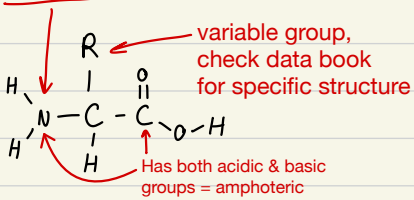
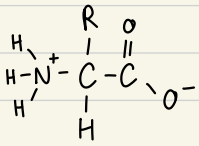
PROTEINS

2-amino acids- general structure



Zwitterion



- 2 functional groups ionised
- No overall charge
- Zwitterions of ionisable amino acids except arginine have unionised R-groups

R-group classifications (highlighted atom = site of (de)protonation of ionisable R-groups)

alanine	Ala	non-polar
arginine Zwitterion has ionised R-group & -COOH, not ionised -NH₂ & -COOH	Arg	More basic than -NH₂ basic
asparagine	Asn	polar
aspartic acid aspartate when deprotonated	Asp	acidic
cysteine	Cys	polar (acidic when pH > 8)
glutamic acid glutamate when deprotonated	Glu	acidic
glutamine	Gln	polar
glycine	Gly	non-polar
histidine	His	basic + aromatic (only weakly basic at pH = 7)
isoleucine	Ile	non-polar
leucine	Leu	non-polar
lysine	Lys	basic
methionine	Met	non-polar
phenylalanine	Phe	non-polar + aromatic
proline	Pro	non-polar
serine	Ser	polar
threonine	Thr	polar
tryptophan	Trp	non-polar + aromatic
tyrosine	Tyr	polar (acidic when pH > 10.5)
valine	Val	non-polar

The “acidic” & “basic” classifications describe R-group properties assuming that surrounding pH = 7 (i.e. physiological pH).

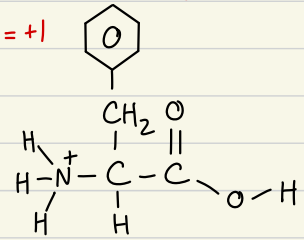
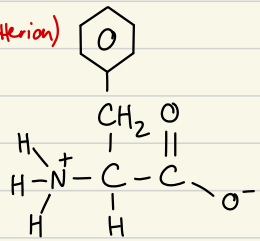
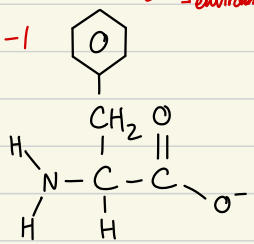
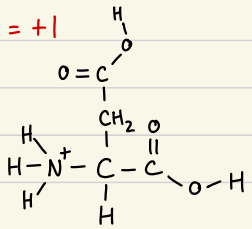
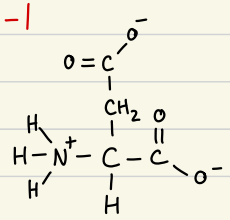
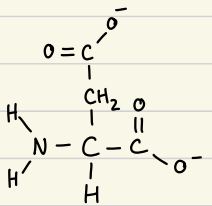
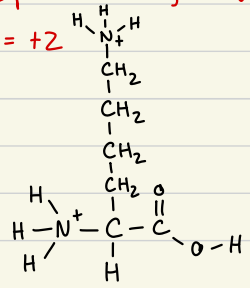
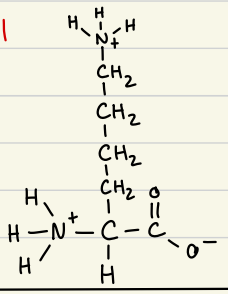
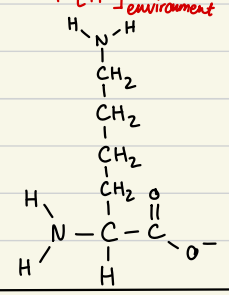
Since pI and pKa aren’t taught in VCE, you’re unlikely to be asked to draw the structures of cysteine and tyrosine at high pH, nor histidine and arginine at physiological pH.

PROTEINS

R-group classification rules

1. Hydrocarbon chains = non-polar
2. Has -COOH in R-group = acidic aka negatively charged
3. Has N in R-group (except tryptophan and amino acids with 1° amide R-groups) = basic aka positively charged
4. Has benzene rings = aromatic
5. All acidic and basic amino acids are also polar

Ionisation by pH

	Low pH (~0)	Physiological pH (~7)	High pH (~14)
Uncharged R-group e.g. phenylalanine	$-NH_2$ protonated to $-NH_3^+$ to ↓ $[H^+]_{environment}$ Net charge = +1 	$-COOH$ deprotonated Net charge = 0 (zwitterion) 	$-NH_3^+$ deprotonated to ↑ $[H^+]_{environment}$ Net charge = −1 
Acidic R-group e.g. aspartic acid	$-NH_2$ protonated to $-NH_3^+$ to ↓ $[H^+]_{environment}$ Net charge = +1 	Both $-COOH$ deprotonated Net charge = −1 	$-NH_3^+$ deprotonated to ↑ $[H^+]_{environment}$ Net charge = −2 
Basic R-group e.g. lysine	Both $-NH_2$ protonated to $-NH_3^+$ to ↓ $[H^+]_{environment}$ Net charge = +2 	$-COOH$ deprotonated Net charge = +1 	Both $-NH_3^+$ deprotonated to ↑ $[H^+]_{environment}$ 

