CARBOHYDRATES

Monosaccharides: cannot be hydrolyzed into simpler units, has C=O (carbonyl group)

→ Water soluble: relatively small, multiple -OH for H-bonding

→ Aldose (C=O at end) vs Ketose (C=O at middle)

→ Ring form vs Linear Chains (Cyclic ring = common, stable)

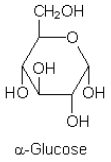
Disaccharides

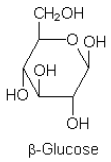
Glucose + Lactose = Galactose

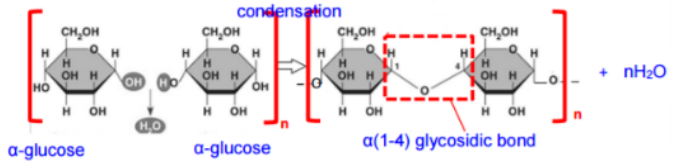
Glucose + Glucose = Maltose

Glucose + Fructose = Sucrose

-Formation of **glycosidic bond** through **dehydration synthesis/condensation rxn**







Polysaccharides:

Polymerisation = <u>condensation of numerous monosaccharides</u>

→ Folded: Compact & ideal for storage

→ Large & insoluble: does not affect φ of cell

→ Structural: Cellulose, Chitin, Pectin

→ Storage: Starch/Glycogen

Starch:

Structure: Amylose helices entangled w/ branched amylopectin

→ compact helical arrangement = more glucose per unit

→ branched arrangement = more hydrolysis sites

→ large structural molecule = relatively insoluble

∴ efficient hydrolysis + compact storage + insolubility

Cellulose:

→ Inversion of alternate β -monomers

→ formation of parallel chains of glucose w/ OH groups projecting from both sides of chains

→ <u>crosslinkage</u> formation between neighbouring parallel chains = microfibril formation

∴ high tensile strength + insolubility

	Cellulose	**Starch**
Monomer	β-glucose monomers	α-glucose monomers
Bond between monomer	Cellulose →β(1-4) glycosidic bond	amylose → α(1-4) glycosidic bond amylopectin → α(1-4) + α(1-6) glycosidic bond
Orientation of monomer	Alternate glucose units are inverted w/ respect to each other	All glucose units in the chain have same orientation
Structure of each molecule	Long, linear unbranched straight chain	amylose → helical/coiled strand or amylopectin → coiled branched molecule
Bonds between molecules	Hydroxyl groups projecting outwards in both directions allow interchain hydrogen bonding	No interchain hydrogen bonding in starch
Branching	No branching	branching

Glycogen

→ More highly branched than starch, shorter chains

→ Long-term storage molecule (less ease of hydrolysis)

	Cellulose	**Starch**
Function	structural support/high tensile strength (cell wall)	compact energy storage molecule
Reason	Many long straight chains interact/ crosslink via hydrogen bonding forming bundles of microfibrils	Long helical strands of α-glucose makes it compact allowing packing of many glucose units per unit volume

Common Mistakes:

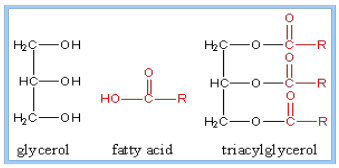
1. Monomer isomers → arise from **same** linear monomer unit

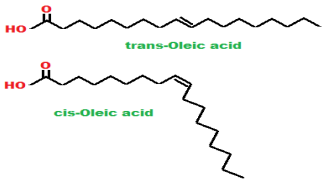
LIPIDS

Lipids → non-polar, insoluble in water vs. <u>soluble in non-polar organic solvents</u>

Triglycerides
→ macromolecules formed by **glycerol** and **fatty acids**

→ **Glycerol**: polar + forms H- bonds w/ water
→ **Fatty Acids**: long non-polar, hydrophobic hydrocarbon chains w/ <u>COOH carboxyl group</u>

