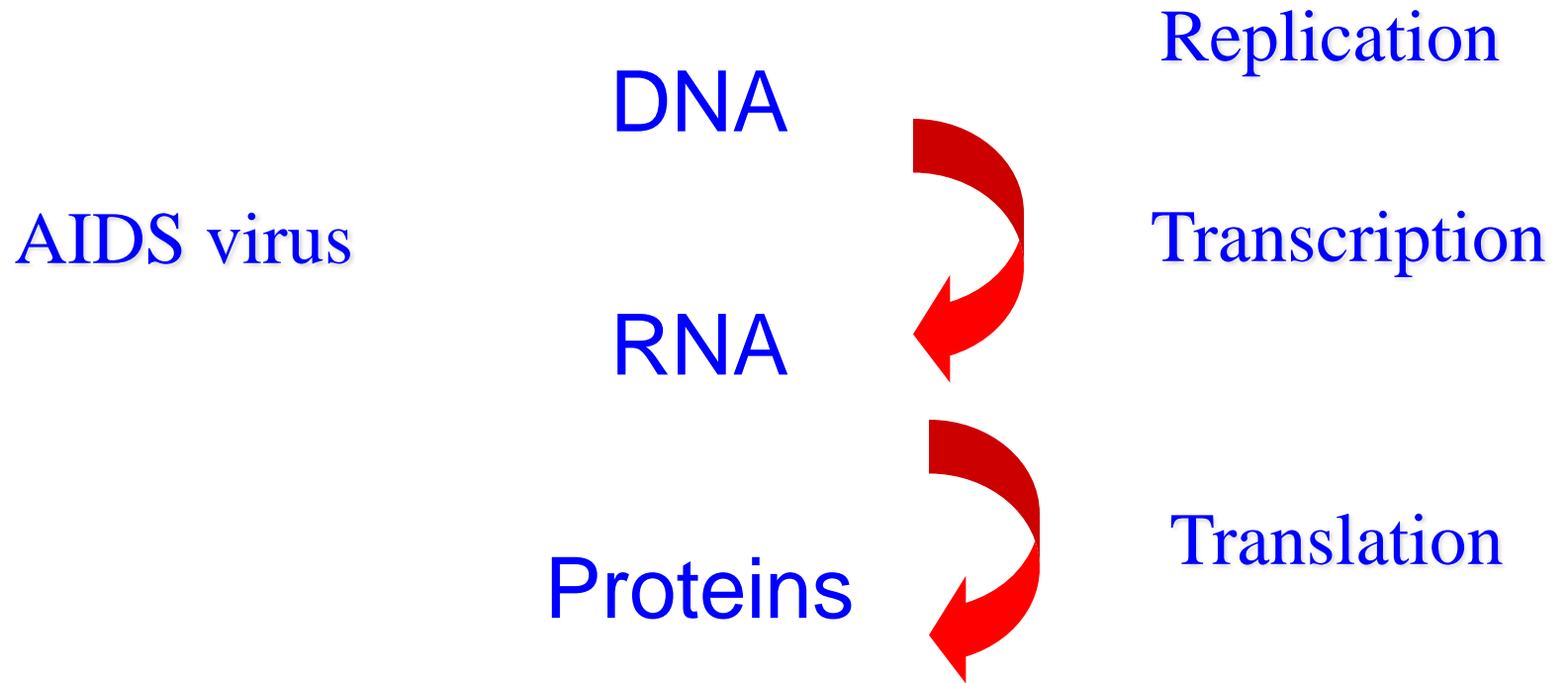


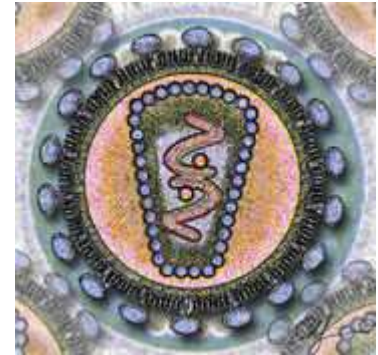
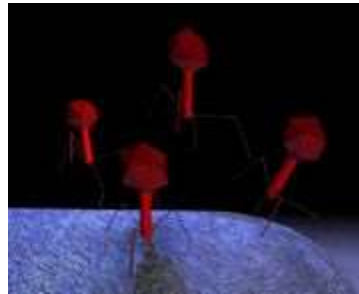
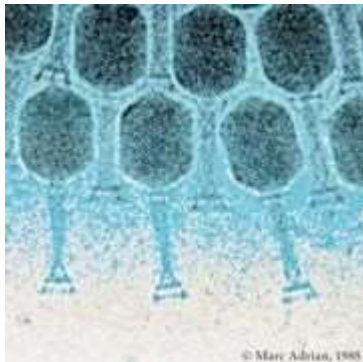
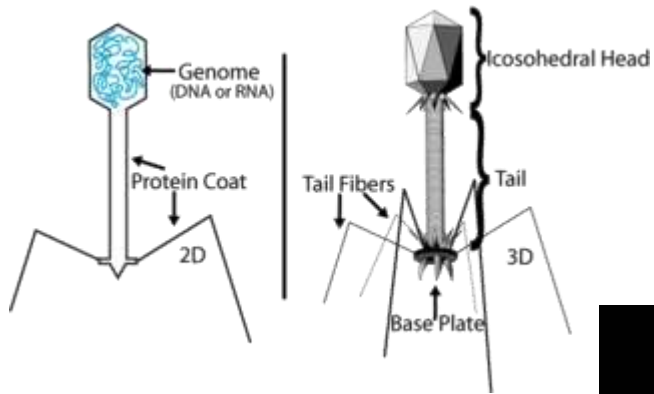
Central Dogma



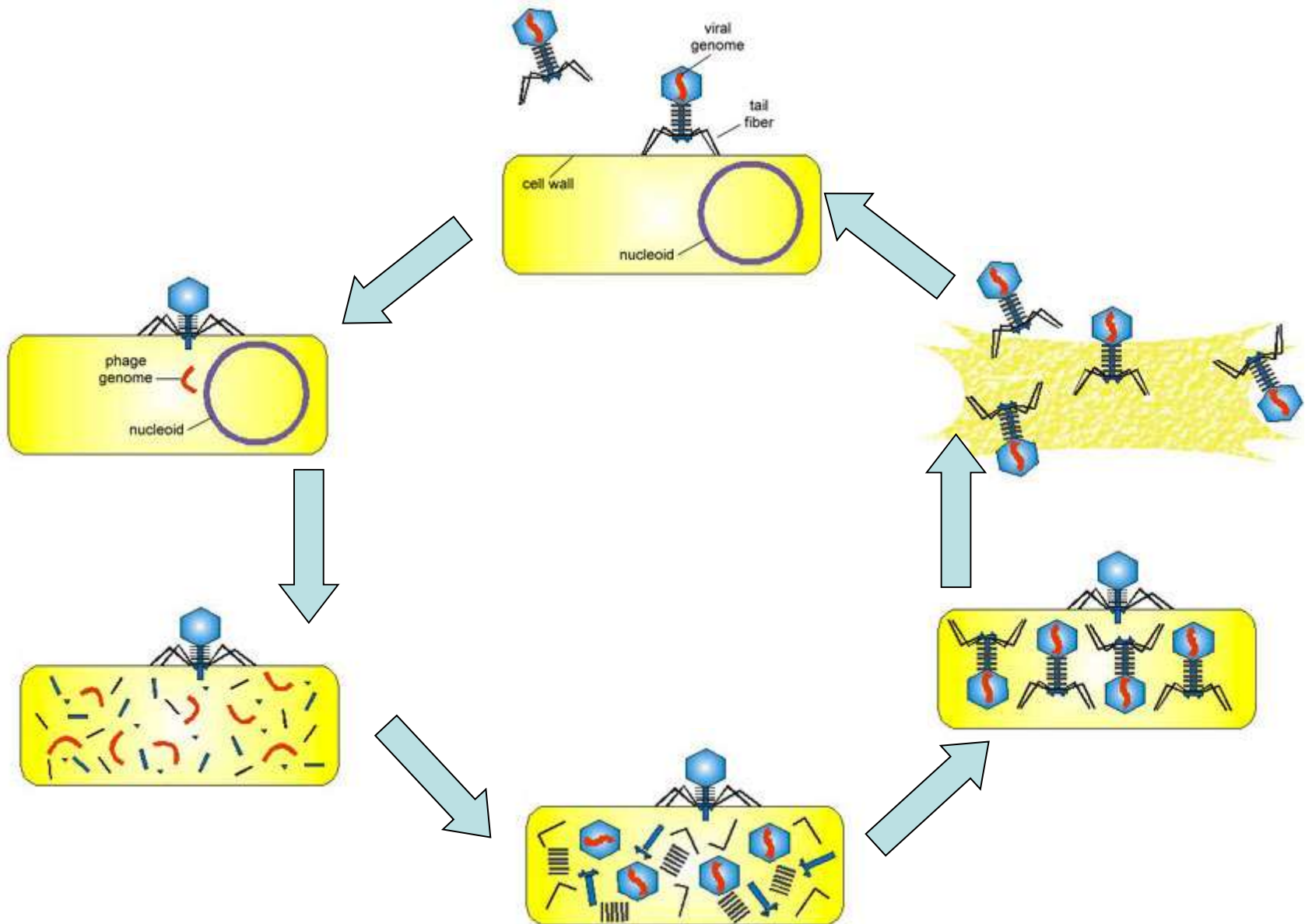
Life

- Replication: reproduction
- Function: catalytic functions
- RNA world:
- Virus is not alive

Virus



Virus Reproduction



- Eukaryotic cells are about 1000 times larger than bacteria cells and also have a membrane enclosed nucleus containing their DNA, and several other internal structures known as organelles.

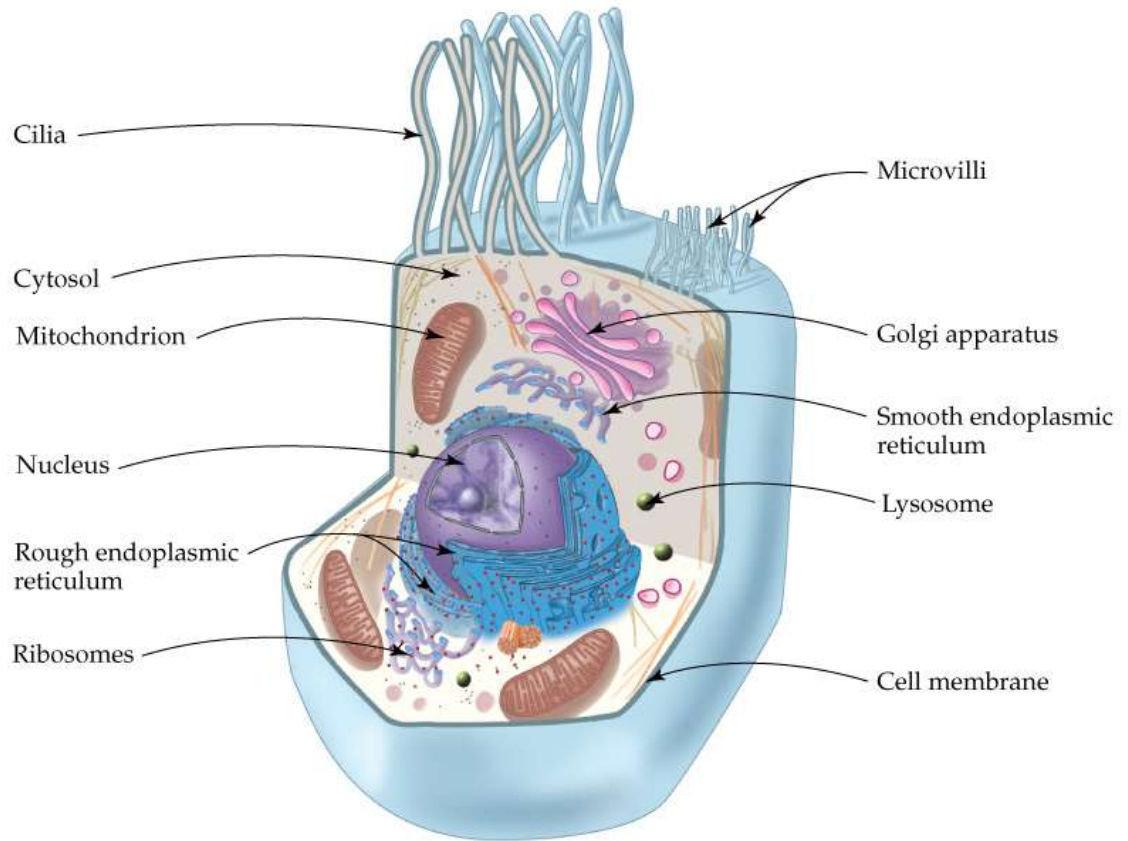
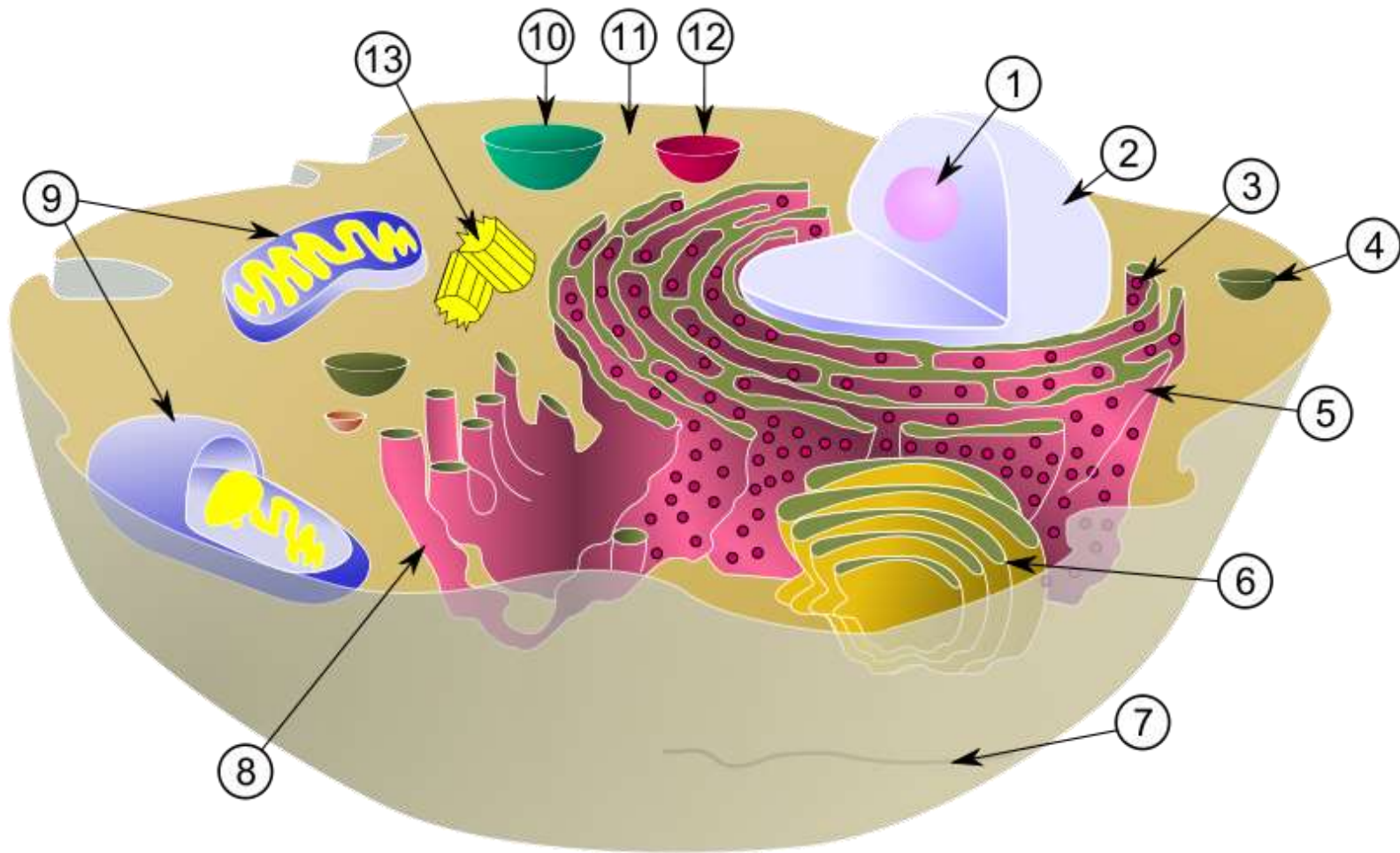


Fig 21.3 A generalized eukaryotic cell.



•Schematic showing the cytoplasm, with its components (or *organelles*), of a typical animal cell. Organelles: (1) nucleolus (2) nucleus (3) ribosome (4) vesicle (5) rough endoplasmic reticulum (6) Golgi apparatus (7) cytoskeleton (8) smooth endoplasmic reticulum (9) mitochondria (10) vacuole (11) cytosol (12) lysosome (13) centriole.

nucleus



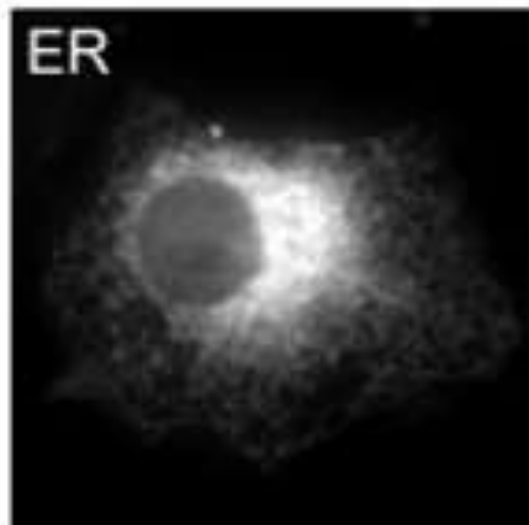
nucleolus



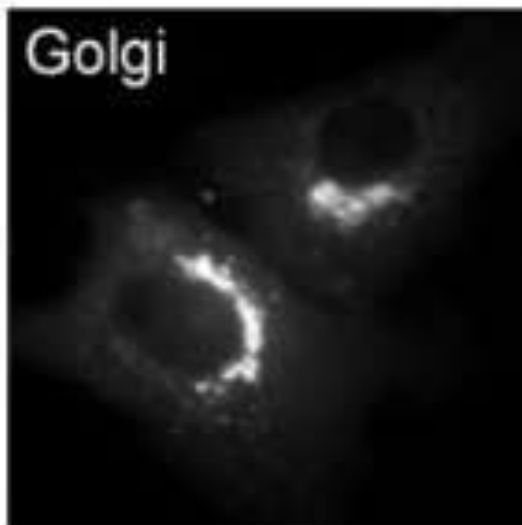
nuclear envelope



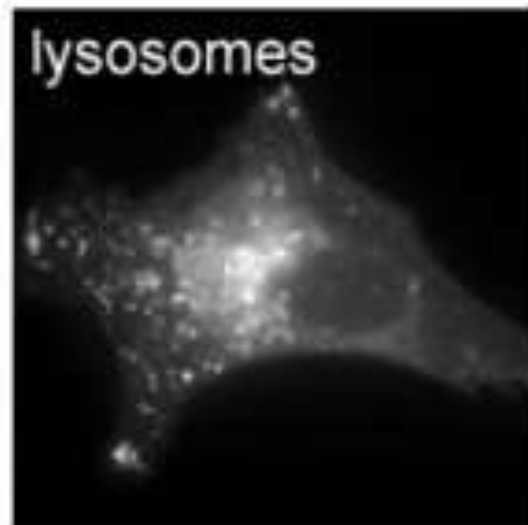
ER



Golgi



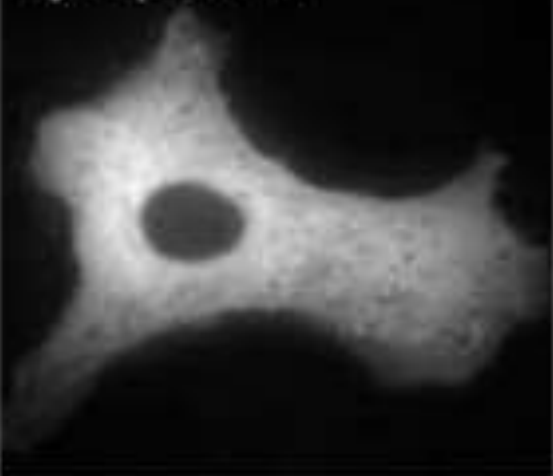
lysosomes



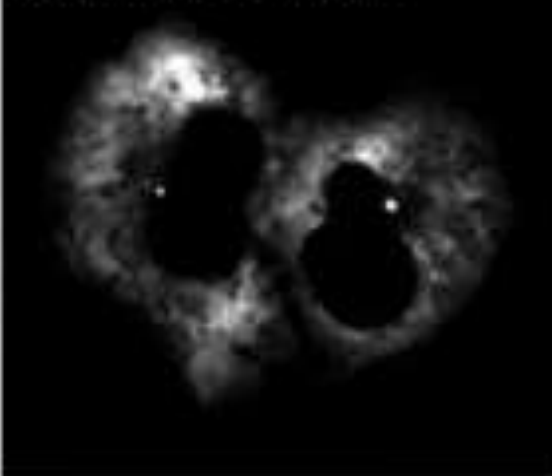
plasma membrane



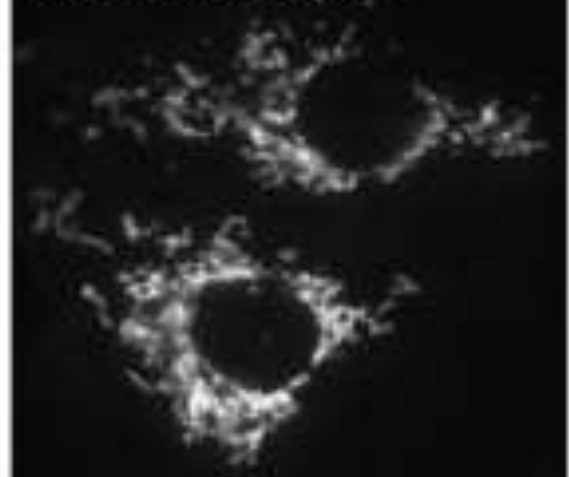
cytoplasm



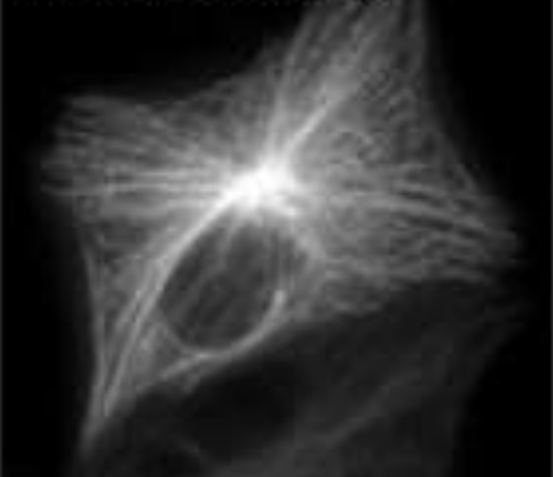
centrosomes



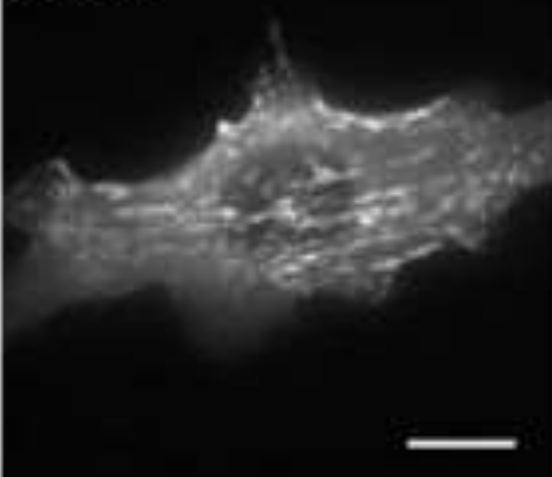
mitochondria



microtubules

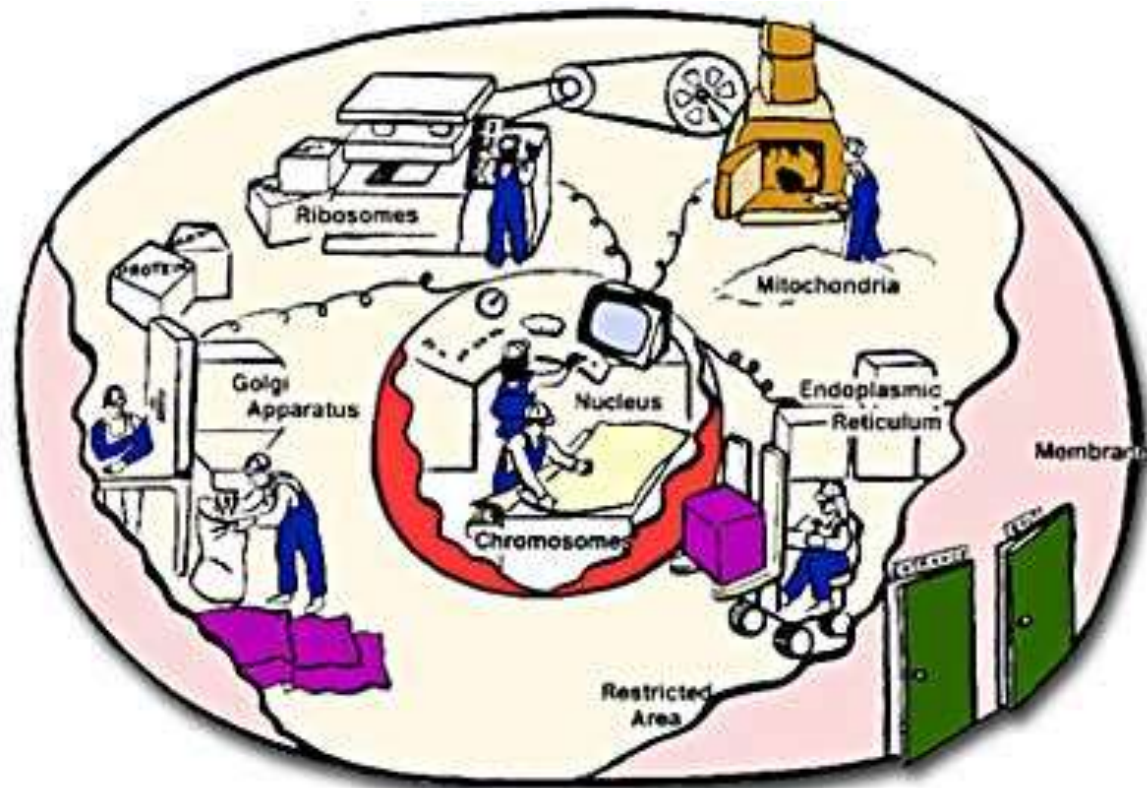


actin



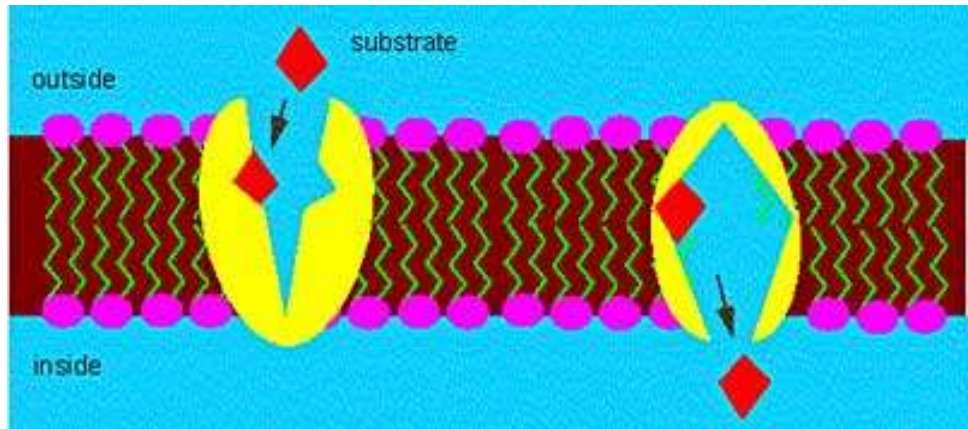
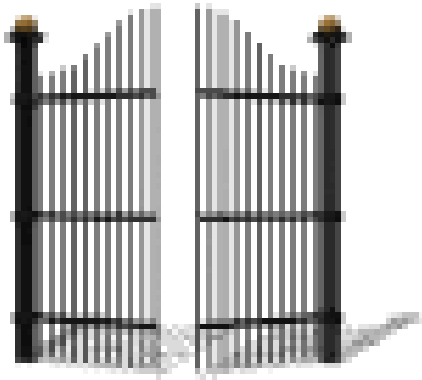
with friendly permission of Jeremy Simpson and Rainer Pepperkok

