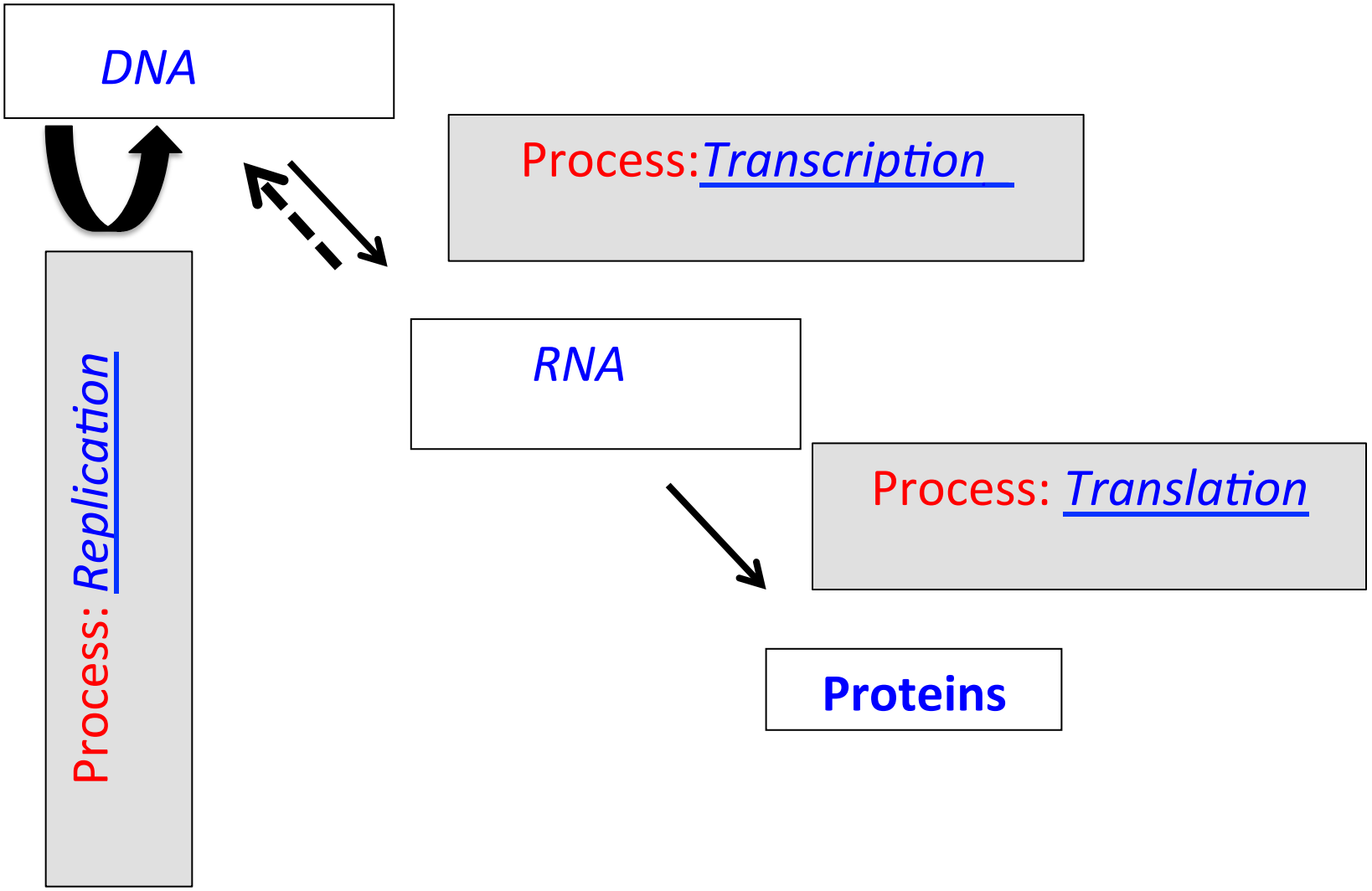
