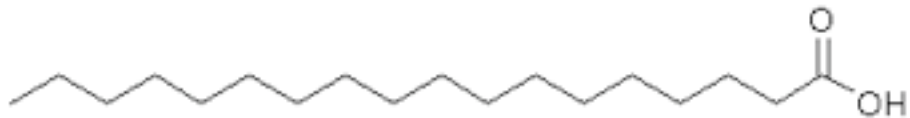
Fatty acid chains



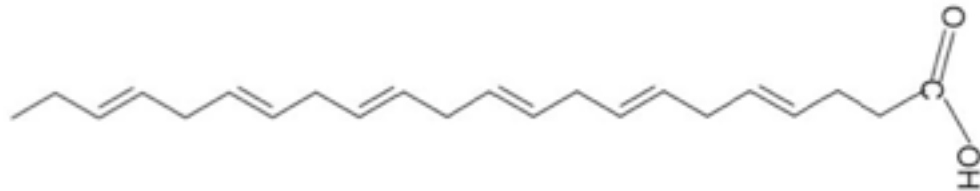
Oleic acid: monounsaturated C18
(18:1)



Palmitic acid: saturated C16
(16:0)



Stearic acid: saturated C18
(18:0)



Docosahexaenoic acid: saturated C22
(22:6)

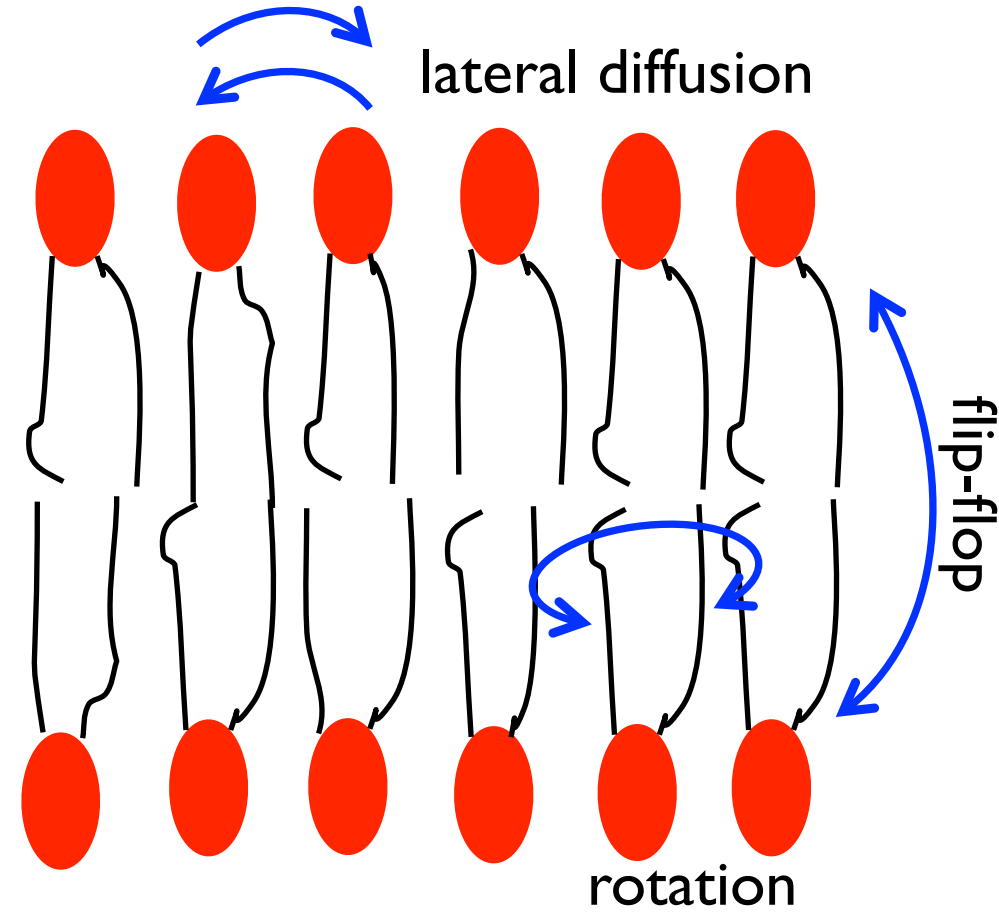
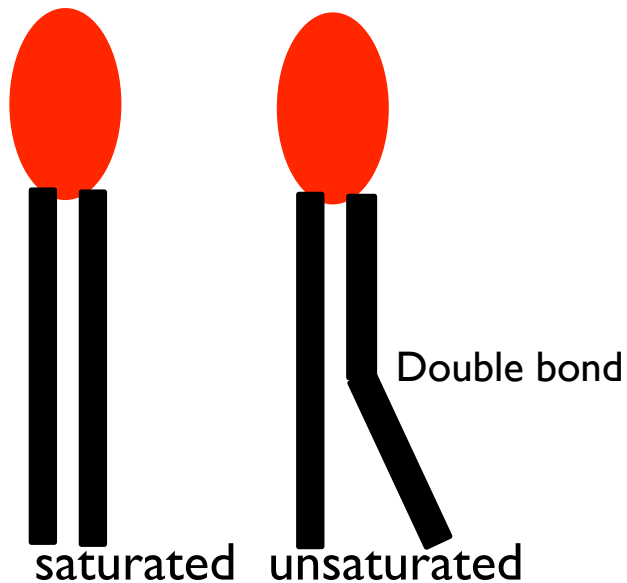
Lipids can have two fatty acid chains of unequal length one or more chains can be unsaturated

Lipids can have a rich variety by varying: fatty acid chain length, degree of saturation, polar head group etc.,

Membranes: Fluid Nature

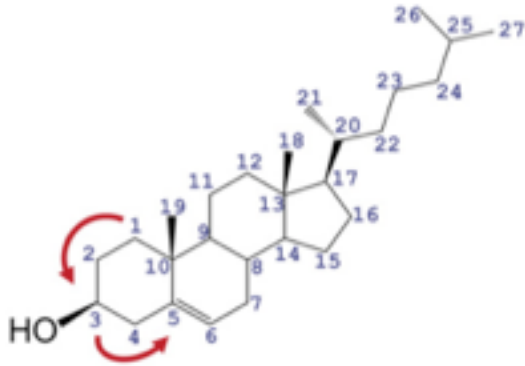
Fluidity: ease with which lipid molecules move within plane of membrane

- depends on lipid composition, temperature
- regular packing leads to less fluidity; unsaturation increases fluidity



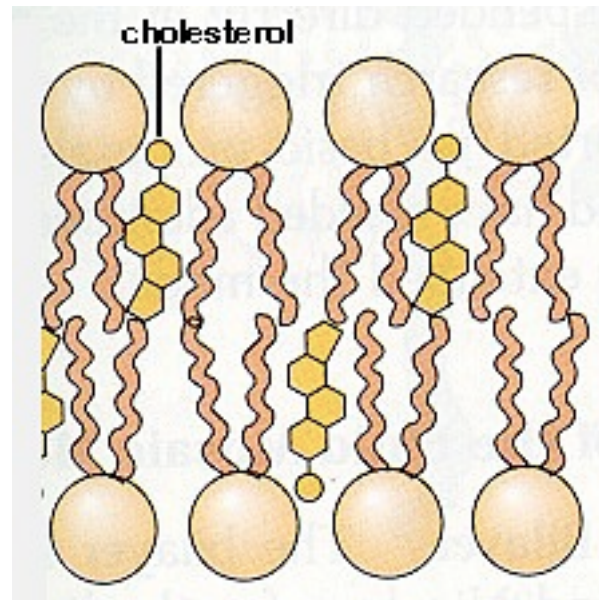
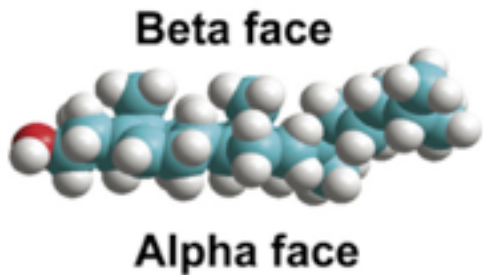
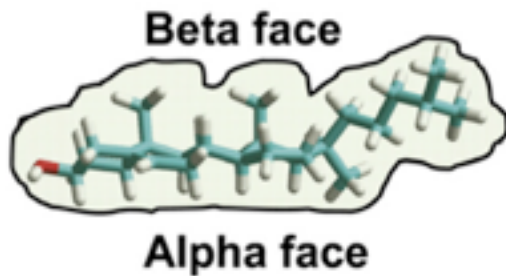
Membrane fluidity plays role in: cell signalling, movements of newly formed lipid molecules, cell division, cell fusion etc,

Cholesterol: a regulator lipid



Cholesterol is one of the most abundant lipid molecules
most cells (animal) have ~ 20-50% cholesterol

Regulates the fluid-like nature of membranes, hence affects
membrane dynamics. At low temperature, increases fluidity
and high temperatures decreases fluidity



Lipid Composition: Plasma membrane



Percentage of Total Lipid by Weight

Lipid	Liver Plasma Membrane	Erythrocyte Plasma Membrane	Myelin	Mitochondrion (inner and outer membranes)	Endoplasmic Reticulum	<i>E. coli</i>
Cholesterol	17	23	22	3	6	0
Phosphatidyl-ethanolamine	7	18	15	35	17	70
Phosphatidylserine	4	7	9	2	5	trace
Phosphatidylcholine	24	17	10	39	40	0
Sphingomyelin	19	18	8	0	5	0
Glycolipids	7	3	28	trace	trace	0
Others	22	13	8	21	27	30

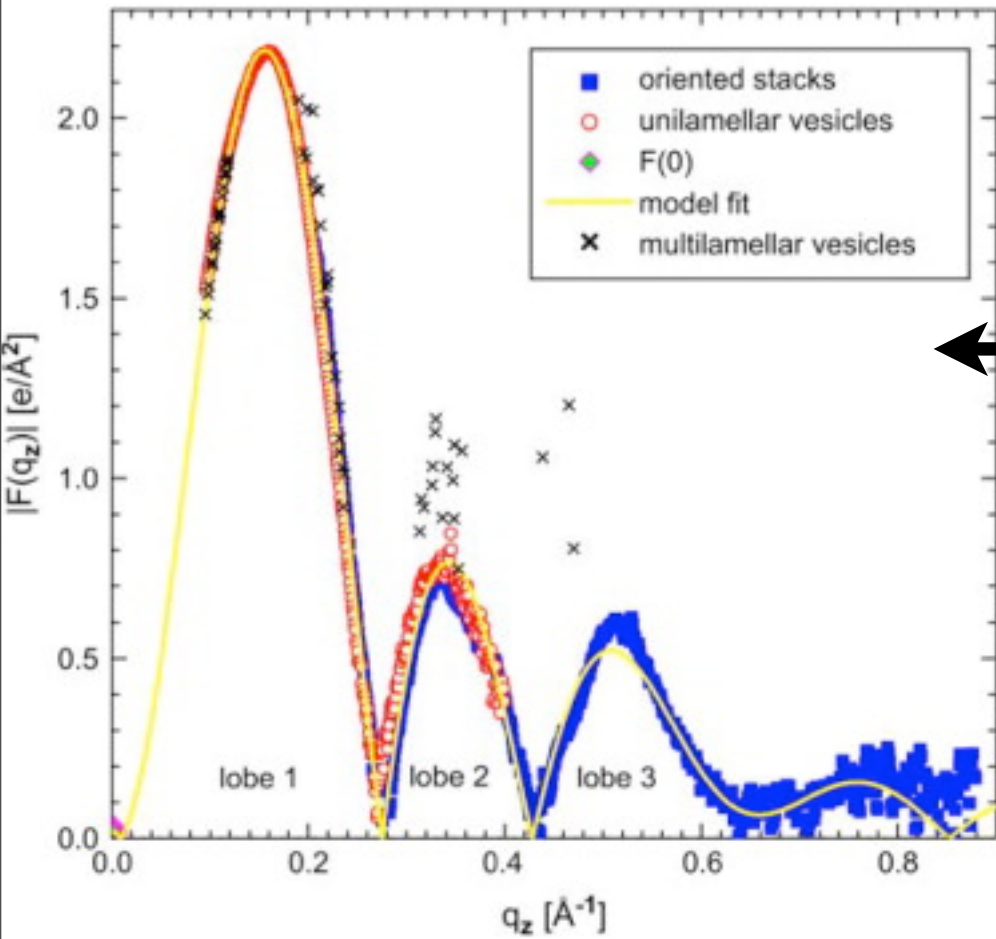
Membranes: what can be measured?