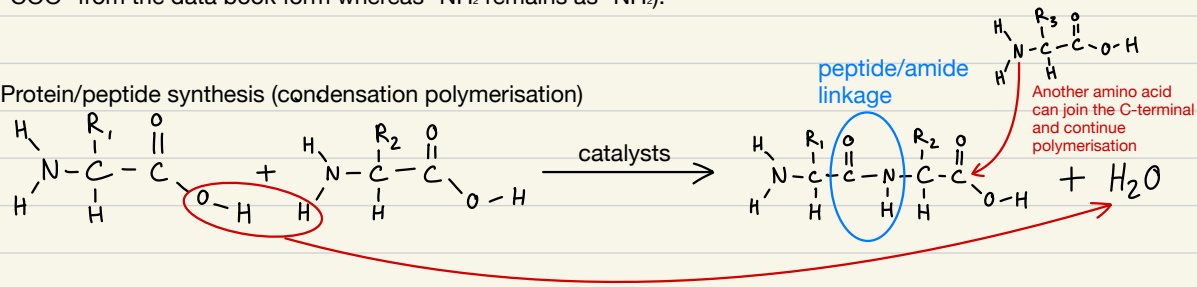
PROTEINS

Memorisation Hack: Use Le Chat's Rule

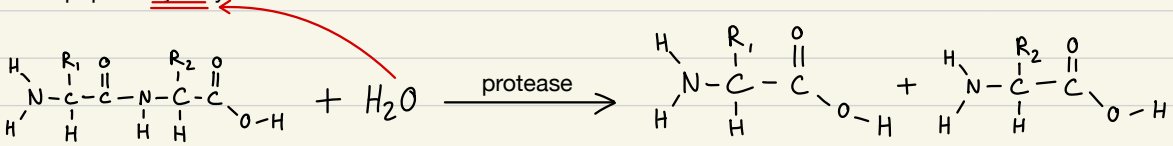
Low pH: To partially oppose the excess of H+ in the environment, the amino acid will act as a base such that all its ionisable functional groups will uptake H+ and be in the protonated state (e.g. -COOH will remain -COOH and $-NH_2$ changes to $-NH_3+$ from the data book form).

High pH: To partially oppose the deficiency of H+ in the environment, the amino acid will act as an acid such that all its ionisable functional groups will donate H+ and be in the deprotonated state (e.g. -COOH will become -COO- from the data book form whereas $-NH_2$ remains as $-NH_2$).

Protein/peptide synthesis (condensation polymerisation)



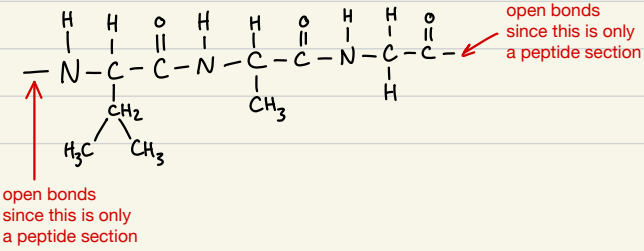
Protein/peptide hydrolysis



Random bits to memorise

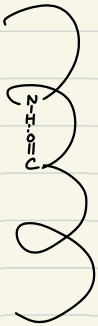
- Essential amino acids can't be produced by the human body and must be supplied in the diet (no need to memorise which ones are essential).
- By convention peptide sequences (e.g. -Val-Ala-Gly-) are written from N-terminal to C-terminal.

The sequence would be drawn as:

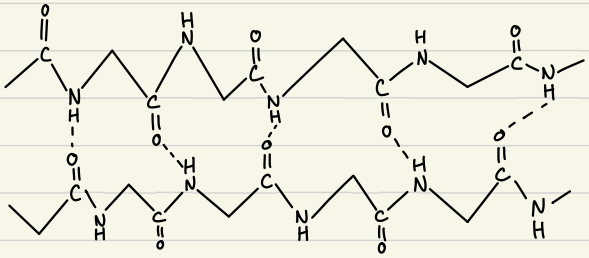


PROTEINS

- 1° structure: Amino acid sequence, held together by peptide/amide linkages.
- 2° structure: H-bonding between C=O and N-H of non-adjacent amino acid residues, forming α-helices and β-pleated sheets. H-bonding in R-groups **aren't** involved in 2° structure.

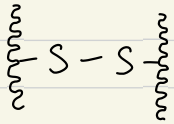


α-helix

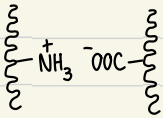


β-pleated sheets

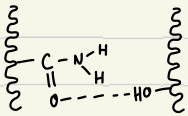
- 3° structure: Covalent bonds, H-bonds, ionic interactions and dispersion forces between R-groups of non-adjacent amino acid residues that give the protein its 3D shape.