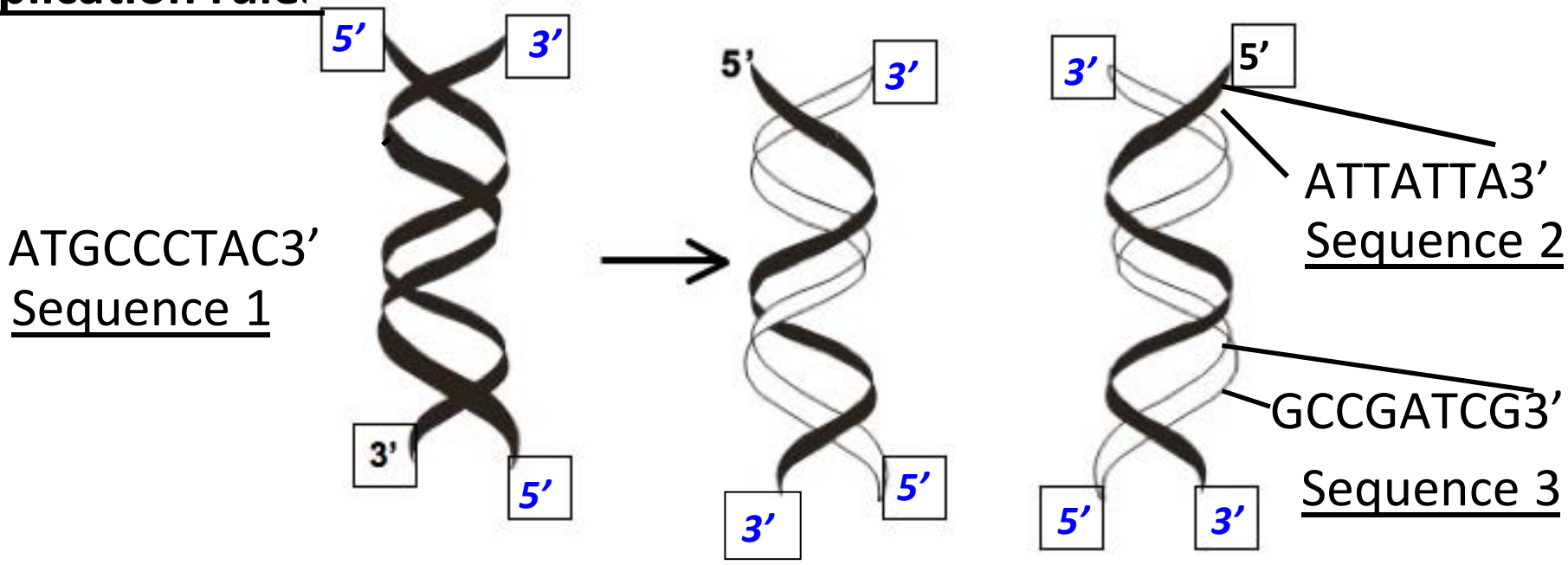
# Central Dogma