- average area/lipid
- membrane thickness
- electron density profile
- order parameters $S_{CD} = \left\langle \frac{3}{2} \cos^2 \theta - \frac{1}{2} \right\rangle$
- tilt angle of hydrocarbon chains
- pressure profiles
- permeation of various small molecules across membranes
- diffusion of lipid molecules $\frac{1}{N_L} \sum_{\forall i} (x_i(t) - x_i(0))^2 + (y_i(t) - y_i(0))^2$
- surface tension across membranes $\gamma = \frac{1}{2} \left\langle L_z \left(P_{zz} - \frac{1}{2} (P_{xx} + P_{yy}) \right) \right\rangle$
- electrostatic potential change

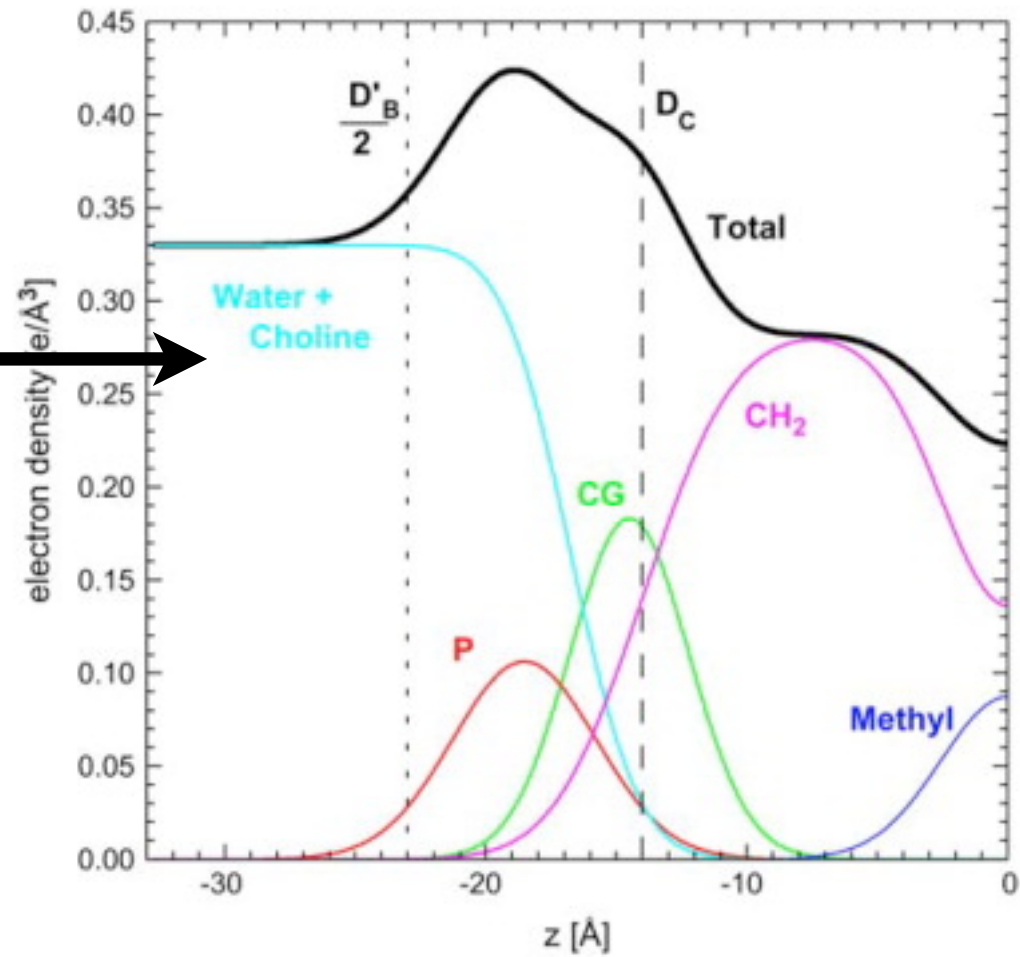
$$\Delta\Psi(z) = \Psi(z) - \Psi(\pm\infty) = -\frac{4\pi}{\epsilon_0} \int_{\pm\infty}^z dz' \int_{\pm\infty}^{z'} \rho(z'') dz''$$

Membranes: Density profiles

Bilayer Form Factor for DPPC (50°C)



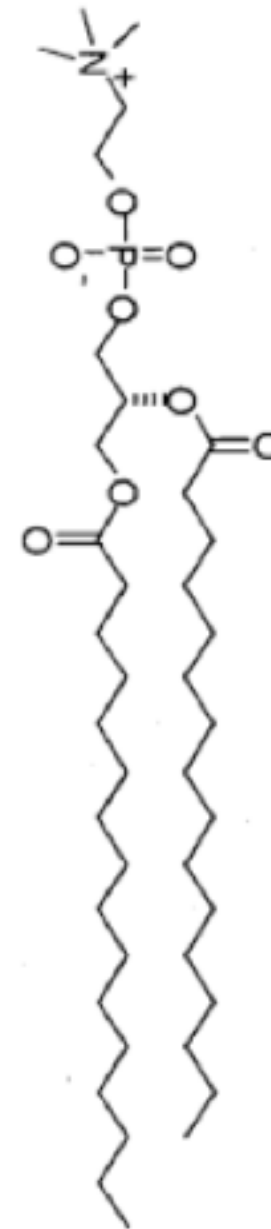
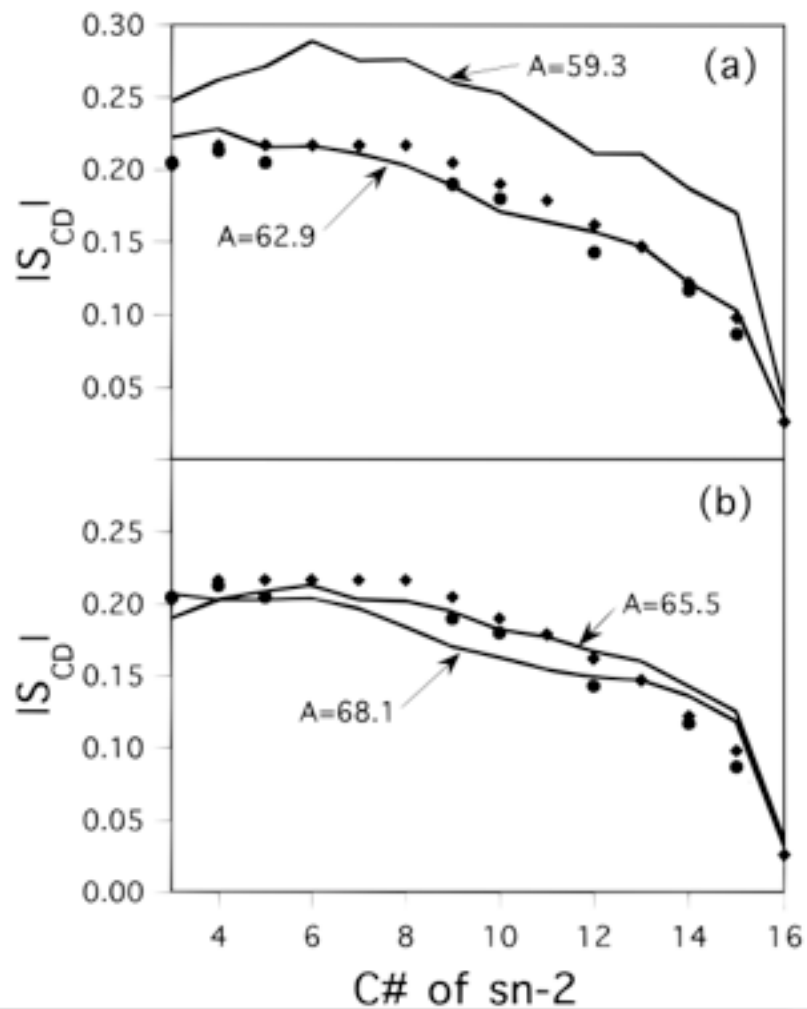
Density profile for DPPC (50°C)



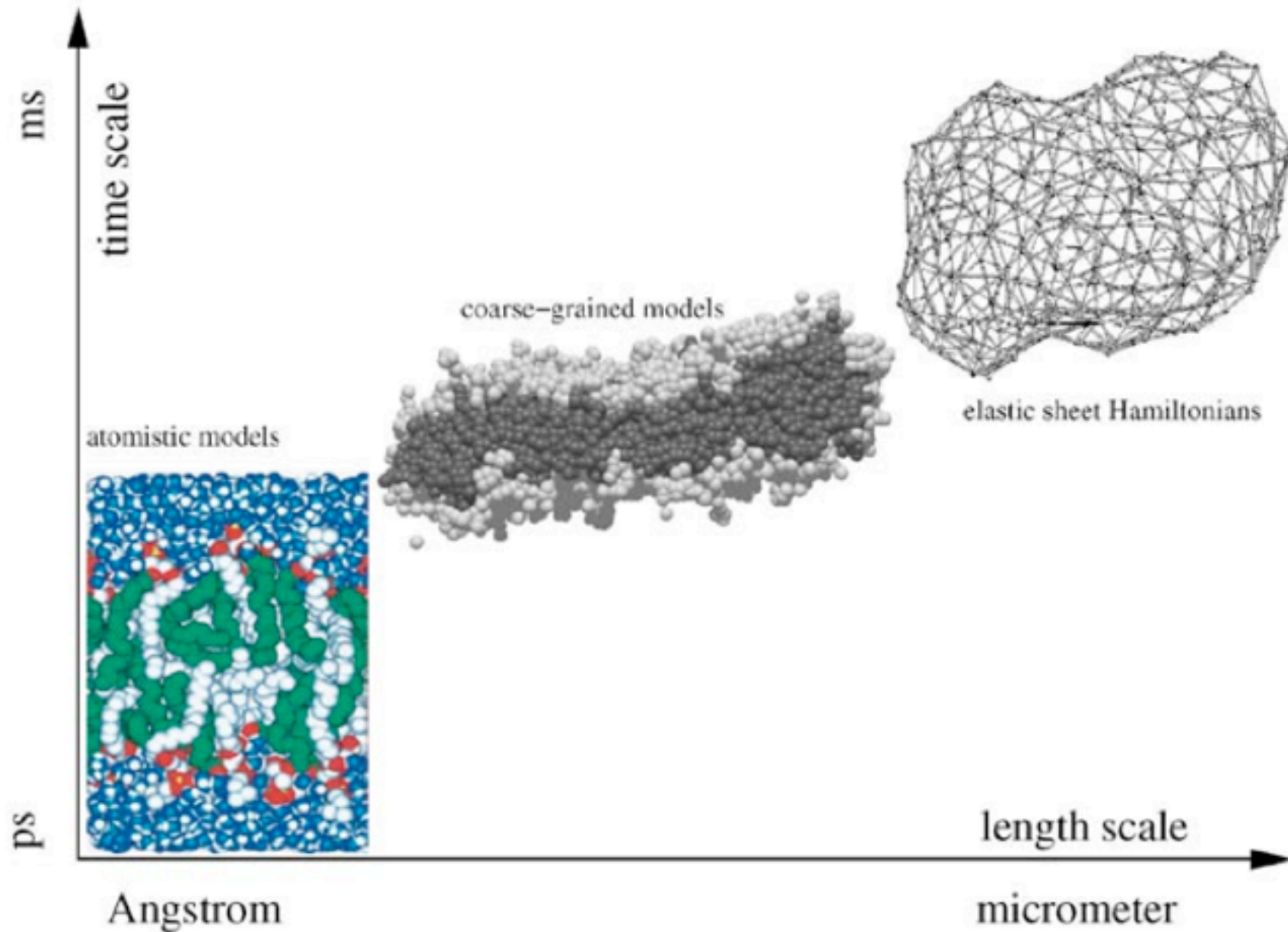
X-ray scattering

Membranes: Deuterium order parameter

$$S_{CD} = \left\langle \frac{3}{2} \cos^2 \theta - \frac{1}{2} \right\rangle$$



Membranes: length and time scales



Lipid Simulations over time

Molecular Dynamics Simulation of a Bilayer of 200 Lipids in the Gel and in the Liquid-Crystal Phases

Helmut Heller,[†] Michael Schaefer,[‡] and Klaus Schulten^{*}

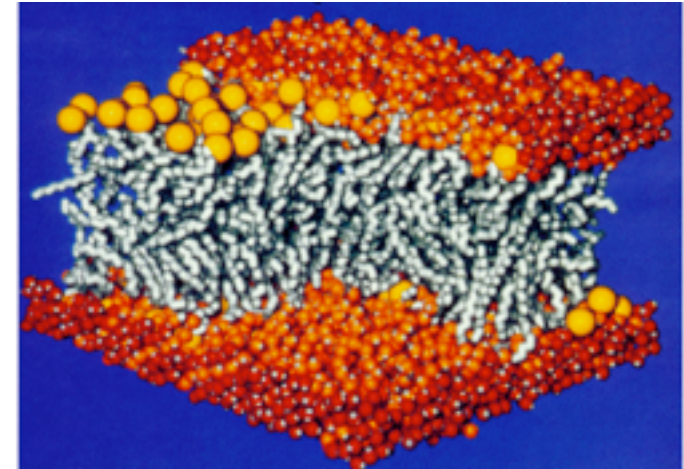
Beckman Institute and Department of Physics, University of Illinois,
405 North Mathews Avenue, Urbana, Illinois 61801

J. Phys. Chem. 1993, 97, 8343–8360

System: palmitoyloleoylphosphatidylcholine(POPC)

System size: 200 lipids Program/force-field: EGO/CHARMM

Simulation time: **263 ps** Electrostatics: Long-range



Molecular structure of the lecithin ripple phase

Alex H. de Vries*, Serge Yefimov, Alan E. Mark, and Siewert J. Marrink

Molecular Dynamics Group, Department of Biophysical Chemistry, University of Groningen, Nijenborgh 4, 9747 AG Groningen, The Netherlands

