

Biochemistry Exam

Molecular Biology

Lecture 1 – An Introduction to Protein Synthesis

- Up to 90% of cellular energy can be spent on protein synthesis
- Proteins are folded versions of a linear chain of amino acids
- Amino acids are joined by covalent peptide bonds
- A polypeptide chain has an N-terminus (the end NH₃ group) and a C-terminus (the end COO⁻).
- There are 20 naturally occurring amino acids

Transcription → the process of making an RNA copy of a DNA sequence.

Translation → the process by which the nucleotide sequence of an mRNA is used as a template to join amino acids in a polypeptide chain in the correct sequence.

Types of RNA:

- Messenger RNA (mRNA) → synthesized from a DNA template during transcription and used as a template for protein synthesis.
- Transfer RNA (tRNA) → RNA molecules that carry amino acids to the ribosome for polymerization. Each tRNA molecule has a 3-nucleotide sequence called an anticodon that is complementary to the codon in mRNA to ensure the correct amino acids are recruited in the correct order.
- Ribosomal RNA (rRNA) → the RNA component of the ribosome that catalyses protein synthesis.
- Micro RNA (miRNA) → involved in post-transcriptional regulation of gene expression.

Why codons are groups of 3:

- Three is enough to provide the variation necessary to code for the 20 standard amino acids, with no extra waste of space and energy.

The genetic code:

- Highly degenerate → means that there is more than one triplet that could specify the same amino acid, for example, CGU and CGC both code for arginine.
- Where several different codons specify more than one amino acid, variability is most frequently observed at the third base. This is called the wobble base.
- Start codons → almost all translation begins with an AUG codon which codes for methionine.
- Stop codons → three codons don't code for any amino acid and when they occur in mRNA they halt translation (UAA, UAG, UGA).

Reading frames:

- Open reading frames → segments that don't have a stop codon for at least 50 codons.
- Every mRNA has three possible reading frames, because after three nucleotides the codons are the same again.
- The same RNA sequence can give completely different polypeptides based on the reading frame used.
- We can guess the nucleotide sequence from the protein sequence by using protein sequencing. The sequence of the amino acids can be determined but we can only guess at the nucleotide sequence due to the fact that the genetic code is degenerate and some amino acids are coded for by multiple codons.

Mutations:

- Errors that occur spontaneously during DNA replication that lead to permanent changes in the sequence.
- Mutations are only inherited if they occur in germ-line cells (egg, sperm, precursor cells).
- Mutations can be good (e.g. evolution) or bad (e.g. cancer).
- Point mutation → a mutation involving a single base substitution. Keeps the reading frame in tact but the protein may still be altered.
- There are 3 types of point mutations:
 1. Silent mutation → the altered codon corresponds to the same protein.
 2. Missense mutation → the altered codon corresponds to a different proteins.
 3. Nonsense mutation → the altered codon corresponds to a stop codon.
- Insertion → the addition of one or more nucleotide base pairs into a DNA sequence.
- Deletion → the deletion of one or more nucleotide base pairs from a DNA sequence.
- Insertions and deletions can change the reading frame, resulting in a mutant protein.

Lecture 2 – An introduction to Protein Synthesis (Part 2)

tRNA molecules:

- tRNA molecules have arms that each play an important role:
 1. D arm → the recognition site for aminoacyl tRNA synthetases
 2. T arm → acts as the recognition site for the ribosome
 3. A arm → contains the anticodon that is critical for mRNA recognition.
 4. CCA arm → a sequence at the 3' end that binds with the amino acid.

Charging tRNA molecules:

- Attaching the correct amino acids to tRNA molecules.

This process is controlled by enzymes called aminoacyl tRNA synthetases