Relation between DNA, RNA and proteins



**Replication rules**




Label 5' and 3' (strands are anti-parallel).

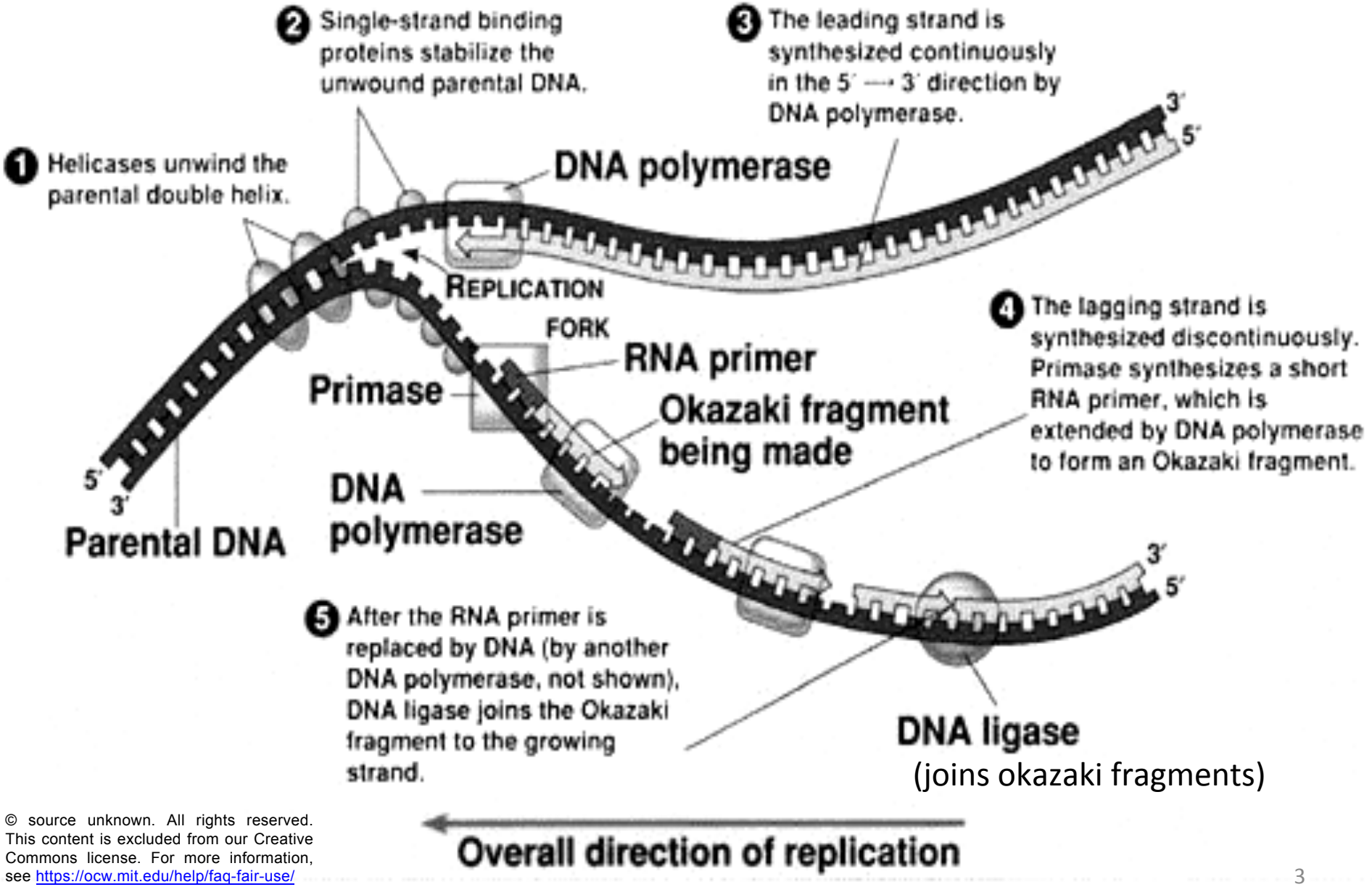
Circle one. Replication is Conservative or *Semiconservative*.