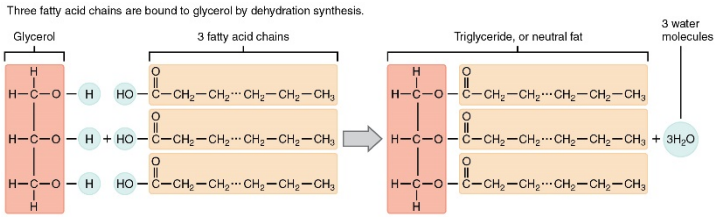




Main Fxn: Energy Storage
→ occupies <u>less volume per unit mass</u> than carbohydrates
→ yield <u>more energy</u> through oxidation of fatty acid chains
→ compact & insoluble in water YET easily hydrolysed
∴ compact, insoluble, more energy than carbohydratres

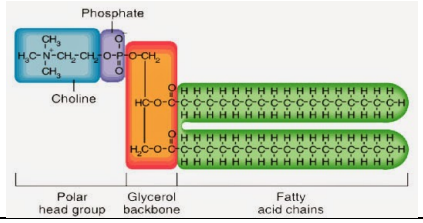
Additional fxn.
→ Source of metabolic water
→ Thermal insulation
→ Buoyancy in marine animals

Saturation: only C-C single bonds
→ C=C forms **kinks** (cis not trans double bonds)
→ longer fatty acid chains + fewer double bonds
= less insoluble + higher melting point (due to increased **hydrophobic interaction**)



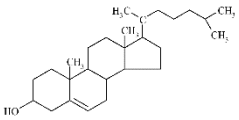
Phospholipids:
2 NPHHC + 1 glycerol backbone – 3rd OH group of glycerol attached to -ve charged phosphate grp.

→ Amphipathic: hydrophilic phosphate head + hydrophobic fatty acid chains



Properties:
→ Formation of **partially permeable membranes w/ phospholipid bilayers**
→ Hydrophobic core shielded from water
→ Hydrophobic tail of phospholipids acts as barrier to polar and charged molecules/ions
→ Hydrophilic phosphate grp. Interacts w/ water

Steroids: carbon skeleton w/ 4 interconnected rings (e.g. cholesterol, vitamins, testosterone**)**



Properties:
→ amphipathic: hydrophobic four-ringed structure w/ hydrophilic OH group

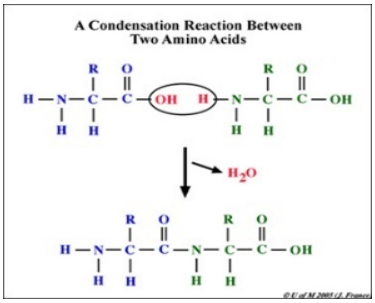
Functions:
→ Align w/ phospholipids in membrane
→ **Regulate membrane fluidity** by preventing excessive fluidity at high temperatures, freezing at low temperatures;

Common Mistakes:
1. Fatty acids: **non-polar**, insoluble and **produces water when oxidized**
2. Emulsion test: white precipitate → fats present

PROTEINS

AA: aa

→ Chiral C atom w/ H,
→ Amine group (-NH_2)
→ Carboxyl group (-COOH)
→ Variable R domain



Dipeptides

→ AA undergo **condensation rxn.** to form polypeptides w/ **peptide bond**
→ OH from COOH + H from NH2 = 1 H2O removed

R groups:
→ neutral AA = electrically neutral R groups
→ non-polar R groups (hydrophobic aa)/polar R groups (hydrophilic aa)
→ electrically-charged aa = acidic aa w/ COOH groups or basic aa w/ OH groups

Zwitterions:
→ ionized aa accept and donate H+ from carboxyl/amine grp.
→ +/- charge on same aa = buffer ability (aa = amphoteric, donate/accept H+)

