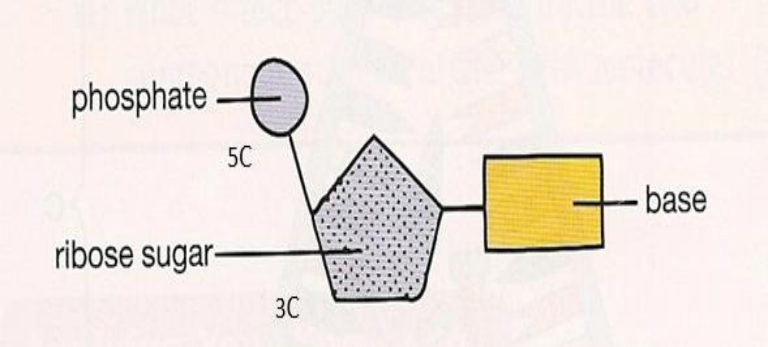
Transcription and Translation of DNA

Genotype – our genetic constitution (makeup) is determined (controlled) by the sequence of bases in its genes

Phenotype – determined by the proteins synthesised when genes are expressed (copied)

Gene expression – involves transcription and translation

RNA – ribonucleic acid is involved in both processes



Each nucleotide is composed of ribose sugar, an organic base and a phosphate group

Differences between DNA and RNA –

1. RNA has ribose instead of deoxyribose
2. RNA has uracil instead of thymine
3. RNA is a single strand, DNA is double stranded

Back to DNA . . . .

Characteristics are the result of biochemical processes controlled by enzymes

Enzymes are made of protein – made up of polypeptide chains composed of amino acids

<u>Genetic code</u>

Sequence of bases along DNA represents a sequence of 'codewords'

Each DNA stand bears a series of 'base triplets' arranged in a particular order for coding for proteins needed by an organism

Genetic information for making protein is on the DNA in the nucleus

Assembly of amino acids into polypeptides takes place in the cytoplasm

Remember, DNA is double stranded and is too big to leave the nucleus

So,

A molecule of mRNA is 'transcribed', copied out, from a section of DNA

mRNA meets another nucleic acid tRNA, transfer RNA

Genetic information is changed into or 'translated' into protein

Transcription and 'primary transcript'

'Promoter' – region of DNA where transcription is initiated

RNA polymerase is enzyme responsible for transcription

As the enzyme moves along the gene from the promoter, it brings about the synthesis of mRNA

mRNA has nucleotide sequence complementary to one of the two DNA strands

RNA polymerase adds nucleotides to the 3' end of the growing mRNA molecule

A 'terminator' region is reached and the m RNA becomes separated from the DNA template

Stages of Transcription

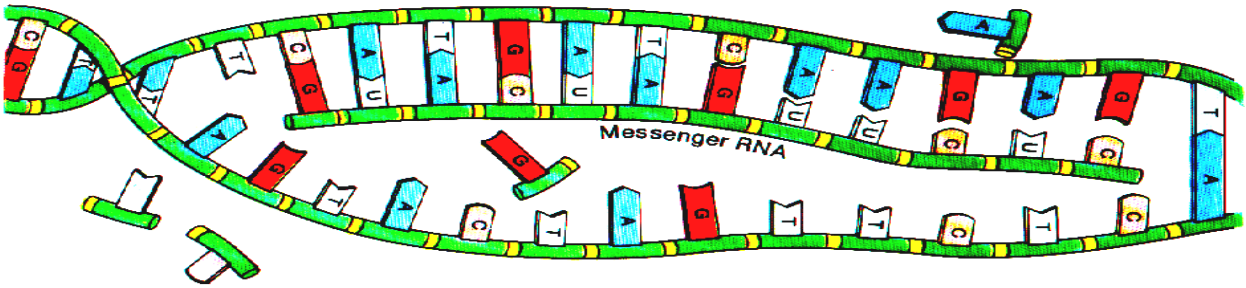
Stage 1 – DNA double helix unwinds

Stage 2 – weak hydrogen bonds breaking between bases, causing DNA strands to separate

Stage 3 – free RNA nucleotides (moving freely in the nucleus) find complimentary pair on the DNA strand

Stage 4 – weak hydrogen bonds are formed between the new bases pairing

Stage 5 – strong chemical bonds are formed between the new RNA nucleotides, opposite the DNA. This allows a new strand to be formed



Stage 6 – weak hydrogen bonds are breaking between DNA & RNA, allowing mRNA to break from the DNA template

Stage 7 – new mRNA strand is ready to be transported out of the nucleus into the cytoplasm

Stage 8 – weak hydrogen bonds reunite the two original DNA strands into a double helix again.

