

Molecular Genetics I (chapter 8)

Task 1 (error in the task: there is no arrow in the textbook indicating the origin of replication!)

the lagging strand: 5'-TTAACGCG

ATGGTCT-3'

TACCAGA-5'

the leading strand: 3'-AATTGCGC

DNA helicase moves directionally along the DNA phosphodiester backbone and separates the two annealed strands using energy derived from ATP hydrolysis. Helicase opens up the DNA at the replication fork.

DNA polymerase moves along the old (template) strand in the 3'-5' direction and creates a new strand from an RNA primer and nucleotides. RNA primers are removed and replaced with DNA by DNA polymerase I.

DNA ligase seals the gaps between two DNA fragments by catalyzing the formation of a phosphodiester bond between them.

RNA-polymerase primase makes an RNA primer, or short stretch of nucleic acid complementary to the template, that provides a 3' end for DNA polymerase to work on.

Okazaki fragments: As opposed to the continually synthesized leading strand, the lagging strand is synthesized in small fragments called Okazakiho fragments, which all need their own primer, while the leading strand needs just one primer.

RNA primer: a short RNA molecules created by primase that is needed by DNA polymerase to start synthesizing the new strand. A typical primer is about five to ten nucleotides long. The leading strand can be extended from one primer alone, whereas the lagging strand needs a new primer for each of the short Okazaki fragments. RNA primers are removed and replaced with DNA by DNA polymerase I.

Task 2

the coding strand: 5'-TTA-ACG-CGA-TGG-TCT-3'

- the noncoding strand: 3'-AAT-TGC-GCT-ACC-AGA-5'
- the mRNA: 5'-UUA-ACG-CGA-UGG-UCU-3'
- the polypeptide: Leu-Thr-Arg-Trp-Ser

Task 3

- 5'-AUG-AAA-AAA-AAA-AAA-AAA-AAA-AAA-AAA-AAA-AAA-AAU-GAA-AAA-AAA-AAA-AAA-AAA-AAA-AAA-AAA-UGA3'

Met-Lys-Lys-Lys-Lys-Lys-Lys-Lys-Lys-Lys-Asn-Glu-Lys-Lys-Lys-Lys-Lys-Lys-Lys-Lys-Lys-Lys-Lys-STOP

b. 5'-AUG-UUU-UUU-UUU-UUU-UUU-UUU-UUU-UUU-UUU-UUU-UUU-UUU-UUU-UUU-UUU-UUU-UUU-UUU-UUA-UGA3'

Met-Phe-Phe-Phe-Phe-Phe-Phe-Phe-Phe-Phe-Phe-Tyr-Val-Phe-Phe-Phe-Phe-Phe-Phe-Phe-Phe-Leu-STOP

c. 5'-AUG-CCC-CCC-CCC-CCC-CCC-CCC-CCC-CCC-CCC-CAU-GCC-CCC-CCC-CCC-CCC-CCC-CCC-CCC-CCA-UGC-CCC-CCC-CCC-CCC-CCC-CCC-CCC-CCC-AUG- ... 3'

(Met-Pro-Pro-Pro-Pro-Pro-Pro-Pro-Pro-Pro-His-Ala-Pro-Pro-Pro-Pro-Pro-Pro-Pro-Pro-Pro-Cys-Pro-Pro-Pro-Pro-Pro-Pro-Pro-Pro-Pro) ... indefinitely

d. 5'-AUG-GGG-GGG-GGG-GGG-GGG-GGG-GGG-GGG-GGG-GAU-GGG-GGG-GGG-GGG-GGG-GGG-GGG-GGG-GGG-GGG-GGG-GGA-UGG-GGG-GGG-GGG-GGG-GGG-GGG-GGG-GGG-GGG-AUG- ...3'

(Met-Gly-Gly-Gly-Gly-Gly-Gly-Gly-Gly-Gly-Asp-Gly-Gly-Gly-Gly-Gly-Gly-Gly-Gly-Gly-Gly-Trp-Gly-Gly-Gly-Gly-Gly-Gly-Gly) ... indefinitely

Task 4

combinations of U and C

a. UUU, UUC, UCU, CUU, CCC, CUC, UCC, CCU

b. UUU $\frac{8}{27}$, UUC $\frac{4}{27}$, UCU $\frac{4}{27}$, CUU $\frac{4}{27}$, CCC $\frac{1}{27}$, CUC $\frac{2}{27}$, UCC $\frac{2}{27}$, CCU $\frac{2}{27}$

c. Phe $\frac{12}{27}$, Ser $\frac{6}{27}$, Pro $\frac{3}{27}$, Leu $\frac{6}{27}$

Task 5

(Note, that the DNA sequence represents the coding strand)

a. AAAGA deletion at codons 1309-1311

wt: GAA-AAG-ATT-GGA-ACT-AGG = Glu-Lys-Ile-Gly-Thr-Arg

mt: GAT-TGG-AAC-TAG = Asp-Trp-Asn-STOP

frameshift mutation leading to premature termination of amino acid chain

b. C to T at codon 1339

wt: CAG = Gln

mt: TAG = STOP

nonsense mutation leading to premature termination of amino acid chain

c. A to T at codon 1349

wt: AGG = Arg

mt: TGG = Trp

missense mutation, different amino acid is incorporated in the newly synthesized protein

Task 6

5'-AGGATATGTTACTCTAAA(A)CAT-3' (the sequence in the textbook has one more A, but it is crossed so I assume it should not be there)

5'-AGG-ATA-TGT-TAC-TCT-AAA-CAT-3'

a. 7

b. tRNA anticodons: UCC-UAU-ACA-AUG-AGA-UUU-GUA

(if we accept the additional A in the sequence then: UCC-UAU-ACA-AUG-AGA-UUU-UGU)

Task 7

NH₂-Met-Glu-Trp-COOH

the coding (sense) strand: 5'-ATG-GAA-TGG-3' or 5'-ATG-GAG-TGG-3'

the noncoding (antisense) strand: 3'-TAC-CTT-ACC-5' or 3'-TAC-CTC-ACC-5'

the mRNA: 5'-AUG-GAA-UGG-3' 5'-AUG-GAG-UGG-3'

the polypeptide: Met-Glu-Trp

Met: AUG (only)

Glu: GAA or GAG

Trp: UGG (only)