

DNA and RNA Structure

Learning objective 6.1.A Describe the structure and function of DNA and RNA.

Name:

Date:

Period:

Use the tool **Two Strands, One Rule**. Part 1 uses **Build the partner strand**, Part 2 uses **Where Chargaff comes from** and Part 3 uses **Which molecule is it?**. Almost everything in this topic follows from one rule — **A pairs with T, G pairs with C** — plus the fact that the two strands run in opposite directions. Derive rather than memorise.

Part 1 • Write the partner strand

Work each row out on paper first: take the complement of the given strand, then **reverse it**, because the partner is read from the other end. Then check with **Build the partner strand**.

Given strand (5'→3')	Complement	Partner strand (5'→3')	GC %	H-bonds
ATGCCGTA				
GGCCTAAG				
TTAATTAA				
GCGCATGC				

1. Explain what “antiparallel” means, and why the partner strand has to be written backwards.

2. Two of your strands have the same length but different hydrogen-bond totals. Identify them and explain the difference.

Part 2 · Where Chargaff's rules come from

Open **Where Chargaff comes from** with **ATGCGATACG** in the box. Record the base counts twice — once counting your strand only, and once counting both strands.

	A	T	G	C	A = T?	G = C?
One strand only						
Both strands						

3. State Chargaff's rules, including the condition under which they hold.

4. Explain why counting both strands makes $A = T$ unavoidable, rather than merely likely.

5. A double-stranded DNA sample is 32% guanine. Calculate the percentage of each of the other three bases, and show your reasoning.

Part 3 • Which molecule is it?

Switch to **Which molecule is it?**. For each sample, answer the two questions in order and then name the molecule.

Sample	Thymine or uracil?	So it is	Complementary bases equal?	So it is
Sample 1				
Sample 2				
Sample 3				
Sample 4				

6. Explain why neither question on its own is enough to identify a nucleic acid.

7. A student says “uracil means RNA, and RNA is single-stranded.” Using your table, explain what is right and what is wrong about that.

Part 4 · Putting it together

These do not need the tool.

8. Name the three parts of a nucleotide, and state which one differs between one nucleotide and the next.

9. Explain why every base pair joins a purine to a pyrimidine, and what this means for the shape of the double helix.

10. Explain why a region of DNA rich in G and C requires a higher temperature to separate its strands than an AT-rich region of the same length.

11. Compare DNA and RNA in terms of sugar, bases and number of strands, and relate each difference to the job the molecule does.

What the model simplifies

The ladder is drawn flat. Real DNA is a double helix with a major and a minor groove, and the twist matters to the proteins that read it — but nothing on this page depends on the twist, so it is left out.

Hydrogen bonds are counted as two per A-T pair and three per G-C pair. That is the standard figure and it is what makes GC-rich DNA harder to separate, but real melting temperature also depends on which bases are next to each other, on length and on the surrounding salt concentration.

'RNA is single-stranded' is the usual summary and is right about messenger RNA, but a single RNA strand routinely folds back and pairs with itself — that is how transfer RNA and ribosomal RNA get their shapes. One of the identification samples is a genuinely double-stranded RNA, which some viruses have.

Base counts in the identification samples are whole numbers chosen so the arithmetic is checkable. A real measurement would carry error, and 22 against 23 would not by itself rule out a paired molecule.