	Fibrous protein	Globular protein
Shape	Long, straight fibres	Polypeptide chains folded into roughly spherical shape
Presence of OH groups	→ extensive H-bonds formed between residues → large and limited ability to form H-bonds w/ water	→ polar R groups exposed to water molecules (aqueous environment) → soluble: form hydrogen bonds w/water
Constituent AA	Less variety of AA are used	More variety of AA are used
Length of polypeptide	→ polypeptide length and aa sequence may vary between 2 sample →protein is still functional.	→ polypeptide length and aa sequence never vary between 2 sample →protein variation leads to non-function

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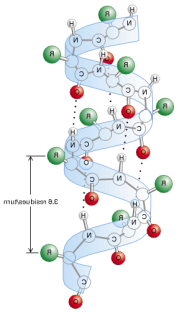
Polypeptides: aa polymers – condensation rxn: peptide bond between aa.
→ N-terminus: end w/ free amino group
C-terminus: end w/ free carboxyl grp

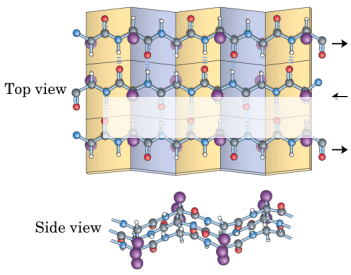
Primary:
→ specific number + sequence of AA in a polypeptide chain linked by peptide bonds

Secondary:
→ α-helix/β-pleated sheet
→ **hydrogen bonding** between -CO and -NH groups of polypeptide backbone



α-helix:
→ single polypeptide wound into a helix
→ **H-bonds** formed between -CO of one AA residue and -NH group of another AA residue (3.6 AA away)
→ R-groups project away from helix

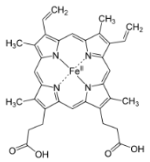
β-pleated sheet:
→ **H-bonds** between CO group of one region and NH group of an adjacent region of a single polypeptide chain,
→ pleated sheet: stable, flexible, high tensile strength



Tertiary:
→ Bonds: hydrophobic interaction, H-bonds, ionic bonds, disulphide bridges-: cysteine w/ sulfhydryl R group
→ Bond formation – between R groups of same polypeptide
→ Extensively folding into specific 3D conformation,

Quaternary:
→ More than 1 polypeptides, same 4 types of interactions/bonds

Haemoglobin:



→ found in RBCs, acts as oxygen-carrier
→ 2 α-globin, 2 β-globin subunits w/ 1 prosthetic haem group each
→ 1 haem group = 1 porphyrin ring + 1 Fe^{2+} ion (binds to 1 O_2 to form oxyhaemaglobin)
→ **water soluble:** hydrophilic amino acid side chains of subunits are on external surface

Cooperative Binding:
→ Subunits move w/ respect to each other
→ formation of 1 oxyhaem increases affinity for other subunits by inducing conformational change in shape of subunits

Sickle Cell:
→ 6th aa changed from glutamic acid (hydrophilic) to valine (hydrophobic)
→ 3D conformation of polypeptide changes → rod-shaped Hb
→ Hb aggregation occurs at low O2 concentrations causes RBC to get sickle shape → higher chance of lysis, capillary damage

Collagen:
→ Tropocollagen: Fibrous structural protein w/ 3 polypeptide chains wound together
→ H-bonds: between AA of adjacent polypeptide chains between NH, CO groups of peptide backbone (high tensile strength)
→ H-bonds: between OH groups of hydroxyproline (insoluble in water)
→ small glycine residues = tight/compact triple helical structure VS. bulky, inflexible proline and hydroxyproline = rigid molecule.
→ covalent cross-links form between lysine residues at the C and N ends of adjacent/parallel tropocollagen molecules; collagen fibrils lie in bundle up to form collagen fibres;

ENZYMES

Enzymes:

1. globular proteins, chemically unaltered reusable catalysts that increase rate of rxn.
2. lowers activation energy by forming ES-complex

Active site:

→ Enzyme 1^0 structure ⇒ substrate-specific 3D conformation with specific region of substrate binding