5392–5396 | PNAS | April 12, 2005 | vol. 102 | no. 15

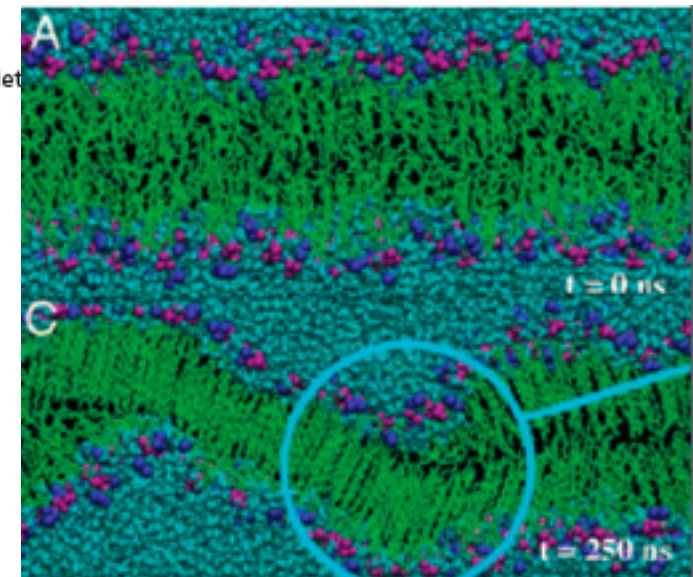
System: Dipalmitoylphosphatidylcholine(DPPC)

System size: 256 lipids

Simulation time: **250 ns**

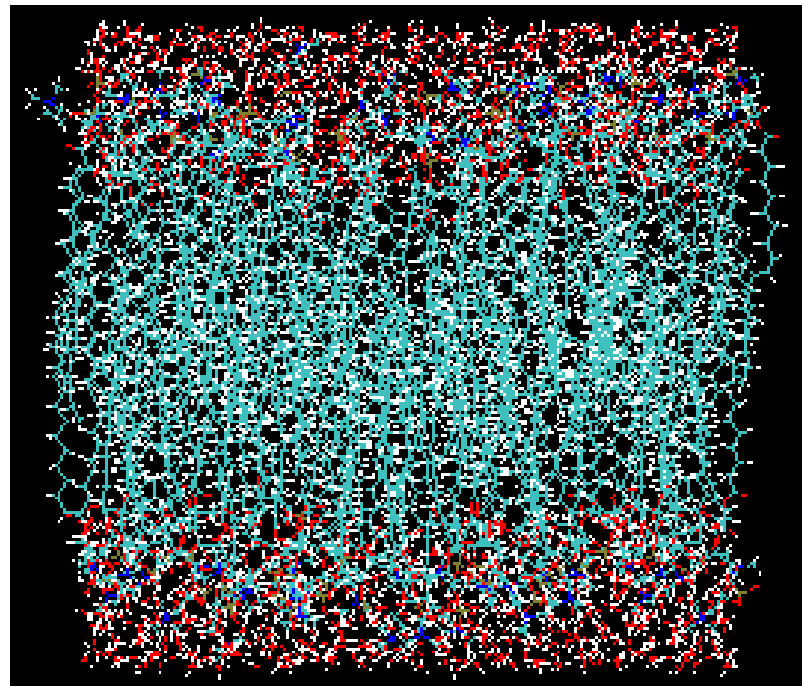
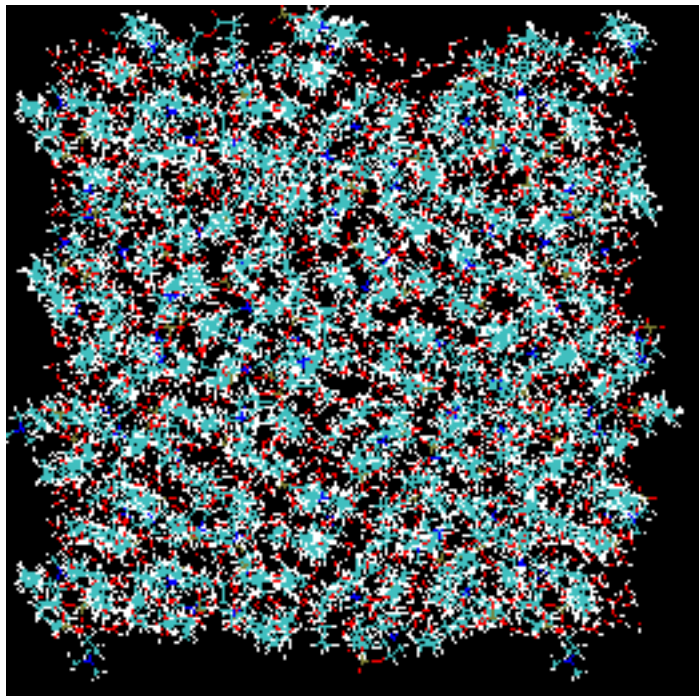
Program: GROMACS

Electrostatics: Long-range



Membrane: Setup

- unlike proteins, no initial coordinates available
- make your own structures or look for existing bilayer patches
- hack into existing lipid topologies to build new ones
- CHARMM 27 force field has lipid topologies/parameter files
- VMD has membrane plugin (very limited)



Force Field

In the context of molecular mechanics, a **force field** (also called a forcefield) refers to the **functional form and parameter sets** used to describe the potential energy of a system of particles (typically but not necessarily atoms).

Many body potential

$$m_i \frac{d^2 \mathbf{r}_i}{dt^2} = - \frac{\partial V(\mathbf{r}^N)}{\partial \mathbf{r}_i} \quad (i = 1, \dots, N)$$

$$V(\mathbf{r}^N) = \sum_b k_b (r - r_b)^2 + \sum_\theta k_\theta (\theta - \theta_0)^2 + \sum_\omega k_\omega (\omega - \omega_0)^2 \\ + \sum_\phi k_\phi (1 - \cos(n\phi - \delta)) + \sum_{i < j} 4 \epsilon_{ij} \left[\left(\frac{\sigma_{ij}}{r} \right)^{12} - \left(\frac{\sigma_{ij}}{r} \right)^6 \right] + \sum_{i < j} \frac{q_i q_j}{r}$$

from Wiki

How to get parameters ?

Parameter set:

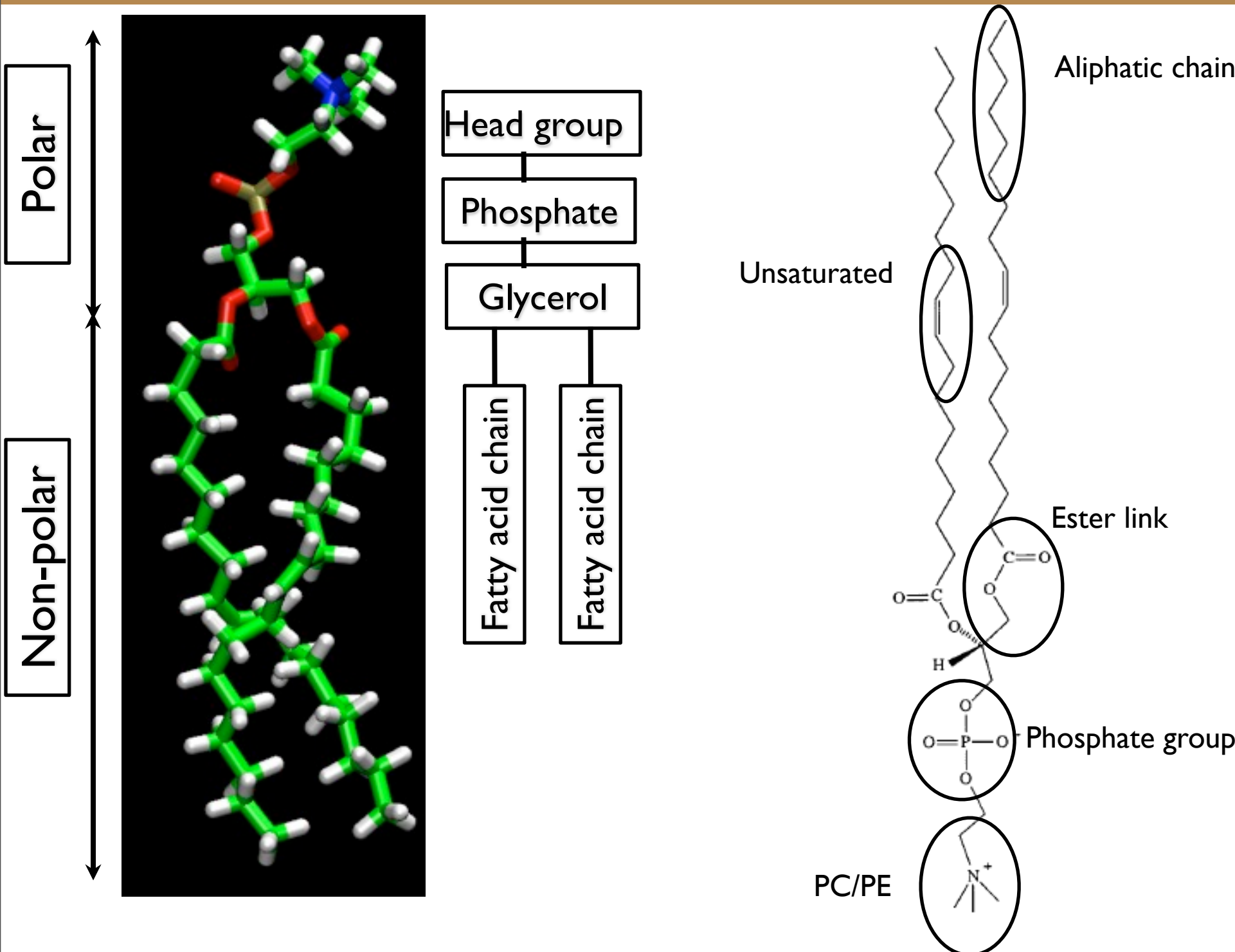
mass, van der waals radius, partial charges, equilibrium bond lengths, angles, dihedrals, force constants

Target data:

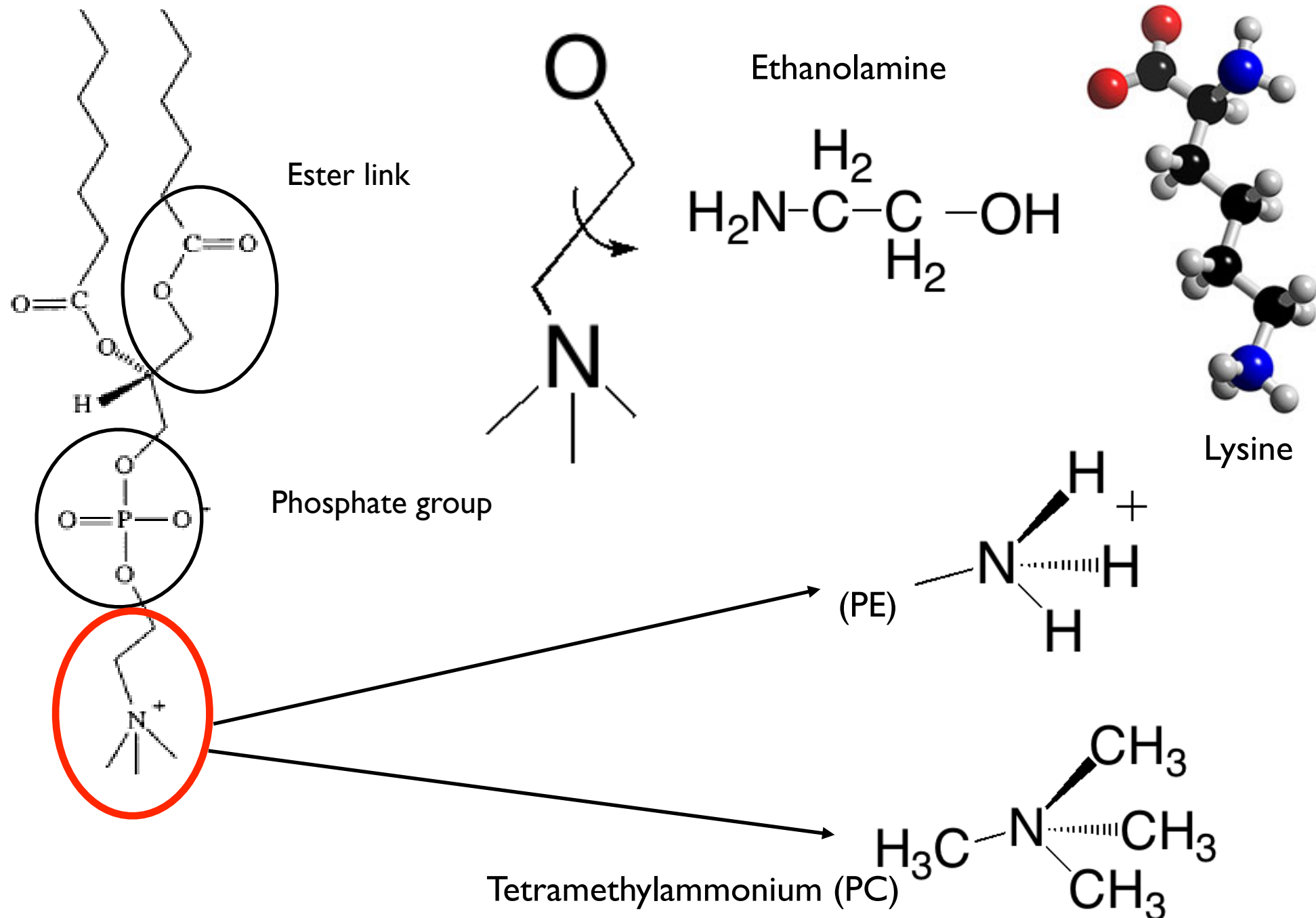
Experiments **&/** high-level quantum mechanics calculations like

IR, Raman, NMR, X-ray crystallography, microwave, heats of vaporization, enthalpies, *ab initio* calculations, normal mode analysis

