



LEVEL 4

SEMESTER 2

MODULE CODE: SHSS4068

MODULE TITLE: THE SCIENCE OF NUTRITION

ASSESSMENT TYPE: ESSAY

ASSESSMENT/COMPONENT: 1

COMPONENT WEIGHTING: 100 %

WORD COUNT: 3000

MODULE TUTOR: David Gardner

SUBMISSION DETAILS: by 3.00 pm through turnitin

- Complete all 3 essays to be submitted through Turnitin UK via moodle.
- Each essay to be no more than 1000 words, excluding figures, tables and references.

By 28th February 2020

Describe the hormonal and enzyme regulation of the digestion process.

or

Describe the digestive process with particular reference to gut flora and bioavailability.

By 27th March 2020

Describe the mechanisms of cell signalling.

or

Describe the processes of gene expression.

By 1st May 2020

Describe the roles and importance of vitamins or minerals during energy catabolism.

or

With reference to a specific vitamin or mineral discuss the implications of deficiency and toxicity.

Assessment Criteria

Details relating to the specific requirements levels grading for the essays are provided in the generic level descriptor provided on moodle.

Specific details and an example session will be provided during lectures.

School of Sport, Health & Outdoor Education

Assessment Feedback Sheet

Student No./Name:

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?	The attempt to make a topic that is complicated easier to read.								
Which aspects do you consider could have been improved in this piece of work?	I found this to be a hard topic to learn and write about, I wanted to push myself. I found it extremely hard to find references for this assignment so better references could possibly be used.								
What have you found most satisfying whilst undertaking this submission?	Improving my understanding of gene expression.								
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:		

Assignment Checklist

- ✓ Please complete the **Personal Evaluation** section of the Assessment Feedback sheet, add your name and details, and paste the whole of this assignment document into the front of your assignment
- ✓ Submission is a **single .pdf file, clearly labelled** with your name and module code
- ✓ Font style - Times New Roman, size -12 for text and 14 for headings
- ✓ Ink colour – black only
- ✓ Line spacing – 1.5 line spacing and 2cm- 2.5cm page margins
- ✓ Quotations more than three lines to be indented 1 line spacing
- ✓ One line space between paragraphs, paragraphs must be left aligned
- ✓ Pagination (your assignment should have **page numbers**)
- ✓ All tables and figures are internally referenced and have a title
- ✓ **Word count** checked and written at end of text (before references and any appendix)
- ✓ Assignment is within 10% of the word limit (excluding references and any appendices)
- ✓ **All** references in the text are included in the reference list
- ✓ **Correct referencing as described in UWTSD Harvard Referencing Handbook on the Library website** <https://www.uwtsd.ac.uk/media/uwtsd-website/content-assets/documents/library-and-learning-resources/infoskills/harvard-eng.PDF>
- ✓ Correct spelling and punctuation, using **UK English**
- ✓ Grammar and syntax correct- double check anything that has a green line under it
- ✓ I have read my assignment out loud to myself and it makes sense and is easy to read
- ✓ Somebody else has read my work and it makes sense to him or her!
- ✓ **I have checked and I have not plagiarised**

**Failure to follow these guidelines will
cost you marks!**

The Process of Gene Expression

Gene expression is an important process within the body and is fundamental for life, it is the process of which gene information is used to create a product that is normally a protein however, in non-protein genes, it creates Ribonucleic acid (RNA) (Schwanhäusser et al 2011). RNA has three different roles within protein synthesis the first being a messenger RNA which carries genetic information gathered from DNA, the second being a transfer RNA which transports amino acids to a ribosome and thirdly being a ribosomal RNA, which turns amino acids into protein chains (Lodish et al 2000). Gene expression is a complicated process comprised of many processes such as; transcription, splicing, translation, folding and exocytosis (Gibney and Nolan 2010).

Transcription is the first stage of gene expression where an exact copy of an RNA molecule is made from a DNA molecule (Gibney and Nolan 2010). Important protein factors are needed for transcription to begin such as RNA polymerase, a molecule used to synthesise chains of amino acids, is used to bind to part of the DNA to create an mRNA (messenger RNA), the proteins are able to recognise a DNA sequence and overlap that with the RNA polymerase sequence (Gibney and Nolan 2010) (Miglani, G. S. 2013). An mRNA's role is to carry copies of genetic code for a gene from the nucleus and into the cytoplasm, where it is then used to produce proteins. (OpenStax 2013).

