NAME TEACHER

**NQA**

Nayland Qualification Authority

## Level Two Biology, 2014

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| **Demonstrate understanding of gene expression**  Credits: 4 |

### Suggested Time: 40 minutes

**Instructions**

* Answer all questions in the spaces provided.
* You must hand this examination paper to the supervisor at the end of the examination.
* Check that this paper has all 5 pages numbered and in the correct order.

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| Achievement Criteria. (for assessors only) | | | | | |
| Achievement | | Achievement  with Merit | | Achievement  with Excellence | |
| Demonstrate understanding of gene expression |  | Demonstrate in-depth understanding of gene expression |  | Demonstrate comprehensive understanding of gene expression |  |
| Overall Level of performance: | | | |  | |

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Assessor’s use only

You are advised to spend 40 minutes answering the questions in this booklet.

**QUESTION ONE: BASE PAIRING**

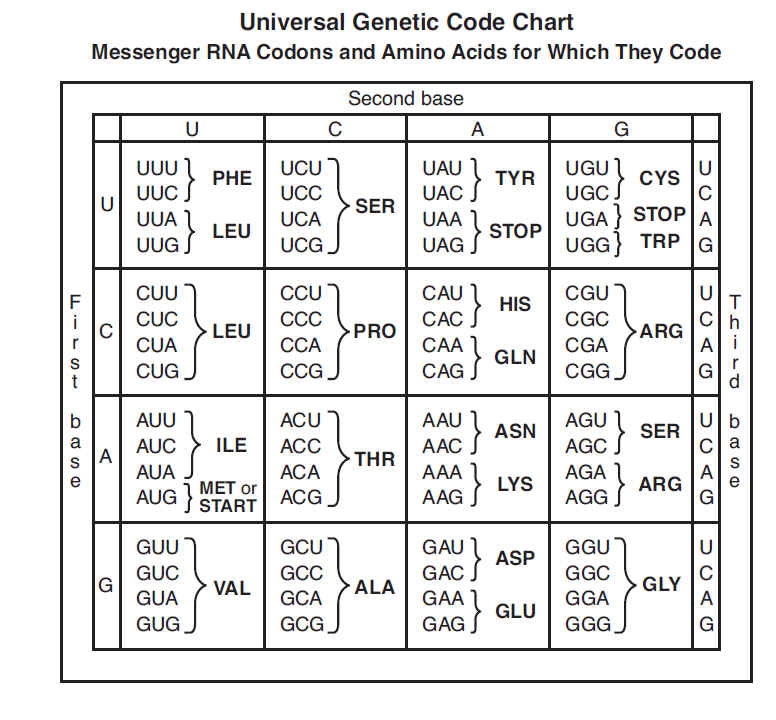
Maintaining the nature of the genetic code through replication and gene expression relies on successful complementary base pairing.

Discuss your understanding of the significance of complementary base pairing to gene expression. In your answer:

* Describe the structure of both **DNA** and **RNA** nucleotides and provide an account of all **complementary base pair** combinations observed during **transcription**.
* Explain how the **coding** and **template** strands of DNA relate to the product of transcription.
* Relate the role of **triplets**, **codons** and **anti-codons** to the process of translating one strand of mRNA.

Assessor’s use only

**QUESTION TWO: TAY SACHS MUTATION**

Tay Sachs Disease is caused by the build up of proteins called gangliosides inside nerve cells causing cell death.

Assessor’s use only

The HEXA gene on chromosome 15 codes for a gene product that normally helps to catalyse the breakdown of these harmful ganglioside proteins.

People born with Tay Sachs have a mutation in the HEXA gene which involves the insertion of four base pairs into the HEXA gene.

(a) Complete the **codon sequence** resulting from transcription of the section of the **normal HEXA allele** shown below.

DNA CGT ATA TCC TAT GCC CCT GAC …

GCA TAT AGG ATA CGG GGA CTG...

mRNA CGU AUA UCC \_\_\_\_\_ GCC \_\_\_\_\_ GAC ...

polypeptide Arg – Ile – Ser – Tyr – Gly – Pro – Asp ...

(b) Complete the **sequence of amino acids** resulting from the translation of the section of **mutated Tay Sachs HEXA allele** shown below.

DNA CGT ATA TC**T ATC** CTA TGC CCC TGA C...

GCA TAT AG**A TAG** GAT ACG GGG ACT G...

mRNA CGU AUA UCU AUC CUA UGC CCC UGA C...

polypeptide Arg – Ile – Ser – Ile – \_\_\_\_\_– Cys – \_\_\_\_\_ - Stop

(c) Explain how the insertion of four base pairs into the HEXA gene affects the **process of translation** and the **structure** of the gene product for children born with the Tay Sachs allele (you may refer specifically to alleles in parts (a) and (b))

Assessor’s use only

(d) Discuss the significance of the Tay Sachs mutation. In your discussion:

* Explain how a mutation in DNA can negatively affect the **catalytic role** of an enzyme
* Analyse the effect of the Tay Sachs mutation on the **third amino acid** to provide evidence of **redundancy due to degeneracy** in the genetic code

Assessor’s use only