

DNA replication · supported focus

International Baccalaureate · IB Diploma · Biology · SL

Scope and prerequisites

Supported SL focus. First assessment 2025; current subject brief acquired; full Biology guide not acquired. Remaining guide, assessment and practical requirements retain their recorded holds.

Prerequisites: read the stated quantities and units, use arithmetic and the model conditions below. Each lesson develops its own method before independent transfer.

These are original or explicitly fictional teaching examples, not actual measurements or completed assessed learner investigations.

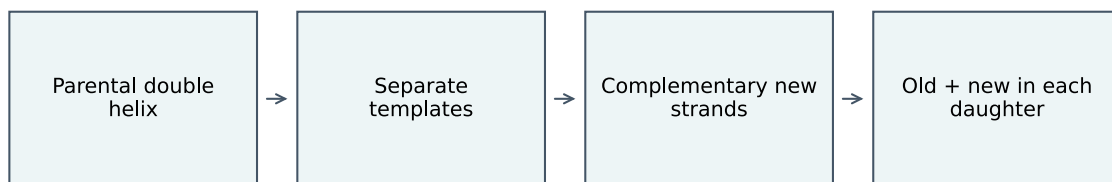
DNA replication: retain one strand in each daughter molecule

■ What would explain this observation?

- After DNA replication, each daughter double helix contains one pre-existing strand and one newly synthesized strand. Copying a molecule is different from expressing its information.
- Start with a prediction. State the quantities or features you would compare, then decide what evidence could distinguish two explanations.

■ Build the model

- DNA replication is semi-conservative. Complementary base pairing supports copying of the base sequence: adenine pairs with thymine and cytosine with guanine. The strands have opposite orientations. Helicase separates paired strands, while **DNA polymerase** DNA builds new DNA using a template and available nucleotides.
- **semi-conservative replication** : DNA copying in which each daughter double helix retains one parental strand; **DNA polymerase**: An enzyme that synthesizes DNA using a template.



■ Choose evidence that can test it

- Complementary bases support copying of the template sequence. Distinguish DNA copying from transcription into RNA and from separation of chromosomes in cell division. The labelled-strand prediction assumes complete replication rounds and no exchange or degradation of the original material. Detailed fork direction and fragment mechanisms remain in the separate HL preparation case pending guide review.
- Use labelled strand models or an attributed experimental diagram. Mark old and new material with both labels and colours so the meaning survives monochrome viewing. Track successive rounds using a stated starting population and assumptions. A classroom model illustrates predictions; it is not direct evidence about enzyme activity or a substitute for experimental results.

■ Work from known quantities

- State the known values and their units. Choose the relation because its assumptions fit this case, then rearrange before substitution.
- Known: one double-stranded molecule contains two labelled original strands. After one complete round in unlabelled nucleotides, two molecules each contain one labelled strand. After two rounds, four molecules exist: two retain one labelled original strand and two contain only unlabelled strands. The fraction containing an original strand is $2/4=50\%$.

Example:

One labelled double helix replicates for three complete rounds in unlabelled nucleotides. What percentage of the eight molecules contain an original strand? Use the same sequence: known quantities → model → relation → substitution → unit and interpretation.

■ Check the conclusion and its limits

- Replication uses DNA as a template to make DNA; transcription uses a DNA template to make RNA. A predicted label distribution assumes complete rounds and no degradation or exchange of the labelled material.
- Return to the original observation. Explain what the result supports, which conditions it assumes, and one way to test a competing explanation.

Warn:

DNA replication and transcription both produce the same type of nucleic-acid product. This claim is false: Replication uses DNA as a template to make DNA; transcription uses a DNA template to make RNA. A predicted label distribution assumes complete rounds and no degradation or exchange of the labelled material.

Key:

DNA replication: retain one strand in each daughter molecule: Complementary bases support copying of the template sequence. Distinguish DNA copying from transcription into RNA and from separation of chromosomes in cell division. The labelled-strand prediction assumes complete replication rounds and no exchange or degradation of the original material. Detailed fork direction and fragment mechanisms remain in the separate HL preparation case pending guide review.