Sequence complementary to sequence 1: 5'*GTAGGGCAT*3'

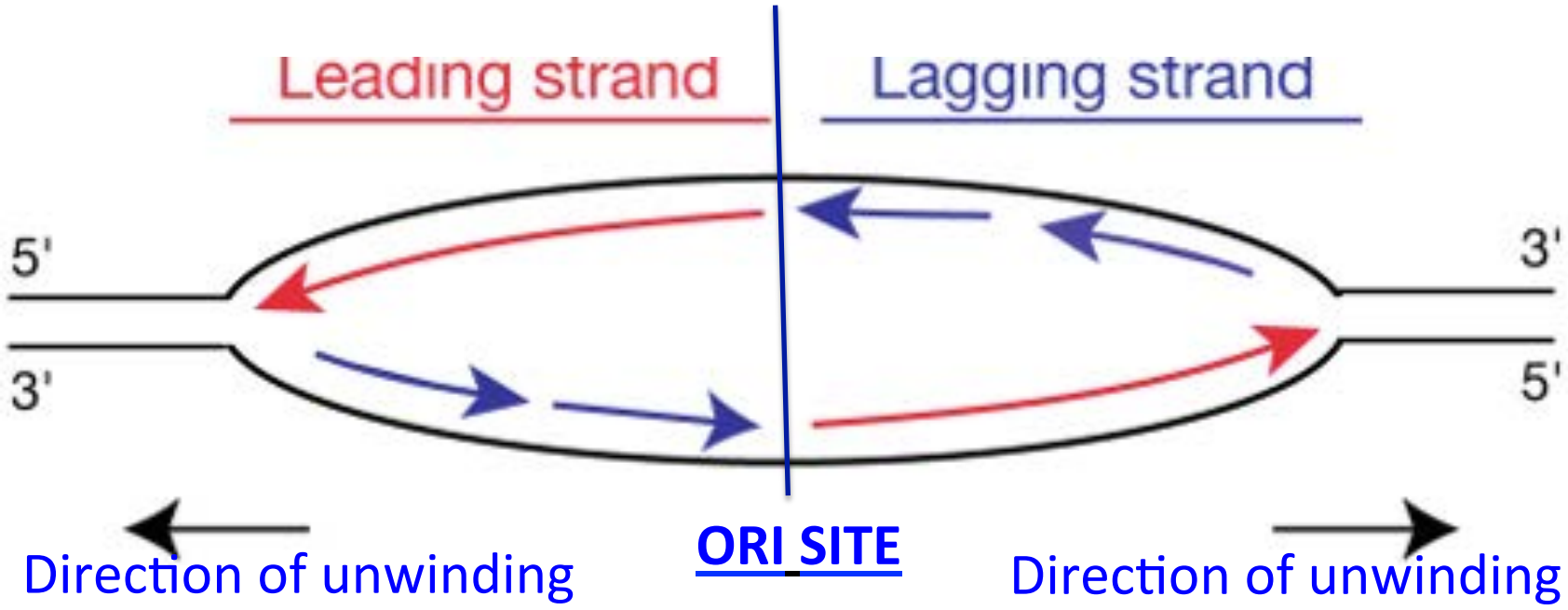
Complementary sequences base pair by *Hydrogen* bonds.

Circle one. Sequence 1/ 2/ 3 is most likely to be the ori site. *Sequence 2*

# Summary slide: Replication steps and enzymes



# Replication is bidirectional




DNA polymerase (DNAP) has a 5'->3' polymerization activity

DNAP in cell is primase dependent, i.e. adds nucleotides to 3'OH end of RNA primer

For the replicating double stranded DNA within a cell….

