

## Initiation

Replication begins at a location on the double helix known as “oriC” to which certain initiator proteins bind and trigger unwinding. Enzymes known as helicases unwind the double helix by breaking the hydrogen bonds between complementary base pairs, while other proteins keep the single strands from rejoining. The “topoisomerase” proteins surround the unzipping strands and relax the twisting that might damage the unwinding DNA. The cell prepares for the next step, elongation, by creating short sequences of RNA called primers that provide a starting point of elongation.

## Elongation

With the primer as the starting point for the leading strand, a new DNA strand grows one base at a time. The existing strand is a template for the new strand. For example, if the next base on the existing strand is an A, the new strand receives a T. The enzyme DNA polymerase controls elongation, which can occur only in the leading direction. The lagging strand unwinds in small sections that DNA polymerase replicates in the leading direction. The resulting small “Okazaki fragments” can contain 1,000 to 2,000 bases in bacteria, but eukaryotes -- organisms having cells with nuclei -- have fragments of only 100 to 200 bases. The fragments terminate in an RNA primer that is subsequently removed so that enzymes can stitch the fragments into an elongating strand.

## Termination

After elongation is complete, two new double helices have replaced the original helix. During termination, the last primer sequence must be removed from the end of the lagging strand. This last portion of the lagging strand is the telomere section, containing a repeating non-coding sequence of bases. Enzymes snip off a telomere at the end of each replication, leading to shorter strands after each cycle. Finally, enzymes called nucleases “proofread” the new double helix structures and remove mispaired bases. DNA polymerase then fills in the gaps created by the excised bases.

### Question 2

Topoisomerase — Relaxes the super-coiled DNA

DNA helicase— Unwinds the double helix at the replication fork

Primase— Provides the starting point for DNA polymerase to begin synthesis of the new strand

DNA polymerase— Synthesizes the new DNA strand; also proofreads and corrects some errors

DNA ligase— Re-joins the two DNA strands into a double helix and joins Okazaki fragments of the lagging strand