A Busy Factory

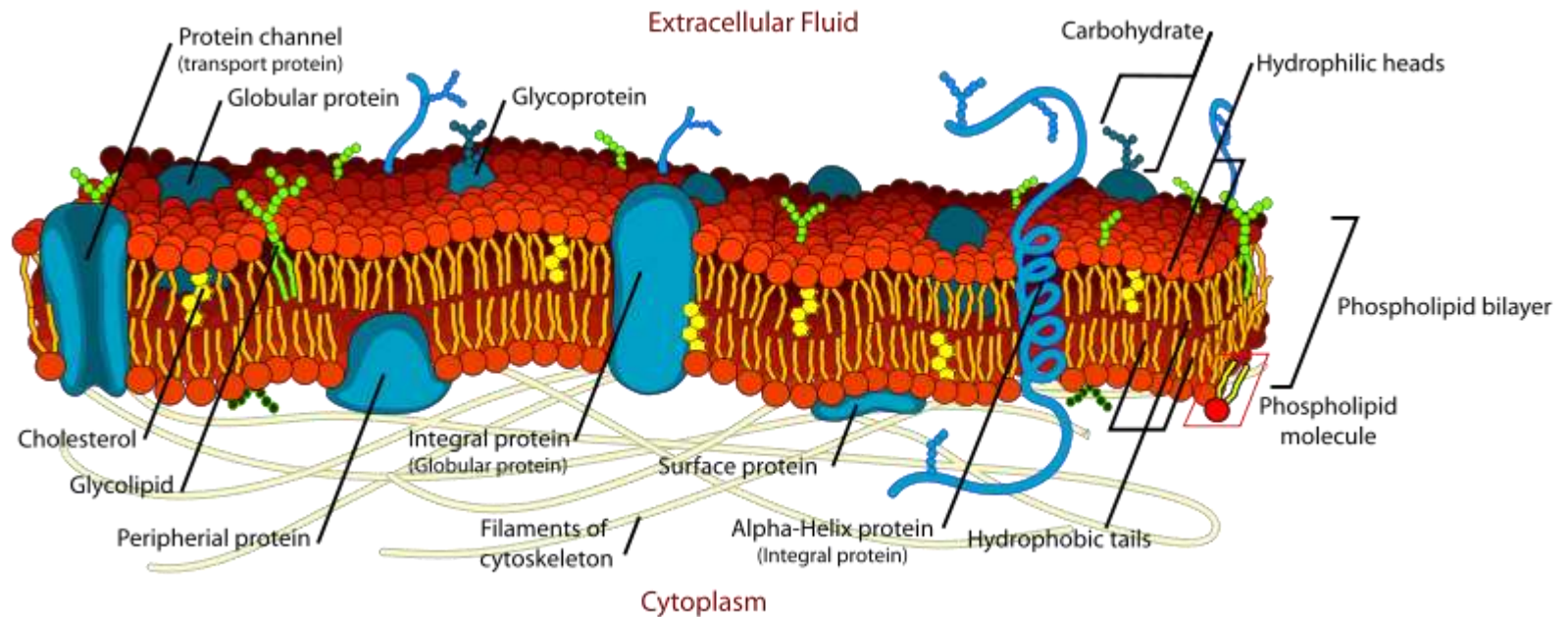


A cell can be thought of as a "factory," with different departments each performing specialized tasks.

The Plasma Membrane

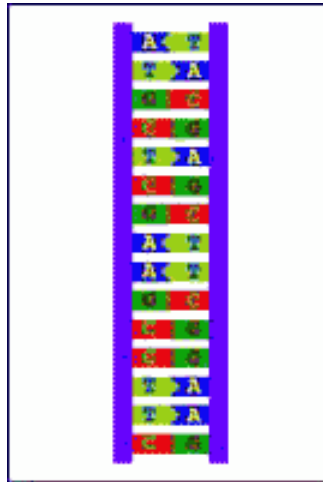


Cell Membrane



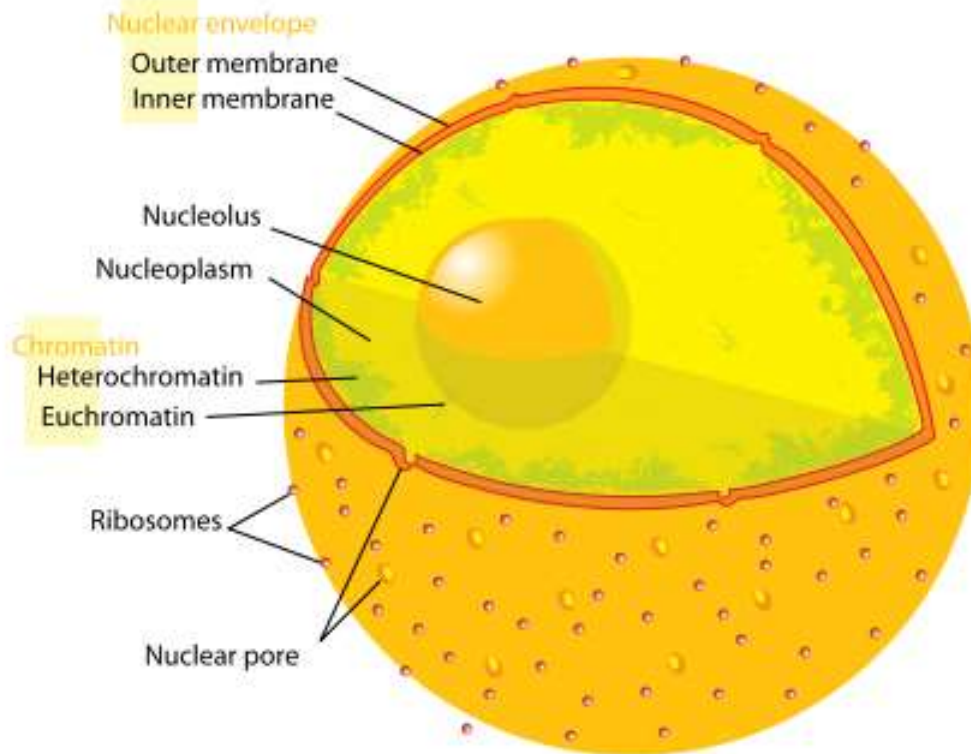
Characteristic diffusivities		
Particle	Typical size	Diffusion constant
Solute ion	10^{-1} nm	$2 \times 10^3 \mu\text{m}^2/\text{s}$
Small protein	5 nm	$40 \mu\text{m}^2/\text{s}$
Virus	100 nm	$2 \mu\text{m}^2/\text{s}$
Bacterium	$1 \mu\text{m}$	$0.2 \mu\text{m}^2/\text{s}$
Mammalian/human cell	$10 \mu\text{m}$	$0.02 \mu\text{m}^2/\text{s}$

The Nucleus



The cell factory contains a large inventory of blueprints dating all the way to its founding. Some of these blueprints are out of date, and some are for parts and products that are no longer made. Part of your job would entail sorting through everything, finding the correct blueprints, copying them, and sending the copies out to the assembly line at the correct time.

Nucleus

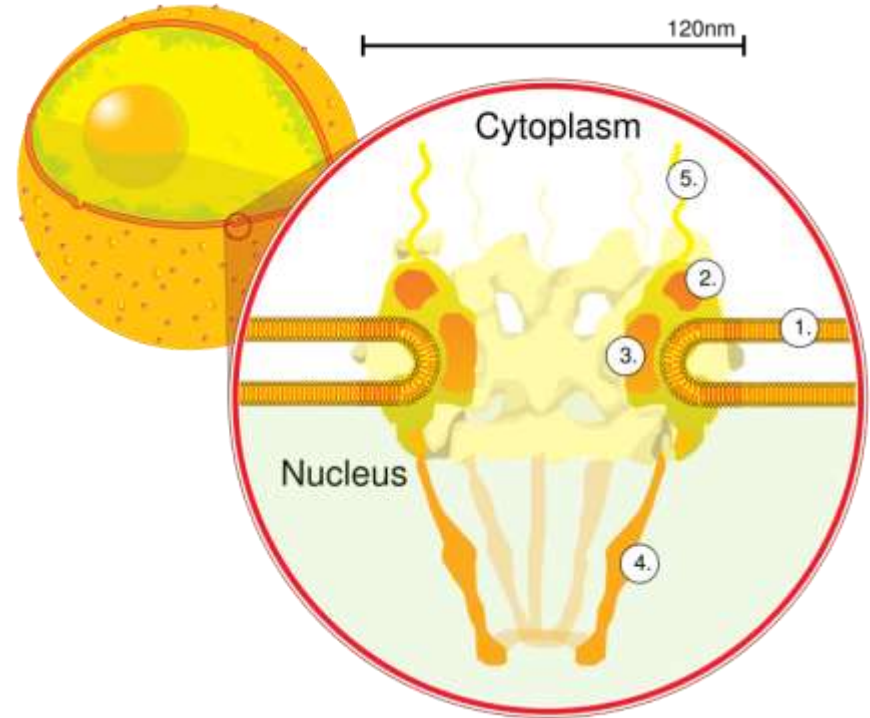


•In cell biology, the **nucleus** is a membrane-enclosed organelle found in most eukaryotic cells. It contains most of the cell's genetic material, organized as multiple long linear DNA molecules in complex with a large variety of proteins such as [histones](#) to form chromosomes. The genes within these chromosomes make up the cell's nuclear genome. The function of the nucleus is to maintain the integrity of these genes and to control the activities of the cell by regulating gene expression.

In cell biology, the **nucleolus** (plural *nucleoli*) is a "sub-organelle" of the cell nucleus, which itself is an organelle. A main function of the nucleolus is the production and assembly of ribosome components

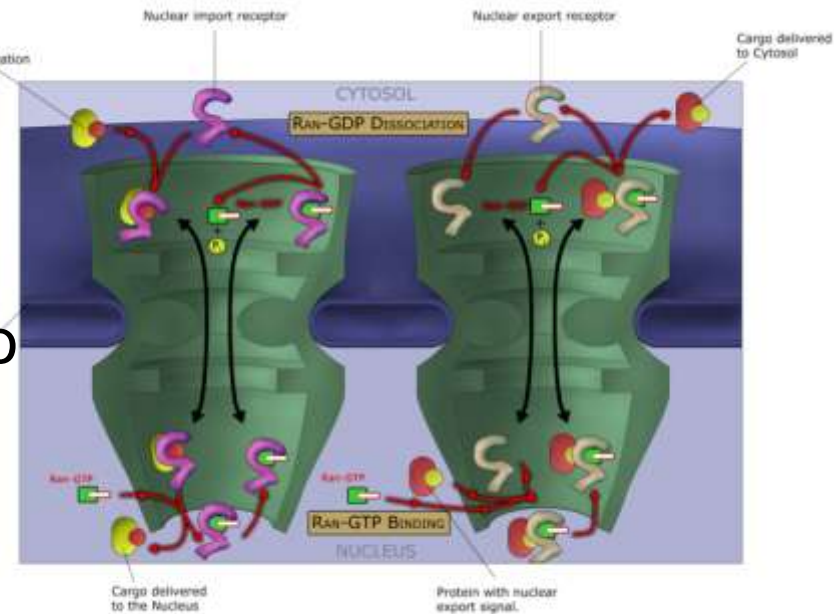
Nuclear pores

Nuclear pores, which provide aqueous channels through the envelope, are composed of multiple proteins, collectively referred to as nucleoporins. The pores are 100 nm in total diameter; however, the gap through which molecules freely diffuse is only about 9 nm wide, due to the presence of regulatory systems within the center of the pore. This size allows the free passage of small water-soluble molecules while preventing larger molecules, such as nucleic acids and proteins, from inappropriately entering or exiting the nucleus. These large molecules must be actively transported into the nucleus instead. The nucleus of a typical mammalian cell will have about 3000 to 4000 pores throughout its envelope

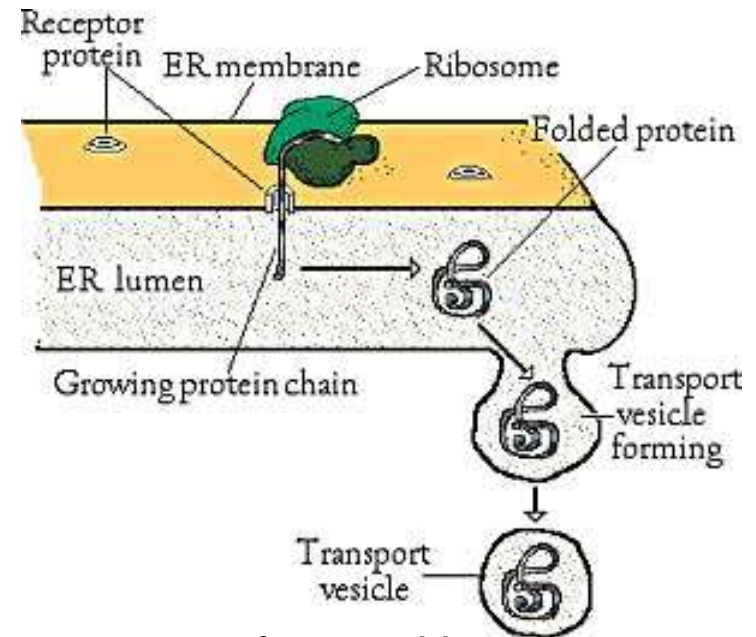
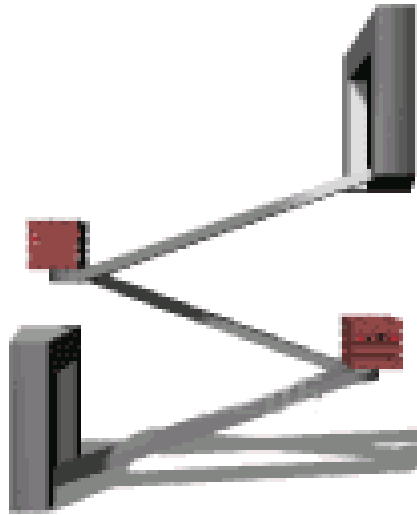


Nuclear localizing sequence (NLS)

- A **nuclear localizing sequence (NLS)** is an amino acid sequence which acts like a 'tag' on the exposed surface of a protein. This sequence is used to confine the protein to the cell nucleus through the **Nuclear Pore Complex** and to direct a newly synthesized protein into the nucleus via its recognition by cytosolic nuclear transport receptors. Typically, this signal consists of a few short sequences of positively charged lysines or arginines. Typically the NLS will have a sequence (NH₂)-Pro-Pro-Lys-Lys-Lys-Arg-Lys-Val-(COOH).



The Ribosomes and the ER

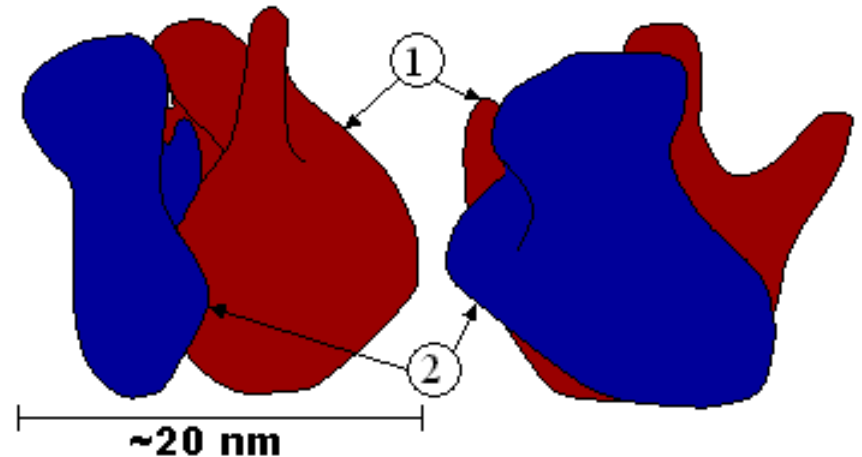


Ribosomes, the workers that build proteins, are manufactured by the nucleolus. They consist of two separate subunits: a large, lower subunit and a small, upper subunit. Ribosomes attach to the rough ER. Now let's take a look at how final processing occurs

The cell has its own assembly line and workers. Within the cytoplasm is a series of large, flattened membranes that fold back and forth on each other and have a very large surface area. This collection of membranes is called the **ENDOPLASMIC RETICULUM**, or **ER**.

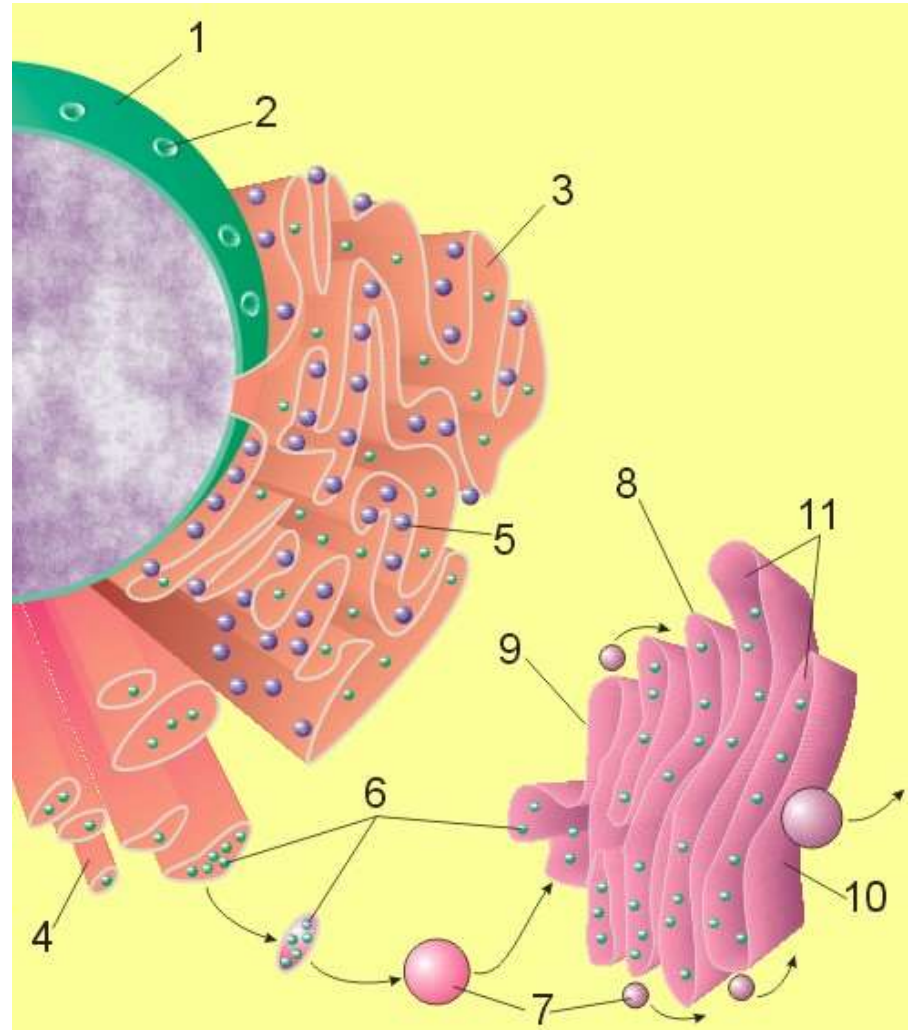
Ribosome

A **ribosome** is a small, dense organelle in cells that assembles proteins. Ribosomes are about 20nm in diameter and are composed of 65% ribosomal RNA and 35% ribosomal proteins (known as a [Ribonucleoprotein](#) or RNP). It translates messenger RNA (mRNA) to build a polypeptide chain (e.g., a protein) using amino acids delivered by Transfer RNA (tRNA). It can be thought of as a giant enzyme that builds a protein from a set of genetic instructions. Ribosomes can float freely in the cytoplasm (the internal fluid of the cell) or bound to the endoplasmic reticulum, or to the nuclear envelope.



Endoplasmic Reticulum

The **endoplasmic reticulum** or **ER** is an organelle found in all eukaryotic cells that is an interconnected network of tubules, vesicles and [cisternae](#) that is responsible for several specialized functions: Protein translation, folding, and transport of proteins to be used in the cell membrane (e.g., [transmembrane receptors](#) and other integral membrane proteins), or to be secreted ([exocytosed](#)) from the cell (e.g., digestive [enzymes](#)); sequestration of calcium; and production and storage of [glycogen](#), [steroids](#), and other [macromolecules](#).^[1] The endoplasmic reticulum is part of the endomembrane system. The basic structure and composition of the ER membrane is similar to the plasma membrane.



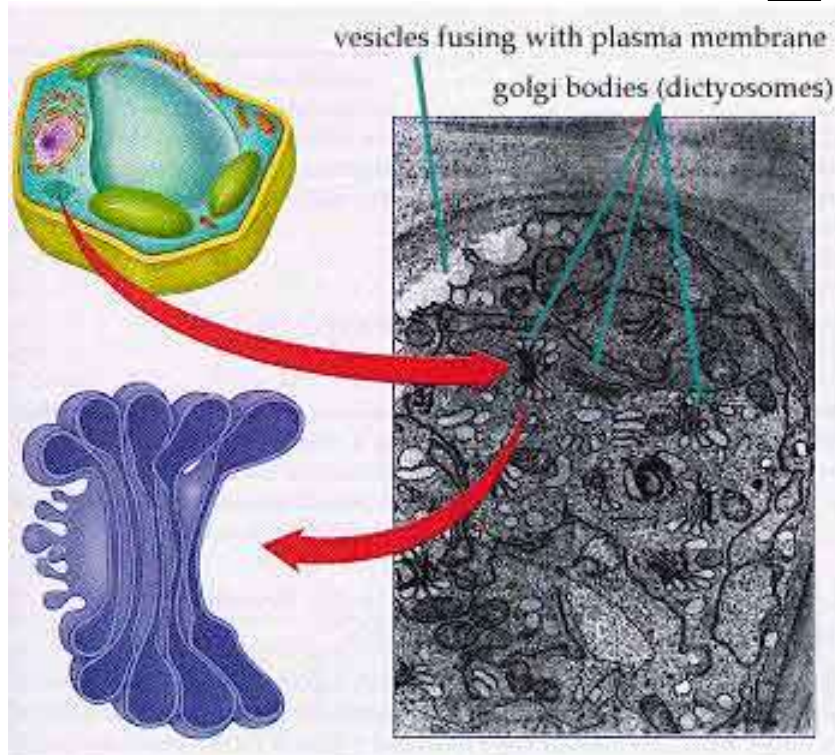
Rough endoplasmic reticulum

- The surface of the rough endoplasmic reticulum is studded with protein-manufacturing [ribosomes](#) giving it a "rough" appearance. But it should be noted that these ribosomes are not resident of the endoplasmic reticulum incessantly. The ribosomes only bind to the ER once it begins to synthesize a protein destined for sorting. The membrane of the rough endoplasmic reticulum is continuous with the outer layer of the nuclear envelope. Although there is no continuous membrane between the rough ER and the Golgi apparatus, membrane bound vesicles shuttle proteins between these two compartments. The rough endoplasmic reticulum works in concert with the Golgi complex to target new proteins to their proper destinations

Smooth endoplasmic reticulum

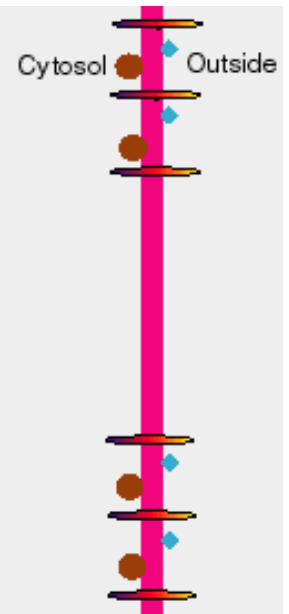
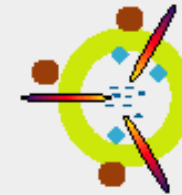
- The smooth endoplasmic reticulum has functions in several metabolic processes, including synthesis of lipids, metabolism of carbohydrates and calcium concentration, and attachment of receptors on cell membrane proteins. It is connected to the nuclear envelope. Smooth endoplasmic reticulum is found in a variety of cell types (both animal and plant) and it serves different functions in each. It consists of tubules and vesicles that branch forming a network. In some cells there are dilated areas like the sacs of rough endoplasmic reticulum. The network of smooth endoplasmic reticulum allows increased surface area for the action or storage of key enzymes and the products of these enzymes. The smooth endoplasmic reticulum is known for its storage of calcium ions in muscle cells.