Long stretches of DNA in a gene do not code for a protein

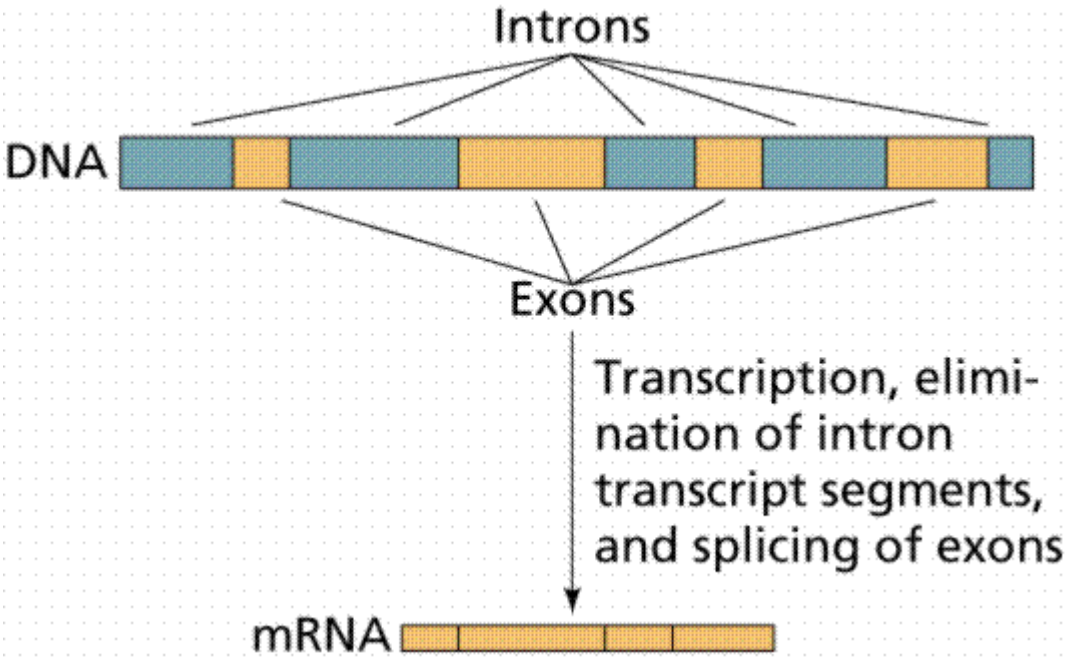
Introns – non coding regions

Exons – coding regions

Introns are ‘cut out’ from the primary transcript and exons are ‘spliced’ together

This forms mRNA with a continuous sequence of nucleotides
This sequence is translated into a sequence of amino acids

RNA Splicing



Translation

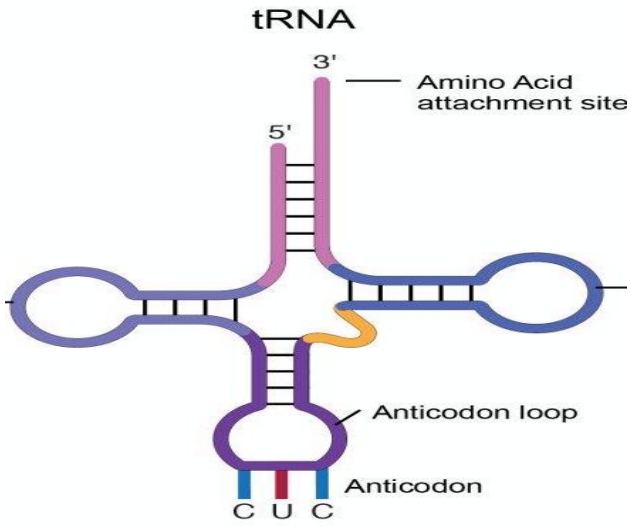
Translation is the synthesis of protein, as a polypeptide chain, under the direction of mRNA

The genetic message, carried by mRNA, is made up of a series of base triplets called codons