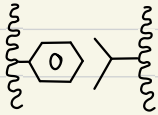
disulfide bridge (covalent bond b/w cysteine residues)



ionic interaction



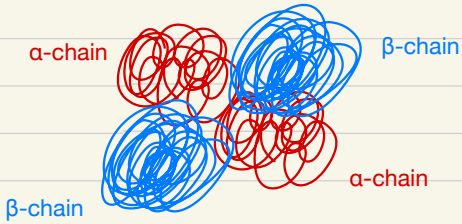
H-bonds



Dispersion forces

aka hydrophobic interactions

- 4° structure: >1 polypeptide chains with 3° structure bound together to form a functional protein.

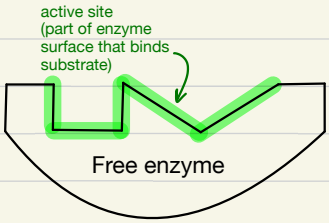


Hemoglobin

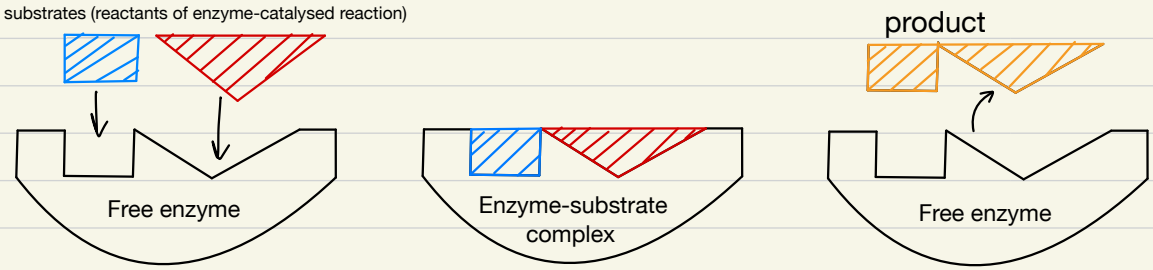
PROTEINS: Enzymes

- Enzymes are catalytic proteins, they speed up reactions by reducing the quantity of required activation energy.

Their names end in -ase e.g. lipase, amylase, protease



LOCK & KEY MODEL



Substrates bind active site which has a complimentary shape to them.

Enzyme-substrate complex formed, corresponding to the transition state on energy profile diagrams.

Product dissociates when reaction is complete. The enzyme was not consumed, meaning that it's catalytic.

- Induced fit model is identical to lock & key except the active site in induced fit only needs to be similar in shape to the substrate (not exactly complimentary as in L & K).
- Under the L & K model, the enzyme can only catalyse the reaction for one specific optical isomer of the substrate as the other optical isomers don't have a complimentary shape/spatial arrangement of atoms to the enzyme's active site.

PROTEINS: Enzymes

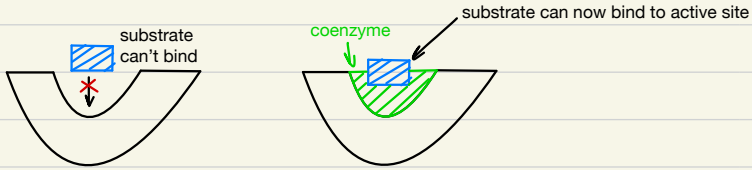
Denaturation marking scheme

2° and 3° structure disruption (must mention H-bonds and specific types of bonding in 3° structure): +1

Active site changes shape: +1

Enzyme is no longer able to bind its substrate and hence loses its catalytic abilities: +1

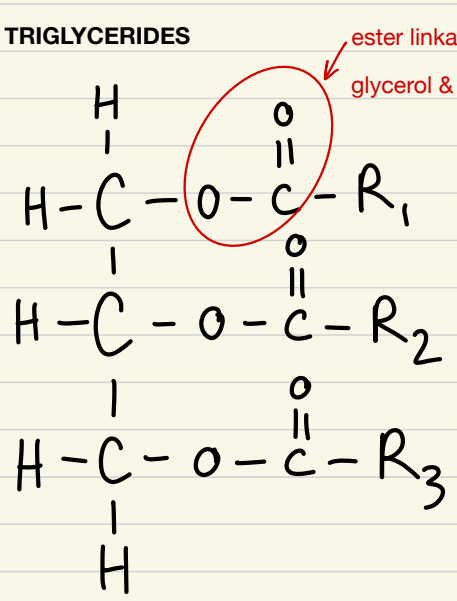
- Denaturation by pH: disrupts H-bonds (2° and 3° structures) and ionises R-groups (disrupts 3° structure by preventing the correct formation of ionic interactions) ∴ Enzymes are very pH-sensitive.
- Denaturation by high temperature: High kinetic energy breaks H-bonds (2° and 3° structures disrupted) and specific covalent bonds e.g. disulfide bonds involved in 3° structure).
- IMPORTANT: denaturation DOESN'T affect 1° structure. Only hydrolysis does.
- Low temperature = low activity due to a smaller proportion of successful collisions.
- Rate of reaction as measured by increase in [products] per unit time OR decrease in [substrates] per unit time is conventionally used to represent enzyme activity.
- Coenzymes modify the active site shape so that an inactive enzyme can bind to the substrate.