The Golgi Apparatus



This animation illustrates how secretion vesicles, arising from the Golgi, fuse with the PM and dump the contents of their lumen outside of the cell. Note that the membrane of the SV turns insideout and becomes new PM.

- Lipid Bilayer (SV)
- Lipid Bilayer (PM)
- Transmembrane Protein
- Peripheral Protein (inside)
- Peripheral Protein (outside)
- Soluble Proteins



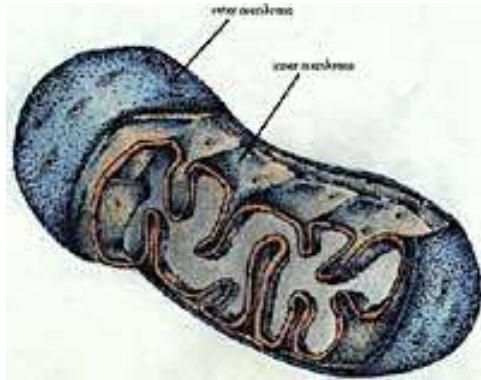
The Golgi apparatus is analogous to the finishing and packing room in a factory. Once the ribosome finishes manufacturing a protein in the rough ER, the protein needs to be prepared for use or export. Special enzymes will trim off any extra amino acids, and then the unfinished protein moves through channels in the smooth ER.

Golgi apparatus

The **Golgi apparatus** (also called the **Golgi body**, **Golgi complex**, or **dictyosome**) is an organelle found in typical eukaryotic cells. It was identified in 1898 by the Italian physician Camillo Golgi and was named after him. The primary function of the Golgi apparatus is to process and package macromolecules synthesised by the cell, primarily proteins and lipids. The Golgi apparatus forms a part of the endomembrane system present in eukaryotic cells.



Mitochondria

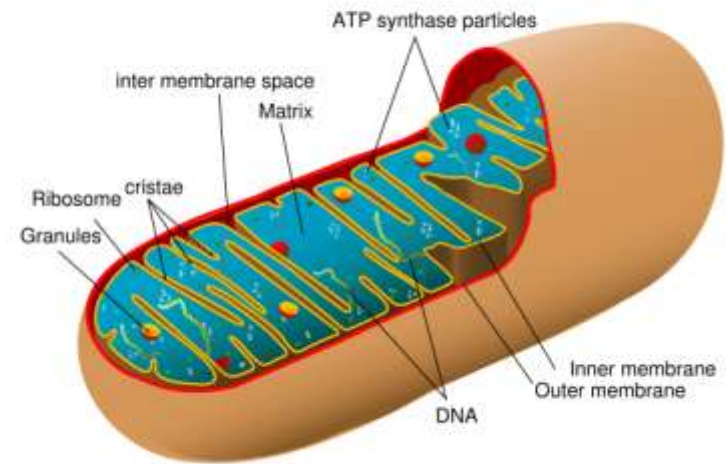
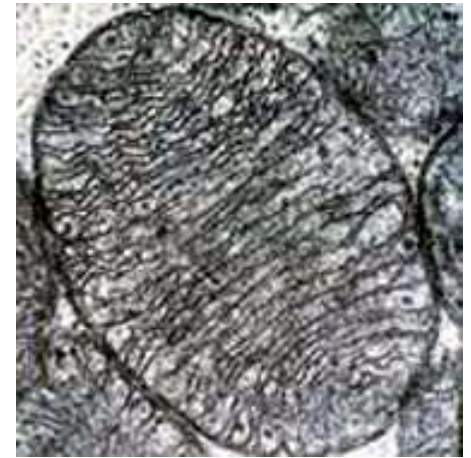


***- ATP -
a Source of
ENERGY***

Like our factory's power plant, mitochondria and chloroplasts transform one form of energy to another. Remember that nearly all the energy used by living things on Earth comes from the Sun. This section discusses how energy is made available for cell processes.

Mitochondrion

- In cell biology, a **mitochondrion** is a membrane-enclosed organelle, found in most eukaryotic cells. Mitochondria are sometimes described as "cellular power plants," because they convert NADH and NADPH into energy in the form of ATP via the process of oxidative phosphorylation. A typical eukaryotic cell contains about 2,000 mitochondria, which occupy roughly one fifth of its total volume. Mitochondria contain DNA that is independent of the DNA located in the cell nucleus. According to the endosymbiotic theory, mitochondria are descended from free-living prokaryotes.



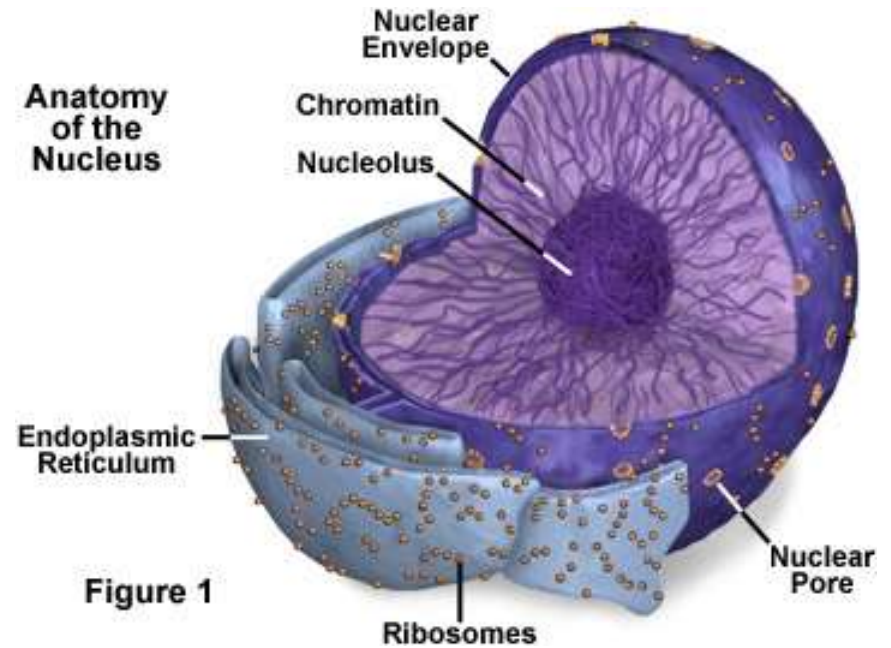
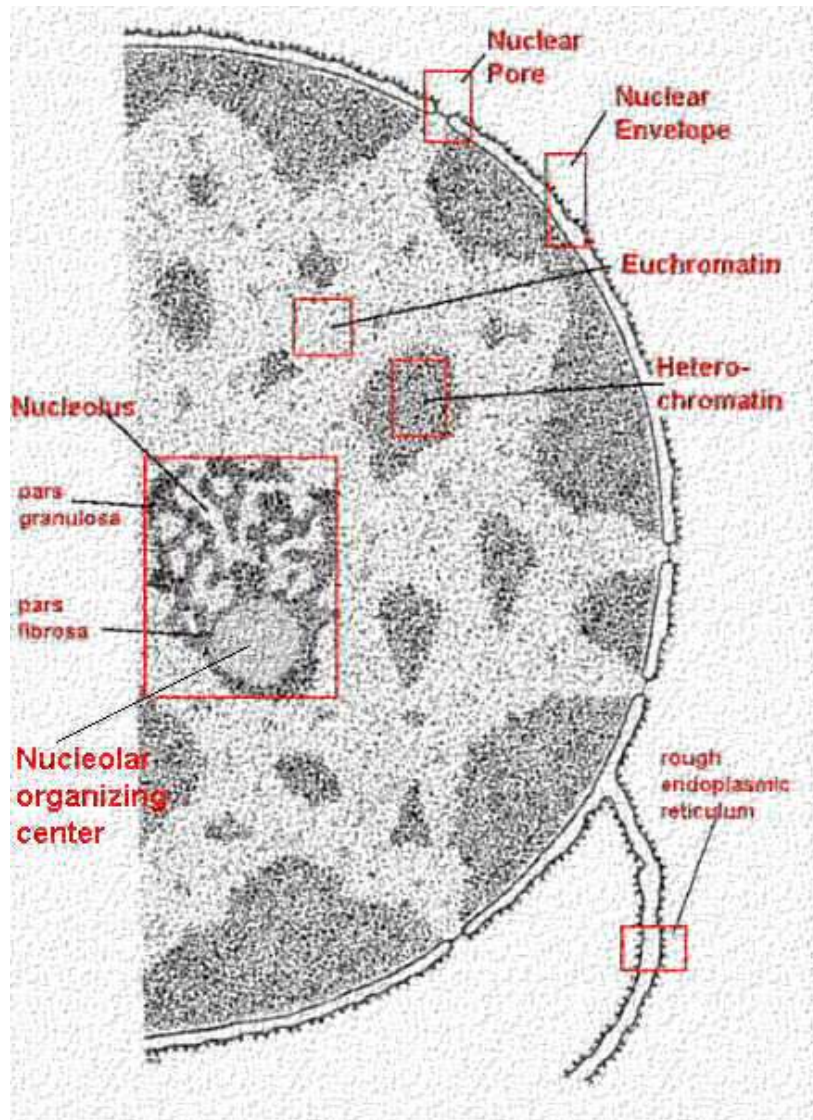


Figure 1

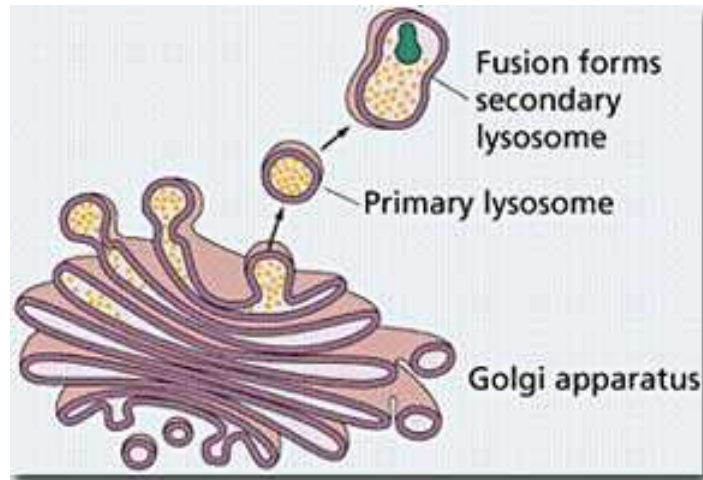
The main roles of the nucleolus are to synthesize rRNA and assemble ribosomes

The main function of the cell nucleus is to control gene expression and mediate the replication of DNA during the cell cycle

Lysosomes

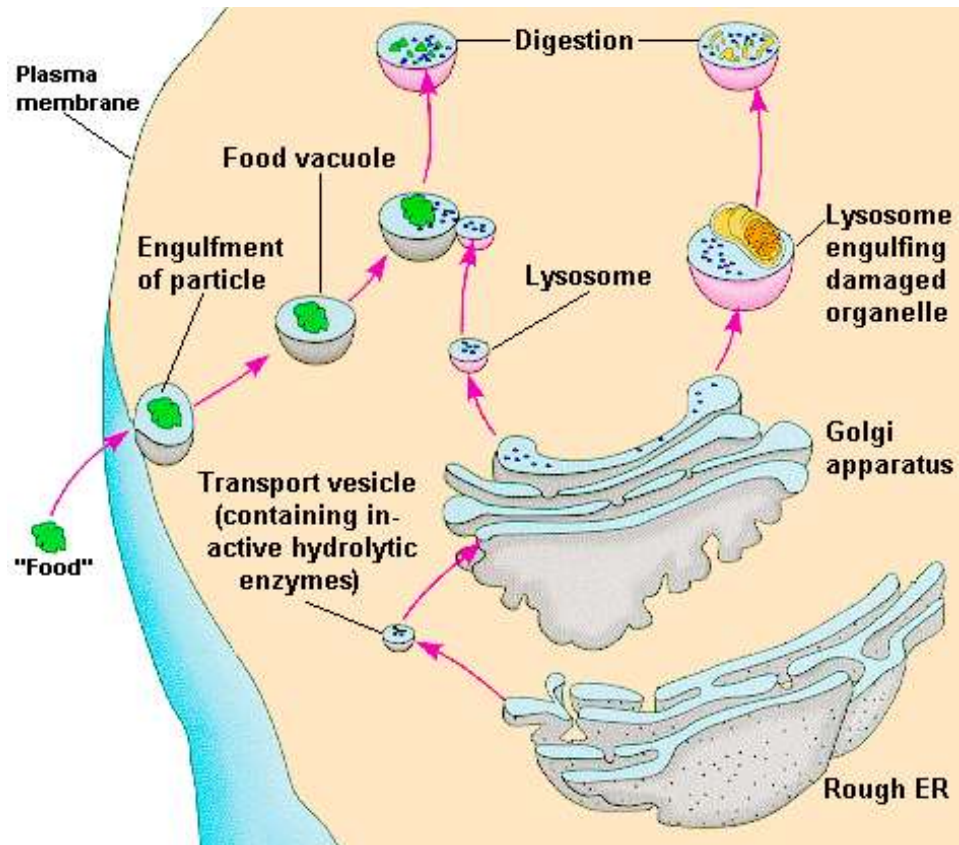
- **Lysosomes** are organelles that contain digestive enzymes (acid [hydrolases](#)). They digest excess or worn out organelles, food particles, and engulfed viruses or bacteria. The membrane surrounding a lysosome prevents the digestive enzymes inside from destroying the cell. Lysosomes fuse with vacuoles and dispense their enzymes into the vacuoles, digesting their contents. They are built in the Golgi apparatus. The name *lysosome* derives from the [Greek](#) words *lysis*, which means dissolution or destruction, and *soma*, which means body. They are frequently nicknamed "suicide-bags" or "suicide-sacs" by cell biologists due to their role in autolysis.

Lysosomes



Lysosomes are responsible for the breakdown and absorption of materials taken in by the cell. Often, a cell engulfs a foreign substance through **ENDOCYTOSIS**, another form of active transport. During endocytosis, the cell membrane puckers up, forms a pouch around materials outside the cell, and pinches off to become a vesicle. If the contents need to be destroyed, lysosomes combine with the vesicle and release their enzymes.

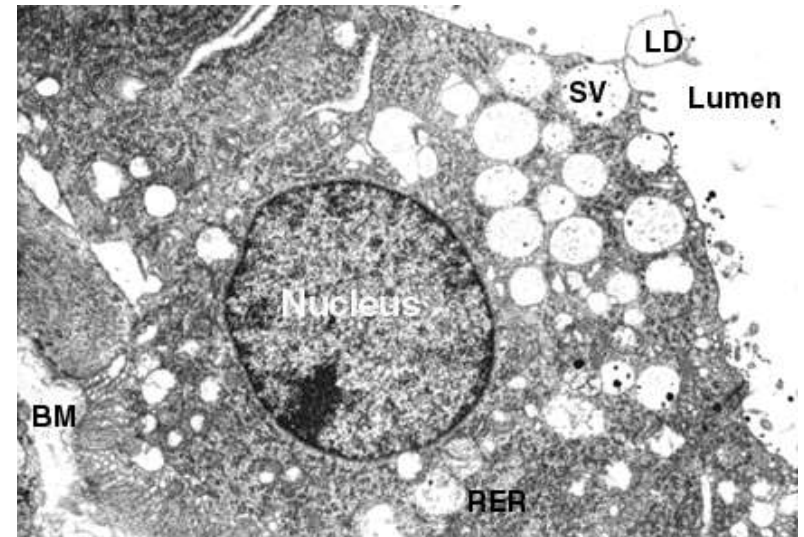
Lysosome



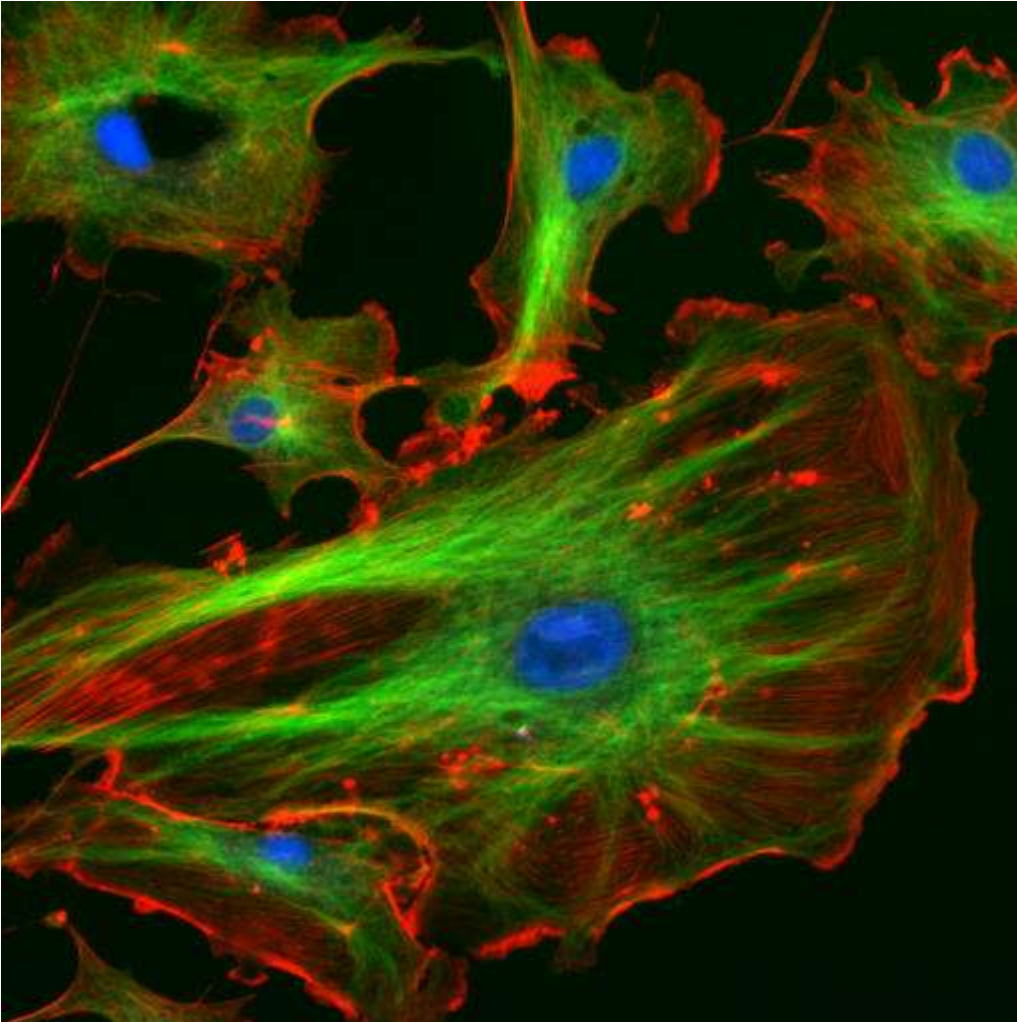
Vesicle

In cell biology, a **vesicle** is a relatively small and enclosed compartment, separated from the **cytosol** by at least one lipid bilayer. If there is only one lipid bilayer, they are called *unilamellar* vesicles; otherwise they are called *multilamellar*. Vesicles store, transport, or digest cellular products and waste.

This biomembrane enclosing the vesicle is similar to that of the plasma membrane. Because it is separated from the cytosol, the intravesicular environment can be made to be different from the cytosolic environment. Vesicles are a basic tool of the cell for organizing metabolism, transport, enzyme storage, as well as being chemical reaction chambers. Many vesicles are made in the Golgi apparatus, but also in the endoplasmic reticulum, or are made from parts of the plasma membrane.

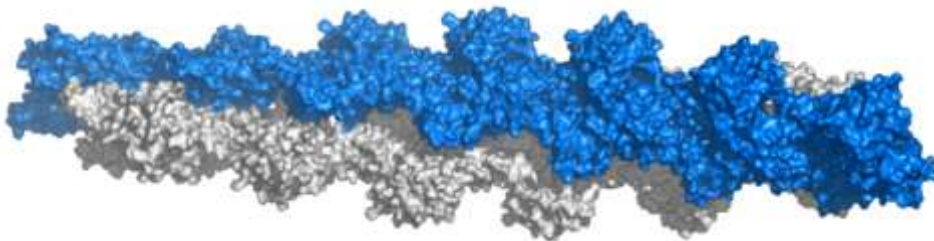
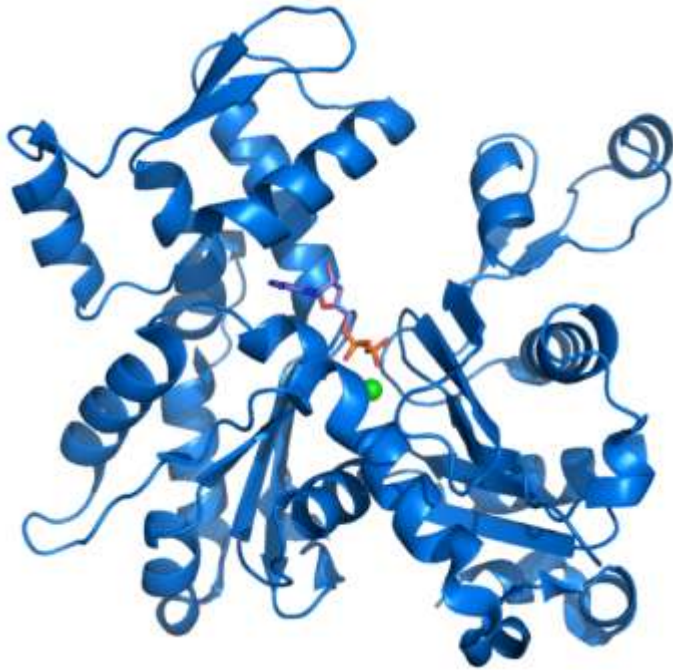


Cytoskeleton



The eukaryotic cytoskeleton. Actin filaments are shown in red, microtubules in green, and the nuclei are in blue.

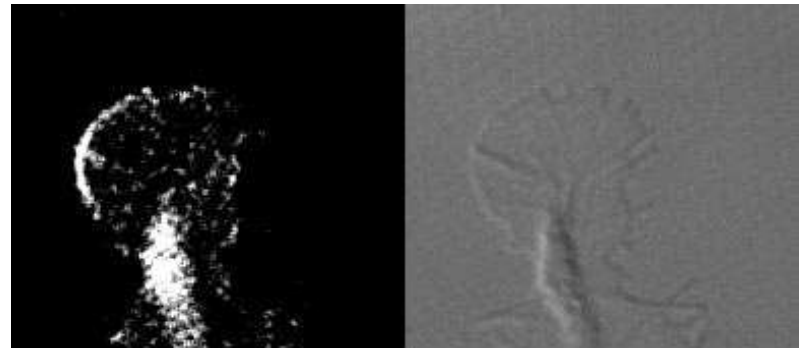
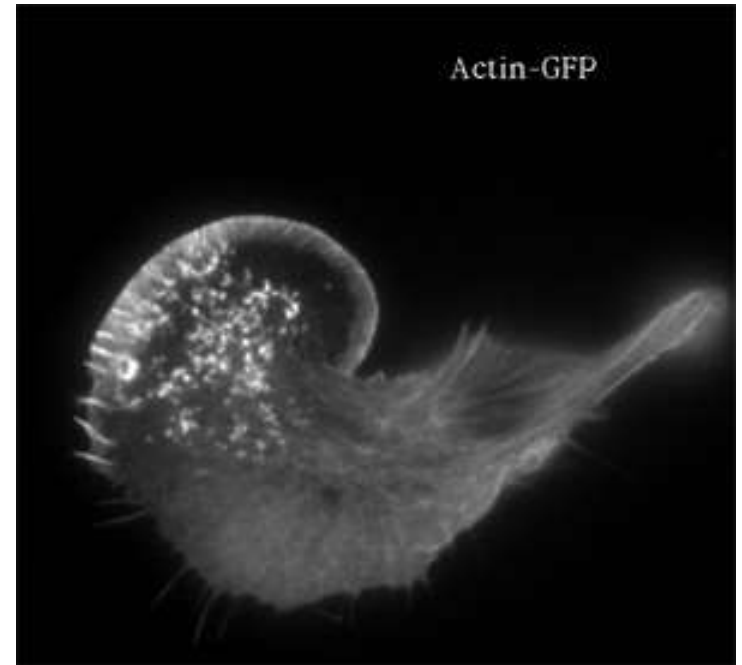
Actin



- **Actin** is a globular structural, 42 kDa, [protein](#) that polymerizes in a helical fashion to form **actin filaments** (or **microfilaments**). These form the cytoskeleton, a three-dimensional network inside the eukaryotic cell. Actin filaments provide mechanical support for the cell, determine its shape, and enable movement of the cell through [lamellipodia](#), [filopodia](#), or [pseudopodia](#). Actin filaments, along with myosin, have an essential role in muscular contraction. In the [cytosol](#), actin is predominantly bound to ATP, but can also bind to ADP. An ATP-actin complex polymerizes faster and dissociates slower than an ADP-actin complex.

