**Topic 1.5 – Nucleic Acids**

**Nucleotides** are formed by a condensation reaction between:

### One or more *phosphate groups* (A).

* A *pentose* sugar (B).
* An organic *nitrogenous base* (contains nitrogen) (C).

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ATP

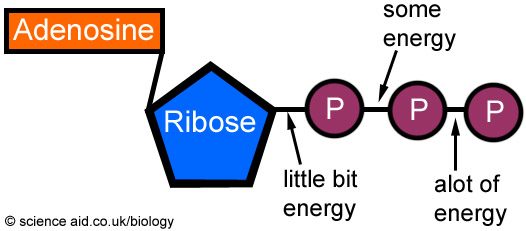
Adenosine *tri*phosphate (ATP) is a **nucleotide**. It is the **universal energy currency of the cell** – It is the common energy source that supplies energy for ***all*** reactions in ***all*** cells in ***all*** organisms.

ATP has 3 phosphate groups, ribose pentose sugar and the nitrogenous base adenine.

Adenine

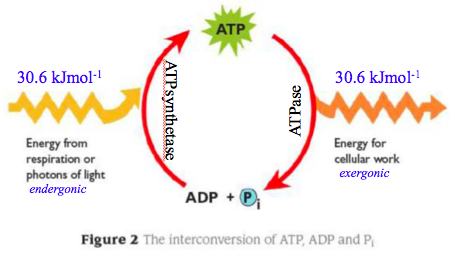
The terminal phosphate bond is unstable and is easily broken by **hydrolysis** (the addition of a water molecule) to release 30.6kJmol-1 energy. As this reaction releases energy it is called an **exergonic reaction**. It is catalysed by an **ATPase enzyme.**

The terminal bond can be re-formed by condensation (the removal of a water molecule) and requires 30.6kJmol-1 energy so this is an **endergonic** reaction. It is catalysed by an **ATP synthetase** enzyme.



The energy-releasing exergonic reactions and the energy-requiring endogonic reactions are always **coupled** together so that energy is **transferred**.

**Top tip** - ATP is produced in the **cytoplasm**, the **mitochondria** (matrix and inner membranes) and in **chloroplasts** (thylakoid membranes).



Advantages of ATP

* ATP is soluble and easily transported e.g. from companion cell to sieve element in phloem.
* ATP is the universal energy source for all reactions, in all cells, in all organisms, increasing efficiency and control by the cell. ATP is the universal intermediary molecule between energy-yielding and energy-requiring reactions in the cell.
* The hydrolysis of ATP to ADP involves a single reaction that releases immediate energy. The breakdown of glucose involves a number of intermediates and it takes much longer for the energy to be released.
* Only one enzyme (ATPase) is needed to release energy from ATP, while many are needed in the case of glucose.
* ATP releases energy in small useable amounts (30.6kJmol-1) when and where needed, whereas glucose contains large amounts of energy that may not be needed immediately.

Uses of ATP

* Metabolic processes to synthesise large organic molecules like polypeptides and DNA
* Active transport
* Muscle Contraction
* Nerve transmission
* Secretion of vesicles

Nucleic acids - DNA (*Deoxyribonucleic acid)* and RNA (*Ribonucleic acid)*

Nucleic acids are built up of repeating **nucleotides**.

DNA nucleotides have deoxyribose sugar and the bases adenine, *thymine*, cytosine or guanine.

RNA nucleotides have ribose sugar and the bases adenine, uracil, cytosine and guanine.

A pyrimidine base must bond with a purine base via complimentary base pairing (A=T, C≡G).