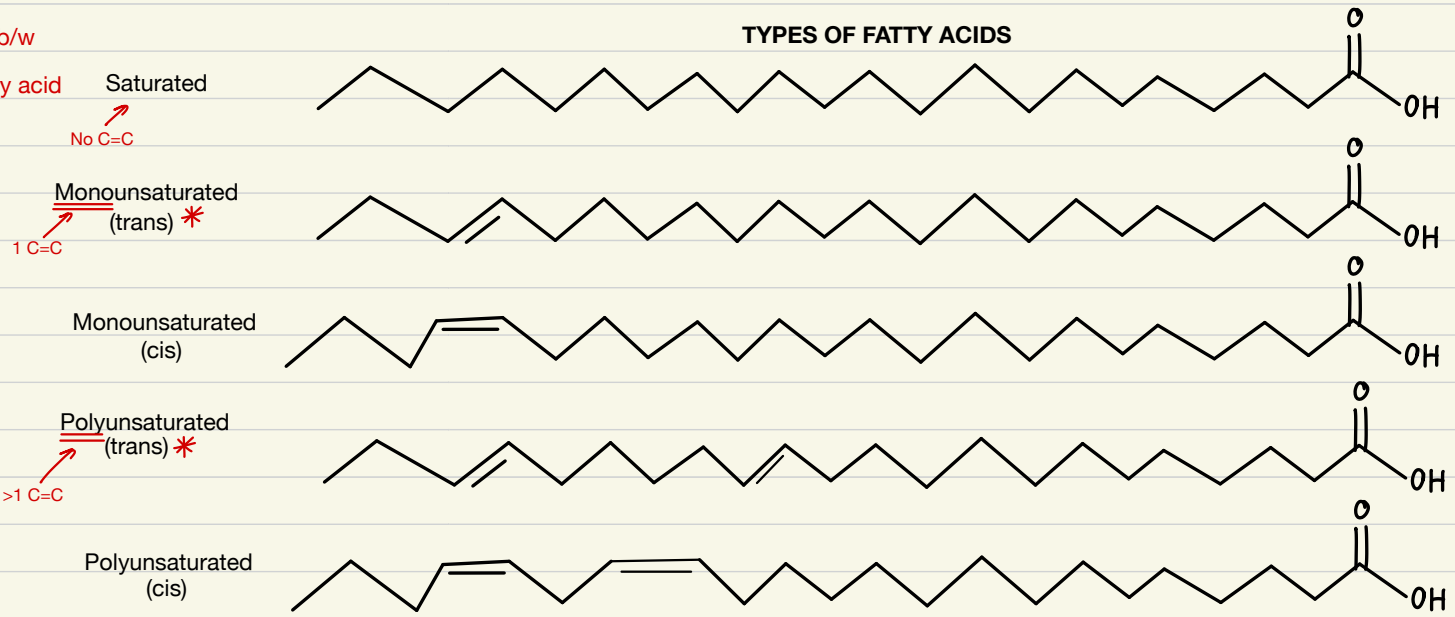
- Many coenzymes are derived from vitamins.
- All coenzymes are cofactors but not all cofactors are coenzymes (e.g. iron in hemoglobin is a cofactor but not a coenzyme).
- Coenzymes can deliver functional groups or e- to an enzyme-catalysed reaction.