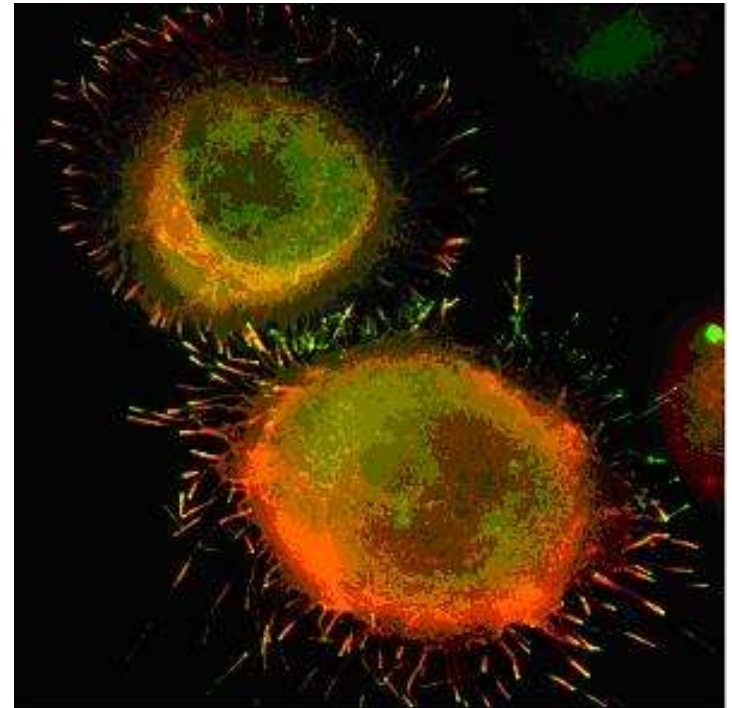
Lamellipodia

- The **lamellipodium** is a cytoskeletal actin projection on the mobile edge of the cell. It contains a two-dimensional actin mesh; the whole structure pulls the cell across a substrate. Within the lamellipodia are ribs of actin called microspikes, which, when they spread beyond the lamellipodium frontier, are called filopodia (Small, et al, 2002). The lamellipodium is born of actin nucleation in the plasma membrane of the cell (Alberts, et al, 2002) and is the primary area of actin incorporation or microfilament formation of the cell. Lamellipodia range from 1µm to 5µm in breadth and are approximately 0.2µm thick. Lamellipodia are found primarily in very mobile cells, crawling at a speeds of 10-20µm/minute over epithelial surfaces..
- The tip of the lamellipodium is the site where exocytosis occurs in migrating mammalian cells as part of their clathrin-mediated endocytic cycle.



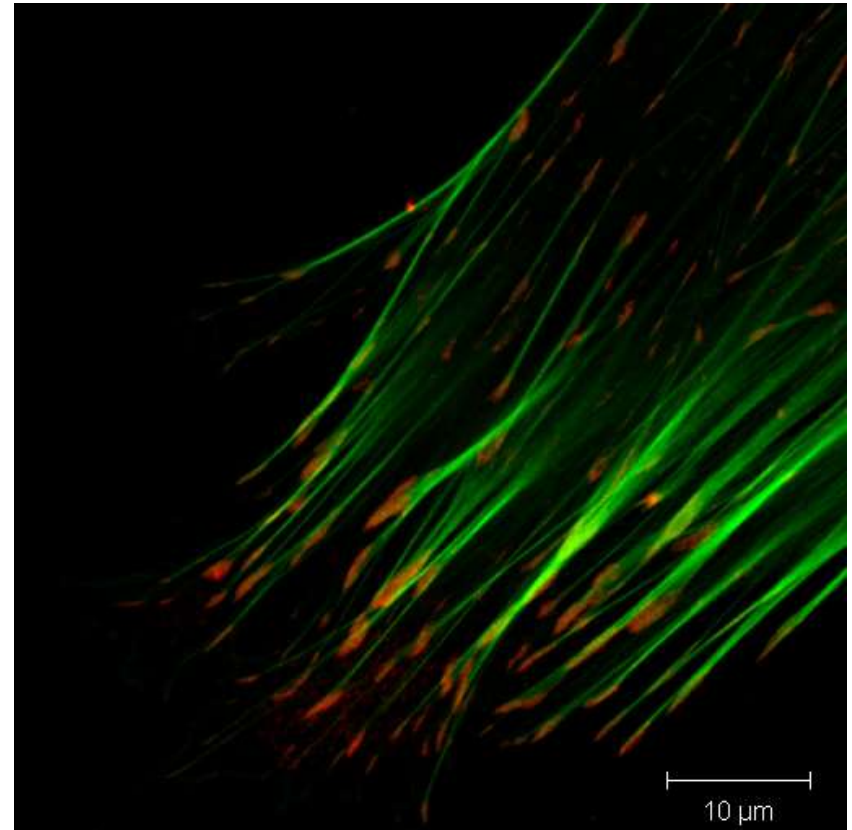
Filopodia

The **filopodia** are slender cytoplasmic projections, similar to [lamellipodia](#), which extend from the leading edge of migrating cells. They contain actin filaments cross-linked into bundles by actin-binding proteins, e.g. fimbrin. Filopodia form focal adhesions with the substratum, linking it to the cell surface. A cell migrates along a surface by extending filopodia at the leading edge. The filopodia attach to the substratum further down the migratory pathway, then contraction of stress fibres retracts the rear of the cell to move the cell forwards.



Focal adhesion

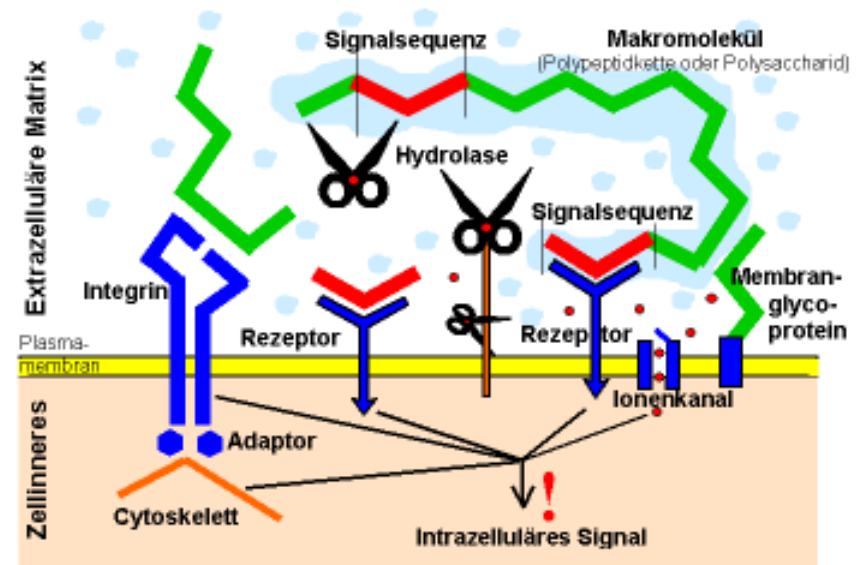
- In cell biology, '**Focal Adhesions**' are specific types of large macromolecular assemblies through which both mechanical force and regulatory signals are transmitted. More precisely, **FAs** can be considered as sub-cellular macromolecules that mediate the regulatory effects (e.g. cell anchorage) of extracellular matrix (ECM) adhesion on cell behavior.



Extra Cellular Matrix

The ECM's main components are various [glycoproteins](#), [proteoglycans](#) and [hyaluronic acid](#). In most animals, the most abundant glycoproteins in the ECM are collagens.

ECM also contains many other components: proteins such as fibrin, [elastin](#), [fibronectins](#), [laminins](#), and [nidogens](#), and minerals such as [hydroxylapatite](#), or fluids such as blood plasma or serum with secreted free flowing [antigens](#).

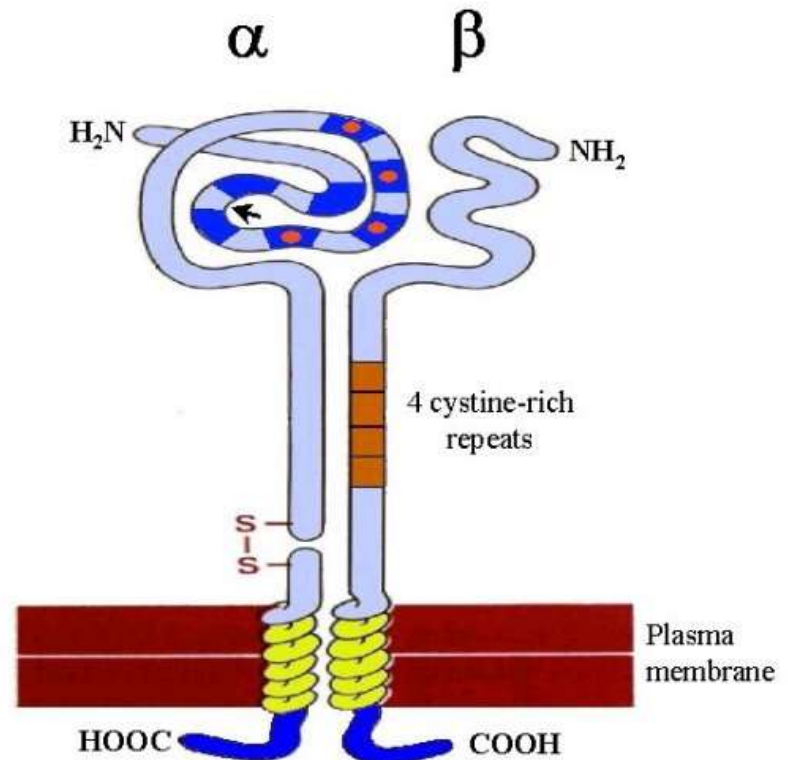


Integrin

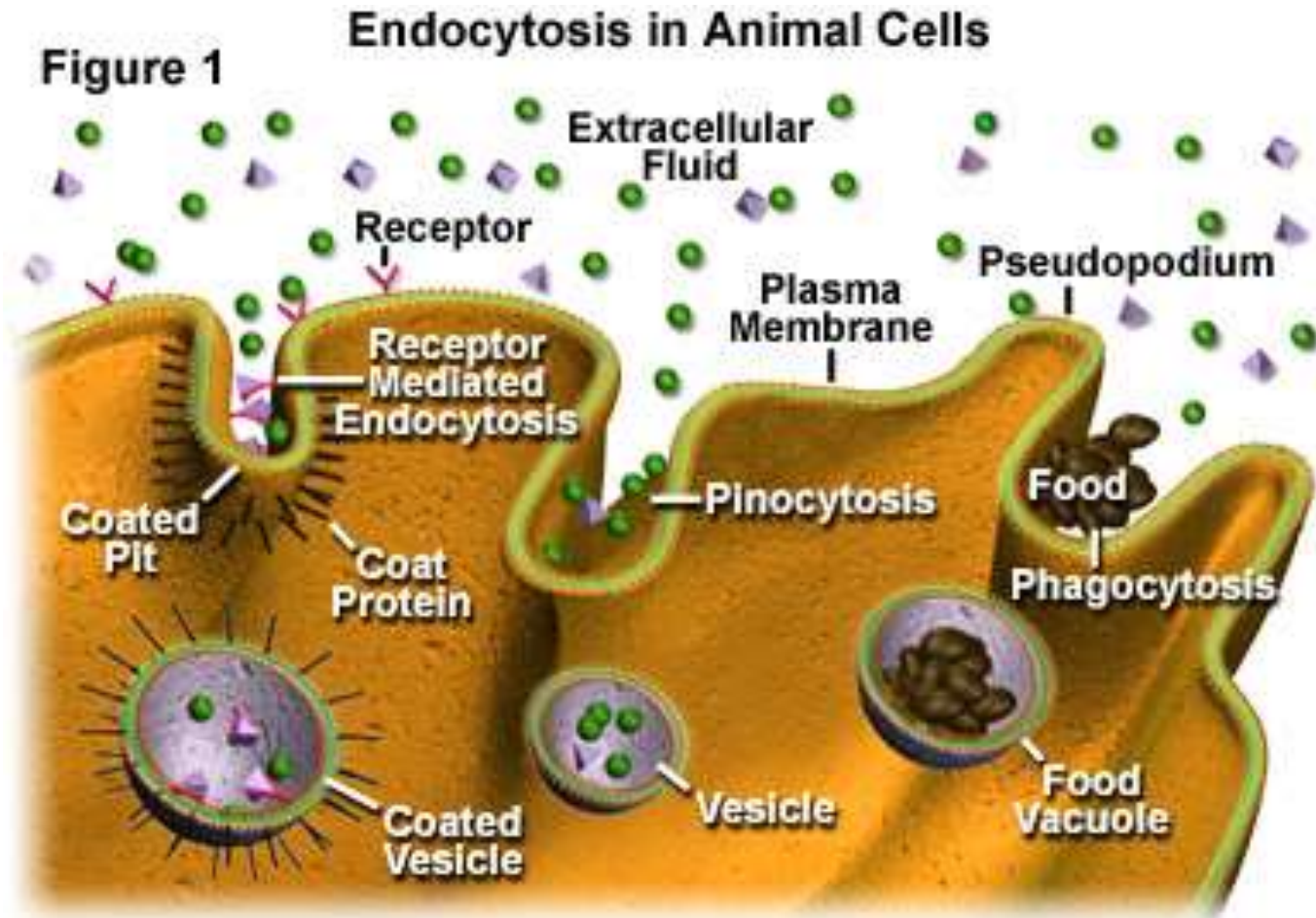
An **integrin**, or **integrin receptor**, is an integral membrane protein in the plasma membrane of cells. It plays a role in the attachment of a cell to the [extracellular matrix](#) (ECM) and to other cells, and in signal transduction from the ECM to the cell. There are many types of integrin, and many cells have multiple types on their surface. Integrins are of vital importance to all [metazoans](#), from humans to sponges.

Schematic drawing of a typical integrin dimer

Arrow shows the region where an I domain is inserted in some α subunits. Not all α subunits are posttranslationally cleaved. Internal disulphide bonds within subunits are not shown. Dark blue regions in the head segment of the α subunit represent homologous repeats. Those with the EF-hand consensus sequence are marked with red circles to denote binding sites for divalent metal ion.



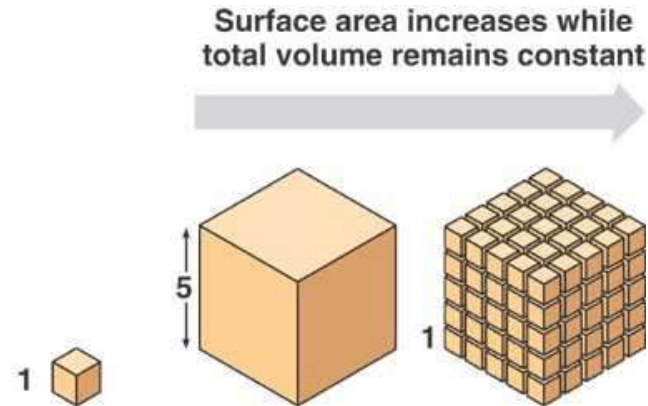
Endocytosis



Nanomaterials

- Metals and Alloys
 - Fe, Al, Au
- Semiconductors
 - Band gap, CdS, TiO₂, ZnO
- Ceramic
 - Al₂O₃, Si₃N₄, MgO, , SiO₂, ZrO₂
- Carbon based
 - Diamond, graphite, nanotube, C60, graphene
- Polymers
 - Soft mater, block co-polymer
- Biological
 - Photonic, hydrophobic, adhesive,
- Composites

Surface to Volume Ratio



Total surface area (height \times width \times number of sides \times number of boxes)	6	150	750
Total volume (height \times width \times length \times number of boxes)	1	125	125
Surface-to-volume ratio (surface area / volume)	6	1.2	6

Surface Energy

One face surface energy: γ

27 cube: $27 \times 6 \gamma$

3 x 9 cube line: 114γ

3 x (3x3) square: 90γ

3 x 3 x 3 cube: 54γ

Surface to Volume Ratio

Au: AAA

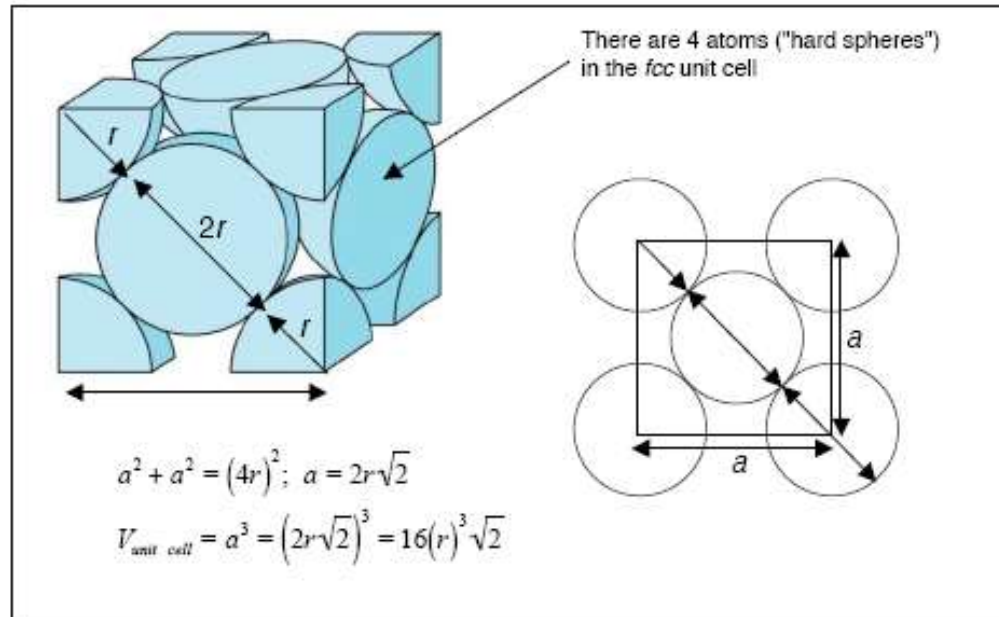
Atomic mass: 196.967

Density 19.31

Radii =0.144 nm

Number of Au atoms in 1 m	$3.4 \cdot 10^9$
Volume of Au atom	$4.19 \cdot 10^{28}$
Surface area Au atom	$7.22 \cdot 10^{19}$
Surface/volume ratio	$1.72 \cdot 10^{-9}$

fcc



$$V_{\text{unit cell}} = a^3 = (2r\sqrt{2})^3 = 16(0.5\text{nm})^3\sqrt{2} = \mathbf{2.828 \text{ nm}^3}$$

$$\frac{10^{27} \text{ nm}^3}{2.828 \text{ nm}^3} = 3.536 \times 10^{26} \text{ nano unit cells}$$

$$\frac{S_{\text{spheres}}}{S_{\text{unit cell}}} = \frac{4.44 \times 10^9 \text{ m}^2}{6.0 \times 10^9 \text{ m}^2} = 0.74$$

$$\text{Collective Area} = 3.536 \times 10^{26} \text{ nano unit cells} \left(\frac{4 \text{ spheres}}{\text{unit cell}} \right) \left(\frac{4\pi r^2}{\text{sphere}} \right) = 4.44 \times 10^{27} \text{ nm}^2$$

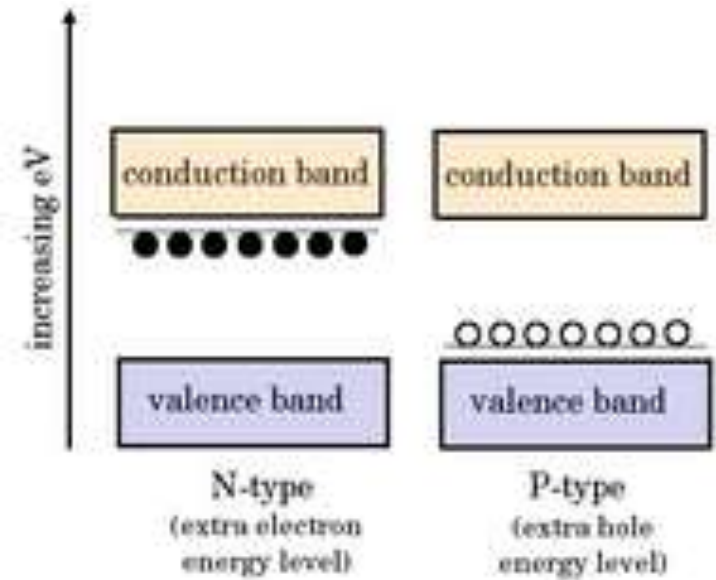
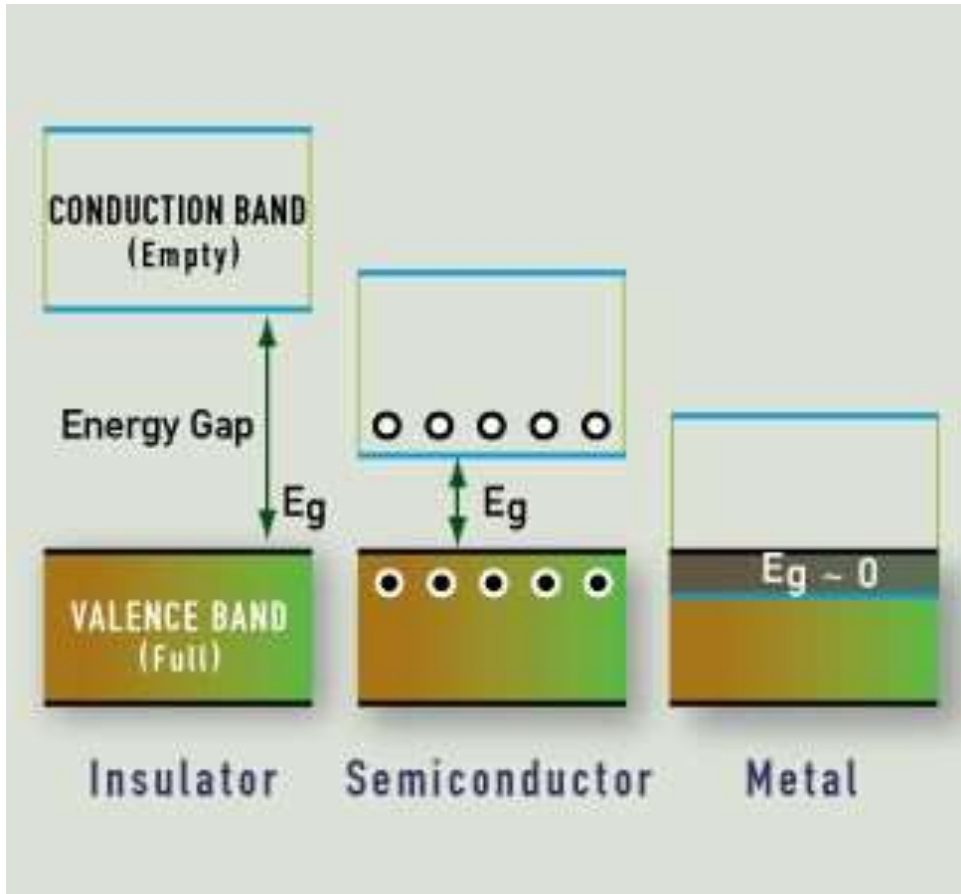
Packing Fraction

$$\text{APF} = \frac{N_{\text{atoms}} V_{\text{atom}}}{V_{\text{crystal}}}$$

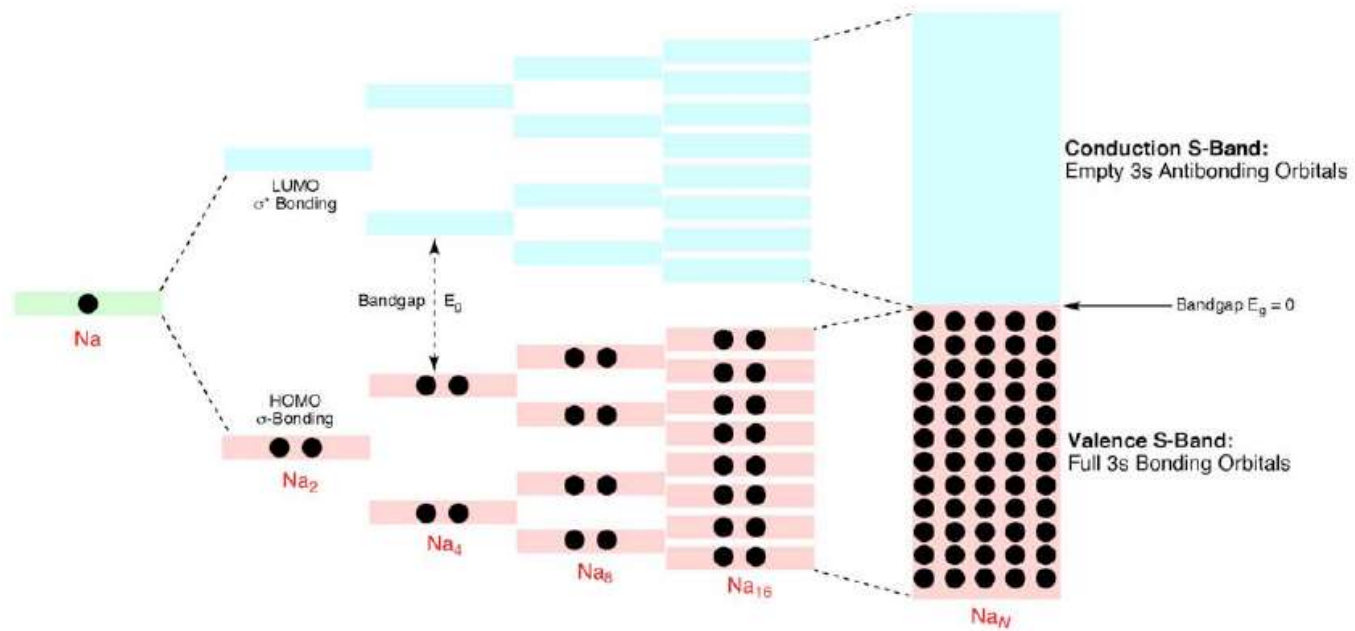
Surfaces

- Collective surface area of nanocube 1 nm
- Porous materials
 - Micropore (<2 nm)
 - Mesopore (2 nm ~ 50 nm)
 - Marcopore (> 50nm)
- Void volume
 - $V_{\text{pore}}/V_{\text{material}}$