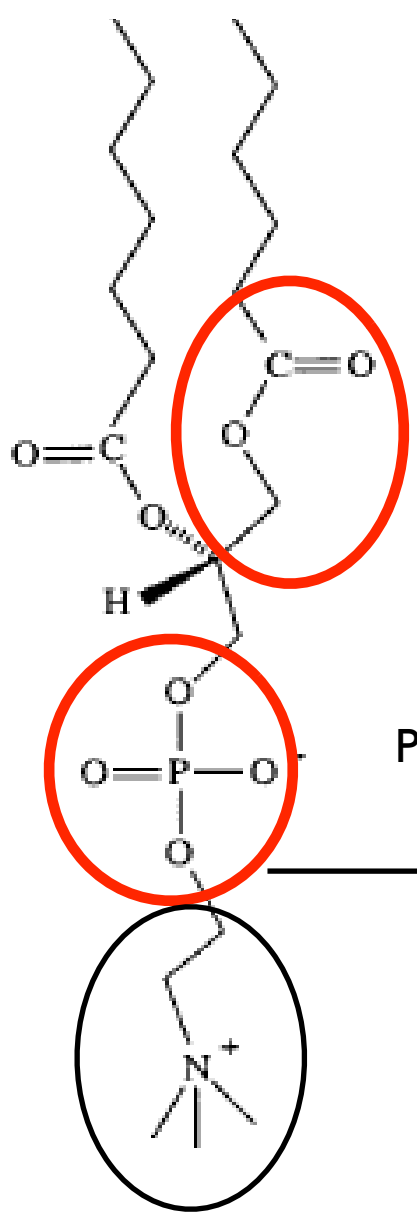
Phospholipid Structure



Head group parameters



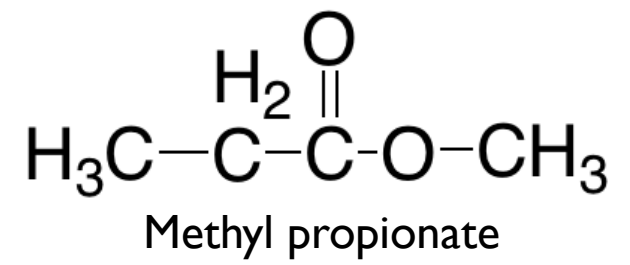
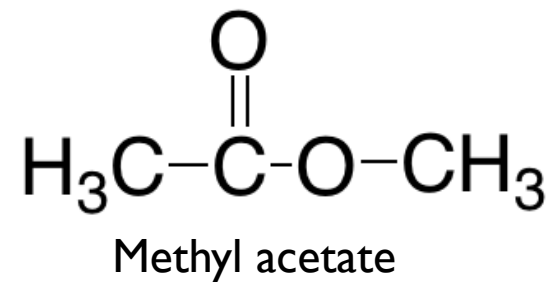
Phosphate/ester group parameters



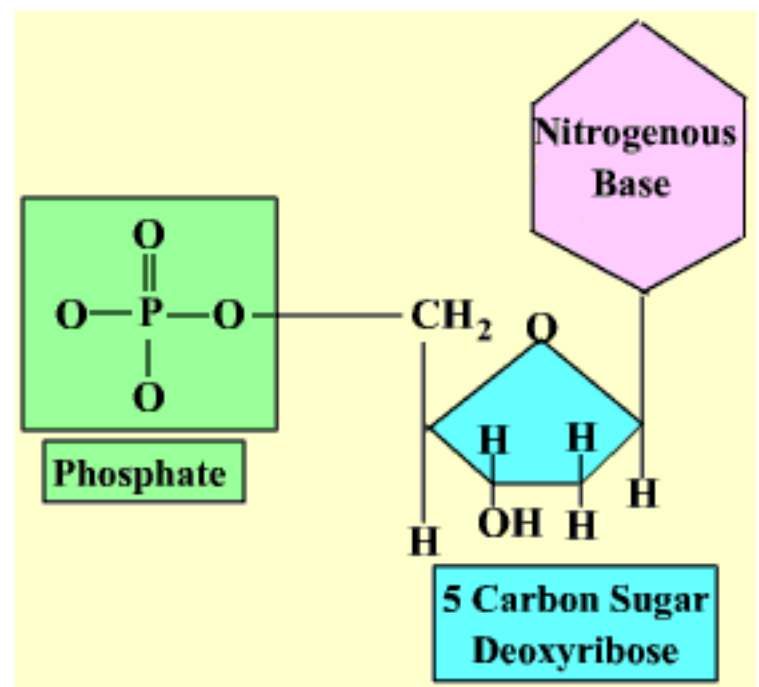
Ester link

Phosphate group

PC/PE



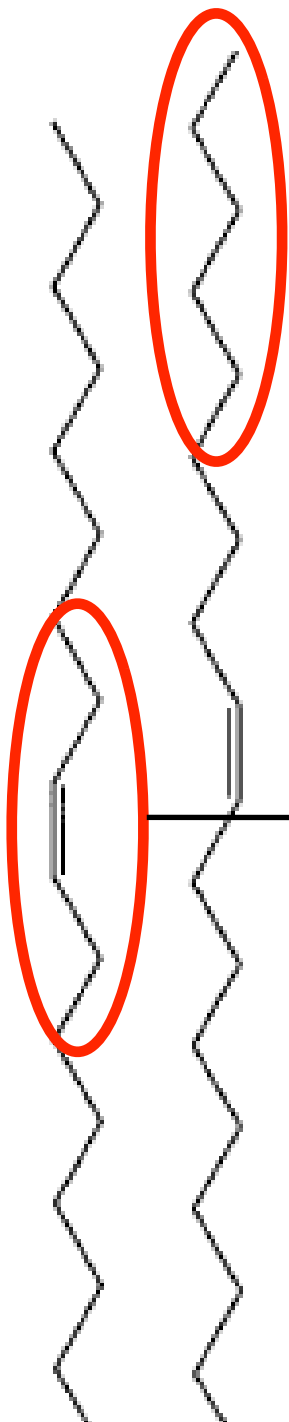
Phosphate group from nucleic acid parameters



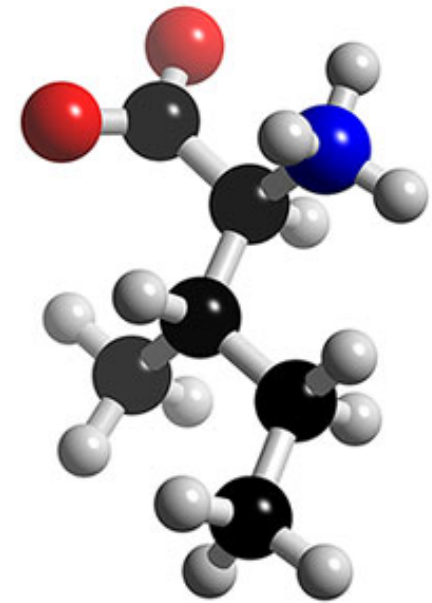
Deoxyribose Nucleotide

<http://www.uic.edu/classes/bios/bios100/lecturesf04am/nuclei1.gif>

Lipid chain parameters

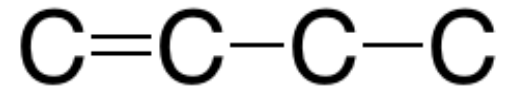


From protein aliphatic side chain groups



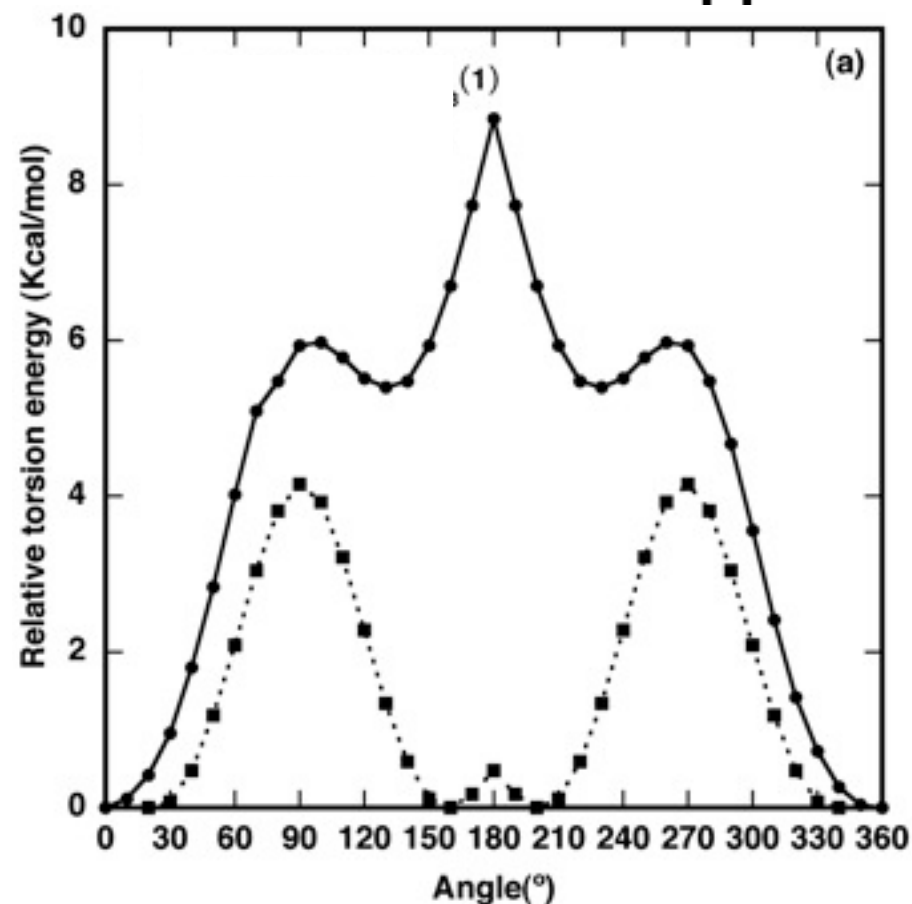
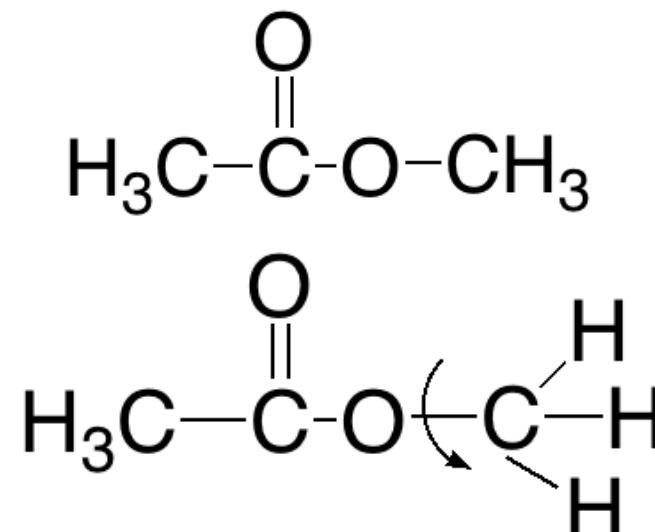
isoleucine

Parameters for unsaturated lipids

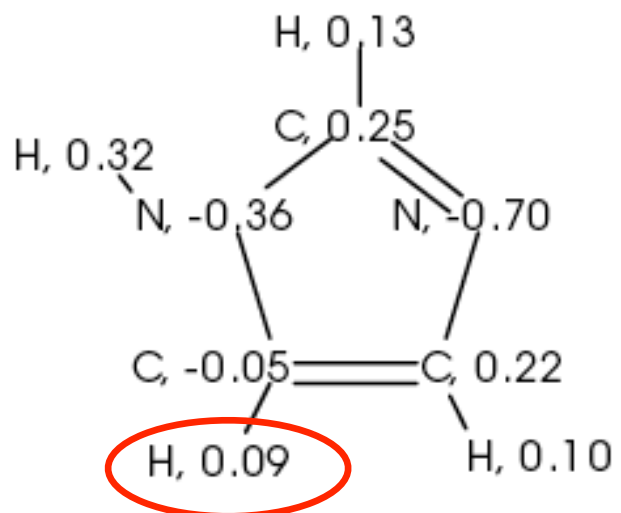


Parameterization

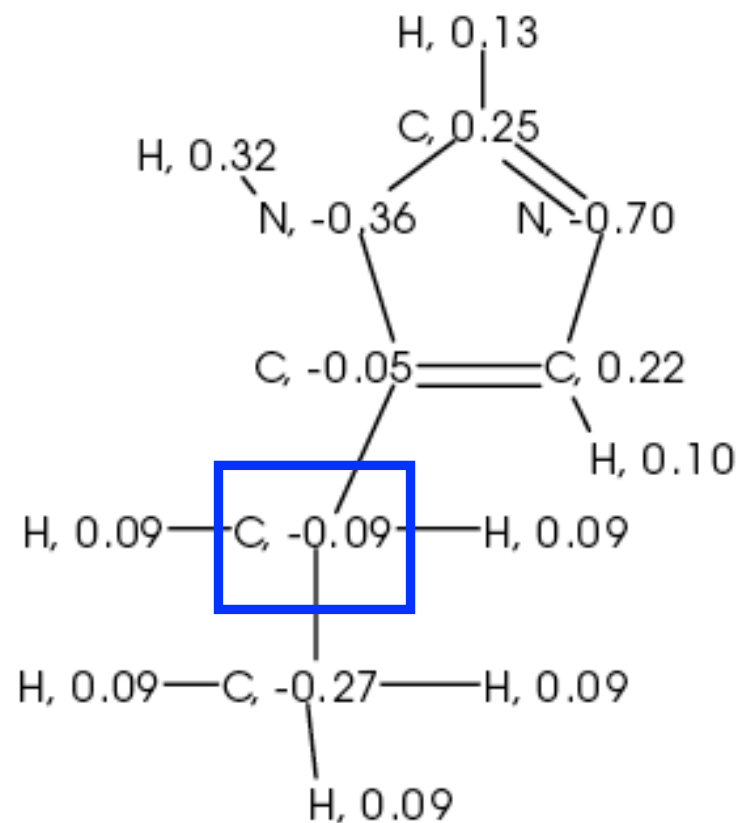
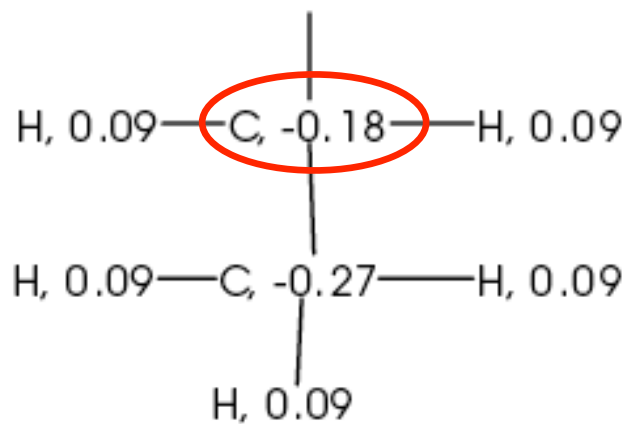
- breakdown into small model molecules
- intra equilibrium values from *ab initio* calculations (high-level of theory)
- intra force constants through 'frequency matching' methods (requires normal mode computation)
- partial charges by different schemes such as Mulliken/RESP (eg., Antechamber program in AMBER/ *ab initio* calculations)
- VDW parameters by analogy and further refined by using target data such as heat of vaporization, densities etc.,