5′ATGAATGTGTGC3′ TOP STRAND
3′TACTTACACACG5′ BOTTOM STRAND

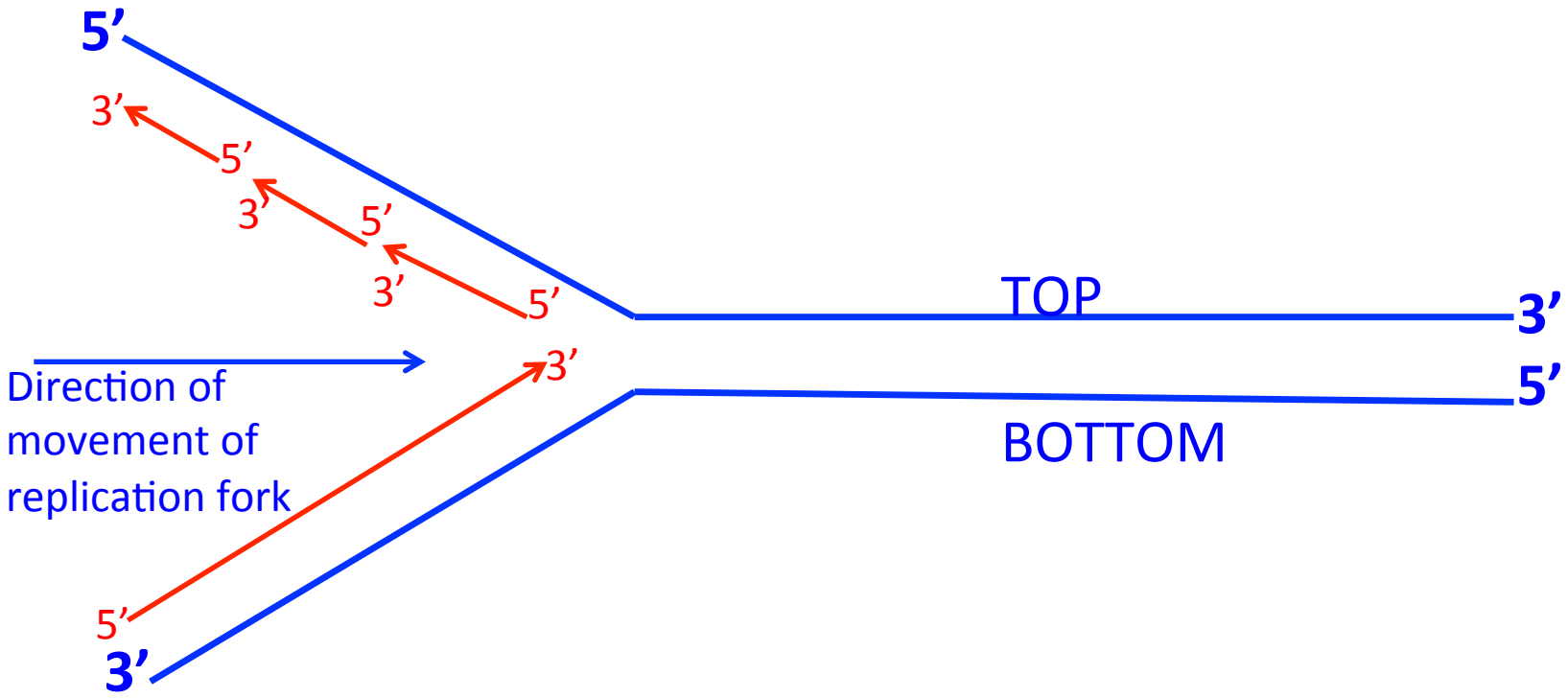
Show the direction of synthesis of new DNA strand by an arrow if the Bottom strand was the template.

Give the complementary base sequence if the TOP strand was the template. ***5'GCACACATTCAT3'***

Give a 5 base long primer if the TOP strand was the template.
**5' _GCACA 3'**

Circle the base on the primer above to which DNAP will add the next (incoming) base. *It binds the "A" at the 3'OH end*