Codon – is the basic unit of the genetic code

tRNA

- t RNA is required for translation
- tRNA is found in the cytoplasm
- tRNA has a 3D structure because it is folded back on itself but is not double stranded
- tRNA has one particular triplet of bases exposed – an anticodon



An anticodon is complementary to a mRNA codon and corresponds with a particular amino acid i.e. its base sequence is **specific to one** of the 20 amino acids

Each tRNA picks up an amino acid from the cytoplasm's amino acid pool

The amino acid is carried by the tRNA to a ribosome and it is added to a growing polypeptide chain

Start and Stop codons

- mRNA codon AUG codes for methionine and acts as a start codon
- mRNA codons UAA, UAG and UGA act as stop codons

Ribosome

Contains enzymes for protein synthesis

Function of a ribosome is to bring a tRNA molecule, bearing an amino acid, into contact with mRNA

Ribosome has one binding site for mRNA

Ribosome has three binding sites for tRNA. These are needed to :-

- hold tRNA carrying the peptide chain
- hold the tRNA carrying the next amino acid allowing it to be joined by peptide bond
- discharge (release) the tRNA from the ribosome

These three sites are called P, A and E

Ribosome binds to the 5’ end of the mRNA so that the start codon, AUG, is in position at binding site P

Next

Molecule of tRNA carrying its amino acid methionine becomes attached, by hydrogen bonds, to site P

mRNA codon at site A ‘recognises’ and forms hydrogen bonds with the anticodon on the tRNA molecule bearing its amino acid

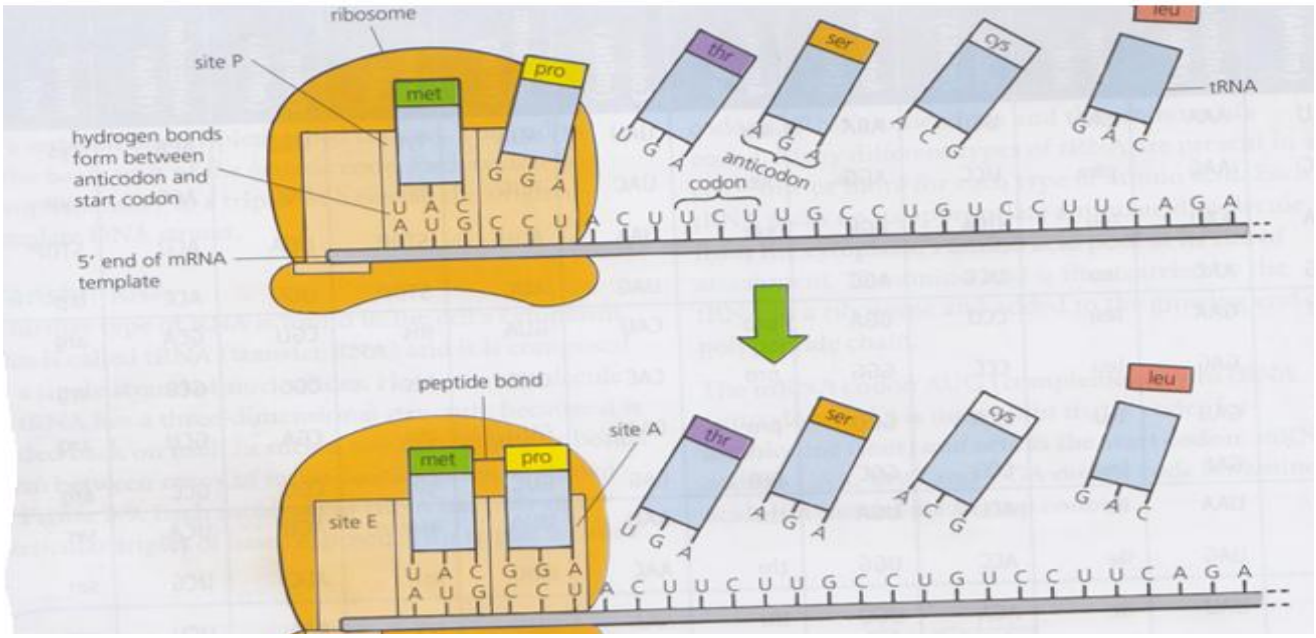
When the first two amino acids are aligned, they become joined by peptide bonds