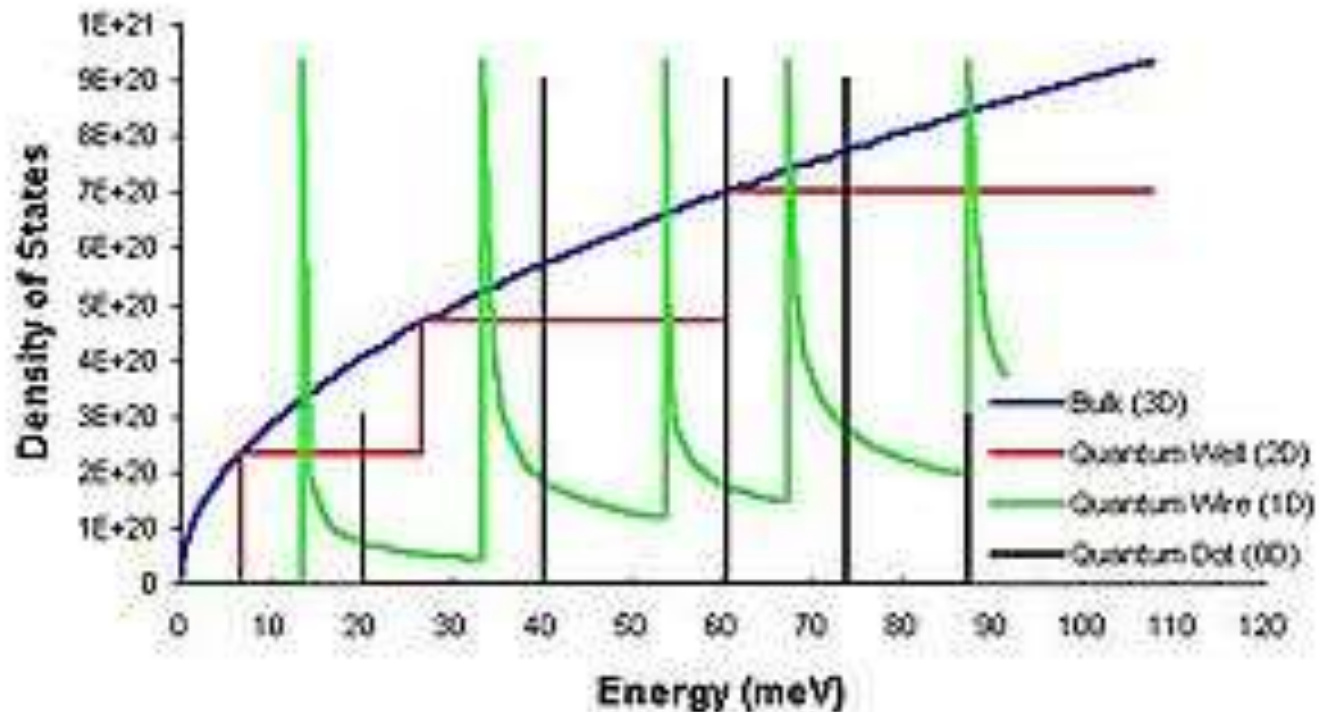
Bandgap



Bandgap



Density of State

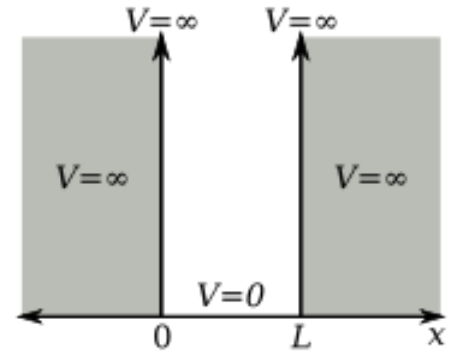


Particle in a Box

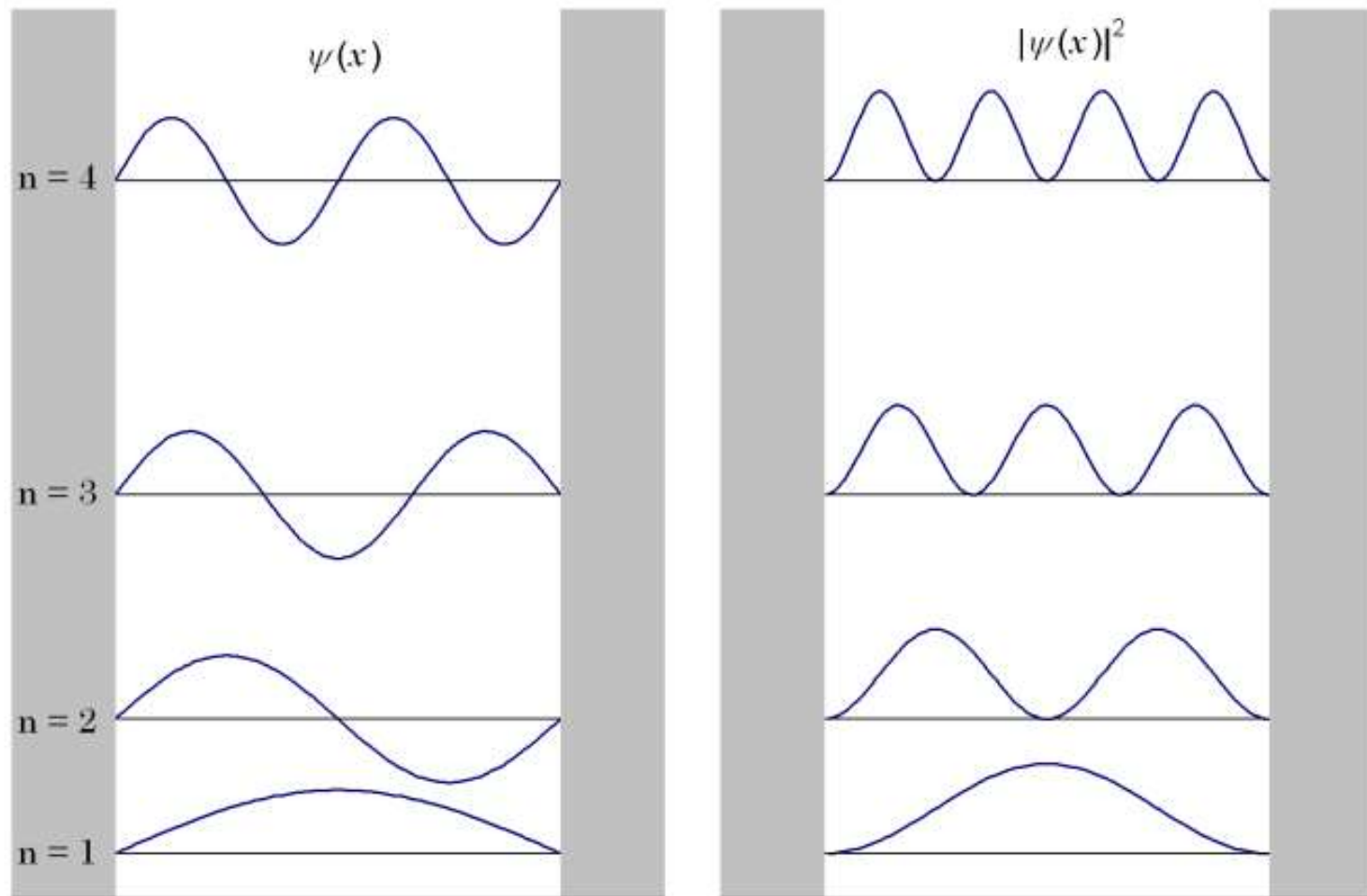
$$-\frac{\hbar^2}{2m} \frac{d^2\psi(x)}{dx^2} + V(x)\psi(x) = E\psi(x) \quad (1)$$

$$\psi_n = \sqrt{\frac{2}{L}} \sin\left(\frac{n\pi x}{L}\right)$$

$$E_n = \frac{\hbar^2 \pi^2}{2mL^2} n^2$$



Particle in a Box



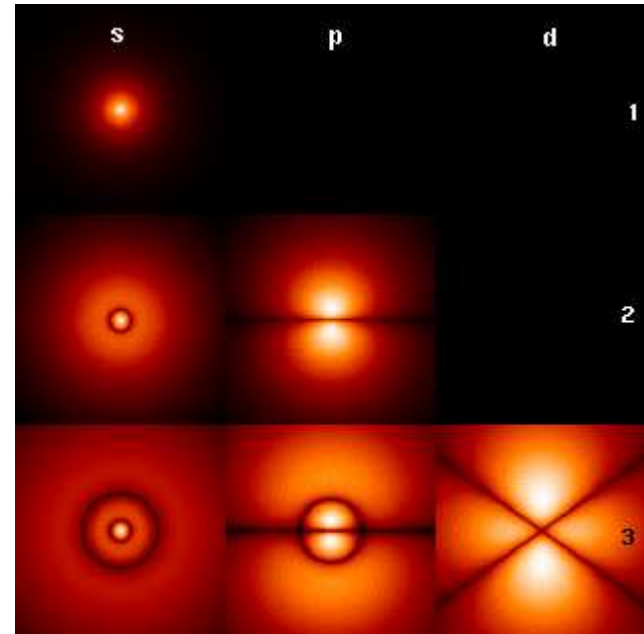
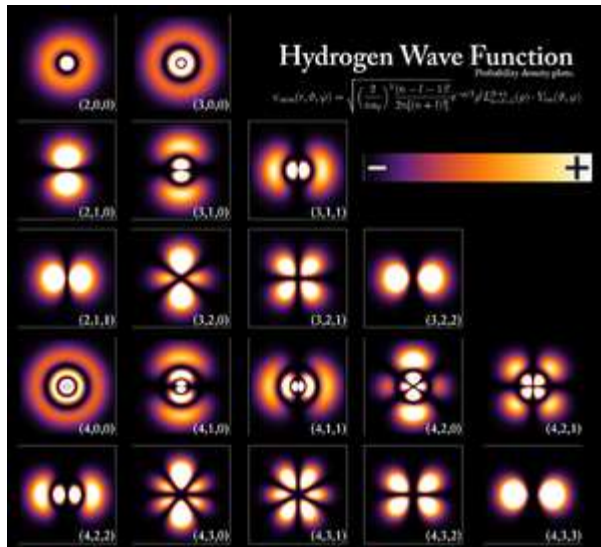
$$\psi_{n_x, n_y} = \sqrt{\frac{4}{L_x L_y}} \sin\left(\frac{n_x \pi x}{L_x}\right) \sin\left(\frac{n_y \pi y}{L_y}\right)$$

$$E_{n_x, n_y} = \frac{\hbar^2 \pi^2}{2m} \left[\left(\frac{n_x}{L_x}\right)^2 + \left(\frac{n_y}{L_y}\right)^2 \right]$$

$$\psi_{n_x, n_y, n_z} = \sqrt{\frac{8}{L_x L_y L_z}} \sin\left(\frac{n_x \pi x}{L_x}\right) \sin\left(\frac{n_y \pi y}{L_y}\right) \sin\left(\frac{n_z \pi z}{L_z}\right) \quad (22)$$

$$E_{n_x, n_y, n_z} = \frac{\hbar^2 \pi^2}{2m} \left[\left(\frac{n_x}{L_x}\right)^2 + \left(\frac{n_y}{L_y}\right)^2 + \left(\frac{n_z}{L_z}\right)^2 \right] \quad (23)$$

Wave Functions



$$i\hbar \frac{\partial}{\partial t} \Psi(\mathbf{r}, t) = \hat{H} \Psi = \left(-\frac{\hbar^2}{2m} \nabla^2 + V(\mathbf{r}) \right) \Psi(\mathbf{r}, t) = -\frac{\hbar^2}{2m} \nabla^2 \Psi(\mathbf{r}, t) + V(\mathbf{r}) \Psi(\mathbf{r}, t)$$

$$V(r) = -\frac{1}{4\pi\epsilon_0} \frac{Ze^2}{r}$$

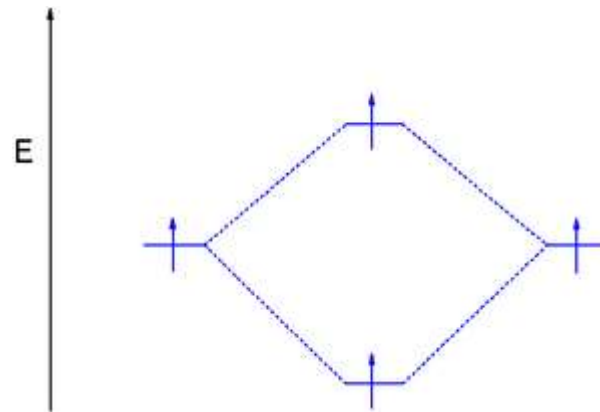
$$\psi_{n\ell m}(r, \vartheta, \varphi) = \sqrt{\left(\frac{2}{na_0}\right)^3 \frac{(n-\ell-1)!}{2n(n+\ell)!}} e^{-\rho/2} \rho^\ell L_{n-\ell-1}^{2\ell+1}(\rho) \cdot Y_\ell^m(\vartheta, \varphi)$$

Linear combination of atomic orbitals molecular orbital method

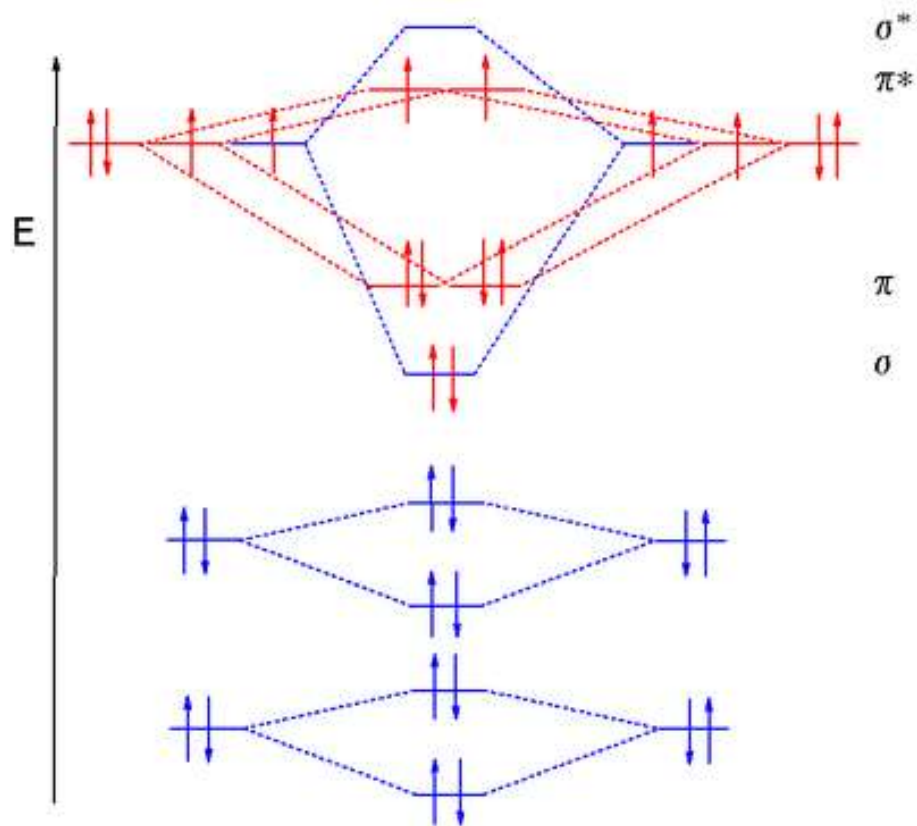
$$\phi_i = c_{1i}\chi_1 + c_{2i}\chi_2 + c_{3i}\chi_3 + \cdots + c_{ni}\chi_n$$

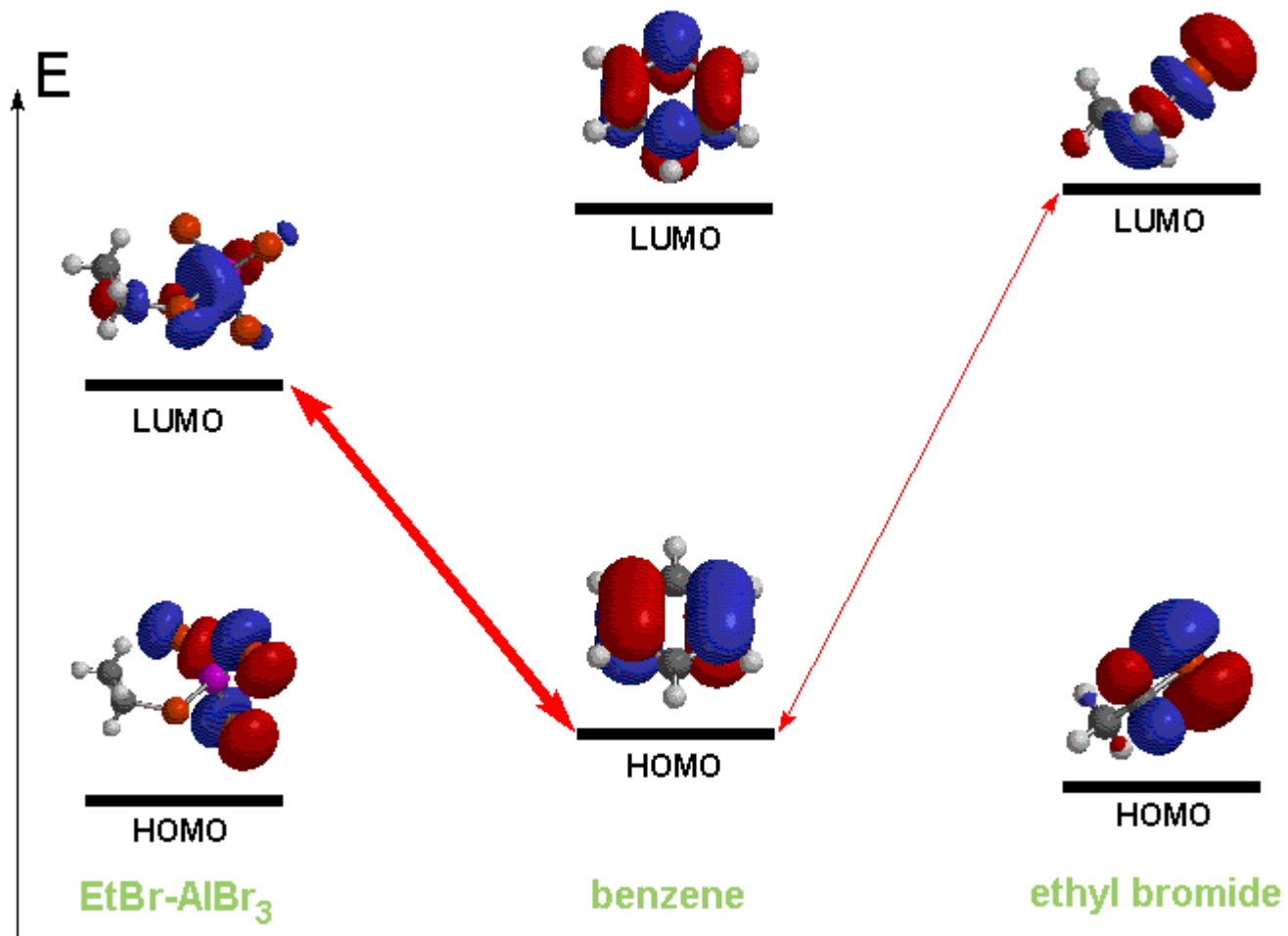
$$\psi_i = \sum_{\mu} c_{\mu i} \phi_{\mu}$$

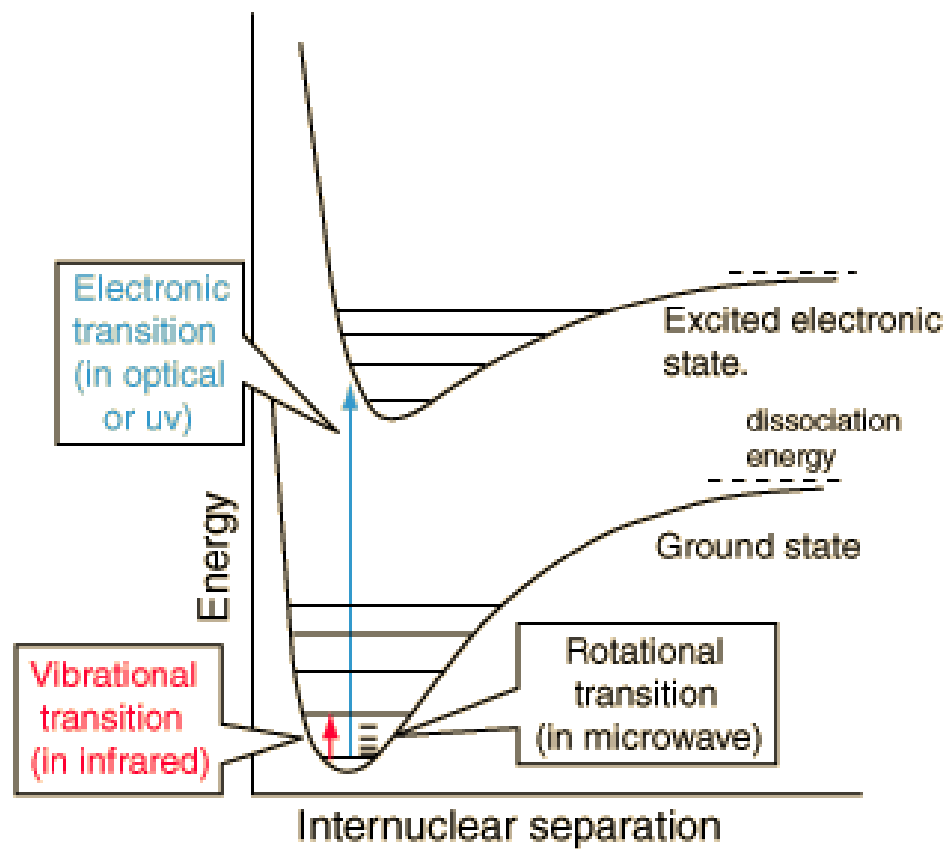
MO \nearrow \nwarrow coefficient of AO_{μ} in MO_i
 \nwarrow \nearrow AO



Oxygen







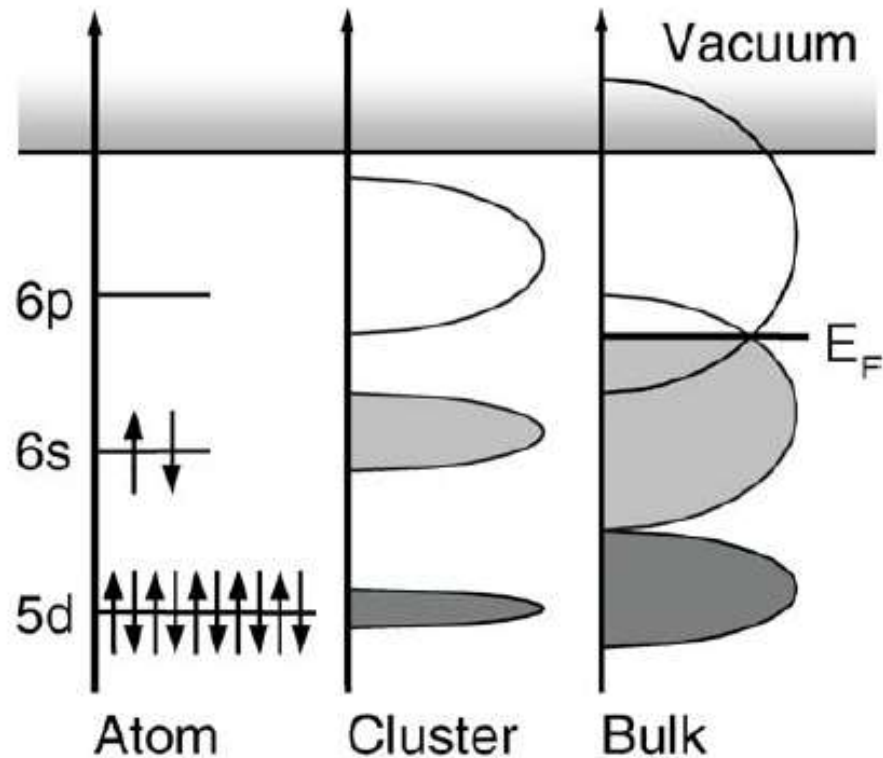


Figure 5 Energy diagram describing a generic Bloch-Wilson MIT in clusters (with specific reference to the energy levels of mercury). For sufficiently large clusters, the *s-p* band gap closes with increasing cluster size (shaded areas represent energy range with occupied electron levels). Overlap leads to a “continuous” DOS at E_F and to an Insulator to Metal transition.