# A replication fork is shown




Template strand for leading strand synthesis: Top Bottom

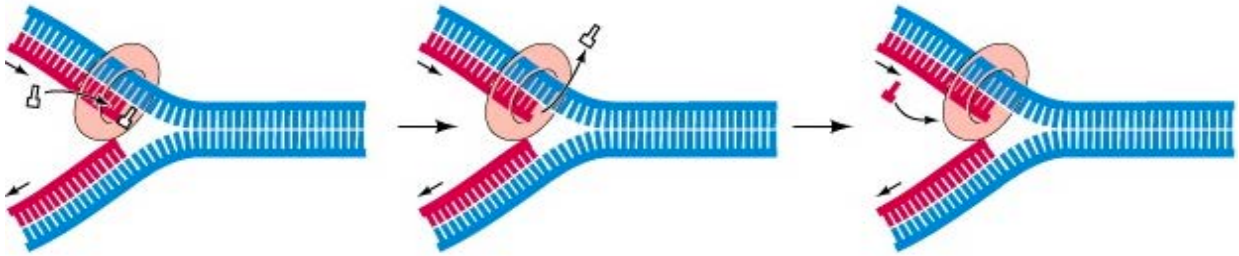
Template strand for lagging strand synthesis: Top Bottom

Draw the new leading strands and okazaki fragments on schematic.

Show the direction of movement of replication fork by an arrow

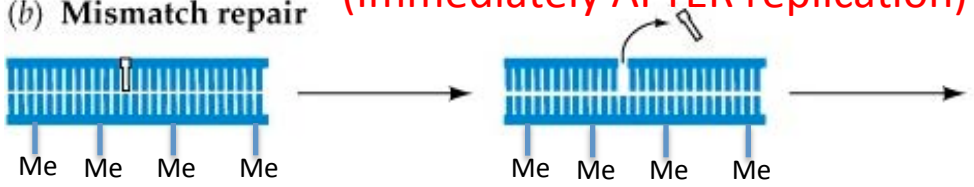
# Summary Slide: DNA Repair mechanisms

(a) DNA proofreading (During replication)



Involves 3'->5' exonuclease and 5'->3' polymerizing activity of DNA polymerase

(b) Mismatch repair (Immediately AFTER replication)



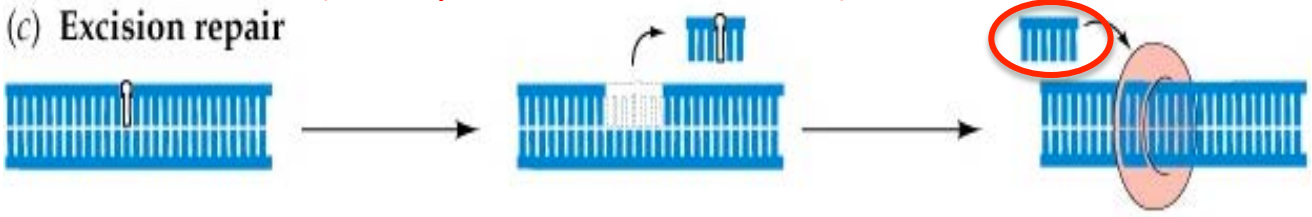

Mismatched base removed

-DNA polymerase adds base
-Ligase seals the gap

Methylated strand

(c) Excision repair (Example: T-T dimerization)

Bases around T-T dimer removed



-DNA polymerase adds bases
-Ligase seals the gap

Sequence of a newly replicated DNA duplex...

5′GTCCAAATGCTAC3′ Hypo-methylated top strand
3′CAGGGTTACGATG5′ Methylated bottom strand

- Sequence can be repaired by:
Proofreading *Mismatch repair* Excision repair

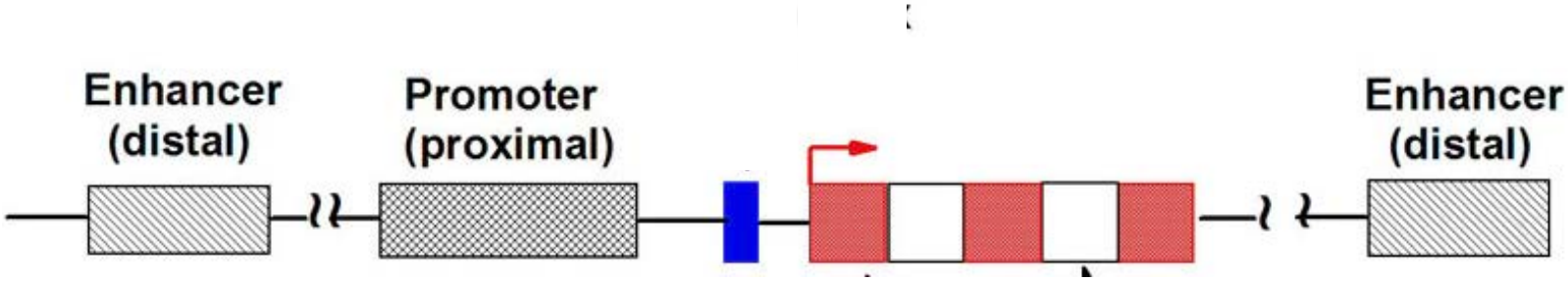
-Circle the incorrect base above. *Underlined"A" is the incorrect base*