Stiching pieces (partial charges)

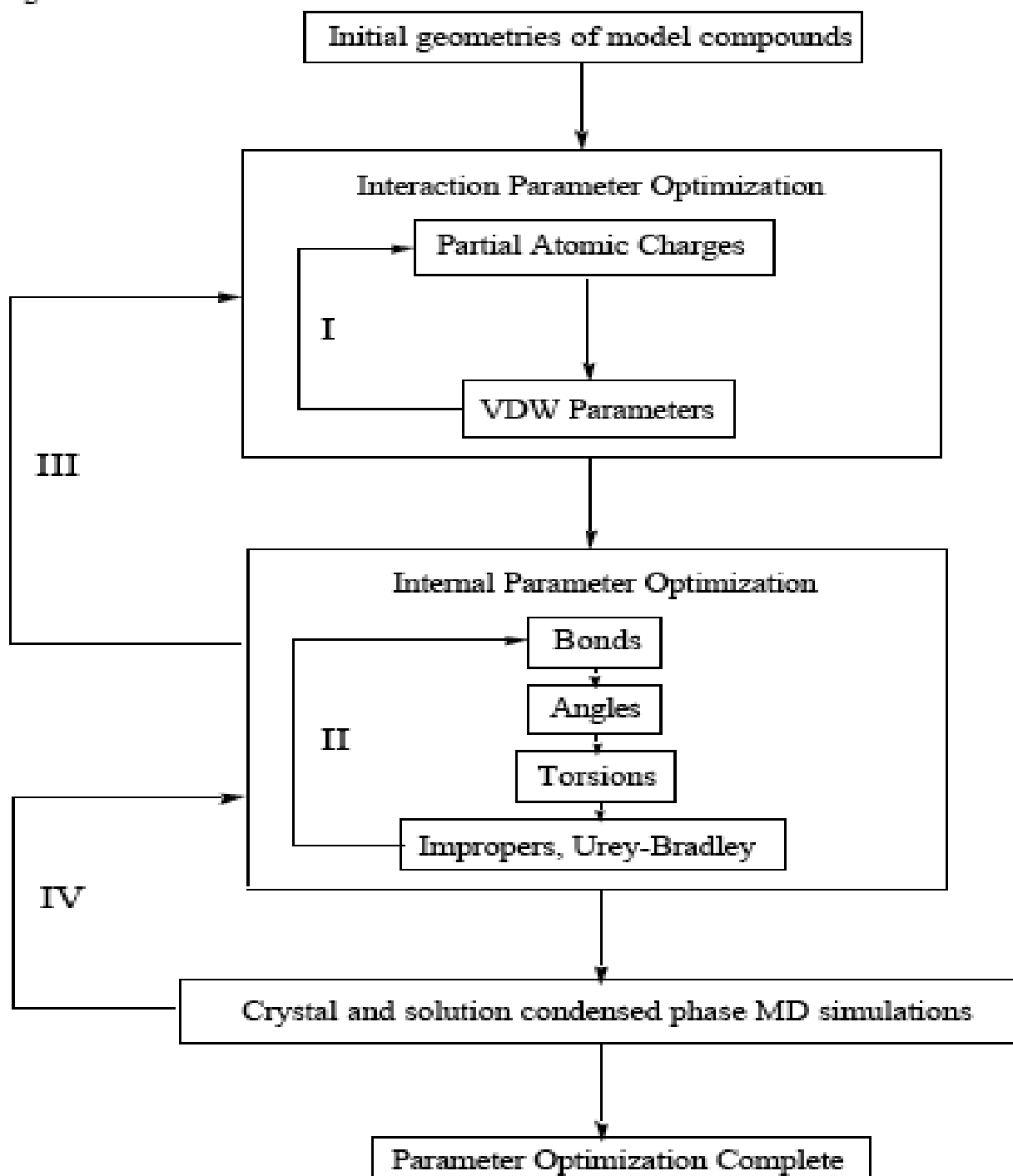


+

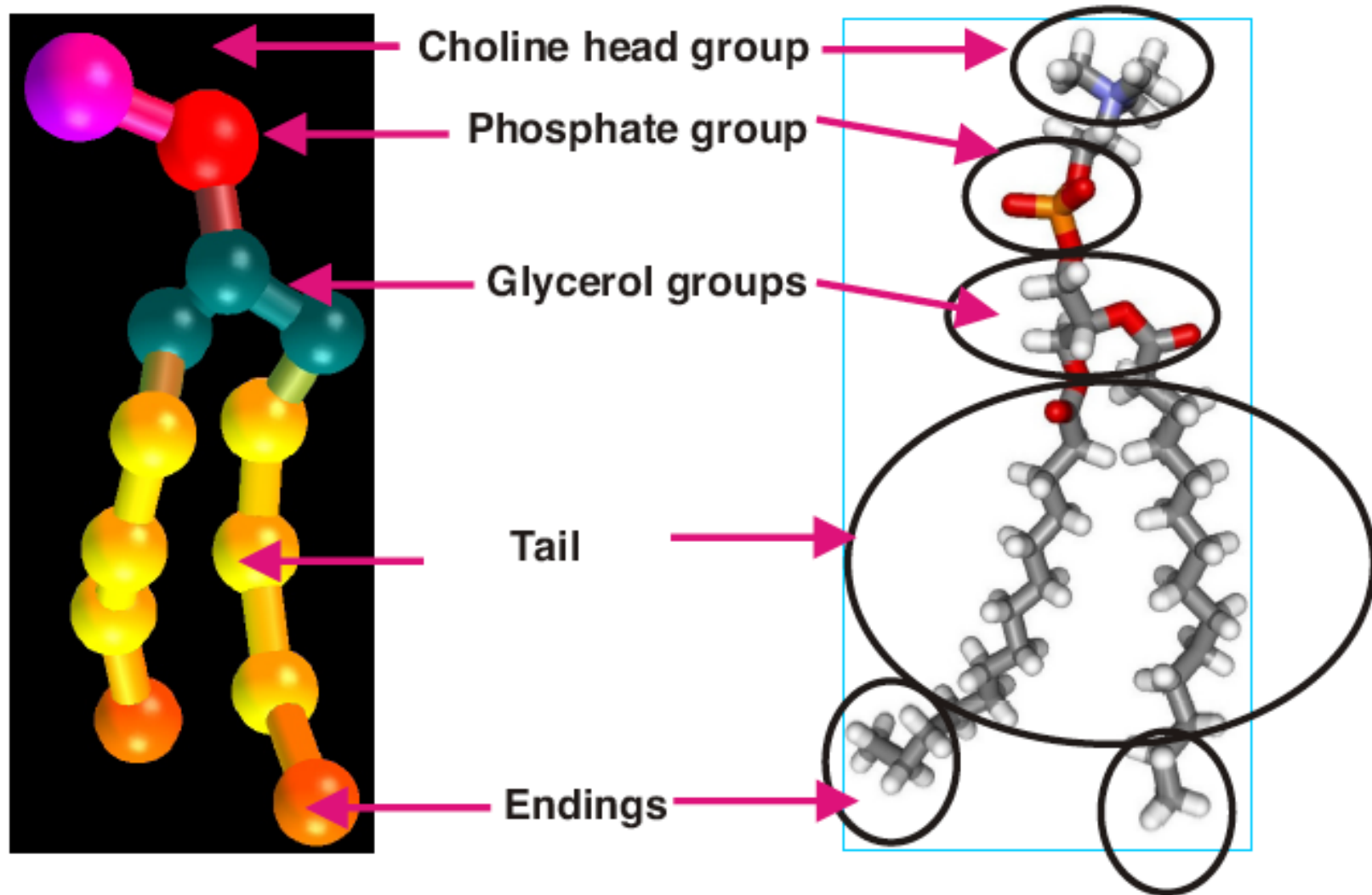


Parameter optimization strategy

Figure 1



Lipid: Coarse Graining



A 3D ribbon diagram of a membrane protein, shown as a yellow-orange ribbon structure. The protein is embedded in a lipid bilayer, which is represented by a grey and white mesh. A green and white ball-and-stick model of a ligand is bound to the protein. Several water molecules, shown as red and white spheres, are scattered around the protein and the ligand. The text "Membrane Proteins" is overlaid in the center of the image.