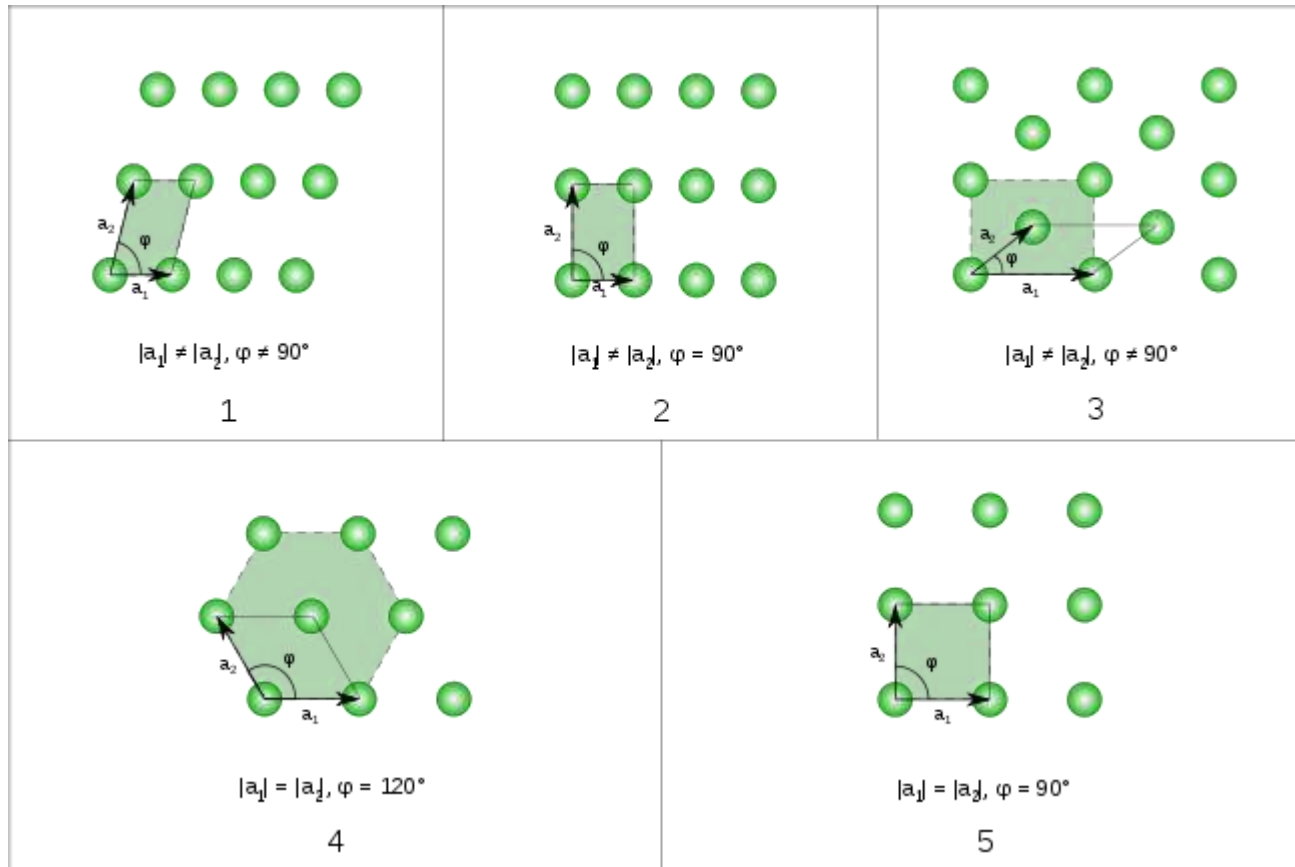
Bloch wave

$$\psi_{n\mathbf{k}}(\mathbf{r}) = e^{i\mathbf{k}\cdot\mathbf{r}} u_{n\mathbf{k}}(\mathbf{r})$$

A **Bloch wave** or **Bloch state**, named after [Felix Bloch](#), is the [wavefunction](#) of a particle (usually, an [electron](#)) placed in a [periodic potential](#).

$$\epsilon_n(\mathbf{k}) = \epsilon_n(\mathbf{k} + \mathbf{K}),$$

The five fundamental two-dimensional Bravais lattices



Unit Cell

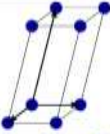
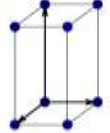
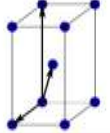
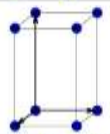
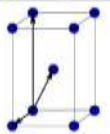
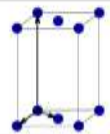
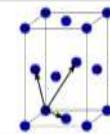
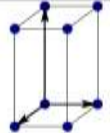
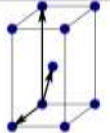
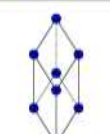
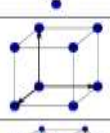
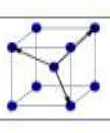
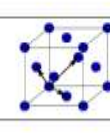
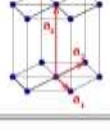
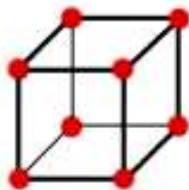
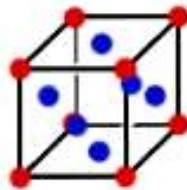
Bravais lattice	Parameters	Simple (P)	Volume centered (I)	Base centered (C)	Face centered (F)
Triclinic	$a_1 \neq a_2 \neq a_3$ $\alpha_{12} \neq \alpha_{23} \neq \alpha_{31}$				
Monoclinic	$a_1 \neq a_2 \neq a_3$ $\alpha_{23} = \alpha_{31} = 90^\circ$ $\alpha_{12} \neq 90^\circ$				
Orthorhombic	$a_1 \neq a_2 \neq a_3$ $\alpha_{12} = \alpha_{23} = \alpha_{31} = 90^\circ$				
Tetragonal	$a_1 = a_2 \neq a_3$ $\alpha_{12} = \alpha_{23} = \alpha_{31} = 90^\circ$				
Trigonal	$a_1 = a_2 = a_3$ $\alpha_{12} = \alpha_{23} = \alpha_{31} < 120^\circ$				
Cubic	$a_1 = a_2 = a_3$ $\alpha_{12} = \alpha_{23} = \alpha_{31} = 90^\circ$				
Hexagonal	$a_1 = a_2 \neq a_3$ $\alpha_{12} = 120^\circ$ $\alpha_{23} = \alpha_{31} = 90^\circ$				

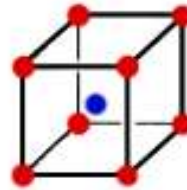
Table 1.1: Bravais lattices in three-dimensions.



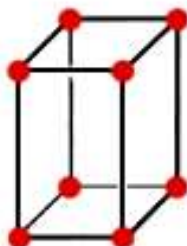
**Simple
cubic**



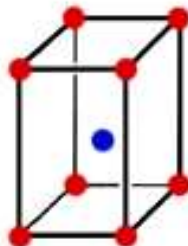
**Face-centered
cubic**



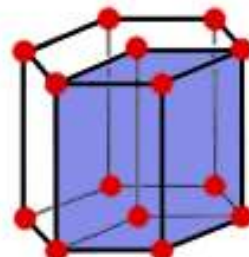
**Body-centered
cubic**



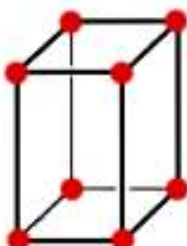
**Simple
tetragonal**



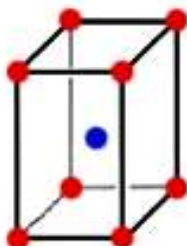
**Body-centered
tetragonal**



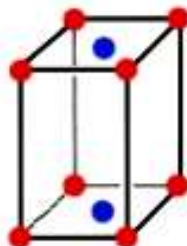
Hexagonal



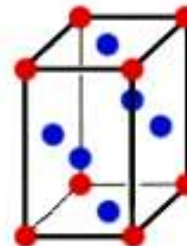
**Simple
orthorhombic**



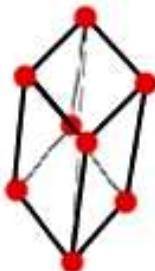
**Body-centered
orthorhombic**



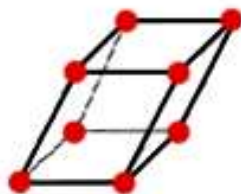
**Base-centered
orthorhombic**



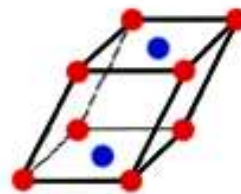
**Face-centered
orthorhombic**



Rhombohedral



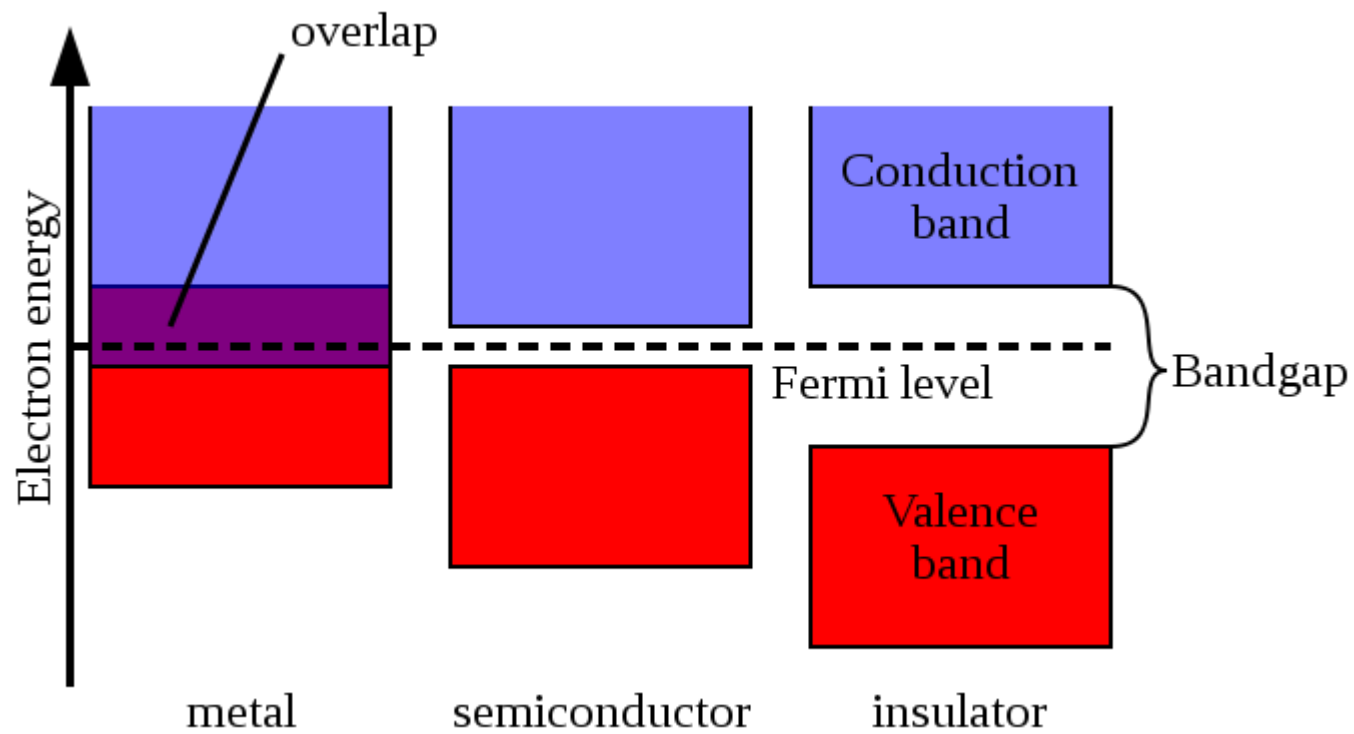
**Simple
Monoclinic**



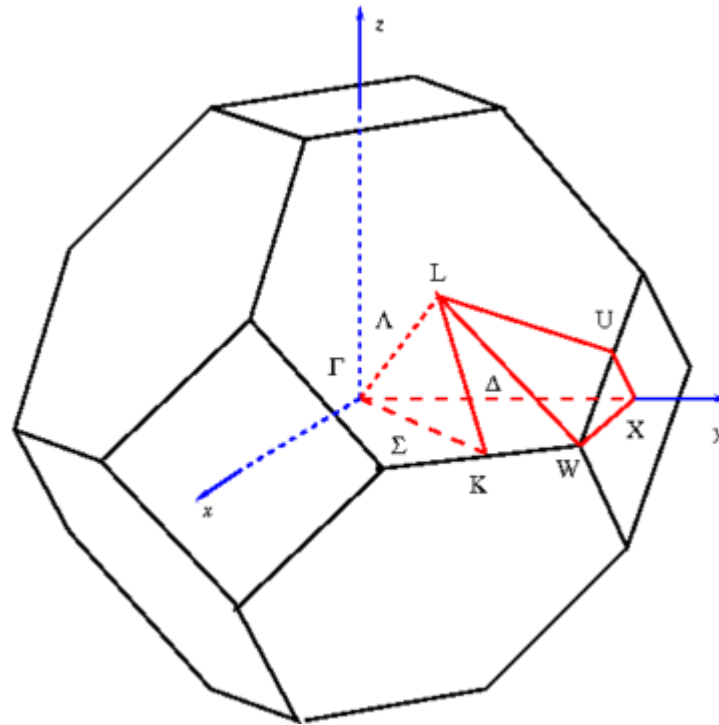
**Base-centered
monoclinic**



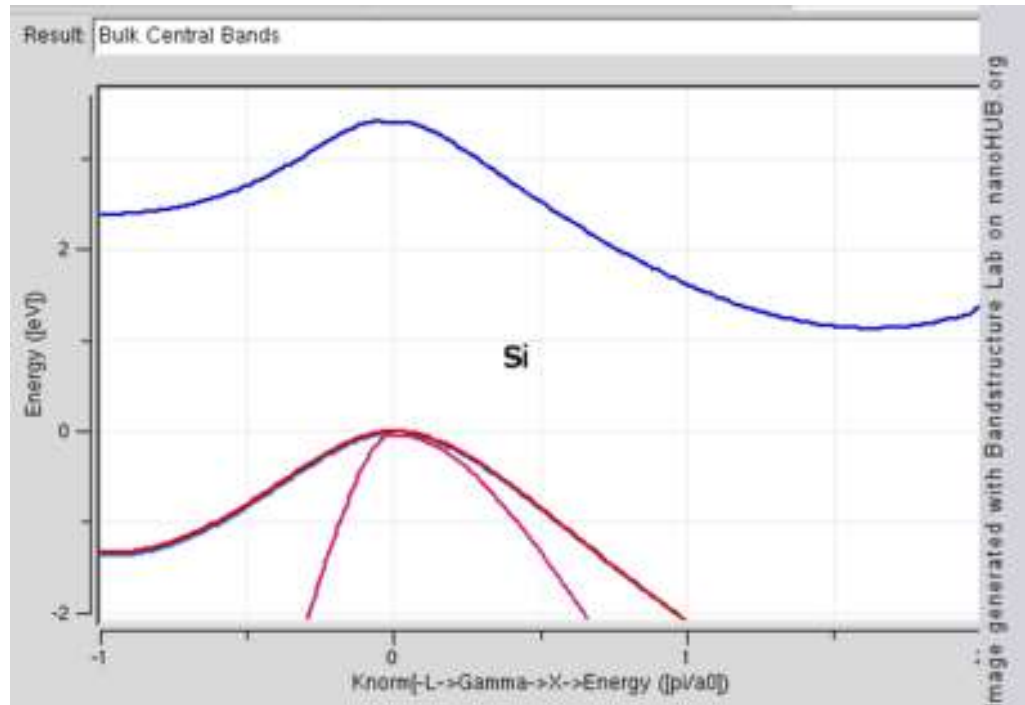
Triclinic



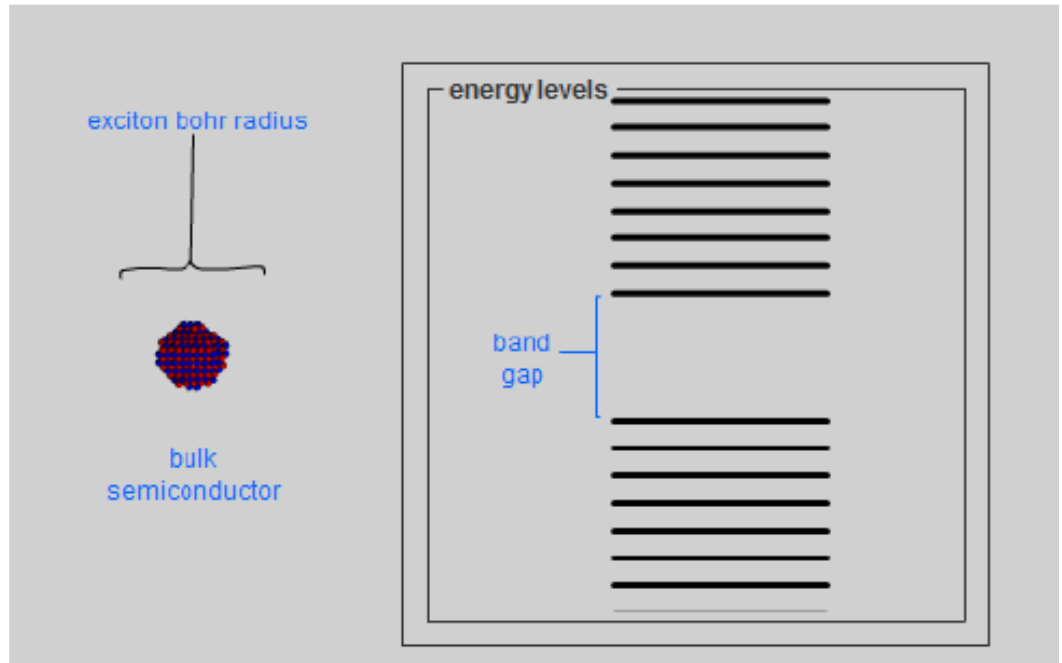
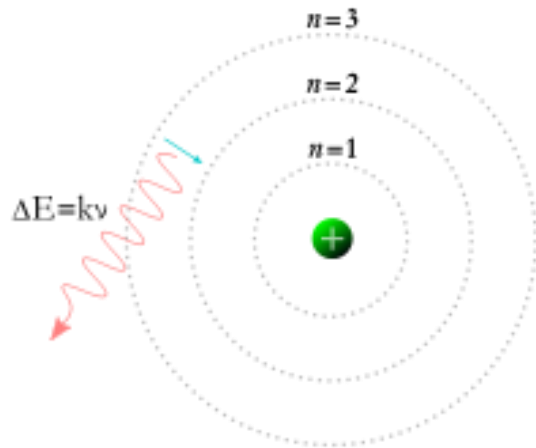
First Brillouin zone of FCC lattice showing symmetry labels



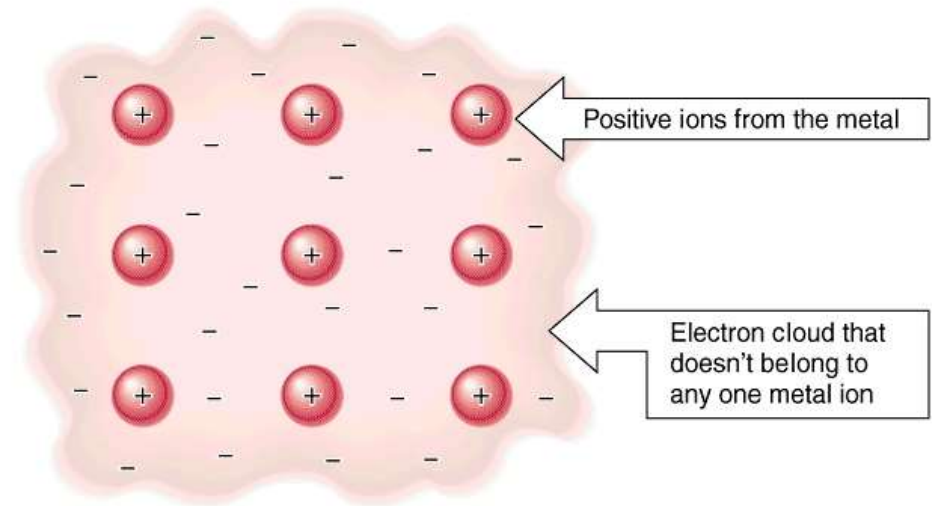
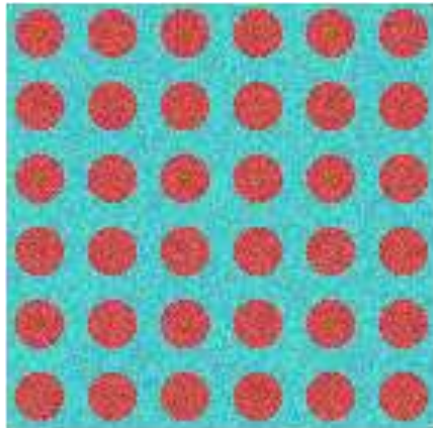
Band Structures



Bohr Exciton Radius



Electron Sea

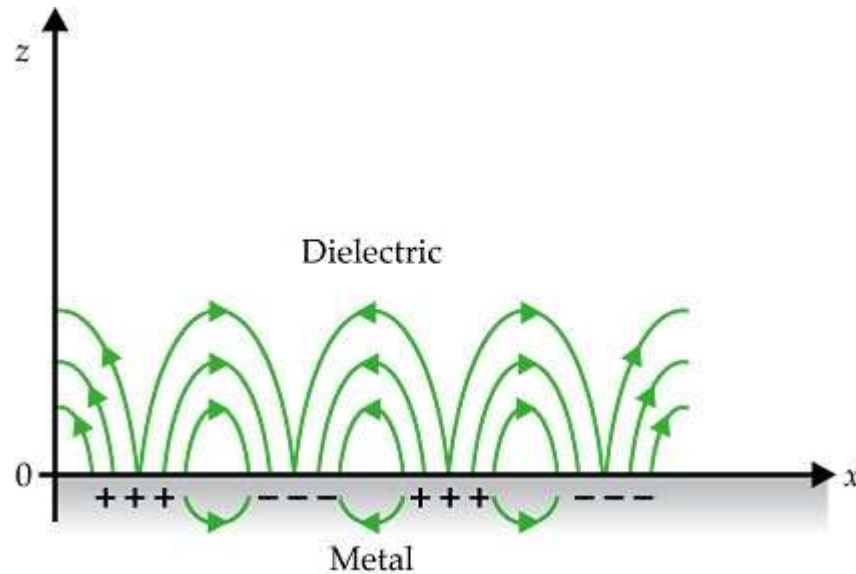


Copyright 1998 by John Wiley and Sons, Inc. All rights reserved.

$$m \frac{d^2 \delta x}{dt^2} = e E_x = -m \omega_p^2 \delta x,$$

$$\omega_p^2 = \frac{n e^2}{\epsilon_0 m},$$

Surface Plasmon



$$\epsilon_m = 1 - \frac{\omega_p^2}{\omega^2}$$

TiO₂

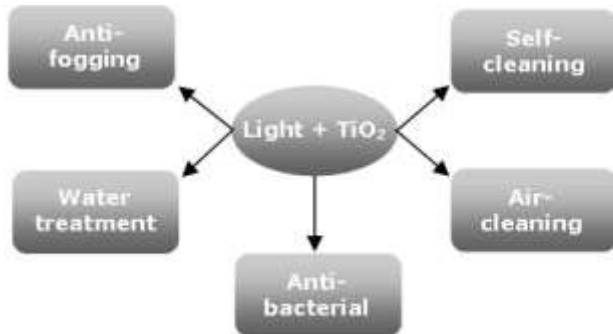
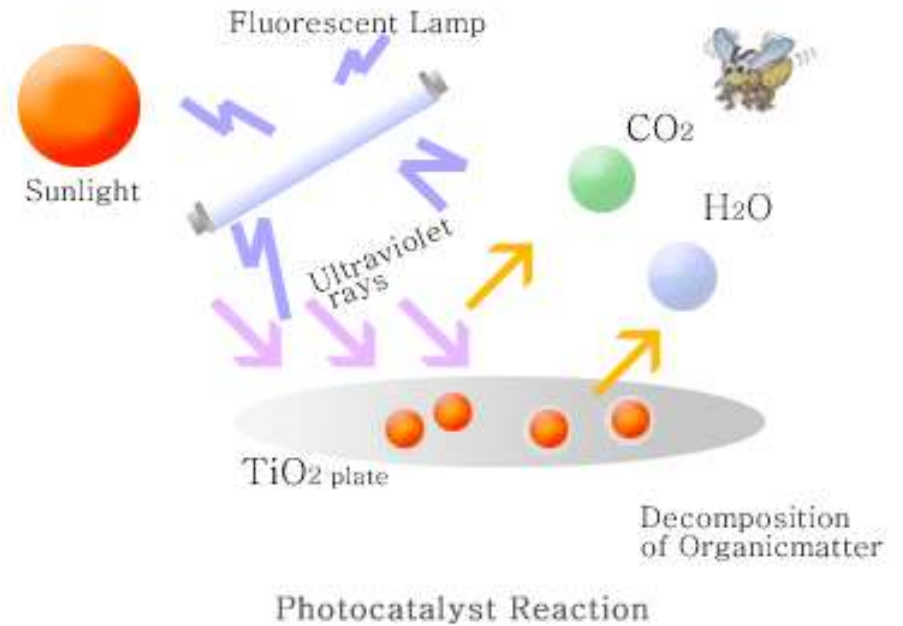
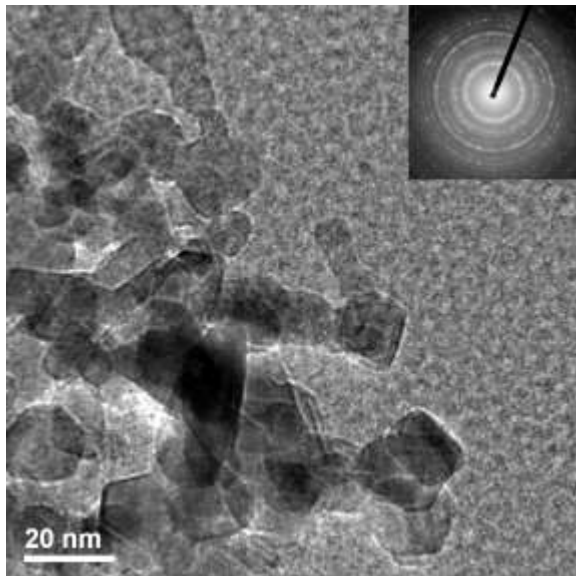
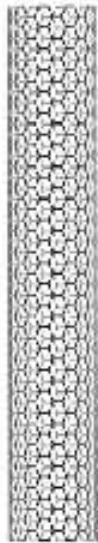


