

School of Sport, Health & Outdoor Education

Assessment Feedback Sheet

Student No./Name: jemima harding

Module Code: SHSS4068**Module:** The Science of Nutrition

Personal Evaluation – to support your academic progress please complete the section below BEFORE submitting your work.										
What do you consider to be the best aspects of this work?										
Which aspects do you consider could have been improved in this piece of work?		Wording flow								
What have you found most satisfying whilst undertaking this submission?										
ASSESSMENT CRITERIA	Learning Outcome	GRADE								
		Poor 0-25%	Unsatisfactory 26-39%	Satisfactory 40 – 49%	Good 50 – 59%	Very Good 60 – 69%	Excellent 70 – 85%	Exceptional 86– 100%	%	
		Theoretical explanation	1							70%
		Use and appropriateness of references	2							20%
		Structure and flow of answer	1							10%
It is expected that students will present work that is proof read, correctly referenced and adheres to the Assessment Checklist . Therefore a range of 0 – 10 marks will be deducted for non-completion of any of the points on the checklist below .										
TUTOR COMMENTS:										
Submission date: via Turnitin		Return date: (at least within 4 weeks)		Tutor:			Mark:			

Process of gene expression

Gene expression is the process by which specific genes are activated to produce a required protein. The nucleus of cells contains DNA, which directs the synthesis of all proteins in the body (Bender, 2017). Molecules of DNA contain coded information in the sequence of nucleotides, which specifies the amino acid sequence of a single polypeptide chain which is known as a gene (Tortora and Derrickson, 2014). A gene is a unit of hereditary information, the total genetic information coded in DNA of an organism is known as a genome (Widemaier, Raff and Strang 2014). Each gene contains sequences of base pairs of adenine (A), thymine (T), cytosine (C) and guanine (G). The genome is distributed in 46, 23 pairs of chromosomes of between. 400 and 3340 genes long, as well as DNA chromosomes contain a special type of proteins called histones (Widemaier, Raff and Strang 2014).

To synthesize a protein the information in DNA is firstly copied which is known as transcription into a strand of a specific molecule called RNA (ribonucleic acid) (Scanlon and Sanders, n.d.). Transcription is taken place in the nucleus, where three DNA nucleotides is copied to a corresponding sequence of three RNA nucleotides which is known as a base triplets, they are then copied into a sequence of codons which are the three successive RNA nucleotides in a strand of RNA (Widemaier, Raff and Strang 2014).

Three kinds of RNA are made from DNA by the aligned ribonucleotides joining together by the enzyme RNA polymerase, which hydrolyses the nucleotide triphosphates, releasing two of the terminal phosphate groups and joining the remaining phosphate in covalent linkage to the ribose of the adjacent nucleotide (Bender, 2017). The sequence of nucleotides that DNA attaches to RNA polymerase are called promoters (Tortora and Derrickson, 2014). The Three kinds of RNA are Messenger RNA (mRNA) which directs synthesis of proteins, Ribosomal RNA (rRNA) joins the ribosomal proteins to make ribosomes and Transfer RNA (tRNA) binds to amino acid and holds it in place on a ribosome until it is incorporated into a protein during translation (Gene Expression - an overview | ScienceDirect Topics, 2020).

During transcription, nucleotides pair in a complementary manner; The nitrogenous base (C) in DNA dictates (G) in the new RNA strand, (T) in DNA dictates (A) in RNA and an A in DNA dictates a uracil (U) in RNA (Widemaier, Raff and Strang 2014). For example if a segment of DNA had the base sequence ATGCAT, the new RNA strand would have the base sequence of UACGUA (Widemaier, Raff and Strang 2014).

Only certain segments of most genes actually code for sequence of amino acids; Exons which are expression regions of the gene are separated by noncoding intervening sequences of nucleotides known as introns (Widemaier, Raff and Strang 2014). RNA must undergo splicing to remove DNA introns, to allow the formation of the continuous sequence of exons which will be translated into proteins This occurs in the nucleus by a complex of proteins and a smaller nuclear RNAs known as a spliceosome which identifies nucleotide sequences at the beginning and end of every intron-derived region in the RNA transcript then removes and splices the exon-derived regions which code for specific amino acids forming another mRNA coding sequence, this occurs in insulin (Gene Expression - an overview | ScienceDirect Topics, 2020). Terminator which is a nucleotide sequence on DNA specifies the end of the gene is reached when RNA polymerase detaches from the transcribed RNA molecule and the DNA strand (Tortora and Derrickson, 2014).

The mRNA passes from the nucleus to the cytoplasm, where one end of the mRNA binds to the small subunit of a ribosome and an initiator tRNA which contains anti-codons that bring the amino acids to the ribosome binds to start the codon on mRNA which begins translation to synthesize proteins (Widemaier, Raff and Strang 2014). Anticodon of incoming tRNA then pairs with the next mRNA codon beside the initiator tRNA, the amino acid on the initiator tRNA forms a peptide bond with amino acid beside it (Tortora and Derrickson,2014). After the peptide bond forms the empty tRNA detaches from the ribosome, and the ribosome shifts the mRNA strand by one codon. As the tRNA bearing the newly forming protein shifts, another tRNA with its amino acid binds to a newly exposed codon (Scanlon and Sanders, n.d.). These steps are repeated over as the protein lengthens. As the ribosomes move along the mRNA other ribosomes called polyribosomes may attach behind and begin translation of the mRNA (Tortora and Derrickson,2014). When ribosome reaches a stop codon, protein detaches from the final tRNA which then vacates the ribosome and the ribosome splits into its large and small subunits (Widemaier, Raff and Strang 2014).

Alterations in the DNA sequence in a cells genome that spells out a genetic message in DNA is known as mutations, this can be caused by chemical radiation such as x-rays as they can break the chemical bonds in DNA; Point mutation is the simplest type where a single base is replaced by a different one, for example the base sequence C-G-T is the DNA triplet for the amino acid alanine. If G is replaced by A the sequence becomes the code for valine C-A-T (Tortora and Derrickson,2014).

Majority of proteins that are synthesized remain the cell to provide structure and function for the cell's survival (Widemaier, Raff and Strang 2014).However some are secreted as they are too large to diffuse through cell membranes into the extracellular fluid, where they act as signals to other cells or provide material for forming the extracellular matrix (Bender, 2017). For secreted proteins the first 15 to 30 amino the emerge from the ribosome acts as a recognition signal known as the signal peptide (Tortora and Derrickson,2014).

The binding of the signal recognition particle to a specific membrane protein on the surface of the rough endoplasmic reticulum, restarts the process of protein assembly (Scanlon and Sanders, n.d.).

Word count:993

References:

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