Membrane Proteins

Membranes: Permeability

Charged ions

Na⁺, Cl⁻



Large uncharged molecules

Amino acids



Small uncharged polar molecules

H₂O, ethanol



Small hydrophobic molecules

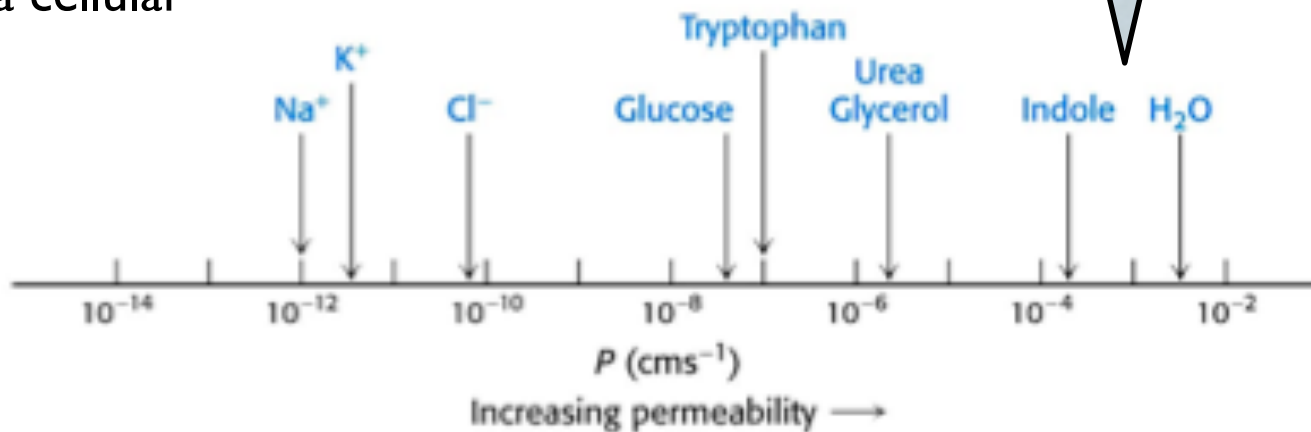
O₂, C₂, N₂, benzene



Extra cellular

Membrane

Intra cellular

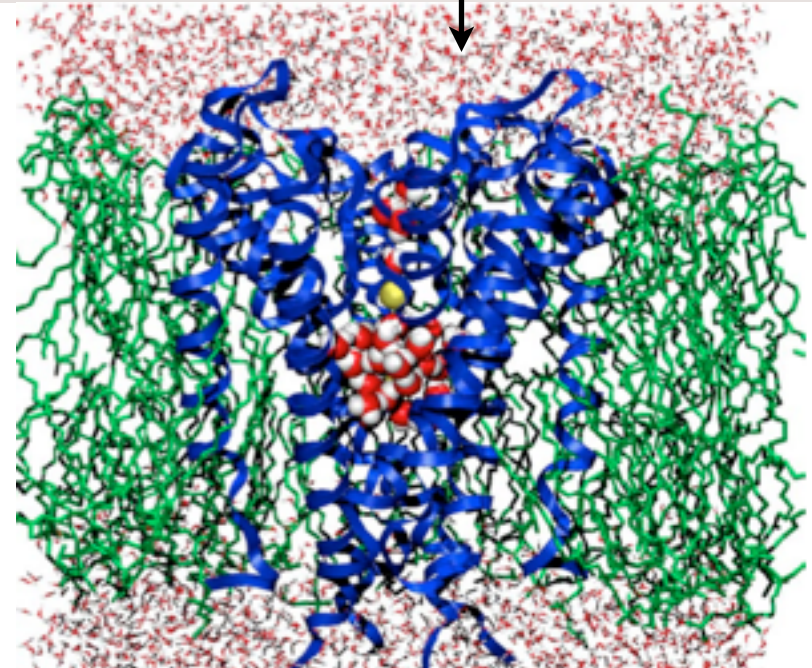
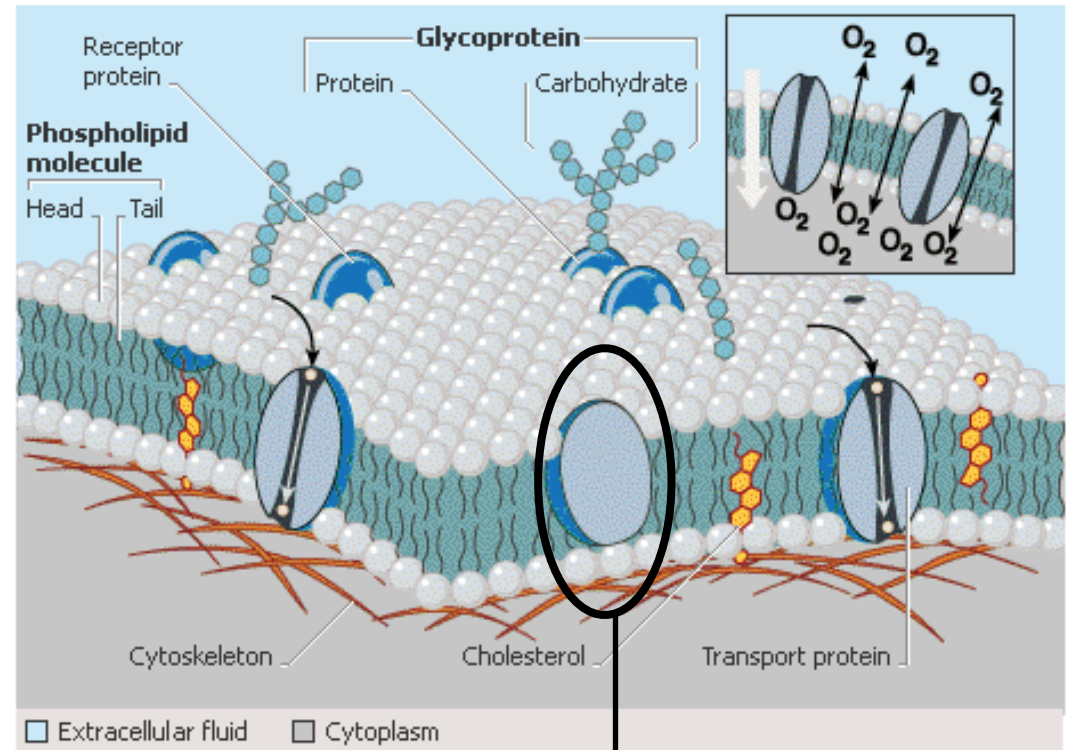
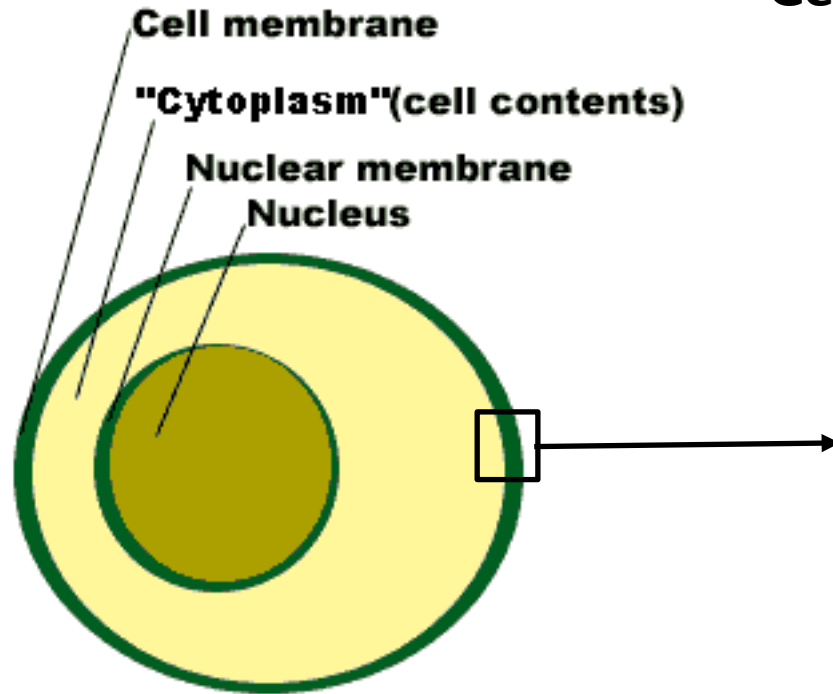


- movement of ions in and out of cells essential for life
- ion flows mediate processes such as signalling, electrical signals in nerves, muscles, pH balance etc.,
- ion currents cause changes in membrane potential

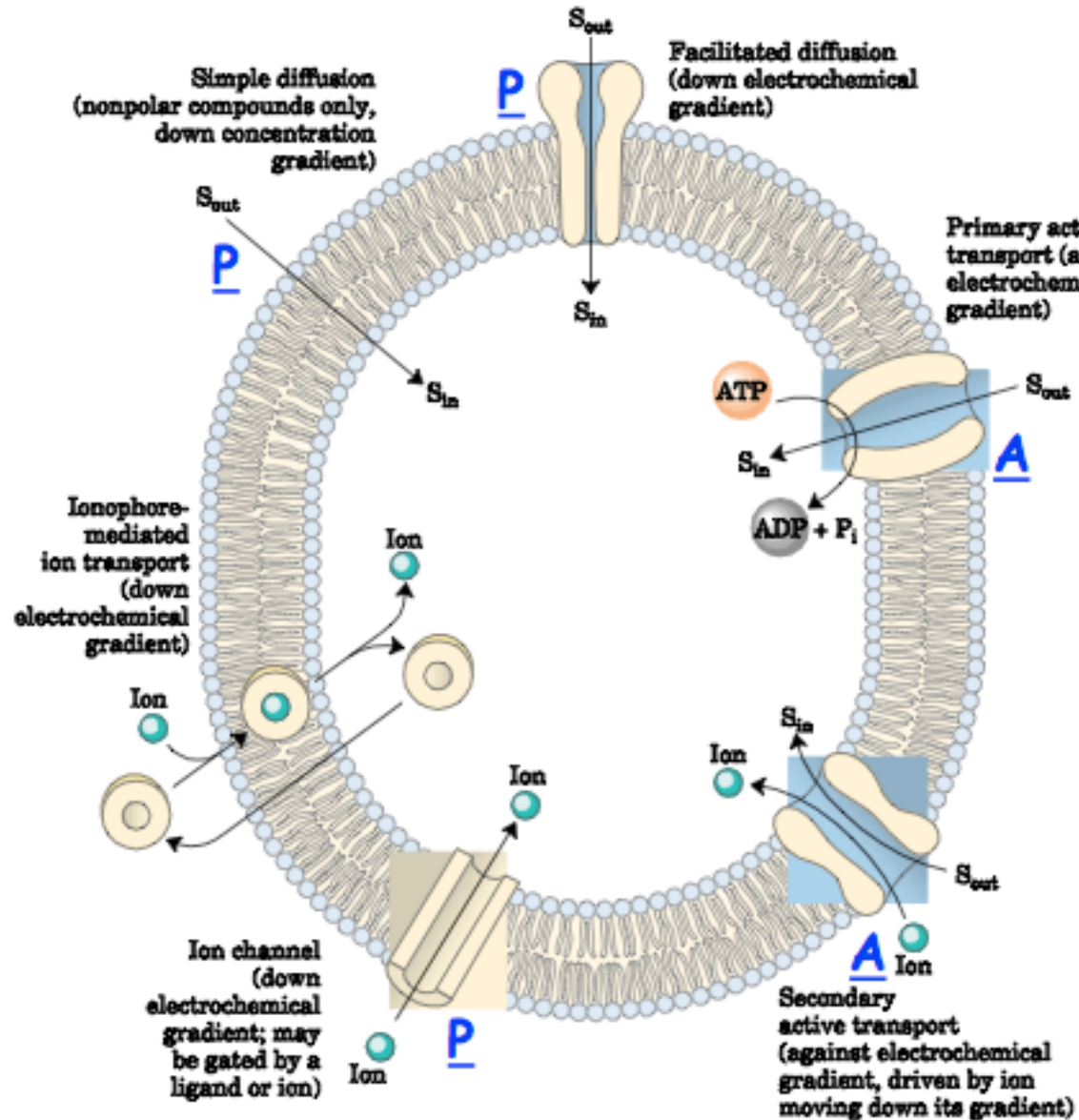
Specialized transport proteins are required.....

Perspective

Cell membrane



Ion transport across membranes

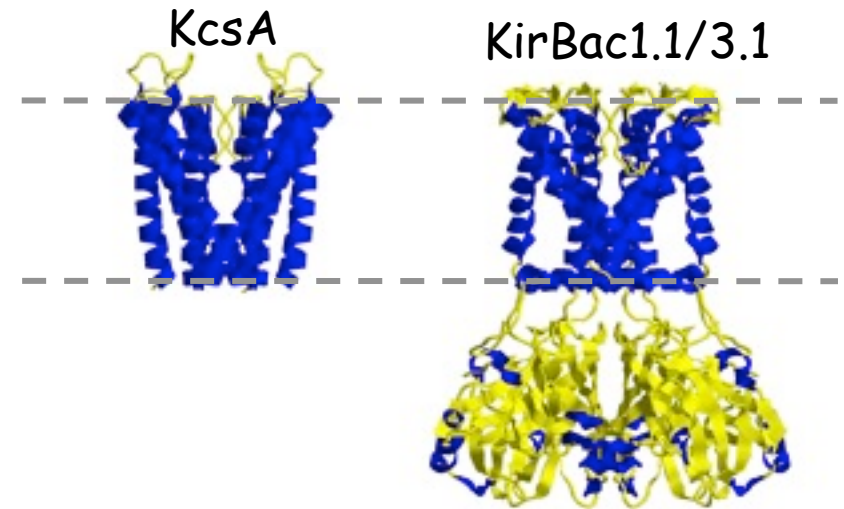
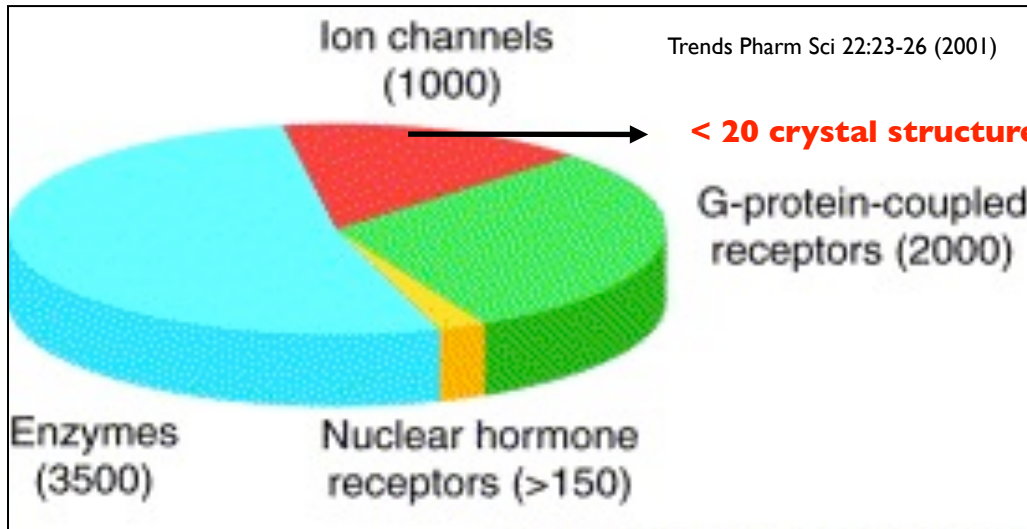