Figure 1. Major areas of activity in titanium dioxide photocatalysis



Carbon



SWNT



Poly-C₆₀

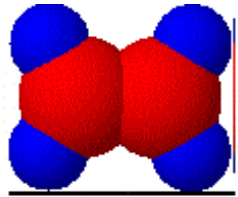


C₆₀

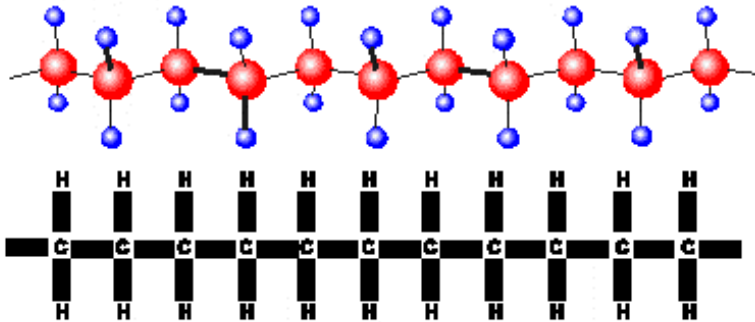
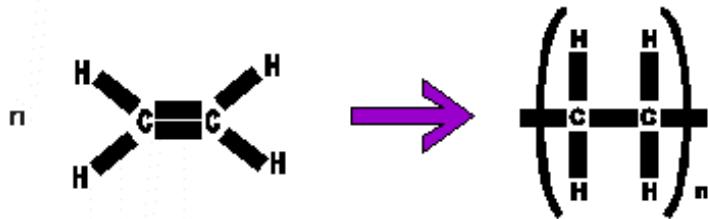
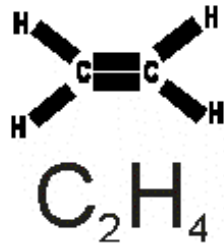


Nanodiamond
~ 2-10 nm

Polymer

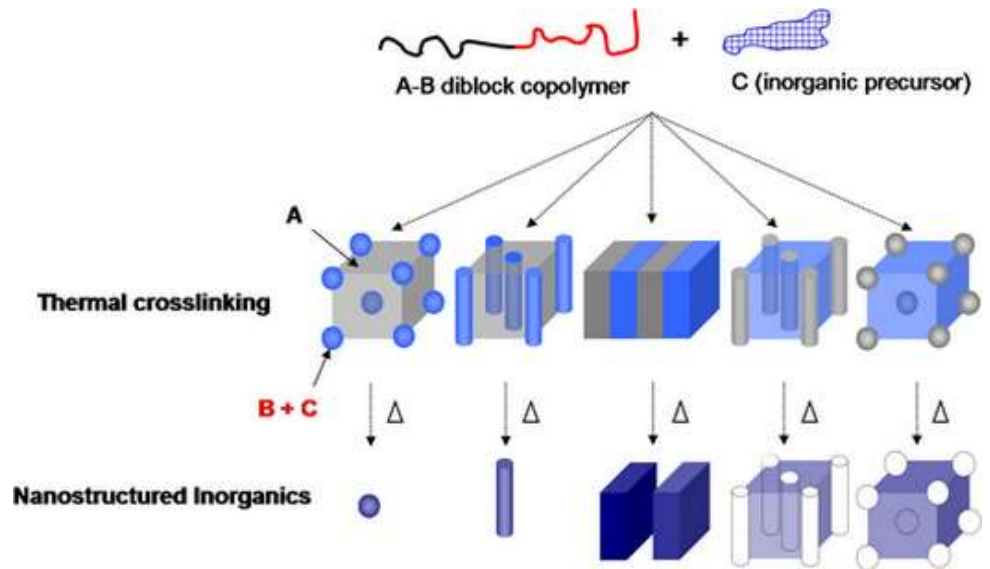


a monomer ethene

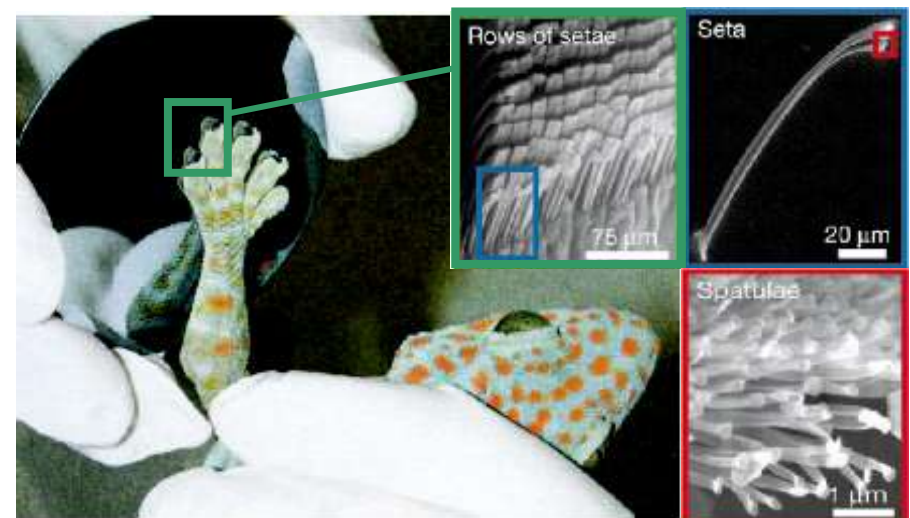
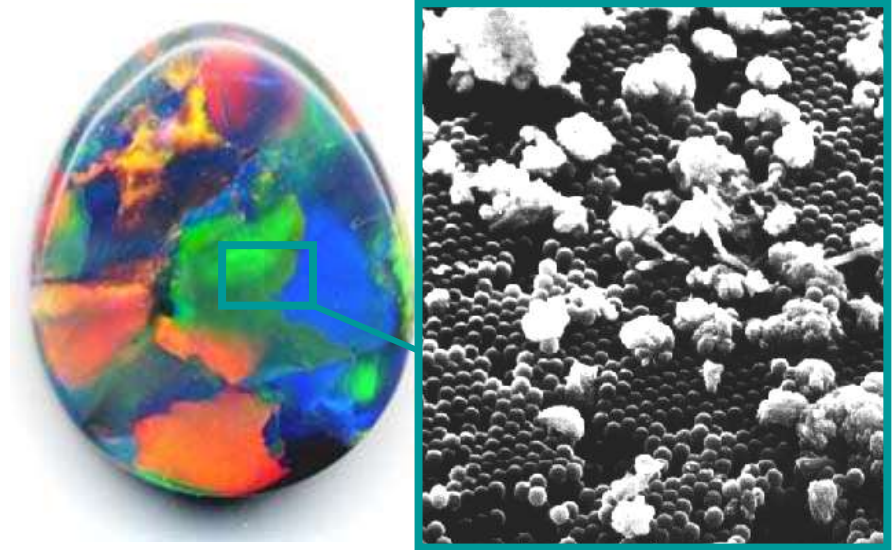
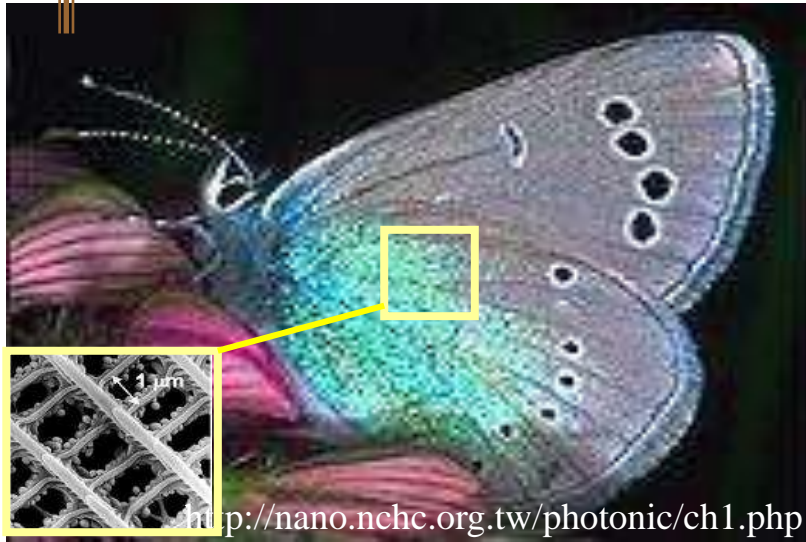


a polymer

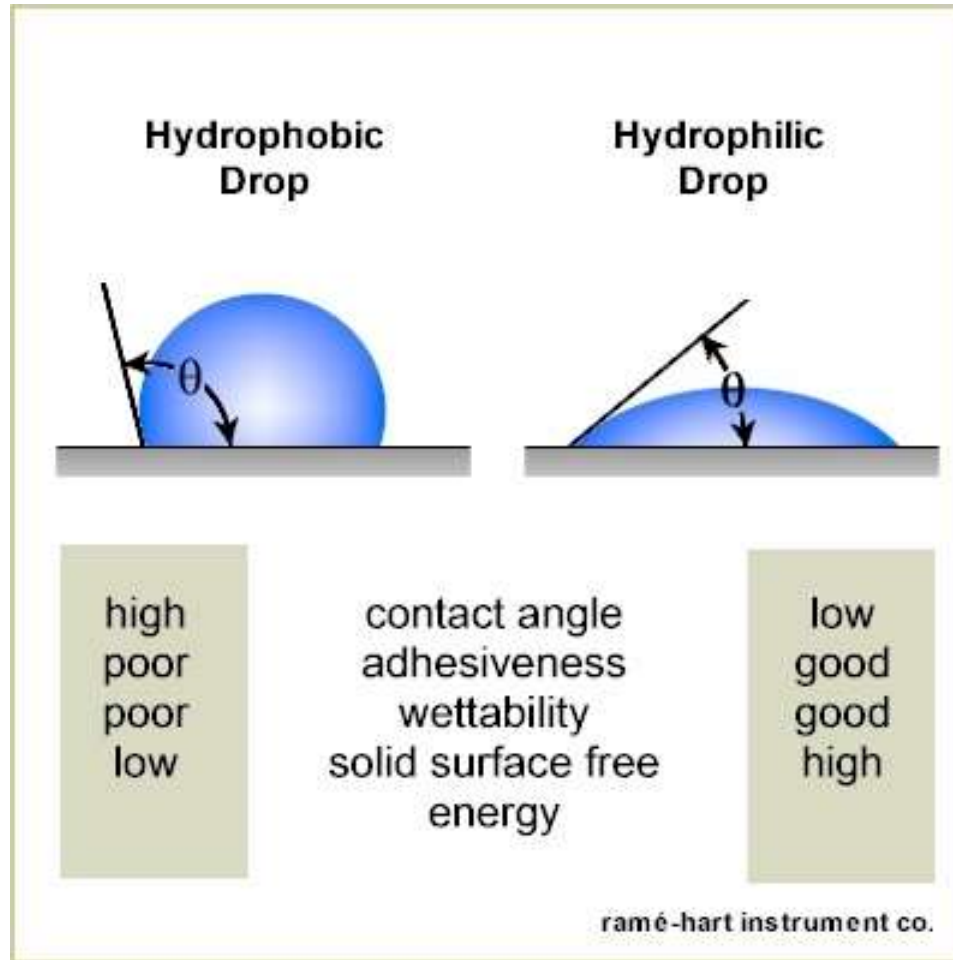
poly(ethene)



Nature Materials

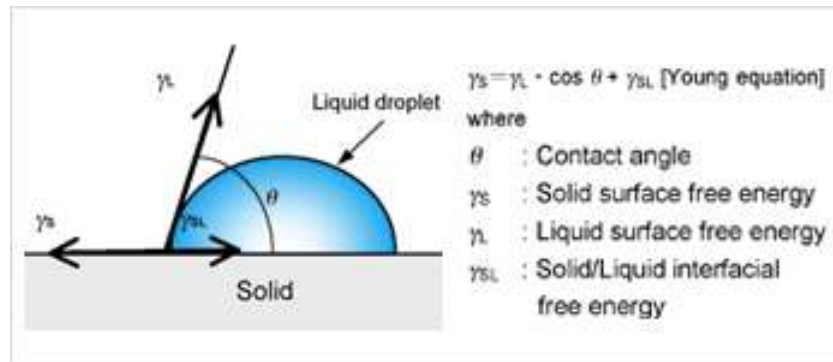


Contact Angle



Young's Equation

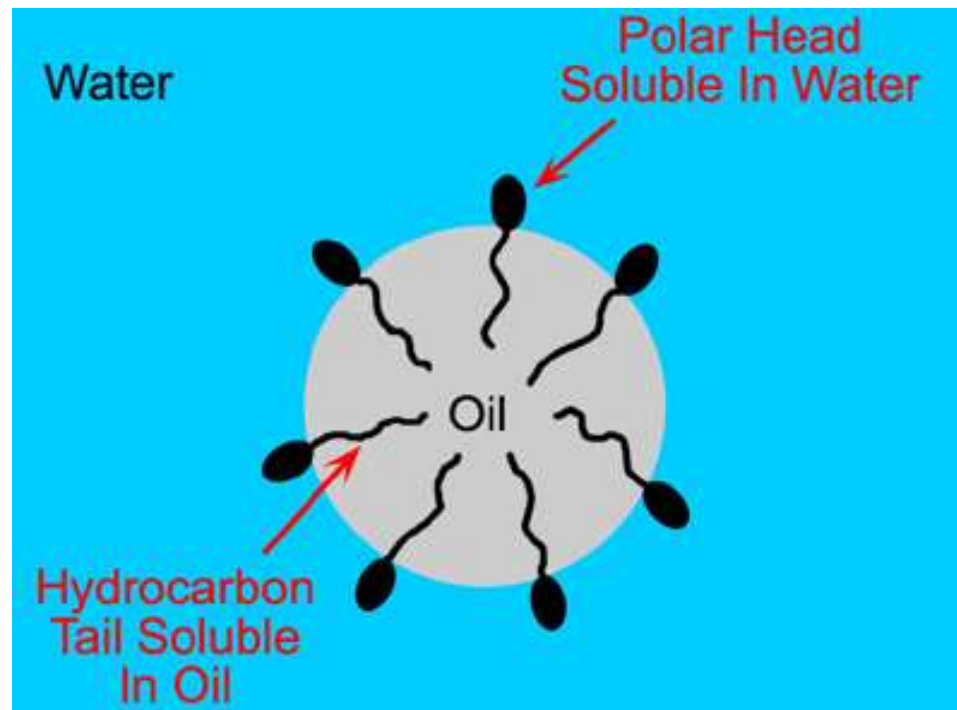
$$\gamma_{SL} + \gamma_{LV} \cos \theta_c = \gamma_{SV}$$



Surface Energy Minimization

- Surfactants
- DLVO
- Polymeric
- Nucleation
- Ostwald Ripening
- Sintering
- Restructure

Surfactant



DLVO Theory

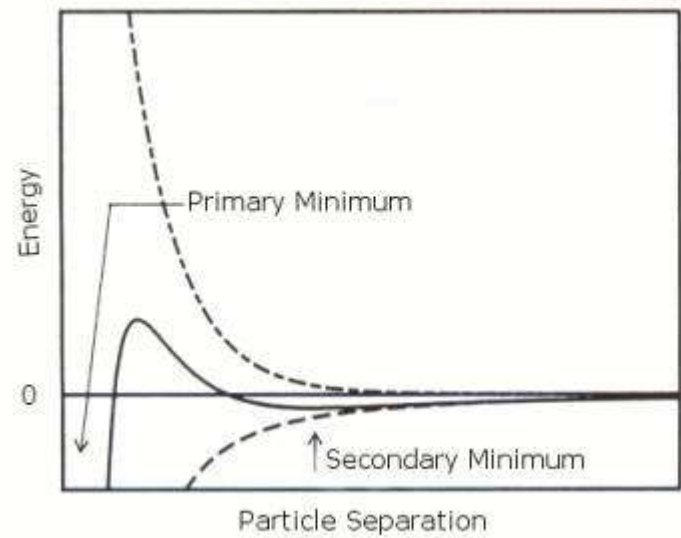
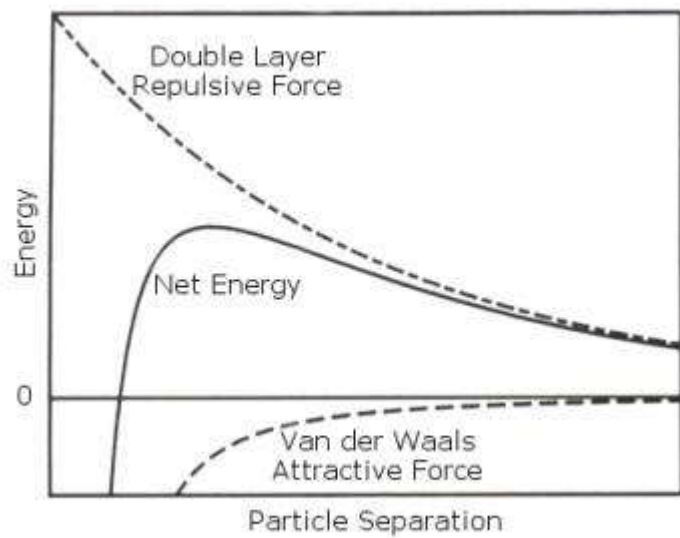
$$V_T = V_A + V_R + V_S$$

$$V_A = -A/(12 \pi D^2)$$

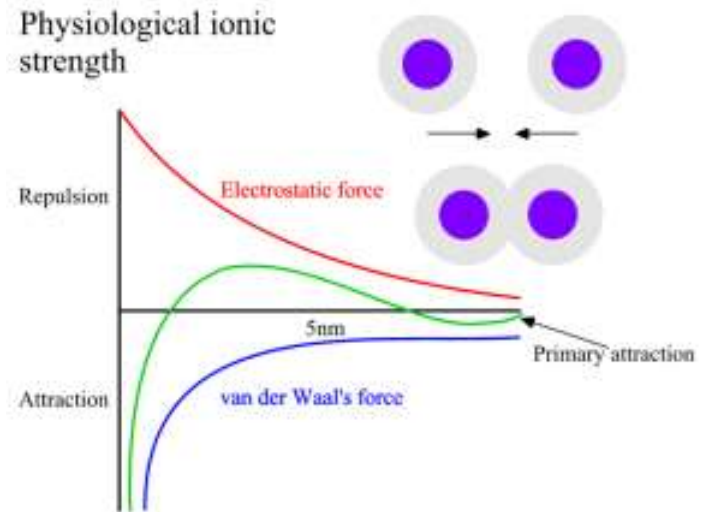
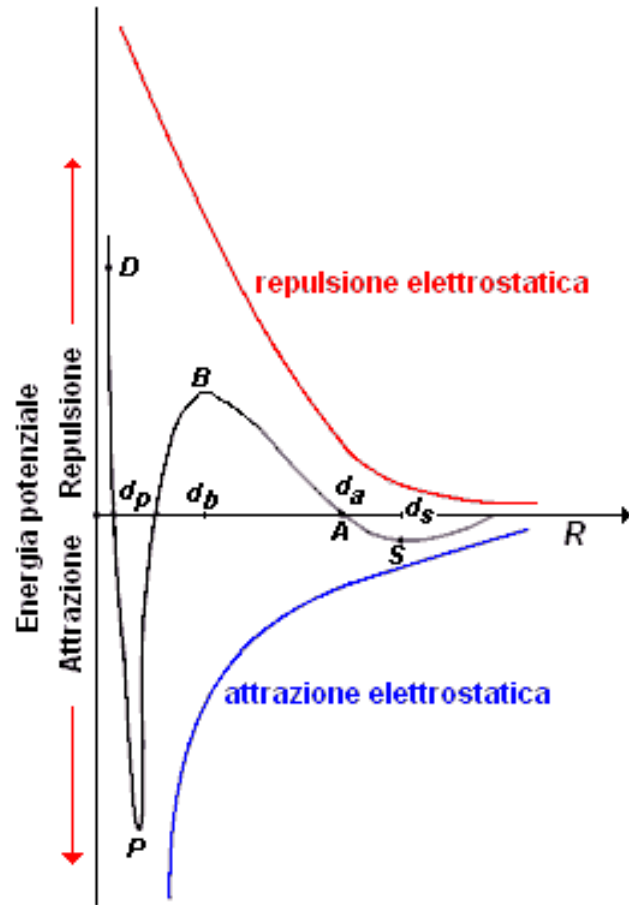
A is the Hamaker constant and D is the particle separation

$$V_R = 2 \pi \epsilon a \xi^2 \exp(-\kappa D)$$

a is the particle radius, π is the solvent permeability,
 κ is a function of the ionic composition and ξ is the zeta potential



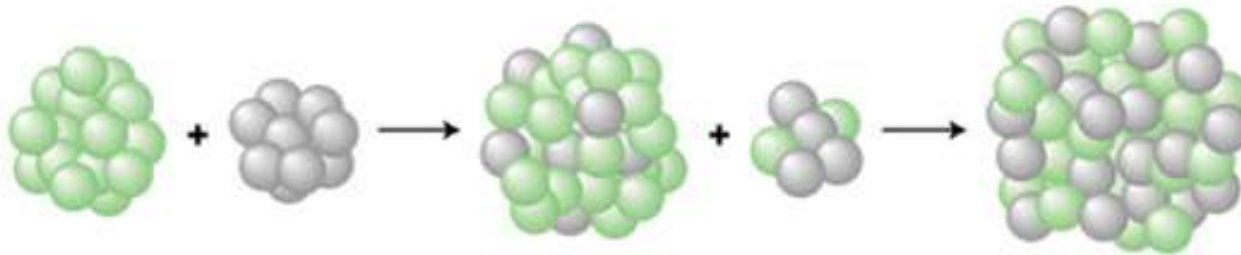
DLVO Theory



a Coalescence



b Ostwald ripening



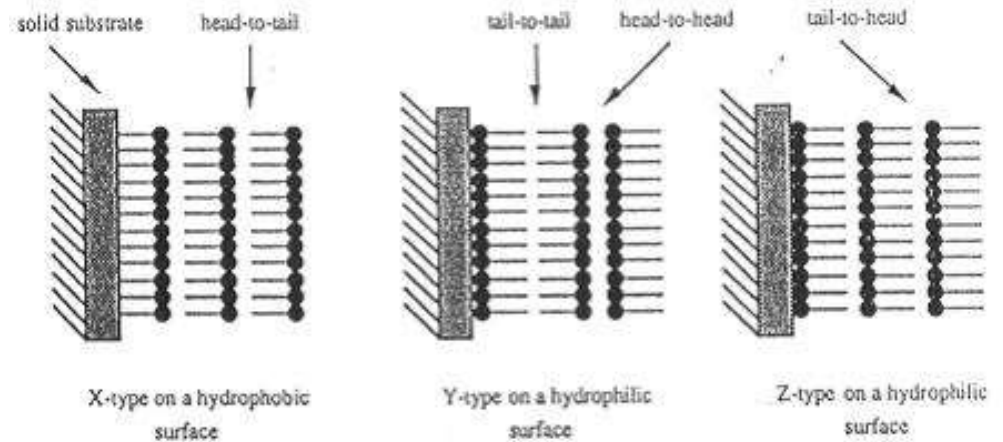
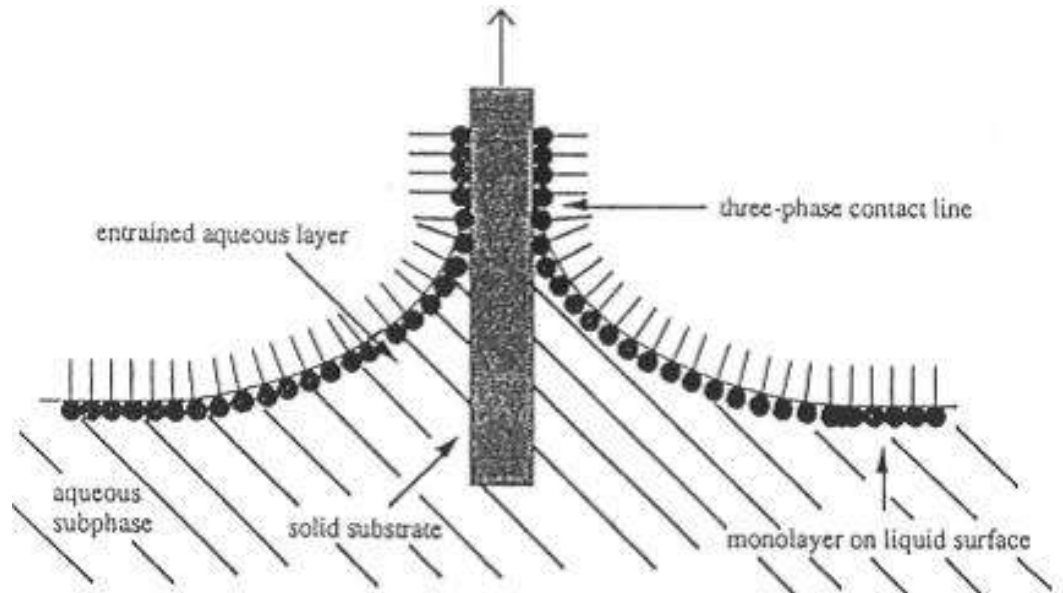
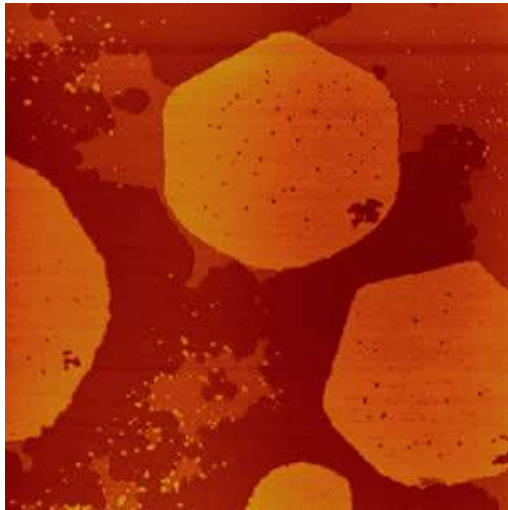
Two main mechanisms are shown here: **a**, coalescence sintering, and **b**, Ostwald ripening sintering. Coalescence sintering occurs when two clusters touch or collide and merge to form one bigger cluster. In contrast, Ostwald ripening sintering occurs by evaporation of atoms from one cluster, which then transfer to another. This is a dynamic process — both clusters exchange atoms, but the rate of loss from the smaller cluster is higher, because of the lower average coordination of atoms at the surface and their relative ease of removal. Thus big clusters get bigger at the expense of smaller clusters, which shrink and eventually disappear. The latter process is the usual form of sintering for metal clusters on a supported surface that are well spaced apart, although coalescence can occur for a high density of clusters. In general, the presence of the surface results in SMORS (surface-mediated Ostwald ripening sintering) in which material is transferred from one cluster to another by diffusion across the surface, and not through the gas phase.