* *Pyrimidine* bases are single ring structures: cytosine, thymine and uracil
* *Purine* bases are double-ring structures: adenine and guanine

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| ***DNA*** | ***RNA*** |
| Two anti-parallel polynucleotide chains, double helix | One polynucleotide chain, single helix |
| Deoxyribose pentose sugar | Ribose pentose sugar |
| Thymine base | Uracil base |
| Complimentary base pairing A=T, C≡G (bases occur in equal mass or percentages) | No complimentary base pairing as only one chain |
| Function: DNA replication in dividing cells and protein synthesis | Function: Protein synthesis – 3 forms mRNA, rRNA and tRNA |

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| ***Type of RNA*** | ***Description and function*** |
| Messenger RNA (mRNA) | Long single-stranded molecule synthesised in the nucleus by Transcription. It carries the genetic code from the DNA to the ribosomes in the cytoplasm. Each strand of mRNA contains the genetic code for one gene. Each gene codes for a particular polypeptide. |
| Ribosomal RNA (rRNA) | Ribosomes are synthesised in the nucleolus and are composed of rRNA and proteins. Ribosomes leave the nucleus via the nuclear pores. Ribosomes are the site of protein synthesis and are involved in Translation. |
| Transfer RNA (tRNA) | tRNA is a small single stranded molecule folded into a clover leaf shape. Each tRNA molecule has an amino acid binding site CCA. At the opposite end of the tRNA molecule there is a triplet of bases called an **anticodon**. tRNA molecules transport amino acids to the ribosomes. |

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**DNA replication**

In DNA replication, **DNA helicase** breaks the hydrogen bonds between the bases in the helix, unwinding the DNA exposing unpaired bases. **DNA polymerase** then forms bonds between free DNA nucleotides and their complimentary bases on the parent strands.

**Two identical DNA molecules are formed -** each made up of one newly synthesised chain and one chain from the original molecule. This is the **semi-conservative hypothesis** proposed by **Meselson and Stahl.**

The genetic code

The genetic code is a linear, triplet, non-overlapping, degenerate, universal code for the production of polypeptides. Amino acids are coded for by triplets of bases in the DNA. The DNA is transcribed to produce codons in mRNA and then translated to produce a sequence of amino acids.

**Protein synthesis**

The transcription of DNA to produce messenger RNA

In the nucleus, DNA helicase breaks the hydrogen bonds between the bases in the helix, unwinding the DNA, exposing unpaired bases on the template strand.

In the nucleus DNA helicase breaks the hydrogen bonds unwinding the DNA, exposing unpaired bases on the template strand. RNA polymerase forms bonds between free RNA nucleotides and their complimentary bases on the parent strand until a stop sequence is reached. A molecule of **pre-mRNA** is produced containing coding exons and non-coding introns. Post-transcription modification removes the introns to produce functional mRNA.

If the introns remained a different protein could be produced and the molecular mass of the mRNA would be heavier.

Eukaryotic genes are usually discontinuous genes with coding exons and non-coding introns.

Prokaryotic genes are usually continuous genes, lacking non-coding sequences.

The translation of mRNA using ribosomes to synthesise proteins in the cytoplasm

Ribosomes have two attachment sites for tRNA (on the larger sub unit) and one attachment site for mRNA (on the smaller sub unit). Each activated tRNA molecule carries a specific amino acid.

The Ribosome binds to the start codon on the mRNA. tRNA molecules bind to the ribosome through codon-anticodon interactions. A peptide bond is formed between the two amino acids. The ribosome moves along the mRNA one codon at a time. This continues until a stop codon is reached.

Beadle & Tatum’s **one gene – one polypeptide hypothesis** states that one gene codes for a single polypeptide (The quaternary protein haemoglobin has four different polypeptide chains, therefore four genes are needed to code for haemoglobin. Collagen has three alpha helices (secondary protein structure) but they are identical, therefore one gene is sufficient.)

The polypeptide is further modified post-translation to produce a fully functional protein. The endoplasmic reticulum transports the polypeptide to the Golgi bodies which folding them in secondary and tertiary structures using bonding between variable R groups. Some proteins have carbohydrates, lipids or phosphates added to them e.g. haem added to haemoglobin. Golgi bodies package proteins into secretory vesicles and are released at cell membrane by exocytosis