LIPIDS/FATS

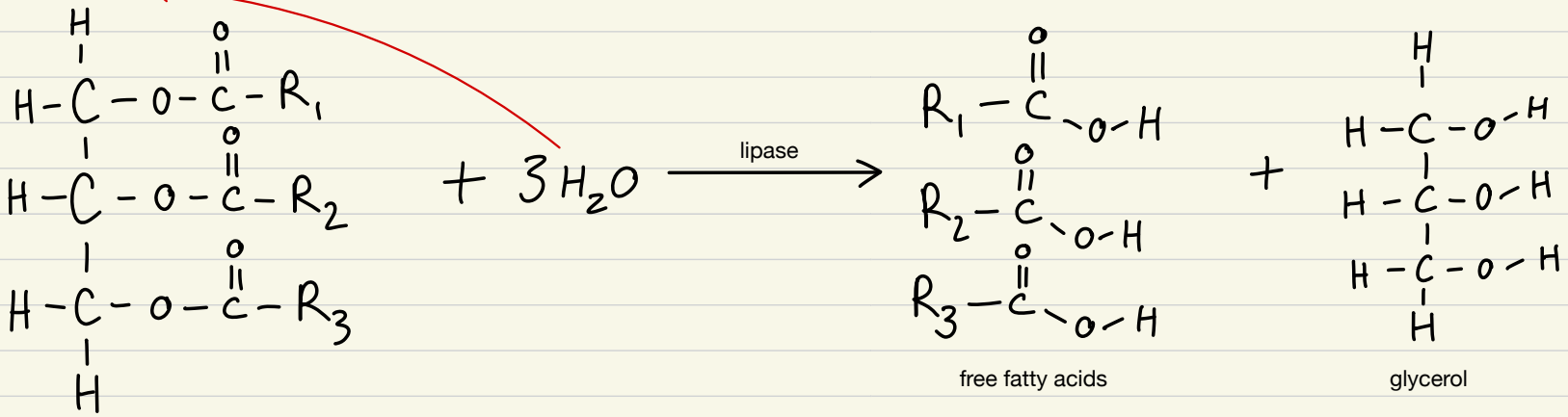
TRIGLYCERIDES



TYPES OF FATTY ACIDS



Triglyceride Hydrolysis (similar to 1st step of biodiesel synthesis)



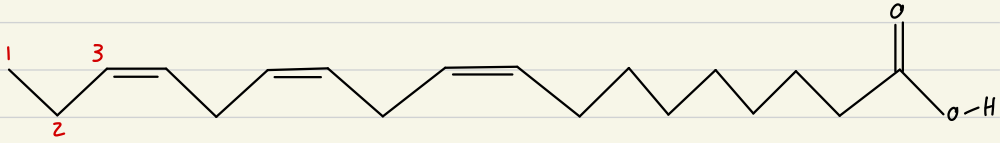
free fatty acids

glycerol

* Trans fats **AREN'T** naturally-occurring and have similar properties to saturated fats.

LIPIDS/FATS

- ω-3 fatty acids have a C=C at the 3rd to last carbon e.g. linolenic acid.



- ω-6 fatty acids have a C=C at the 6th to last carbon e.g. linoleic acid.

Saturation

- Given the formula C_xH_YCOOH, # of C=C = X - 0.5Y + 0.5
- More unsaturated = lower MP and BP since the kinks in the carbon chain prevents unsaturated fatty acid molecules from approaching each other, which reduces the strength of intermolecular forces present. Since saturated fatty acids also have more atoms than unsaturated ones of the same carbon chain length, there are more dispersion forces between saturated fatty acid molecules compared to between molecules of unsaturated fatty acids. Hence saturated fatty acids are usually fats (solid at room temperature) whereas unsaturated ones are usually oils (liquid at room temperature).
- More unsaturated = more reactive since C=C can participate in addition reactions and can be cleaved more easily during the process of oxidative rancidity.

Oxidative rancidity

Initiation (formation of reactive radical species through exposure to oxidising agents or radiation e.g. UV light): 1st lot of infected zombies starting the zombie apocalpyse

Propagation (radicals oxidise other chemicals producing even more radicals): Zombie bite victims turn into zombies themselves

Termination (free radicals react with each other to generate non-radicals): Zombies are cured by biting each other

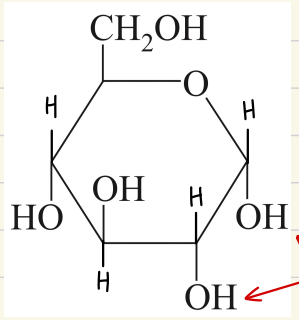
LIPIDS/FATS

- Antioxidants slow oxidative rancidity since they're reductants that are oxidised in preference to the fatty acids to produce free radicals that assist in the termination step. This is similar to galvanising steel with a zinc coating where after preferential oxidation, a zinc oxide layer is formed that protects steel against oxidation/corrosion.
- Essential fatty acids can't be produced by the human body and must be supplied in the diet (all ω-3 and ω-6 fatty acids are essential).

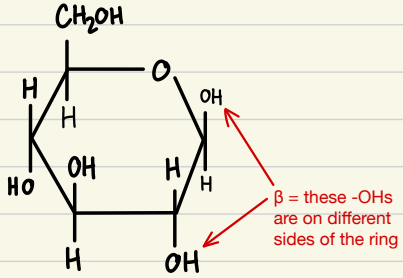
CARBOHYDRATES

STRUCTURES

Monomers (monosaccharides) + Dimers (disaccharides)

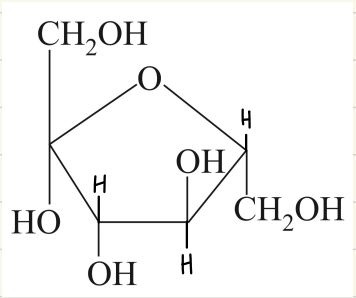


α-glucose

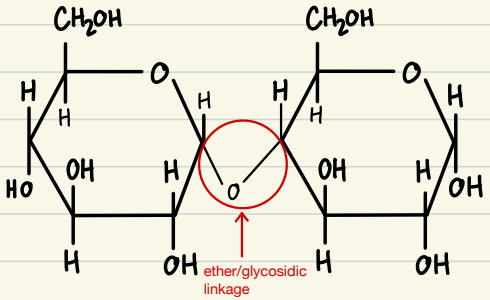


β-glucose

(NOT GIVEN IN DATA BOOK)