Synthesis of Nanoparticles and Surface Modifications

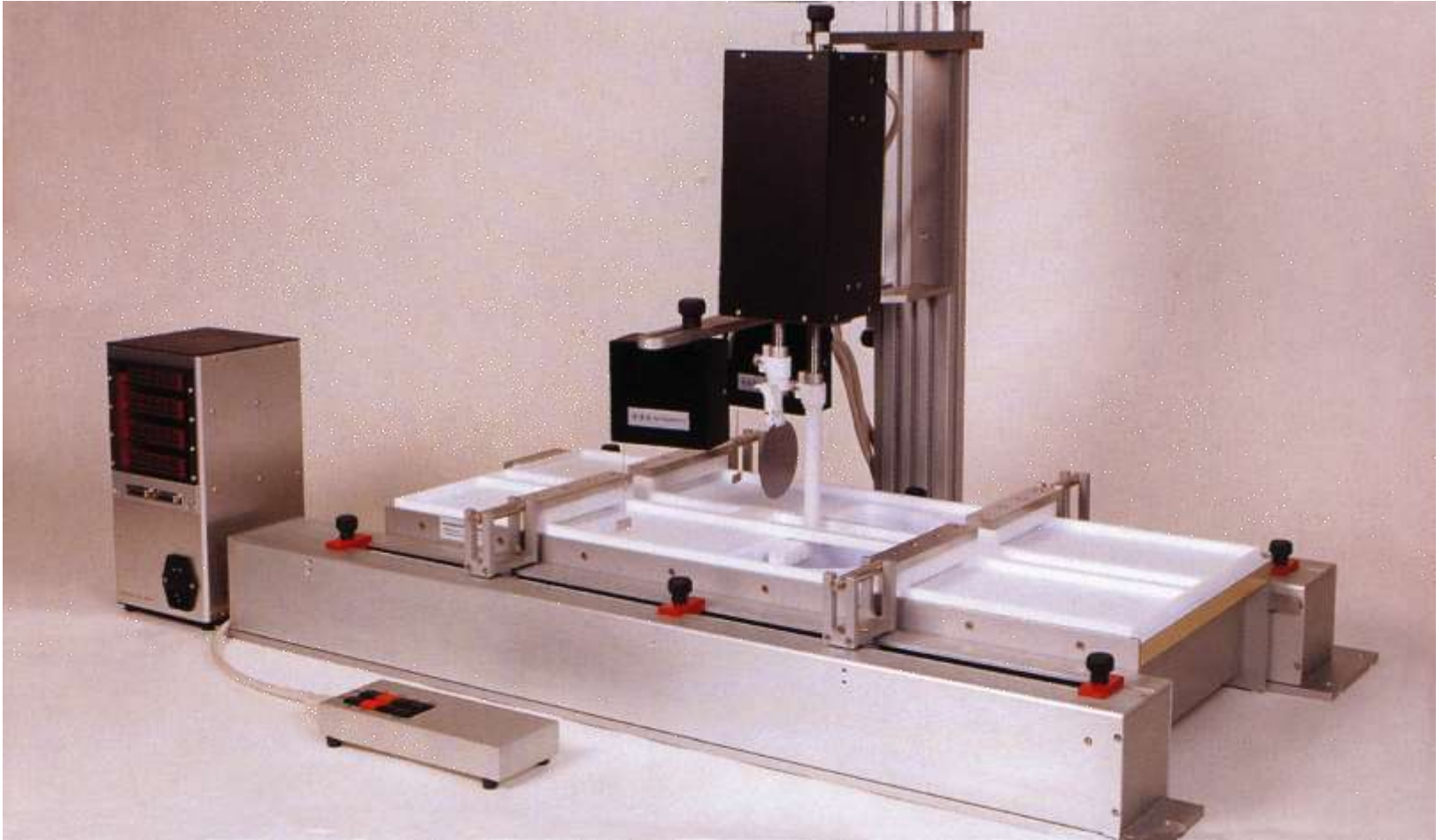
Self-Assembly

- Static assembly
- Dynamic assembly
 - $RT = 8.314 \text{ J/mol} \times 300 = 2.4 \text{ kJ/mol}$
- Driving forces
 - Chemisorption
 - Surface effect
 - Hydrophobic-hydrophilic
 - Intermolecular forces
 - Capillary force

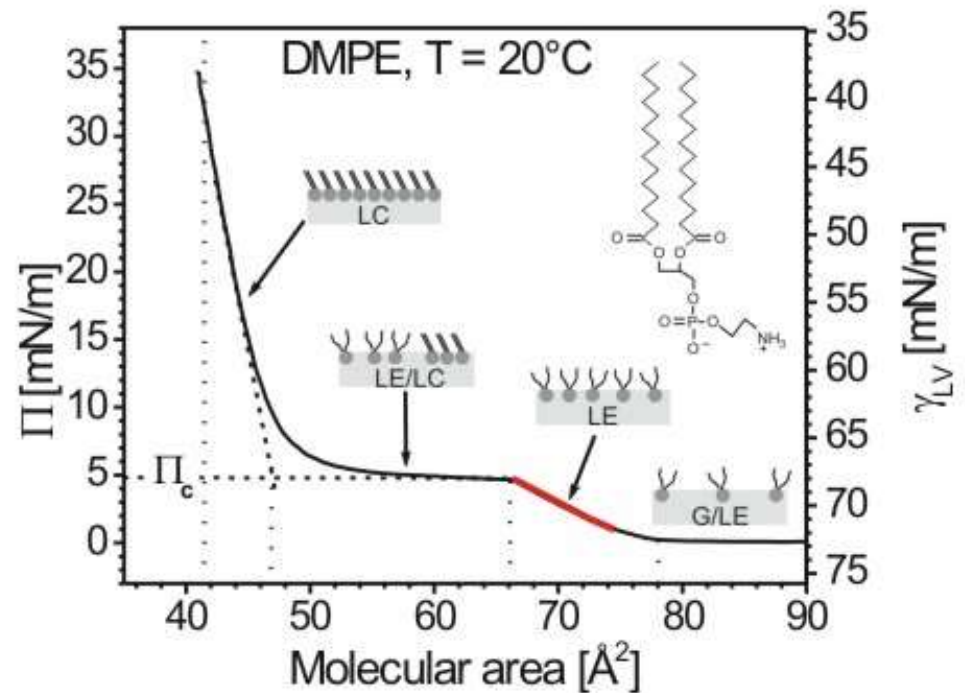
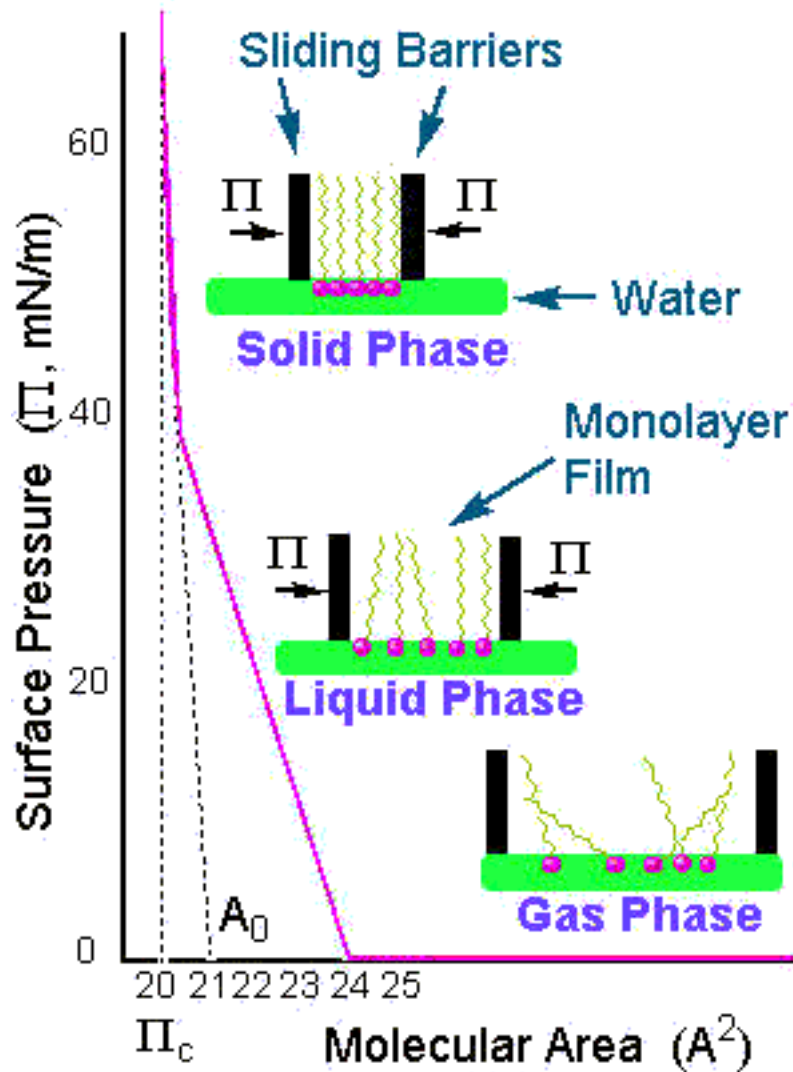
Langmuir-Blodgett Films



Langmuir-Blodgett Films

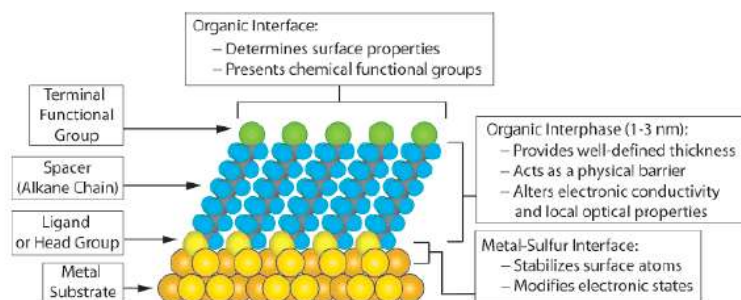


Isotherm



Self-Assemble Monolayer (SAM)

Chem. Rev. 2005, 105, 1103–1169



S-Au 25-30 Kcal/mole
Si-O 190 kcal/mole

Ligand	Substrates	Morphology of Substrate		Ligand	Substrates	Morphology of Substrate	
		Thin Films or Bulk Material	Nanoparticles or Other Nanostructures			Thin Films or Bulk Material	Nanoparticles or Other Nanostructures
ROH	Fe ₃ O ₄	36	35	RSSR'	Ag	89	90
	Si-H	37			Au	20	90-92
	Si				CdS		61
RCOO-RCOOH	α -Al ₂ O ₃	38,39			Pd	30	
	Fe ₃ O ₄		40		Au	93	
	Ni		41,42				
RCOO-OOCR	Ti/TiO ₂	43		RCSSH	Au	94	
	Si(111)H	44			CdSe		95
Ene-diol	Fe ₃ O ₄		45	RS ₂ O ₂ Na ⁺	Au	96	
					Cu	97	98
RNH ₂	Fe ₃	46		RSeH	Ag	99	
	Mica	47			Au	100,101	
	Stainless Steel 316L	48			CdS		60
	YBa ₂ Cu ₃ O _{7-δ}	49			CdSe		102
	CdSe		50	RSeSeR'	Au	103	
RCuN	Ag	51					
	Au			R ₃ P	Au		103
R-NehN'(BF ₄)	GaAs(100)	52			FeS ₂		104
	Pd	52			CdS		104
	Si(111)H	52			CdSe		104
					CdTe		104
RSH	Ag	56	53,54	R ₃ P-O	Cu		105,106
	Ag ₂ Ni ₁₀	55			CdS		104
	AgS		56		CdSe		104
	Au	26	57		CdTe		104
	AuAg		58	RPO ₃ ²⁻ /RPO(OH) ₂	Al	107	
	AuCu		58		Al-OH	108	
	Au ₂ Pd ₁₈		58		Cu ₂ (PO ₃) ₂ (OH) ₂	109	
	CdTe		59		GaAs	110	
	CdSe		60		GaN	110	
	CdS		61,62		Indium tin oxide	111	
	Cu	26	58	RPO ₃ ²⁻	(ITO)		
	FePt		63-66		Mica	112	
	GaAs	67			TiO ₂	113,114	
	Ge	68			ZnO	114,115	
	Hg	69,71			CdSe		116-118
	HgTe		72		CdTe		118,119
	InP	73		RNaC	Al ₂ O ₃	120	
	Ir		74		Nb ₂ O ₅	120	
	Ni	75			Ta ₂ O ₅	121	
	PbS		76-78		TiO ₂	120,122	
	Pd	30	74,79				
	PdAg		58	RHC-CH ₂	Pt	123	124
	Pt	32	80		Si	37	
	Ru		81		Si(111)H	125	
	Stainless Steel 316L	48		RSDX ₂ X = H, Cl, OCH ₂ CH ₃	HfO ₂	126	
	YBa ₂ Cu ₃ O _{7-δ}	82			ITO	127	
	Zn	83			PhO	128	
	ZnSe	84			TiO ₂	113,126,129	
	ZnS		85		ZnO	126,129	
RSAc	Au	86					
	Au		87				
	Au						
	Au	88					

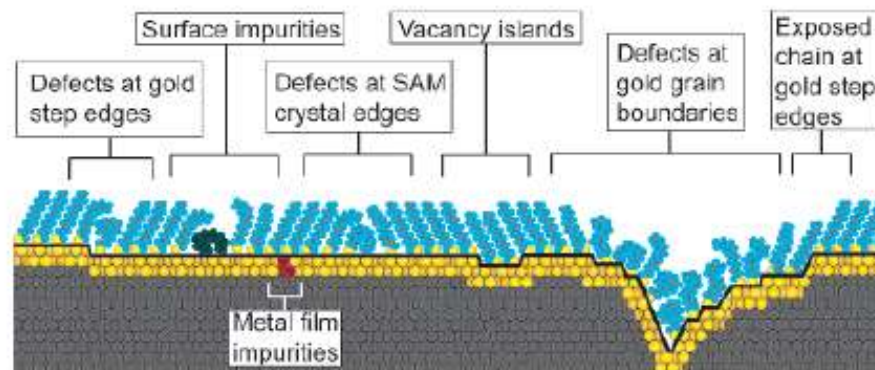
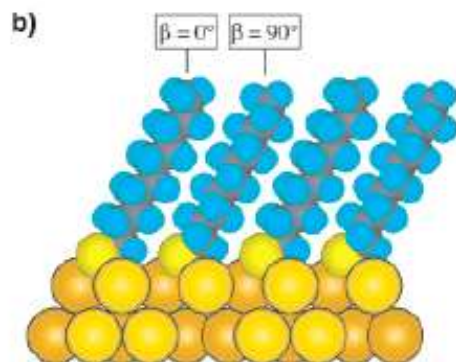
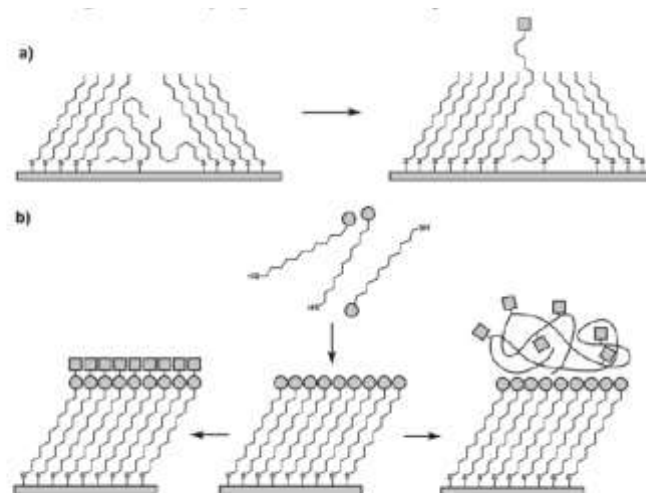
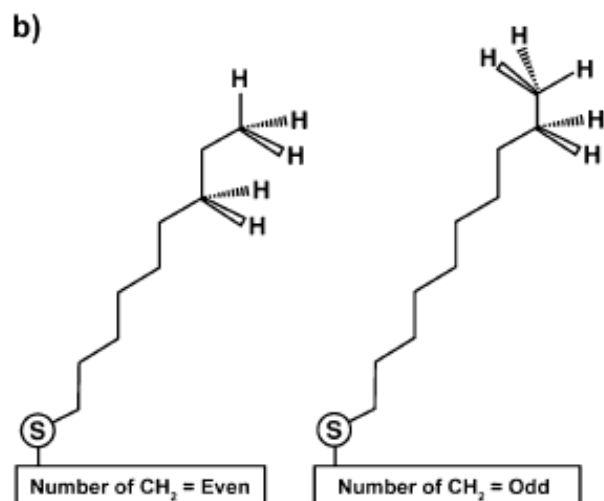


Figure 7. Schematic illustration of some of the intrinsic and extrinsic defects found in SAMs formed on polycrystalline substrates. The dark line at the metal–sulfur interface is a visual guide for the reader and indicates the changing topography of the substrate itself.



^a (a) Insertion of a functional adsorbate at a defect site in a preformed SAM. (b) Transformation of a SAM with exposed functional groups (circles) by either chemical reaction or adsorption of another material.

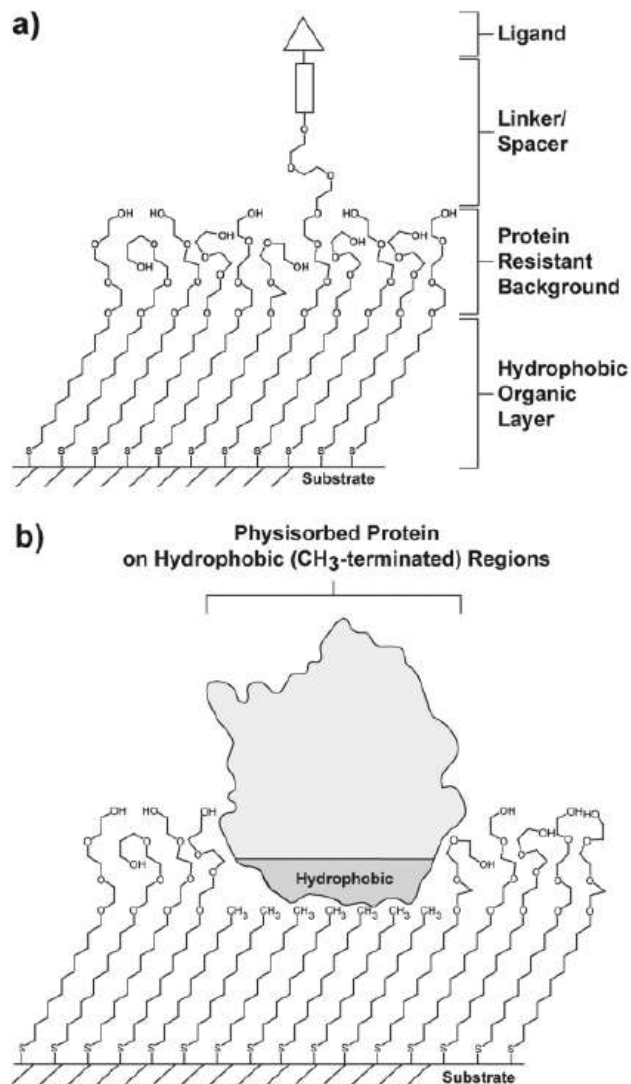


Figure 21. Schematic illustrations of (a) a mixed SAM and (b) a patterned SAM. Both types are used for applications in biology and biochemistry.

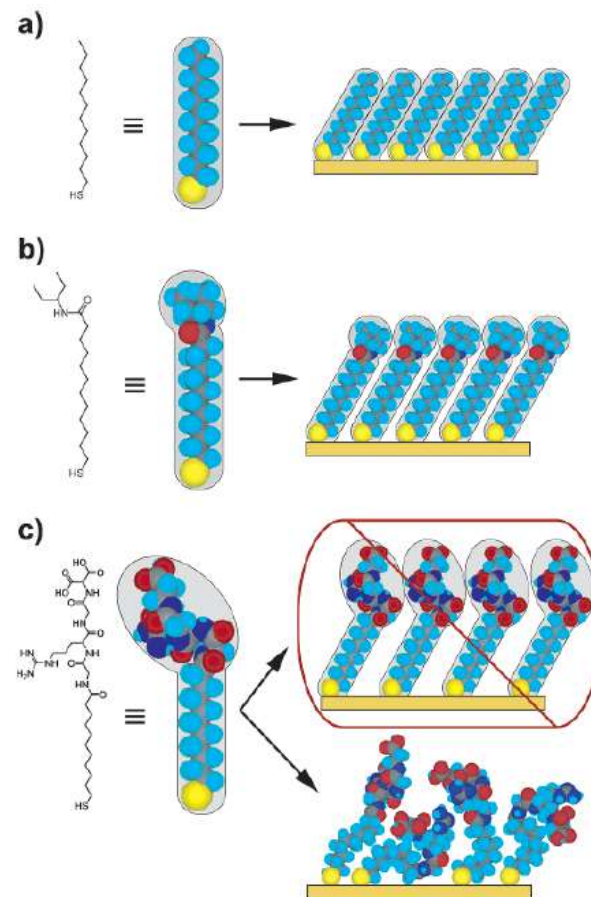


Figure 22. Schematic diagram illustrating the effects that large terminal groups have on the packing density and organization of SAMs. (a) Small terminal groups such as --CH_3 , --CN , etc., do not distort the secondary organization of the organic layer and have no effect on the sulfur arrangement. (b) Slightly larger groups (like the branched amide shown here) begin to distort the organization of the organic layer, but the strongly favorable energetics of metal–sulfur binding drive a highly dense arrangement of adsorbates. (c) Large terminal groups (peptides, proteins, antibodies) sterically are unable to adopt a secondary organization similar to that for alkanethiols with small terminal groups. The resulting structures probably are more disordered and less dense than those formed with the types of molecules in a and b.

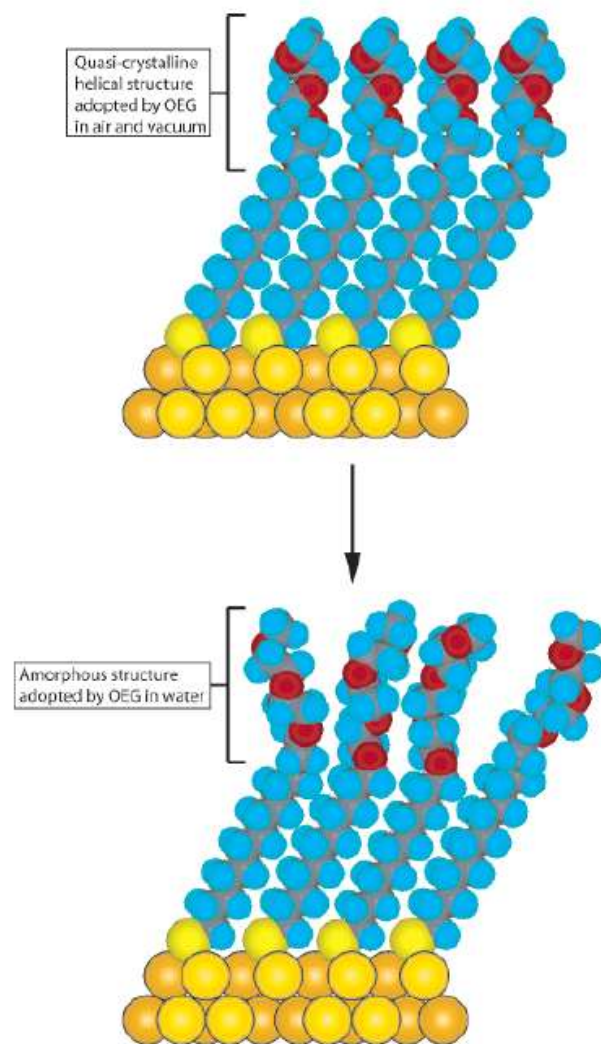
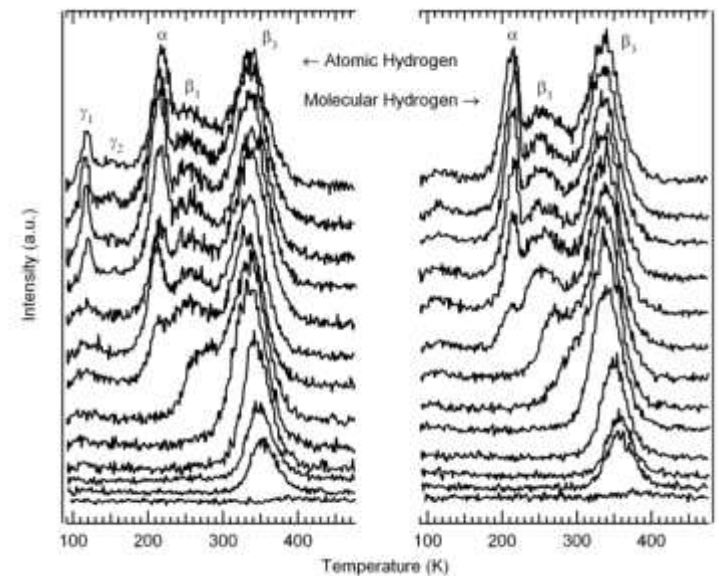


Figure 23. Schematic illustration of the order–disorder transition evidenced by SAMs of alkanethiolates terminated with triethylene glycol. The EG₃ group loses conformational ordering upon solvation in water.

Temperature Programmed Desorption



Self-Assembly

- Substrates
- Interstitial adhesion layer
- Noble metal layer
- Organo-sulfur