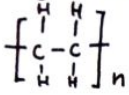
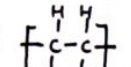
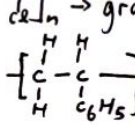
POLYMERS

ADDITION POLYMERISATION

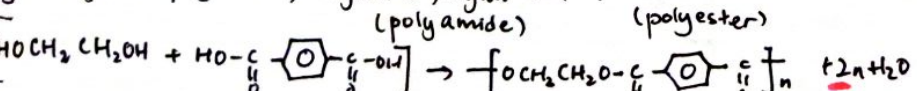
- A process where small molecules called monomers join together to form large molecules (consisting of repeating units.
- repeat unit : 
- Examples :
  - poly(ethene) → plastic food wrap, plastic gloves
  - poly(chloroethene) PVC  → electrical insulators (wire cover), gramophone records
  - poly(phenylethene) polystyrene  → electrical insulator, packaging material.

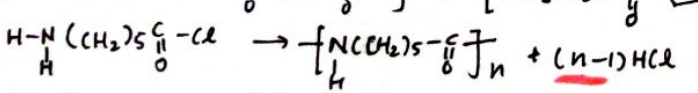
DESIGNING USEFUL POLYMERS

- Low density polyethene (LDPE) 
  - non polar polymer chains interact w/ weak vdw forces.
  - random branching, not closely packed
  - ↓density ↓mp.
- High density polyethene (HDPE)
  - Ziegler-Natta catalyst.
  - straight chains
  - unbranched ∴ SA↑ ∴ vdw forces↑
- Neoprene (synthetic rubber) → monomer : 2-chlorobuta-1,3-diene.
- Latex → monomer : 2-methylbuta-1,3-diene.
  - cross linking chains to make it harder.
  - vulcanisation → sulfur bridges link polymer chains.

CONDENSATION POLYMERISATION

- monomers hv 2 functional group
- empirical formula of polymer ≠ monomer.
- small molecule eliminated.
- Eg. Terylene (polyester), nylon 6, nylon 6,6 (polyamide), poly(lactic acid) (polyester)





DISPOSAL OF POLYALKENES

- no reactive sites ∴ non-biodegradable
- burried in landfill sites (dumping)
  - ↳ x degrade ∴ shortage of land
- incineration
  - ↳ toxic gases eg. HCl from PVC, HCN from poly(propenenitrile)
- use / develop biodegradable plastics / photodegradable plastics
- ♺ & reuse plastics.

HYDROLYSIS

- base / acid
- n (monomers) + 2n H_2O $\xrightarrow{\text{(conc } H_2SO_4 \text{ cat)}}$ n monomer + n monomer
  OR
  2n NaOH → "
- * ammonium salt / dicarbo. salt.

PROTEINS

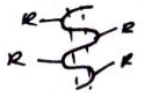
- in polypeptide, always one end w/ free amino group (NH_2) → N-terminal
- one end has free carboxyl (COOH) group → C-terminal.
- unbranched, linear polymer

PRIMARY STRUCTURE

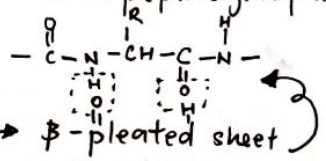
⇒ sequence of amino acids in a polypeptide chain.

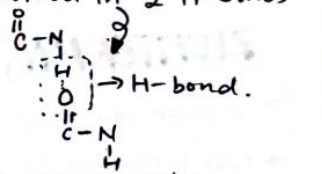
- synthesized from N to C
- position of cysteine residue determines disulphide bridges.

SECONDARY STRUCTURE



- α-helix.
  - coiled in spiral, R groups project outwards
  - each peptide group involved in 2 H-bonds





- β-pleated sheet
  - lengths of chain lie side by side.
  - R-groups point above & below.
  - H-bonds form between adjacent sections.

⇒ regular structural arrangements of the polypeptide chain that result from H-bonding between peptide bond regions of the chain.

TERTIARY STRUCTURE

⇒ overall folding of a polypeptide chain that arises from interactions between amino acid side chains.

- ionic interactions
  - → transfer of H from −COOH to $-NH_2$ to form zwitterions.
- H-bonds.
  - → when 2 groups w/ O-H or N-H
  - * if COOH & NH_2 then ionic
- covalent disulphide bonds.
  - → 2 cysteine R-groups react to form sulphur bridge.

(vdw)

- instantaneous dipole
  - → between R-groups of non polar amino acids.

POLYMERS

QUATERNARY STRUCTURE

=> interactions w/ other polypeptide chains

CLASSIFICATION

→ Globular / Fibrous
H_2O soluble , insoluble

DENATURATION OF PROTEINS

→ changes in environmental factors result in loss of specific 3D structure of protein.

→ Eg → Heat : KE↑ ∴ break H-bonds , ionic
pH : alters COO^- / NH_3^+ , break ionic
Heavy metal ions : highly electrotve ∴ combine w/ COO^-, break ionic
: react w/ -SH groups ∴ break disulphide
mechanical force : H-bonds
organic chemical : vdw
reducing agents : disulphide.

ENZYMES

→ catalytic properties
→ 'cleft' → active site => region where enzyme catalysed reaction occurs.
→ catalytic properties & specificity determined by chemical nature of amino acid R-groups.

PROPERTIES OF ENZYMES

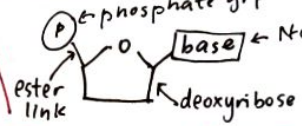
→ specific
→ not used up
→ form ES complexes
→ only small amount needed
→ fast acting
→ affected by temp / pH
→ slowed down / stopped by inhibitors.

SPECIFICITY

→ only 1 specific substrate
→ 'lock & key' mechanism.
→ lower Ea
→ products leave ∴ can reuse.

DNA → sugar-phosphate backbone w/ bases hanging off.

→ strand made by condensation poly.
→ nucleotide



→ Adenine } purines
→ Guanine }
→ Thymine } pyrimidines.
→ Cytosine }

FACTORS AFFECTING ENZYMES

→ dependent on tertiary structure
→ CONC
→ ↓ enzyme ↓ active site ∴ rate↓
→ ↑ enzyme ↑ active site, turnover rate↑
→ TEMP
→ affects speed of molecules, Ea, thermal stability
→ temp↑ , KE↑ , collisions↑
→ more collisions w/ energy > Ea ∴ successful collisions, rate↑
→ > 40°C, disruption of forces ∴ heat denatured.
→ pH
→ affect ionization of amino acid.
→ disrupts 3D arrangement

DNA DOUBLE HELIX

→ 2 strands running in opposite directions
→ H- bonds between bases
→ complementary base pairing.

DNA REPLICATION

→ catalysed by DNA polymerase.
→ H-bonds & vdw forces between base pairs in double helix broken.
→ 2 new strands are formed using original strans as templates
→ each new strand contains complementary sequence of bases as dictated by the order of bases in original strands.
→ semi-conservative replication
↳ each daughter molecule contains one new one old.