→ substrate and active site have complementary conformation and charge

1. Catalytic AA ⇒ catalyse conversion between substrate and enzyme's active site
2. Contact AA ⇒ bind reversibly w/ weak H-bonds + ionic bonds

Models of Action:

1. Lock and Key Hypothesis - enzyme is the lock and substrate is the key

→ catalytic R-groups already in position to act on bonds

2. Induced fit hypothesis: substrate induces a change in shape in enzyme

→ catalytic R-groups at active site brought into precise orientation

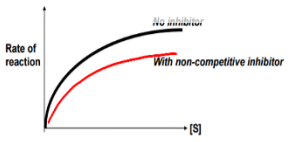
Mode of Action:

→ Enzymes lowers the activation energy barrier

1. **P**roximity ⇒ substrates aligned next to each other in active site for rxn. to occur
2. **O**rientation ⇒ substrate oriented such that its bonds are exposed to attack
3. **S**train ⇒ strains bonds to be broken / distorts the substrate and reduces E_a to achieve transition state
4. Provide a favourable Micro**E**nvironment
5. **D**irect Catalysis ⇒ R-groups of AA residues in active site participate in direct catalysis – e.g. Acid-base catalysis

Competitive Inhibitor: similar charge and shape/ conformation to the substrate

- inhibitor binds to enzyme active site reversibly (w/ weak, non-covalent bonds) and block substrate binding.
- At high [substrate], inhibitor fx. Is negligible since the substrate molecules can effectively out-compete the inhibitor molecules for active sites;



Non-competitive inhibitor: binds to allosteric site (another site on enzyme not active site) either permanently or reversibly (depends on inhibitor)

- Alters shape/conformation of the specific enzyme active site = substrate cannot bind in correct orientation
- Rate of rxn. decreases with ↑ [inhibitor] = cannot be neutralized by ↑ [substrate]

Temperature:

→ Increase in temperature = ↑ KE of enzyme and substrate molecules

→ ↑ frequency of effective collision between substrate and enzyme = more ES complex;

→ ↑ no. of molecules w/ energy to overcome activation energy barrier

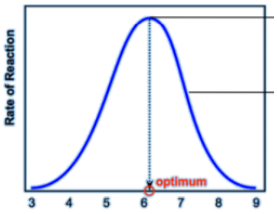
→ Rxn. rate increases with temperature up to the optimum temperature;

Optimal Temperature:

→ maximum no. of effective molecular collisions reached hence max rate of rxn.; =

→ post-optimal thermal agitation breaks H-bonds, ionic bonds and other weak interactions that stabilizes conformation = enzyme denaturation

pH:



→ Optimal pH ⇒ rate of rxn. is at maximum

1. Excess [H+]/[OH-] ions affect ionisation of R groups of AA (COO- -> COOH and excess -OH- = NH3 + becoming –NH2)

→ Disruption of ionic/H-bonds: stabilize specific conformation of active site = denaturation of enzyme

→ pH: change specific charge of R groups of catalytic residues in the active site (affect temporary binding between enzyme and substrate = no enzyme-substrate complex formed)

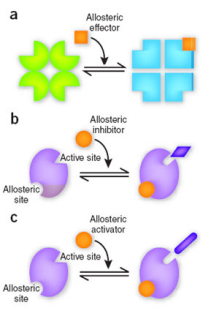
[Substrate]: low conc.: active sites of the enzymes readily available to catalyse rxn. ([substrate] = limiting factor)

- [Substrate] increases = rate of rxn. increases as more active sites occupied by substrates
- At higher [substrate], saturation of active sites = [enzyme] = limiting factor

(Similar for **[enzyme]** – more active sites available)

- K_m (Michaelis constant) = conc. of substrate at ½ V_{max}

Allosteric Regulation: allosteric enzymes regulated by inhibitors/activators



- 2+ subunits – each w/ own active site to bind substrates + allosteric site to bind regulators
- 2 conformational states (oscillation between active/inactive forms = regulator stabilizes respective form)

cooperativity: allosteric enzyme – one subunit binds to substrate, others bind easily to substrate too

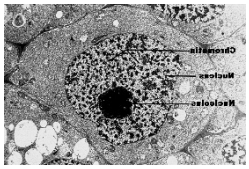
feedback inhibition: end- product inhibition (end-product binds to enzyme early in pathway) = accumulation of end-product = more binding to allosteric site = altered conformation of specific active site = substrate unable to bind = lower rate of rxn.