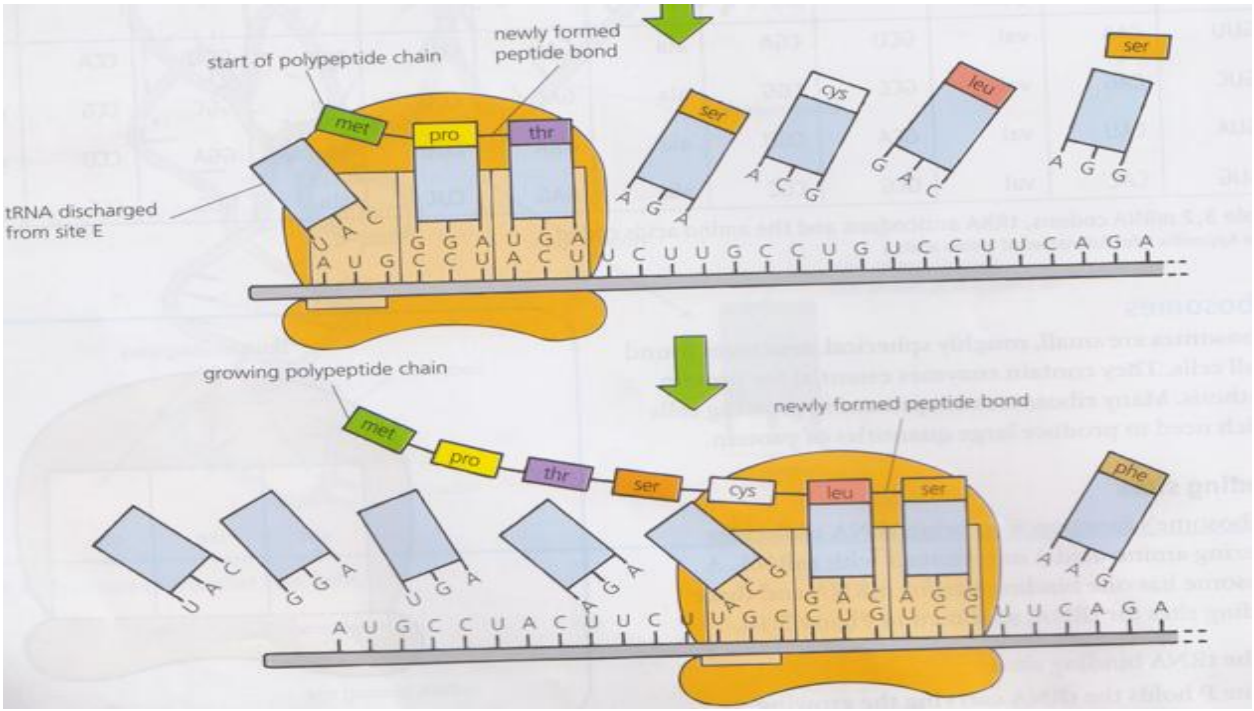
As the ribosome moves along, the t RNA that was at site P is moved to site E and is discharged from the ribosome to be re-used

The tRNA that was at site A is moved to sit P and the vacated site A becomes occupied by the next tRNA carrying an amino acid . . . and so on!

Eventually a ‘stop codon’ is reached (AUU AUC UGA)

At this point, site A becomes occupied by a ‘release factor’ which frees the polypeptide from the ribosome

