



i. A sequence in which the “top” strand read from 5’ to 3’ is the same as the bottom strand read from 5’ to 3’.

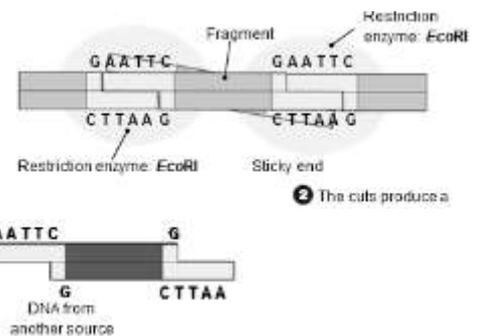
ii. Each different restriction enzyme (and there are hundreds) has its own restriction site. The ends of the DNA produced after being cut with a restriction enzyme can be either “\_\_\_\_\_ or \_\_\_\_\_”

Restriction Enzyme	Restriction site	Sticky or Blunt
EcoRI	5' GAATTC 3' 3' CTTAAG 3'	
BamHI	5' GGATCC 3' 3' CCTAGG 5'	
HindIII	5' AAGCTT 3' 3' TTCGAA 5'	
AluI	5' AGCT 3' 3' TCGA 5'	
SmaI	5' CCCGGG 3' 3' GGGCCC 5'	
HhaI	5' GCGC 3' 3' CGCG 5'	

7. When scientists study a DNA molecule, one of the first things they do is figure out where many restriction sites are. They then create a “\_\_\_\_\_”, showing the locations of cleavage sites for many different enzymes.

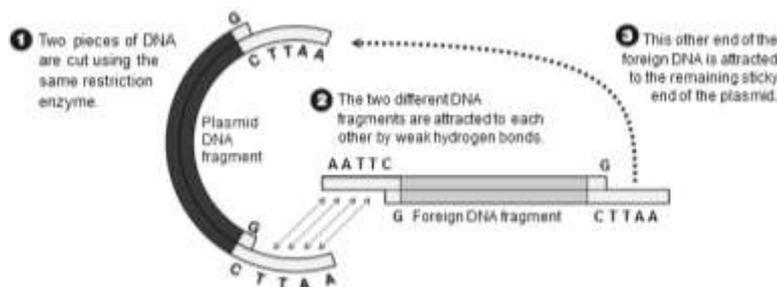
8. DNA cut in such a way to produce ends which may only be joined to \_\_\_\_\_ with a complementary base sequence

- Restriction enzymes cut the \_\_\_\_\_ DNA molecule at its specific recognition site.
- The cut produces a DNA fragment with two \_\_\_\_\_
- The fragments of DNA are joined by \_\_\_\_\_



9. When two matching “sticky ends” come together, they join by a base pairing process called \_\_\_\_\_

- This allows \_\_\_\_\_ from a different source, such as plasmids, to be joined to the \_\_\_\_\_.
- The joined fragments usually form a \_\_\_\_\_ molecule or a \_\_\_\_\_ molecule



10. DNA fragments produced using RE are reassembled by a process called \_\_\_\_\_.

- Pieces of DNA are joined together using the enzyme \_\_\_\_\_