CELL STRUCTURE

Overview: Eukaryotic cell structure – cell surface membrane, nucleus, cytoplasm, cell wall (depends)

1) Nucleus: largest organelle - 5µm diameter, spherical

- surrounded by **double membrane (nuclear envelope)** = 2 phospholipid bilayers w/ numerous nuclear pores (regulate passage of substances into/out of nucleus)



- contains **chromatin/ chromosomes**: hereditary material (DNA) – thin elongated chromatin threads (not in mitosis) = DNA complex + histone proteins VS. **condensed** thicker, shorter chromosomes (before mitosis)
- **chromatin:** most = loosely coiled, diffuse **euchromatin** (unstained) vs. some = tightly coiled, dark stained heterochromatin
- <u>fxn.: contains hereditary material + regulates protein synthesis (thus controls entire cell)</u>

2) Nucleolus: one or more in 1 nucleus = contains DNA, rRNA + proteins

- <u>fxn.: site of **ribosomal RNA synthesis** (to form ribosomes) + **assembly site of rRNA + ribosomal proteins into subunits**</u>

3) Ribosomes = large subunit + small subunit (each subunit = rRNA + proteins)

- ribosomal subunits assembled in nucleolus -> exported out of nucleus into cytoplasm
- ribosomes = freely floating in cytosol (free ribosomes)/ attached to outer surface of **rough endoplasmic reticulum** (bound ribosomes)

(70S ribosome – prokaryotes, chloroplasts, mitochondria vs 80S ribosome – eukaryotes)

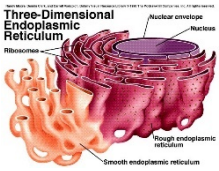
- <u>fxn.: site of **protein synthesis –** translation of mRNA</u>

4) Cell Surface Membrane* - refer to CSM notes

5) Nuclear Envelope – double membrane perforated by nuclear pores (formed by a protein pore complex)

<u>fxn.: allow regulating passage of substance</u>

6) Endoplasmic Reticulum: network of membranous tubules (cisternae) w/ single membrane separating cytosol from cisternal space



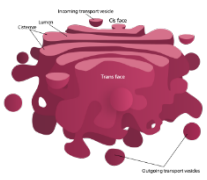
- **Rough ER:** continuous w/ outer membrane of nuclear envelope – flattened, interconnected cisternae + **bound ribosomes** that stud outer surface of membrane

-<u>Translation of mRNA to protein/ protein synthesis by bound ribosomes + glycosylation/modification and transportation of proteins</u>

-**Smooth ER:** Tubular membrane bound sacs called cisternae without bound ribosomes

<u>- Lipid and steroid synthesis + carbohydrate synthesis + detoxification;</u>

7) Golgi Apparatus: single membrane-bound w/ saucer-like membranous cisternae w/ Golgi vesicles



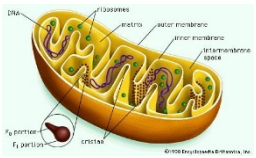
– convex (cis/flat face): vesicles from ER fuse onto GA vs. concave (trans/curved face): vesicles pinch off from GA

- <u>fxn.: glycosylation of proteins/lipids, modification of glycoprotein and glycolipids, formation of lysosomes, production of polysaccharides, sorts and targets materials for secretion</u>

8) Lysosomes: single membrane-bound w/ hydrolytic enzymes – optimal pH (acidic)