active: against concentration gradient, transporters

Passive & Active Transport Across Cell Membranes

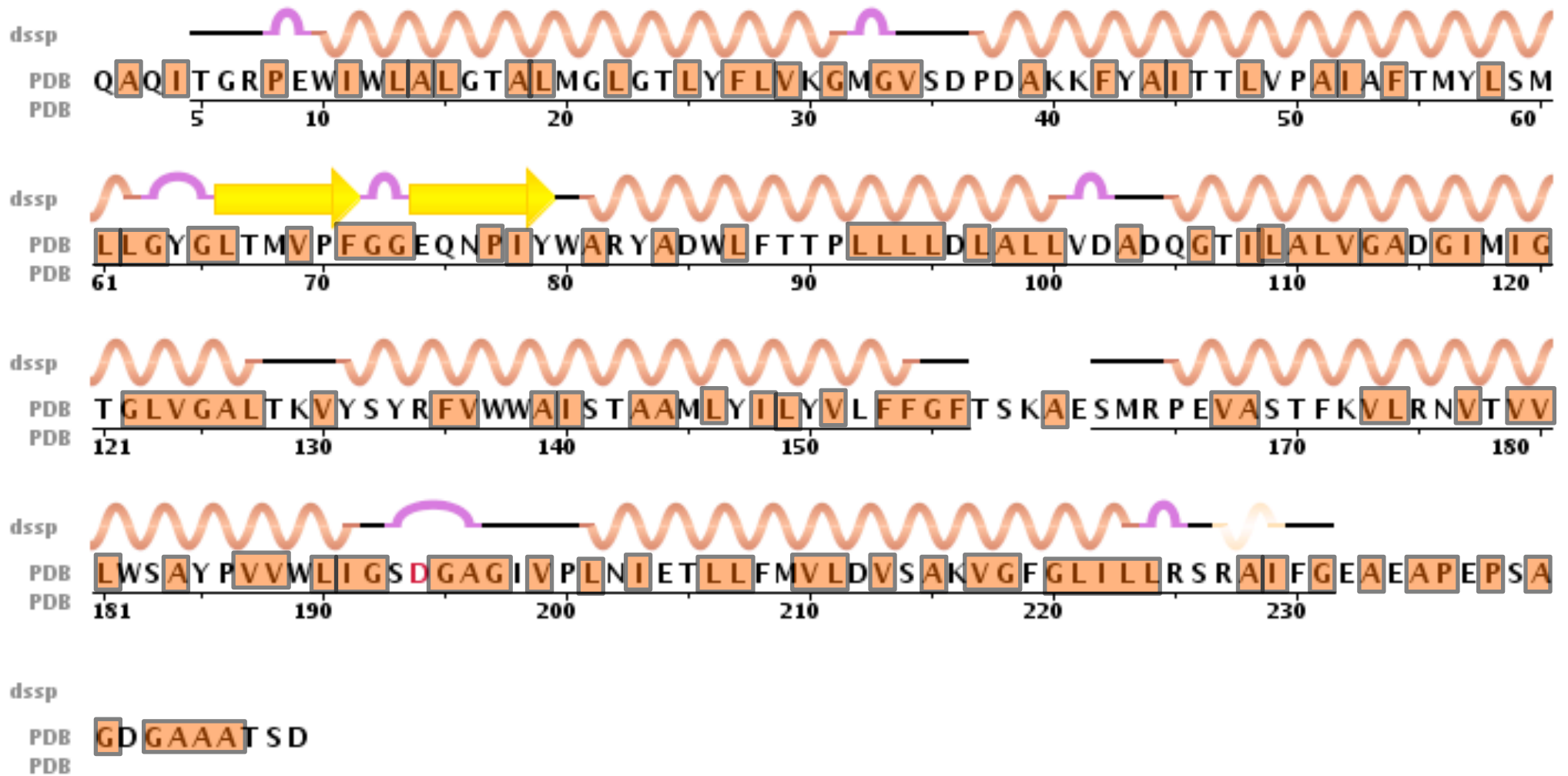
passive: travel down the concentration gradient

Membrane Proteins



- Genomics – Membrane Proteins constitute ca. 25% to 30% of all genes
- Membrane Proteins are implicated in many diseases: Diabetes, Parkinson's, drug resistance (tumours & bacteria) ...
- Membrane Proteins are major drug targets
- ~50% of current drug targets are membrane proteins

Rhodopsin



Nobel Prizes for ion channels:

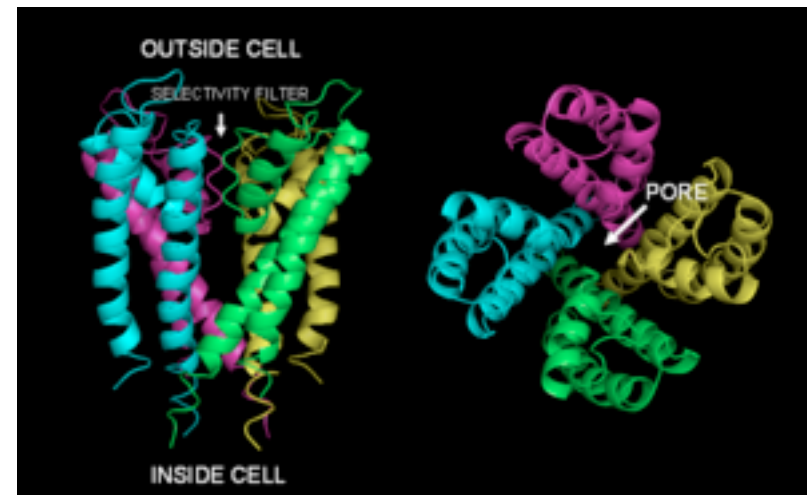
- Alan Hodgkin and Andrew Huxley in (1963)
- Erwin Neher and Bert Sakmann (1991)
- Roderick MacKinnon (2003)

The Nobel Prize in Physiology or Medicine 1963 was awarded jointly to Sir John Carew Eccles, Alan Lloyd Hodgkin and Andrew Fielding Huxley "for their discoveries concerning the ionic mechanisms involved in excitation and inhibition in the peripheral and central portions of the nerve cell membrane".

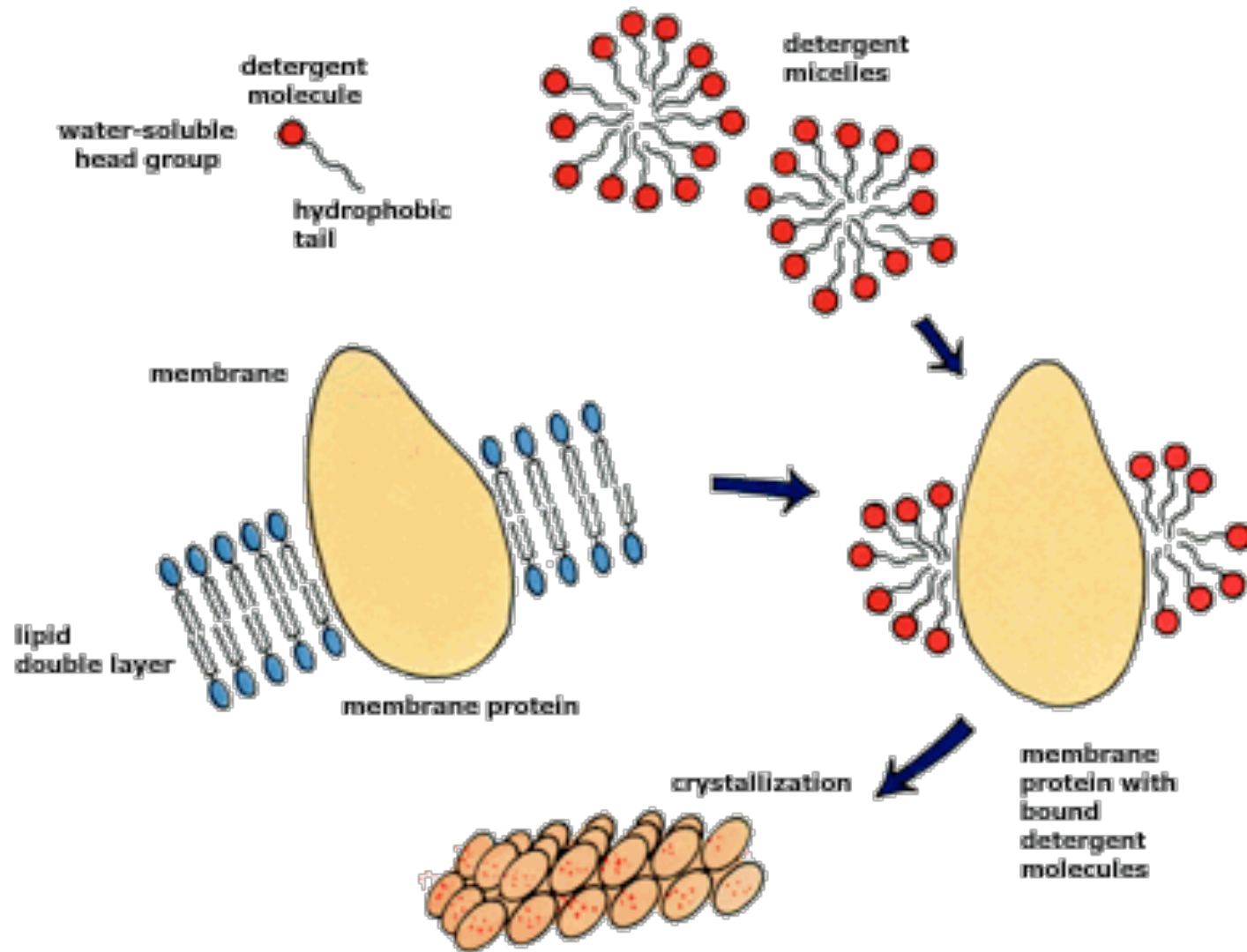


"This year's Laureates, Erwin Neher and Bert Sakmann, succeeded in making a conclusive demonstration that ion channels exist, by developing a technique by which the miniscule currents, flowing through a single ion channel molecule, could be measured."

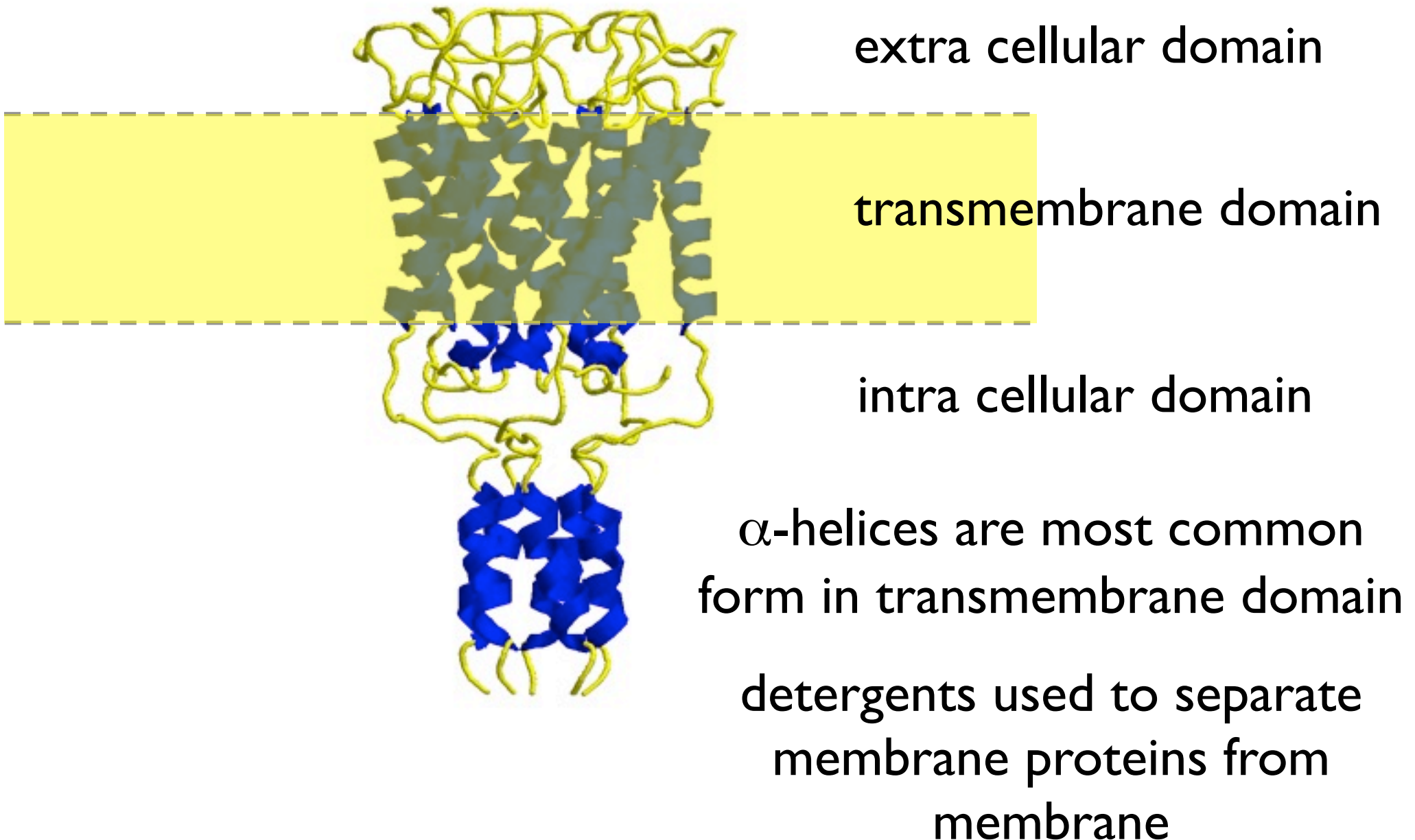
The Nobel Prize in Chemistry 2003 was awarded "for discoveries concerning channels in cell membranes" jointly with one half to Peter Agre "for the discovery of water channels" and with one half to Roderick MacKinnon "for structural and mechanistic studies of ion channels".