-Enzyme(s) removing the incorrect base: *Mismatch repair enzymes*

-Enzyme(s) adding the correct base: *DNA polymerase*

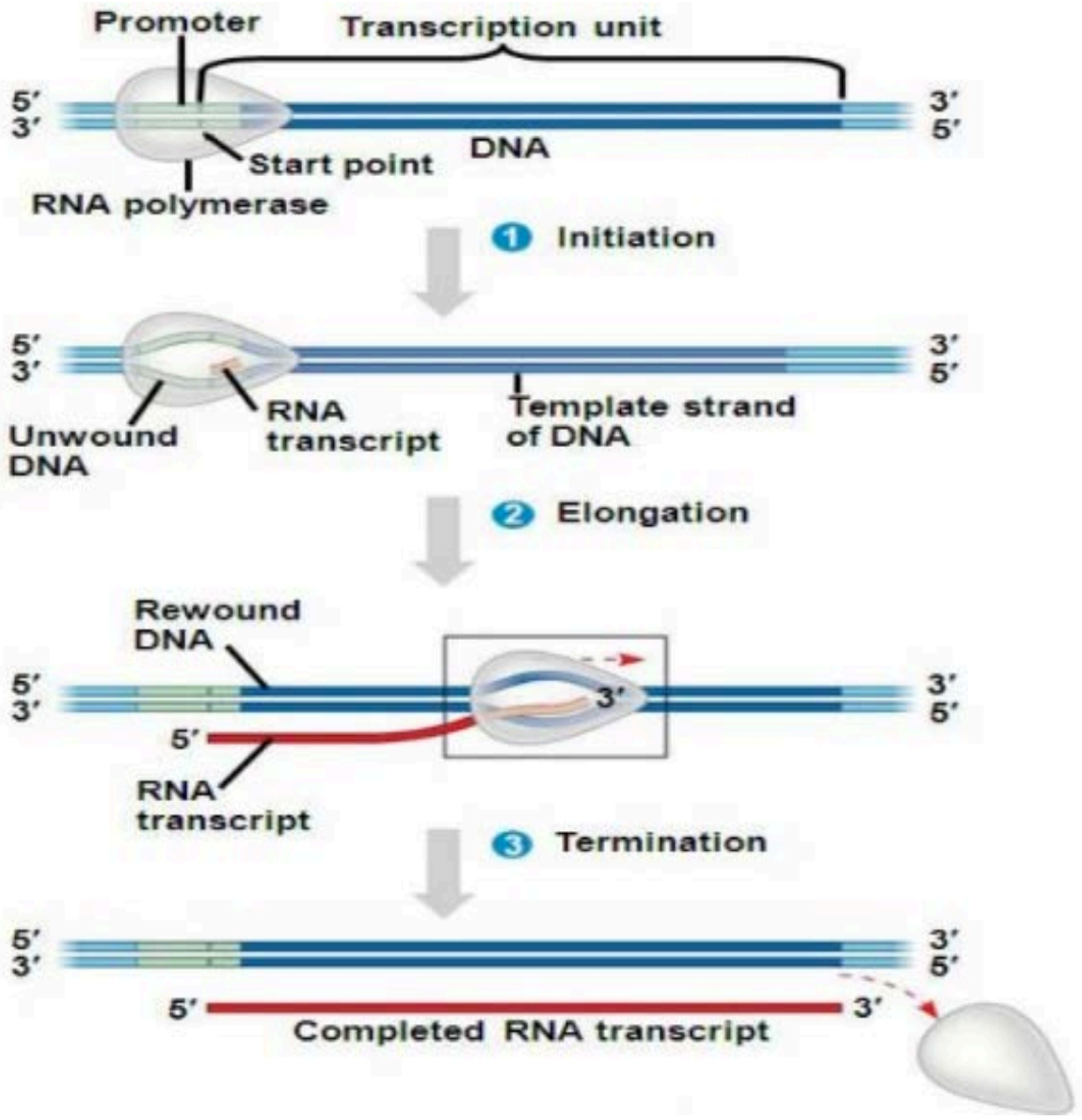
-Enzyme(s) sealing the gap: *DNA ligase*