- storage vesicle to keep enzymes apart & prevent destruction of the rest of the cell
- **Digestion of materials**: digestive enzymes mix w/ contents of vesicles = useful products released into cytosol
- **Autolysis/self-rupture:** self-destruction of cell by release of lysosomal contents within cell
- **Autophagy:** destruction of worn out organelles, digested products returned to cytosol for re-use

9) Mitochondrion: double membrane-bound: outer membrane = **smooth,** inner membrane – highly infolded, numerous **cristae**

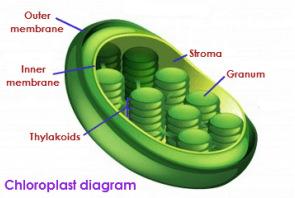


- intermembrane space: between the outer and inner membrane vs. **matrix:** inside inner membrane – **70S ribosomes, circular DNA**

- cristae: large surface area – enzyme attachment **fxn. OP**

fxn.: site of **cellular respiration – generate ATP** vs. **Krebs cycle – matrix** vs. oxidative phosphorylation – cristae

10) Chloroplast: lens-shaped (2µm - 5µm) + double membrane w/ intermembrane space + interconnected sacs = thylakoids (inside chloroplast)

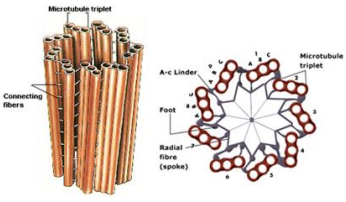


- stacks of thylakoids = **grana** (chrlorophyll + enzymes on thylakoid membrane)
- fluid outside thylakoid = stroma (w/ circular DNA, ribosomes, enzymes, starch grains.
- <u>fxn.: site of photosynthesis</u>

11) Microtubules – hollow rods (25nm diameter) = **tubulin** wall + each tubulin – dimer w/ 2 subunits

- help maintain cell shape (cytoskeleton) / intracellular transport/ chromosome movement in ell division/ strucutrual component of centrioles, cilia and flagella

12) Centrioles – 9 triplets of microtubules (rod-like structure) x2

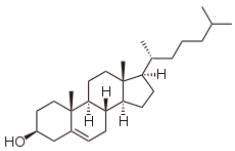


- found in pairs, perpendicular to each other
- organize spindle fibres during cell division
- anchorage for cilia and flagella

CELL MEMBRANE

Phospholipid Bilayer: Around 7.5nm/10^{-9}m thick – present in both prokaryotic/eukaryotic cell.
Phospholipid: A phospholipid = a glycerol molecule + phosphate (PO4-) group = hydrophilic region, 2 hydrocarbon tails / chains = hydrophobic region.
- form **bilayers** in aqueous medium (or micelle)
- held together by **weak hydrophobic interactions/van der Waals forces +** contribute to membrane fluidity

Cholesterol: four ring structure, hydrophobic yet **amphipathic –** hydrophilic OH group (fxn.: regulates membrane fluidity)

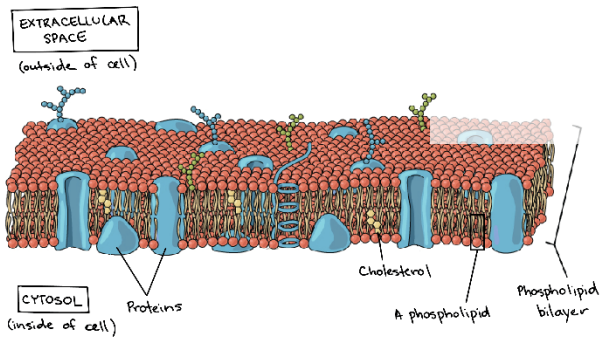


- prevents membrane from being overly fluid at warmer temperatures (cholesterol's rigidity restricts phospholipids' lateral movement)
- prevents membrane from being overly firm at lower temperatures (cholesterol prevents the close packing of phospholipids and hence prevents its solidification/ crystallization)