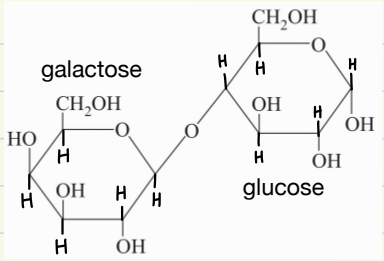


β-fructose

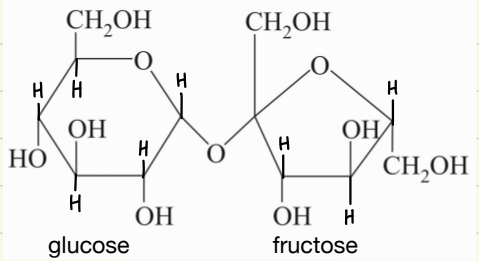


α-Maltose (α-glucose + α-glucose)

(NOT GIVEN IN DATA BOOK)

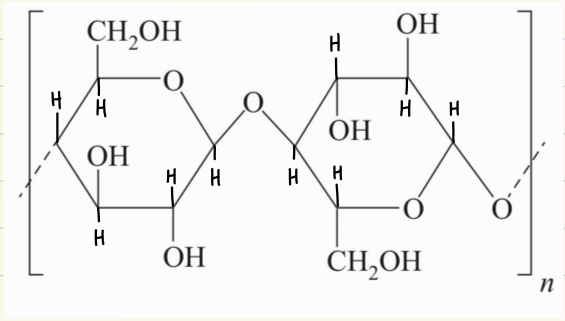


lactose (α-glucose + β-galactose)

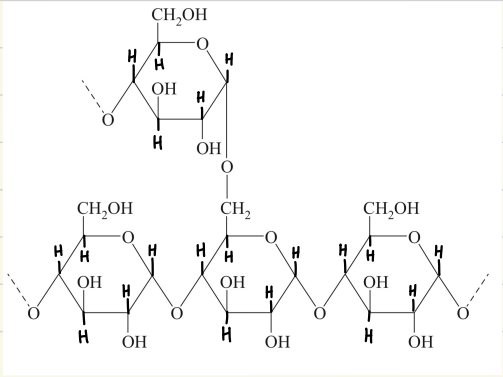


sucrose (α-glucose + β-fructose)

Polymers (polysaccharides)

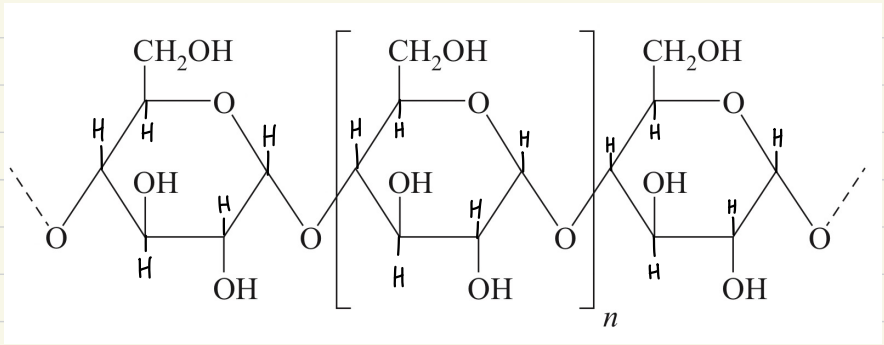


cellulose (β-glucose polymer)



amylopectin (α-glucose polymer)

*glycogen has a similar branched structure to amylopectin



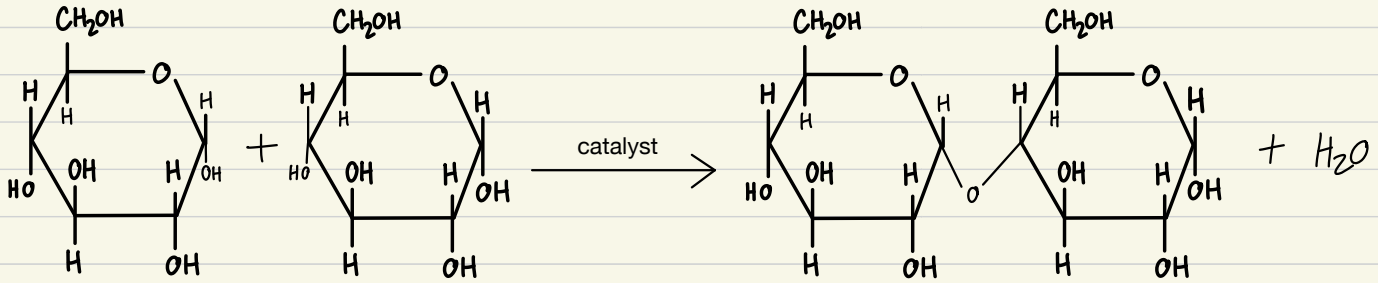
amylose (α-glucose polymer)

