

What is DNA Structure and How Does Replication Work?

Worksheet

DNA structure: two antiparallel strands (5'3' and 3'5') wound in a double helix, with bases adenine-thymine (A-T, 2 H-bonds) and guanine-cytosine (G-C, 3 H-bonds) pairing across. Replication: strands unwind, DNA polymerase III builds new complementary strands on each template (5'3' leading, 3'5' lagging), producing two identical DNA molecules.

Questions

1. If one strand of DNA is 5'-AATGC-3', the complementary strand is:

- A) 5'-AATGC-3'
- B) 5'-CGATT-3'
- C) 3'-TTACG-5'
- D) 3'-GCAAT-5'

2. In semiconservative replication of a double helix, after one round, you have:

- A) two DNA molecules with two new strands each
- B) two DNA molecules, each with one old and one new strand
- C) one DNA molecule with two new strands
- D) four single strands

3. Which enzyme unwinds the DNA double helix?

- A) DNA Polymerase III
- B) Helicase
- C) DNA Ligase
- D) Primase

4. Why is the leading strand synthesised continuously but the lagging strand discontinuously?

- A) The enzymes are different
- B) Different strands run in different directions, and DNA Pol III only works 5'3'
- C) Temperature differences
- D) It's actually arbitrary

5. A template DNA strand is 5'-ATCG-3'. What is the sequence of the newly synthesised complementary strand?

6. In semiconservative replication, how many parental DNA strands are in each of the two daughter DNA molecules?

7. Why is Okazaki fragment synthesis needed on the lagging strand?

8. Define: What are the two strands of DNA called?

9. Define: How many hydrogen bonds hold A-T together?

10. Define: How many hydrogen bonds hold G-C together?

Answer Key

1. C) 3'-TTACG-5' - Antiparallel: new strand is 3'-TTACG-5' (AT, TA, GC, CG).
2. B) two DNA molecules, each with one old and one new strand - Semiconservative: each daughter has 1 parental + 1 new strand.
3. B) Helicase - Helicase breaks hydrogen bonds between base pairs, unwinding the helix.
4. B) Different strands run in different directions, and DNA Pol III only works 5'3' - Template for leading is 3'5'; template for lagging is 5'3'. Pol III only makes 5'3', so lagging needs short fragments (Okazaki).
5. Template: 5'-ATCG-3' New strand synthesises 3'5' antiparallel 5'-CGAT-3' (or read 3'-TACG-5' correctly)
6. Each daughter molecule has: 1 original (parental) strand + 1 newly synthesised strand If you start with 2 parental strands, you end with 2 daughter DNA molecules, each hybrid.
7. DNA Pol III only synthesises 5'3' On the lagging strand, template runs 5'3' So short fragments (Okazaki) are made discontinuously, then ligated.
8. Antiparallel strands: one runs 5'3', the other 3'5', wound in a double helix.
9. Two hydrogen bonds (A-T pair).
10. Three hydrogen bonds (G-C pair is stronger).

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