Membrane crystallization

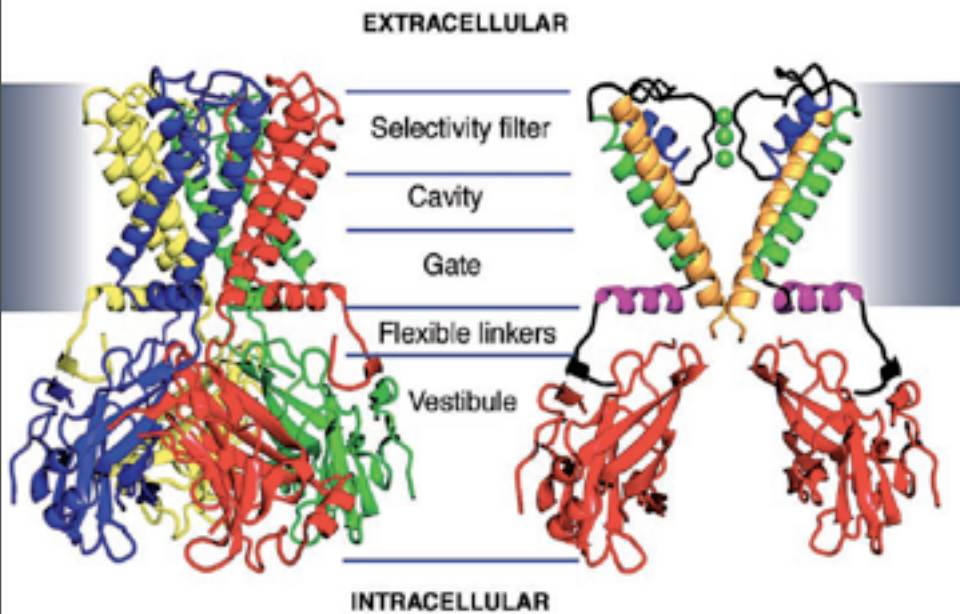


Membrane Proteins

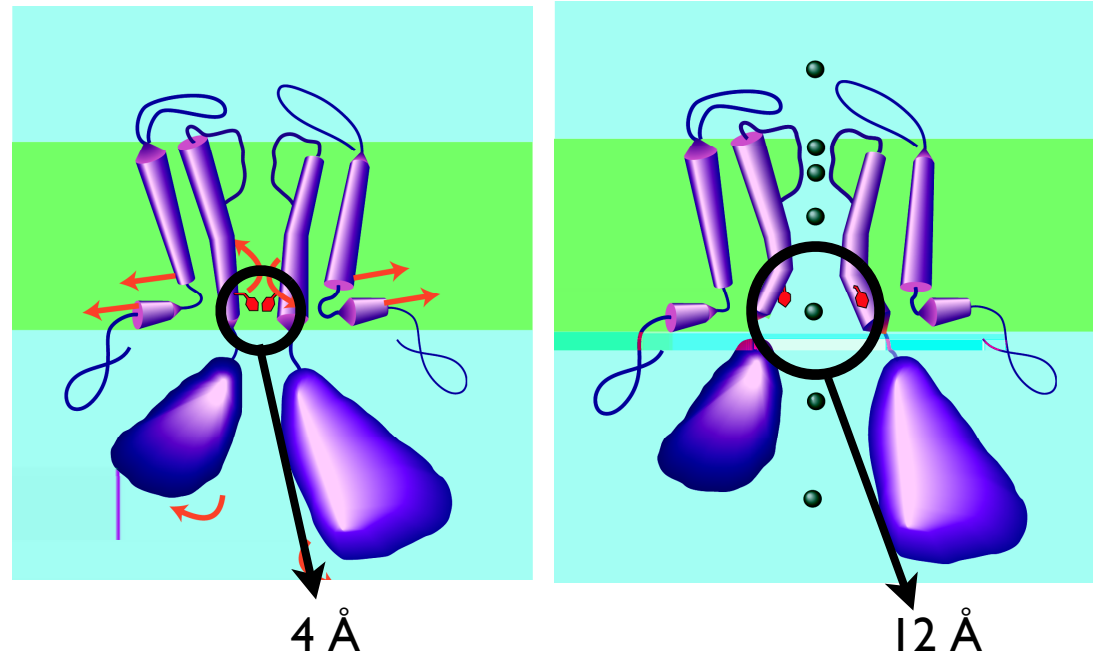


KirBac: Potassium channel

Close structure at 3.65 Å in 2003



Gating: 4 hydrophobic PHE residues

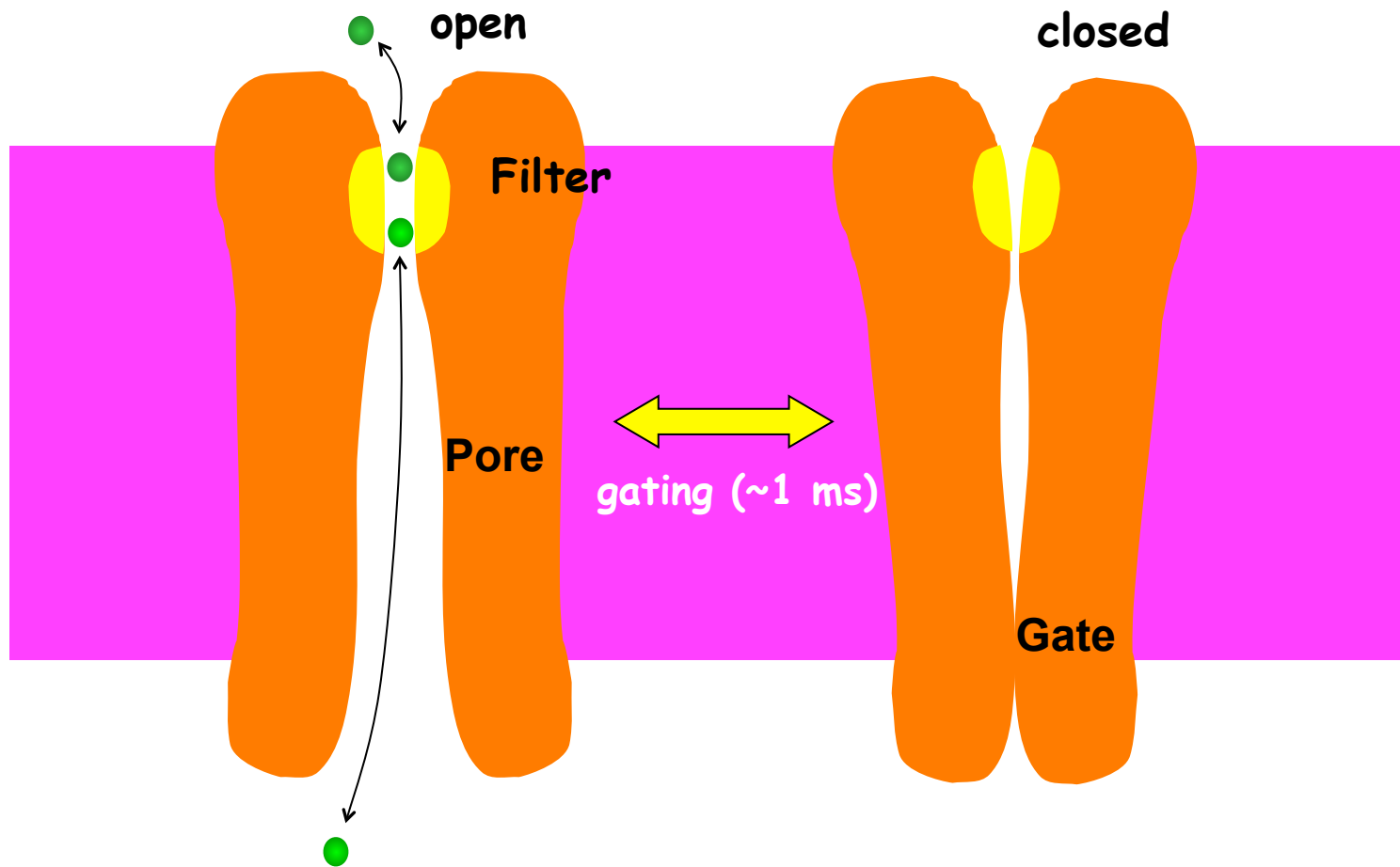


Ubiquitous -
Viruses, Bacteria, Yeast, Plants, Animals

Diverse Functions -
Electrical Excitability, Insulin Release, Cell Volume Control

Well Characterised -
Physiology, Molecular Biology, Structure

Ion Channels: Gating

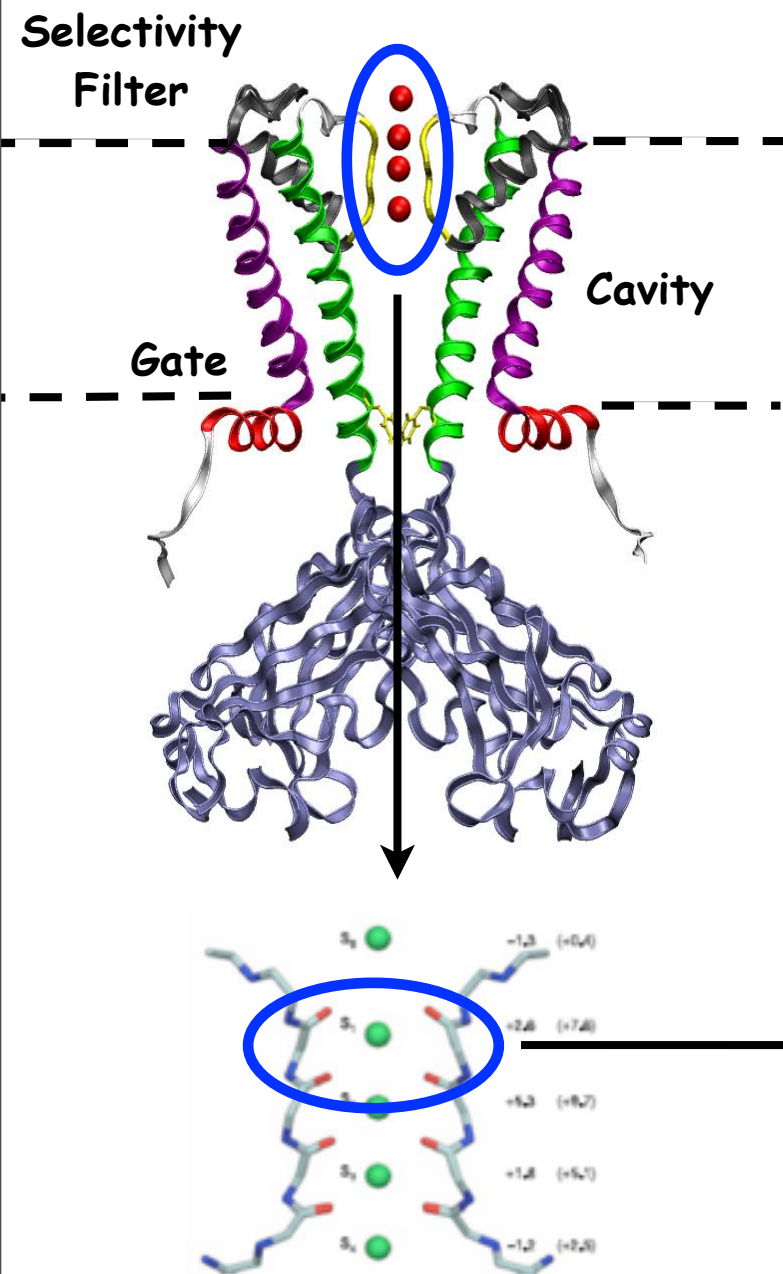


Gating : stimulus-triggered

Stimulus: ligand, voltage, stress

Ion Channels: Selectivity

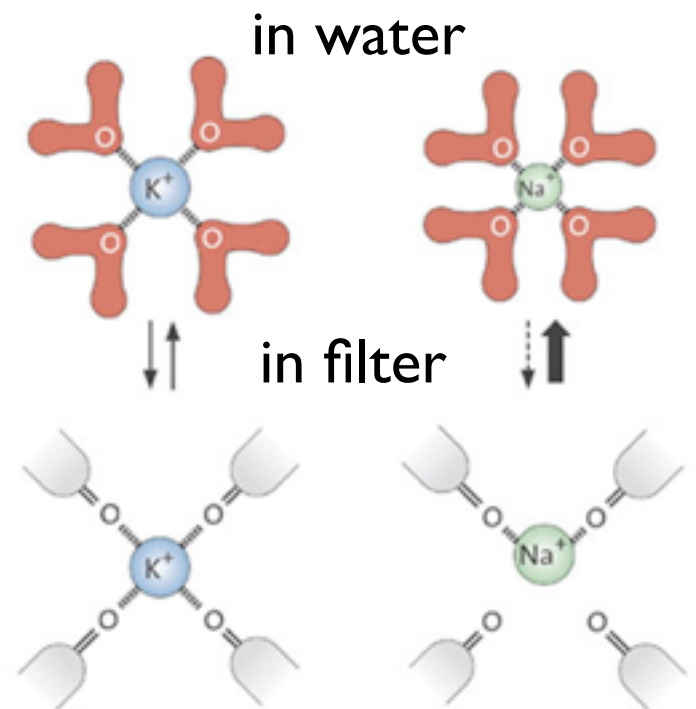
Close structure at 3.65 Å in 2003



Potassium Selective:

K^+ radius = 1.33Å

Na^+ radius = 0.95Å



http://www.bio.miami.edu/~cmallery/150/memb/ion_channels.htm

Continuum Calculations

- Ion flux rate: ~10 million/second
- MD simulation time scale: ~ 100s of ns (10^{-15})
- Probability of permeation events very low
- Electrostatic free energy barrier measurement

Electrostatic free energy to transfer an ion from bulk solution to a point r in the pore of protein:

$$\Delta\Delta G(\mathbf{r}) = [\Delta G^{\text{ic}}(\mathbf{r}) - \Delta G^{\text{c}} - \Delta G^{\text{i}}]$$

$\phi(\mathbf{r}_i)$ is the electrostatic potential at the position of q_i .

$$\Delta G = \frac{1}{2} \sum_i q_i \phi(\mathbf{r}_i)$$

Finite difference Poisson Boltzmann equation:

$$\nabla \cdot (\epsilon \nabla \phi) = -\rho$$

Thank You