CARBOHYDRATES

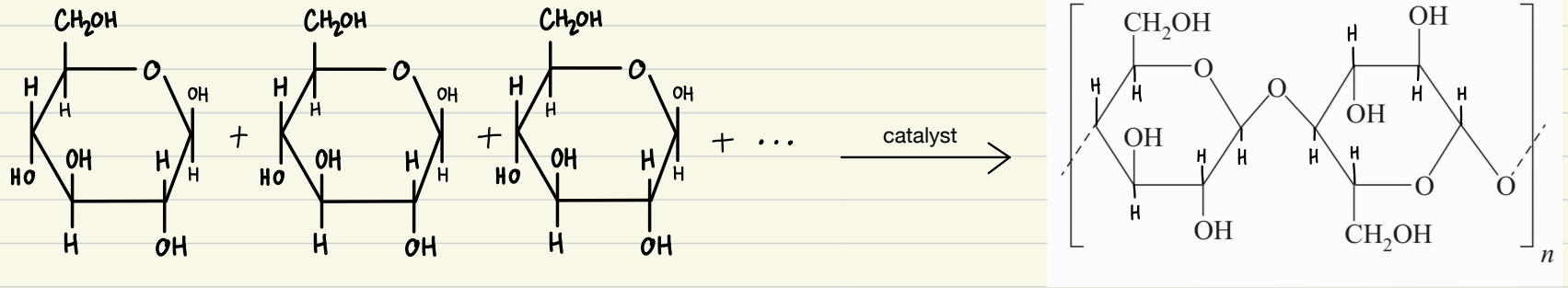
REACTIONS

NEED TO MEMORISE CELLULAR RESPIRATION THERMOCHEMICAL EQUATION: $C_6H_{12}O_{6\,(aq)} + 6O_{2\,(g)} \rightarrow 6CO_{2\,(g)} + 6H_2O_{(l)}$ ΔH = -2860 kJ/mol

Formation of disaccharides $(2C_6H_{12}O_6 \rightarrow C_{12}H_{22}O_{11} + H_2O)$



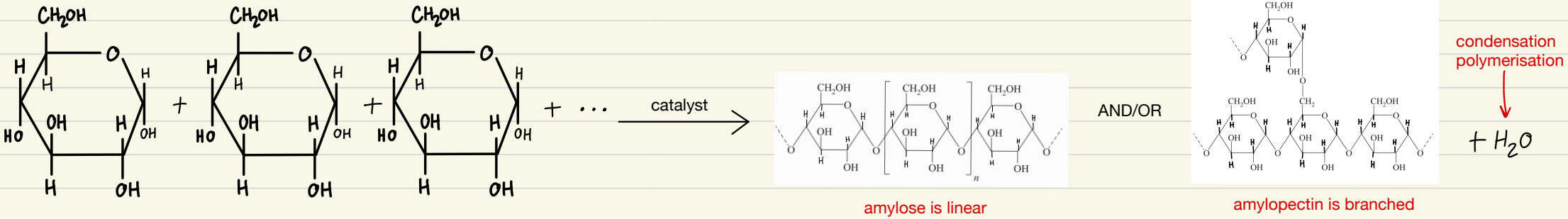
Formation of cellulose $(nC_6H_{12}O_6 \rightarrow C_{6n}H_{10n+2}O_{5n+1} + (n-1)H_2O)$



All β-glucose

cellulose is linear

Formation of starch $(nC_6H_{12}O_6 \rightarrow C_{6n}H_{10n+2}O_{5n+1} + (n-1)H_2O)$



All α-glucose

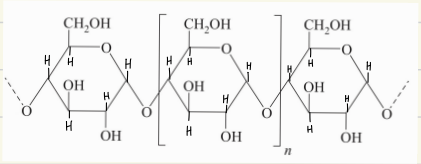
amylose is linear

amylopectin is branched

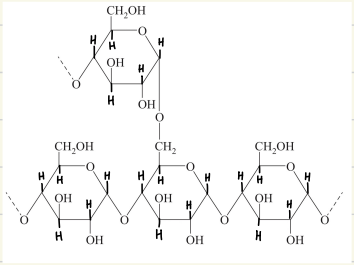
CARBOHYDRATES

REACTIONS CONTINUED

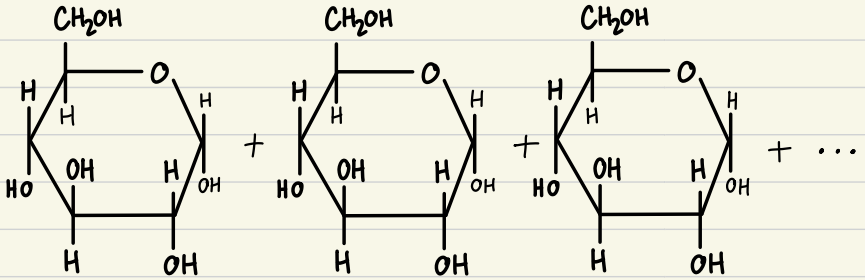
Hydrolysis of starch $(C_{6n}H_{10n+2}O_{5n+1} + (n-1)H_2O \rightarrow nC_6H_{12}O_6)$



AND/OR



$+ H_2O$ —amylase + maltase→



NOTE: Starch hydrolysis actually happens in multiple steps. Amylase hydrolyses amylose/amylopectin to maltose, which is then hydrolysed to glucose by maltase.