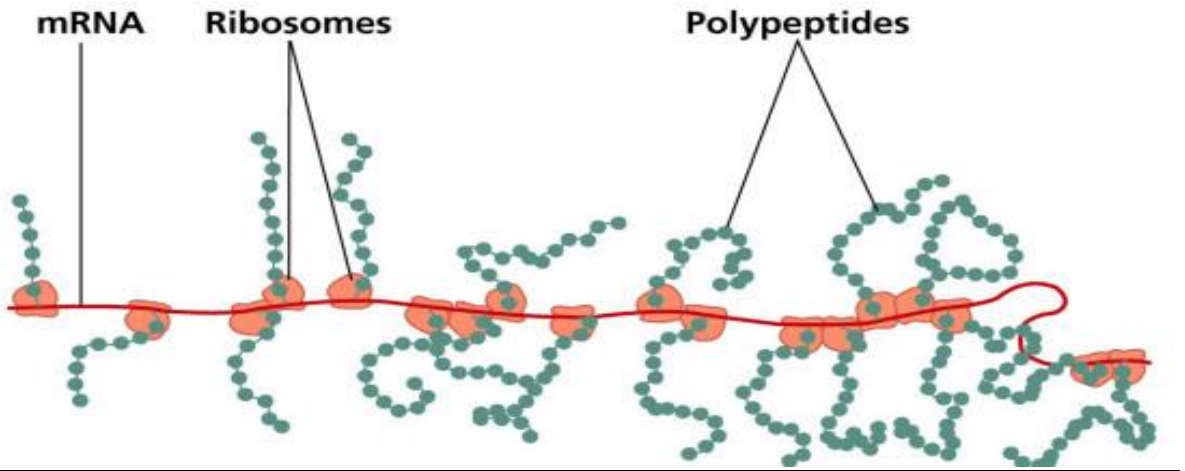




<u>Polyribosome</u> – Not mentioned in arrangements but interesting

Multiple translation is achieved by several ribosomes being attached to the ribosome and translating at the same time

In this way many copies of the polypeptide are made



One gene, many proteins

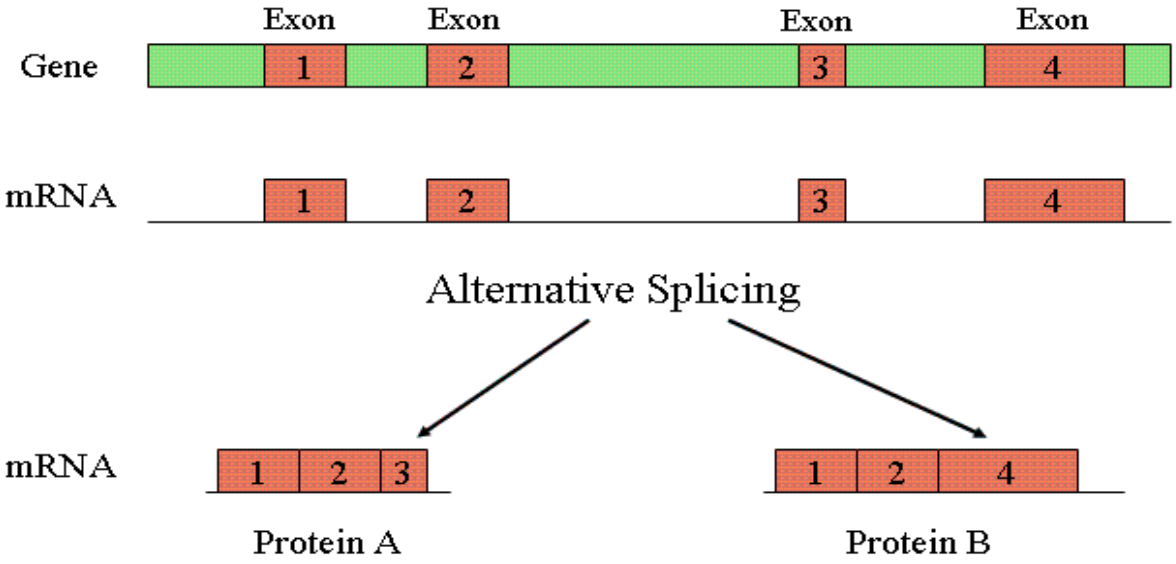
A primary transcript is cut up and its exons are spliced together to form mRNA ready for translation

'Alternative segments' of mRNA may be treated as exons and introns

So, the same primary transcript has the potential to make several mRNA molecules each with a different sequence of base triplets

One gene can code for several different proteins

And, a limited number of genes can give rise to a wide variety of proteins



Post-translational modifications

A single polypeptide chain may be **'cleaved'** (cut) by enzymes to make it active

e.g. Insulin requires the central section to be cut out by protease enzymes – see next slide

A protein's structure can be modified by adding **carbohydrate** or a **phosphate group e.g.**

Mucus – is a glycoprotein, protein with carbohydrate added

P53 is a regulatory protein which is usually inactive

When a cell's DNA is damaged, phosphate is added – this makes it active

P53 active – can repair DNA or bring about cell death

Pro-insulin shown in the diagram opposite is ‘inactive’ and only becomes active when the section shown is ‘cut out’. This process is called ‘cleavage’