Gene splicing happens after the transcription process has been completed, genes are split into two parts; coding sequences (exons) and non-coding sequences (introns) (Miglani, G. S. 2013). This is done by the excisionligase enzyme being used to break down and re-join areas of the gene (Miglani, G. S. 2013). The number of introns within the newly split gene determine whether the gene is a monintron gene which only have one intron or the multintron gene which have multiple introns (Miglani, G. S. 2013). Monintron genes are not used for the next step of gene expression (translation) but are instead involved within tRNA which helps decode a messenger RNA into a protein (Miglani, G. S. 2013). Multintrons however are involved in the process of creating proteins as they are directly translated into proteins through the transcription process (Miglani, G. S. 2013).

Within the gene expression process, translation slows down protein synthesis and is a focus of post-transcriptional regulation (the control and regulation of gene expression) as well as determining the stability of a gene (Gualerzi and Pon 2015). Translation starts by forming an initiation complex (a complete ribosome) where the start codon of the mRNA translation process is decoded by the anticodon in the P-site of the small ribosomal subunit (Gualerzi and Pon 2015). After the gene has been decoded at the small ribosomal subunit, it goes to the large ribosomal subunit allowing it to form an initiation dipeptide (two amino-acid residues) (Gualerzi and Pon 2015). The translation process is the longest process within gene expression, the time it takes to complete the process varies depending on a multitude of factors, but it is also one of the most fundamental as it is the start of protein synthesis (Gualerzi and Pon 2015).

Protein folding occurs within the endoplasmic reticulum and converts an unfolded polypeptide, which was the product of translation, into a three-dimensional folded protein made up of a multitude of amino acids (Kaufman 2004). Pathways from the endoplasmic reticulum avert the gathering of unfolded proteins by increasing the endoplasmic reticulum folding capacity and increasing the speed and efficiency at which misfolded proteins are broken down and removed (Kaufman 2004). It is important for the structure of the protein to be correct to allow it to function, if the protein remains unfolded after the process then it can either become an inactive protein or potentially become toxic (Faure et al 2016). The protein created by the folding process is determined by the sequence of the amino acids, this allows many different proteins to be created via the same process (Faure et al 2016).

The final stage of gene expression is exocytosis which is the way a material (protein in gene expression) from inside of a cell moves to the surface of the cell, this can be either the removal of waste from the cell or secretion (Martin and Hine 2008). The first stage of exocytosis is vesicle trafficking where proteins are transported to the cell's surface via vesicles, once they reach their destination they are tethered and remain there (Vazquez-Martinez et al 2001). The final stage is vesicle fusion has multiple outcomes, the first being proteins becoming entwined within the vesicle membrane which is crucial to the regulation of transporters within the body, the second being the surface of the cell increasing which is important for cell growth and the last being the contents of the vesicles being disbursed in the body (Vazquez-Martinez et al 2001).

The process of gene expression is a fundamental part of the human body, production of proteins, control of protein synthesis and the production of structures of cells (Gibney and Nolan 2010). Gene expression is a long and complicated process containing many different steps that are all required in order for the body to take information from DNA and slowly convert it to a functioning protein, RNA, mRNA or tRNA. Future study of gene expression could be used to improve one's understanding of many functions within the human body as well as helping people who have a gene expression defect.

(911 words)

Reference List

Faure, G., Ogurtsov, A. Y., Shabaline, S. A., Koonin, E. V. (2016) 'Role of mRNA structure in the control of protein folding', *Nucleic Acids Research*, 44 (22), pp10898-10911.

Gibney, E. R., Nolan, C. M. (2010) 'Epigenetics and gene expression', *Heredity*, 105, pp4-13.

Gualerzi, C. O., Pon, C. L. (2015) 'Initiation of mRNA translation in bacteria: structural and dynamic aspects', *Cellular and Molecular Life Sciences*, 72, pp4341-4367.

Kaufman, R. J. (2004) 'Regulation of mRNA translation by protein folding in the endoplasmic reticulum', *Nucleic Acids Research*, 29 (3), pp152-158.

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Miglani, G. S. (2013) *Gene Expression*, Alpha Science International. 1st ed. Swansea: ProQuest Ebook Central.

OpenStax. (2013) *19 3.4 Protein Synthesis*. 1st ed. OpenStax.

Schwanhäusser, B., Busse, D., Li, N., Dittmar, G., Schuchhardt, J., Wolf, J., Chen, W., Selbach, M. (2011) 'Global quantification of mammalian gene expression control', *Nature*, 473 (7347), pp337-42.

Vazquez-Martinez, R., Shorte, S. L., Faught, W. J., Leumont, D. C., Frawley, L. S., Boockfor, F. R. (2001) 'Pulsatile Exocytosis Is Functionally Associated with GnRH Gene Expression in Immortalized GnRH-Expressing Cells', *Endocrinology*, 142 (12), pp5364-5370.