CARBOHYDRATES

RANDOM THEORY TO MEMORISE

- Energy content of macronutrient groups in kJ/g are given in the data book. Note that the mass of fibre i.e. cellulose must be subtracted from the total mass of carbohydrates since humans lack cellulase to hydrolyse it.
- Since the data book says that 1 g of carbohydrates will release 16 kJ of energy when metabolised, the energy content (kJ/g) of sucrose, glucose and fructose must all be similar.
- Glucose and fructose have similar molar energy content (kJ/mol) as they're isomers. Sucrose's molar energy content is around twice that of glucose/fructose as it's a disaccharide.
- Energy is stored as glycogen in animals and starch (mix of amylose and amylopectin) in plants.
- Aspartame is the methyl ester of the Asp-Phe dipeptide (structure given in data book). It's 200x sweeter than sucrose but has the same energy content.
- Lactose-intolerant people can't hydrolyse lactose as they're deficient in the lactase enzyme.
- Glycemic index is a measure of how fast carbohydrates-containing foods can have their carbohydrate content hydrolysed to raise blood glucose levels.
- Glucose is assigned an arbitrary GI of 100.
- Sugary foods e.g. lollies have higher GI than starchy ones e.g. bread since it takes time for the starch in bread to be hydrolysed to glucose, whereas simple sugars in lollies can raise blood glucose levels directly.

Amylose vs amylopectin marking scheme

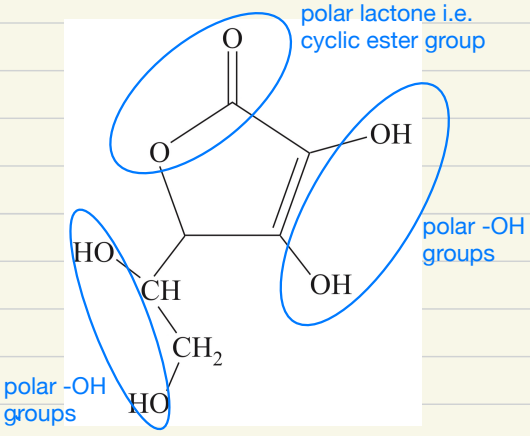
Amylopectin is branched whereas amylose is unbranched: +1

Branches in amylopectin = more surface area available to amylase, which allows it to be hydrolysed to glucose faster than amylose: +1

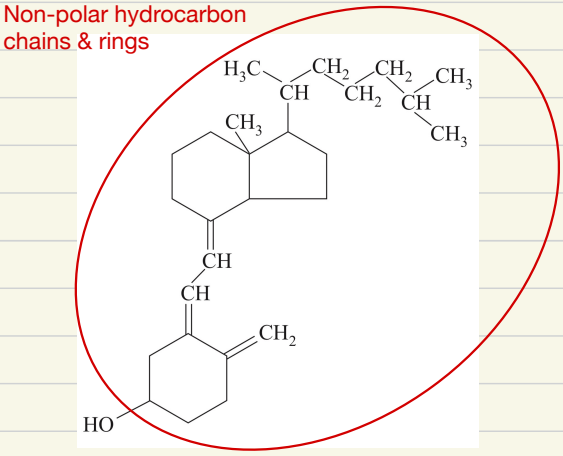
∴ Amylopectin has a higher GI than amylose OR amylopectin-rich foods have higher GI than amylose-rich ones: +1

VITAMINS

- All vitamins except for vitamin D are essential i.e. the human body can't produce them so they must be supplied in the diet.
- Water-soluble vitamins e.g. vitamin C can't be stored by the body whereas lipid-soluble ones e.g. vitamin D can.
- Only need to compare vitamins C and D in terms of structure.
- Many vitamins serve as coenzymes or antioxidants.



Vitamin C (water-soluble)



Vitamin D (lipid-soluble)

CALORIMETRY

chemical calibration ↓ electrical calibration ↓

- Calibration factor = energy (J) / ΔT (°C) = [V (V) x I (A) x t (sec)] / ΔT (°C)
- energy (kJ) = $n_{(calibrating\ chemical)}$ (mol) x molar heat of combustion (kJ/mol)
- Solution calorimetry = heating water with burning food
- Bomb calorimetry is better than solution calorimetry as it's better insulated to minimise heat loss to surroundings which causes underestimations in energy content.