Summary slide: A Eukaryotic gene

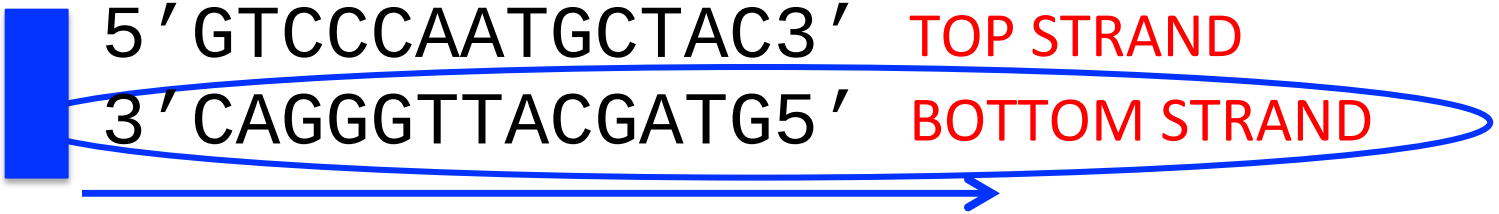



- Enhancer, a distal regulatory element
- Promoter, binding site  for RNA polymerase and transcription factors
- Shaded boxes (after arrow) = exons
- Open boxes (after arrow) = introns

# Summary slide: Transcription



Sequence of a small gene (DNA)...




Transcribed RNA from this gene…

5′GUCCCAAUGCUAC3′ RNA (contains U, not T)

- Circle the template strand on gene (RNA is complementary to the template)

-Draw an arrow in the direction of transcription of this gene (nucleic acid is polymerized 5' → 3')

-Draw a Box to the LEFT or RIGHT of the gene to show the promoter (promoter is prior to transcribed sequence)

-Shade the binding site of RNA polymerase and transcription factors *It's the promoter region*

mRNA sequence corresponding to a small gene...

5′CUCGGAUCGUA3′

- Give the sequence of the corresponding gene.

Promoter


-Arrow the direction of transcription on the gene

-Draw a Box to the LEFT or RIGHT of the gene to show the promoter

-Circle the correct option(s). A mutation in the promoter sequence affects which of the following?

- The rate of transcription
- Amount of protein produced
- Sequence of protein produced

Mark the statements below as True ('T') or False ('F').
In our body…

- All cell types have the same genes *True*
- All cell types express the same genes *False*
- Cell types vary in amount and types of Transcription Factors *True*
- Heat shock can influence/alter the transcription of genes *True*
- Methylation of bases promotes transcription *False*
- Removal of histones promotes transcription *True*
- Histone modifications alter transcription *True*
- Histone and base methylation alter the DNA sequence *False*
- Imprinted genes in a cell are likely silenced *True*
- Imprinting is faithfully maintained through mitosis *True*