Proteins: determine membrane's specific functions
Integral/intrinsic protein: amphipathic – hydrophilic polar/charged R groups + non-polar R groups
- hydrophobic regions lie in hydrophobic core of bilayer vs hydrophilic region (exposed to aqueous medium)
- transmembrane protein (spans entire membrane) vs unilateral protein (halfway across membrane)

Peripheral/extrinsic protein: not embedded, loosely attached to membrane surface/ integral protein (weak ionic/ H-bonds)
- attached to fibres of **ECM** (exterior of membrane) vs. held by cytoskeleton (cytoplasmic side of membrane)

Carbohydrates: glycolipids and glycoproteins = carbohydrates bound to proteins
- carbohydrates project out of cell into **ECM**
- *fxn.: markers for cell-cell recognition (e.g. distinguish cells as 'self'/'non-self' = immune system)*
- *cell-cell recognition = cell adhesion = cells attached to one another to form tissues, organs;*
- *receptor for pathogens to bind to host cells and enter cell*
- *found in myelin sheath = electrical insulation of nerve cell*



Fluid Mosaic Model: fluid state = lateral movement of Plipids, proteins within layer (weak Hphobic interactions) + mosaic = random arrangement of proteins embedded amongst Plipids

Membrane Function:

1) Regulate movement of substances across membrane
- selectively permeable membrane: hydrophobic core = ions, polar/large molecules need transport proteins
= non-polar molecules diffuse through **hydrophobic core**

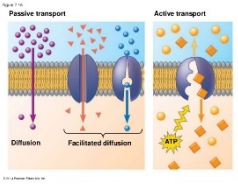
2) Compartmentalization
- formation of unique environments for specialized activities such as enzyme reactions in lysosomes
- establishment of proton gradients within specialized organelles such as mitochondria and chloroplasts (ETC)
- storage of food (e.g. starch in amyloplasts)

3) Protein Localization
- localization of proteins of related function together so that sequential biochemical processes are facilitated
- (e.g. enzymes and proteins are grouped together into PS II and I on chloroplast thylakoid membrane)

4) Increased Surface Area
- Increase surface area for chemical reactions such as the highly folded cristae of mitochondria increase surface area for insertion of electron transport carriers and ATP synthase complexes for oxidative phosphorylation to take place

Transport Across Membrane

1) Simple Diffusion: non-polar molecules + water – direct movement down conc. gradient w/o ATP + proteins
- relies on conc. gradient only = ends in dynamic equilibrium
- *rate factors: molecular size (smaller particle = faster diffusion), solubility in lipid bilayer (non-polar particles = faster diffusion), concentration gradient (steeper gradient = faster diffusion, kinetic energy (higher temperature = faster diffusion), surface area of membrane (more SA = faster diffusion), distance (shorter distance = faster diffusion)*

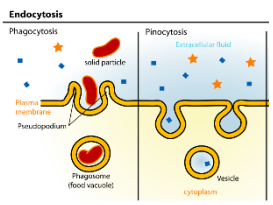


2) Facilitated Diffusion: simple diffusion (no ATP, conc. gradient, passive) BUT w/ transport proteins
- Channel Protein: transmembrane, w/ hydrophilic pore = ions/charged molecules pass through membrane (may be gated)
- Carrier Protein: transmembrane = molecule binds to protein, change channel shape, allow molecule to pass (e.g. glucose)

3) Osmosis: movement of water mol. From region of higher WP to lower WP **through selectively permeable membrane** (simple diffusion – transient pore/facilitate diff – aquaporin)

4) Active Transport:
- Needed when polar, charged molecules or ions are to be transported (against a concentration gradient across the membrane requiring ATP) + needs carrier proteins / pumps and is also solute-specific

5) Bulk Transport: active transport w/o protein channels
- Endocytosis: infolding/extension of CSM = vesicle (carrier)
- Phagocytosis: pseudopodia formation = engulfing **solid** particle = formation of vesicle
- Pinocytosis: invagination of membrane -> **liquids taken up**



- Exocytosis:
macromolecules in vesicles = vesicle fuses w/ membrane = contents released into cytosol