

BI 8 LECTURE 13

REPAIR, ENGINEERING, SUBVERSION, AND EVOLUTION: MANY USES OF DNA RECOMBINATION

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16 February 2016

Reading for this week: Alberts et al. Ch. 5

Unfinished
business: a unique
problem at the end
of linear
chromosomes

how do you prime
replication of the last
few bases of the
lagging strand?

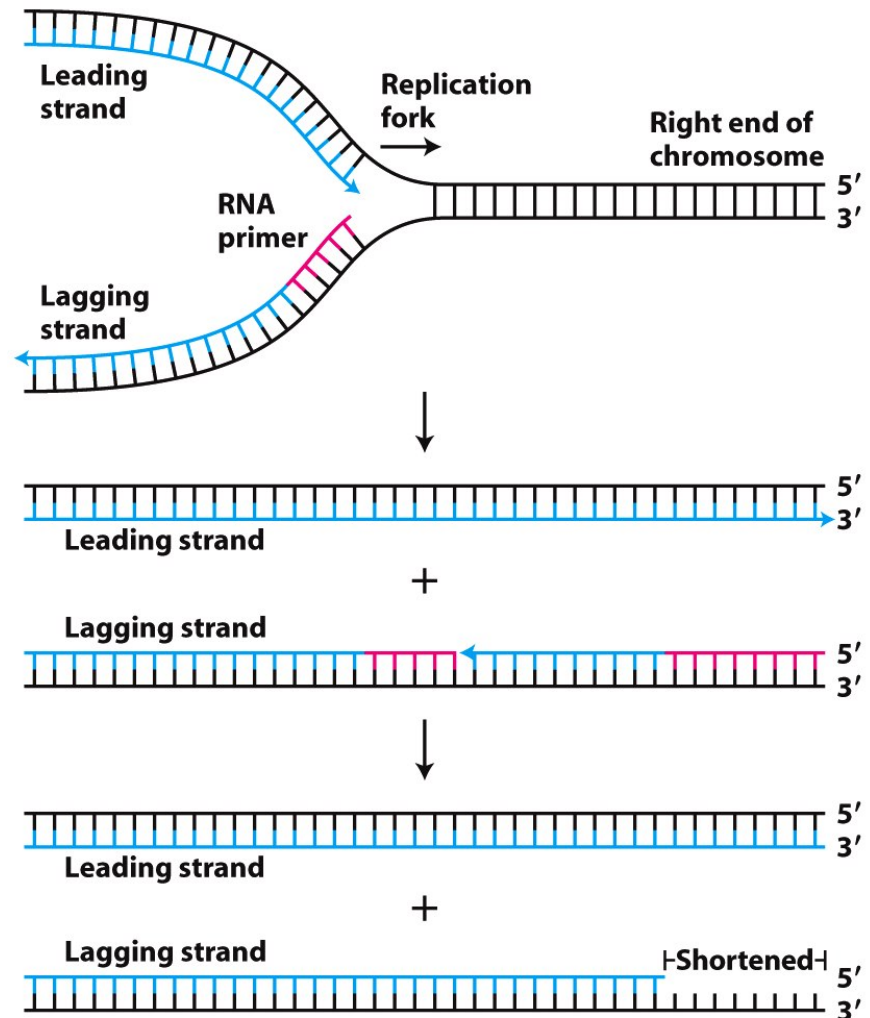


Figure 6-48
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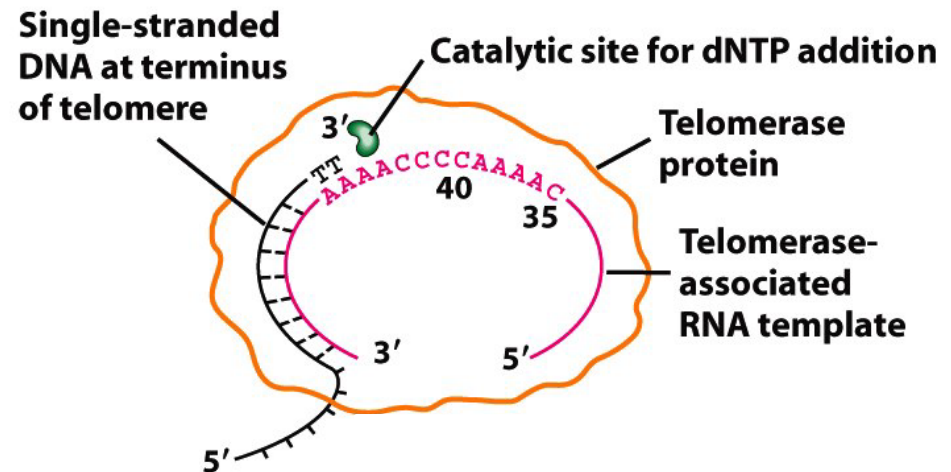
A special simple-sequence repeat element at ends of chromosomes and a special ribonucleoprotein enzyme, **TELOMERASE**, make it possible to solve this problem

Ends of chromosomes consist of tandem repeats of simple sequences:

$(TTAGGG)_n$
($n=800-2500$ in human germ cells, declining in differentiated cells with age)

$((TG)_{1-3}(TG)_{2-3})_n$
($n= 50-75$ in brewer's yeast *Saccharomyces cerevisiae*)

Telomerase uses these repeats as templates to restore ends and may even extend the number of repeats at certain cell cycles



Telomerase is a “reverse transcriptase”: a DNA polymerase that uses RNA template... and in this case the RNA template is part of the telomerase enzyme

Using repeat sequences, telomerase makes RNA templates for elongation of terminal lagging-strand template beyond original end

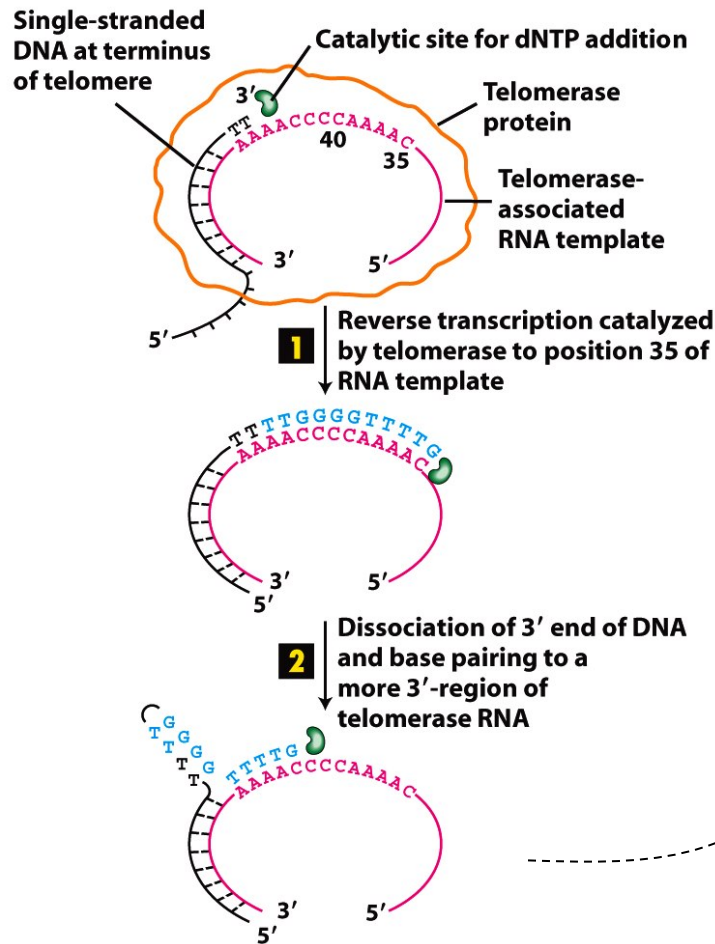


Figure 6-49 part 1
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Plenty of DNA now for primase, DNA pol to work on!

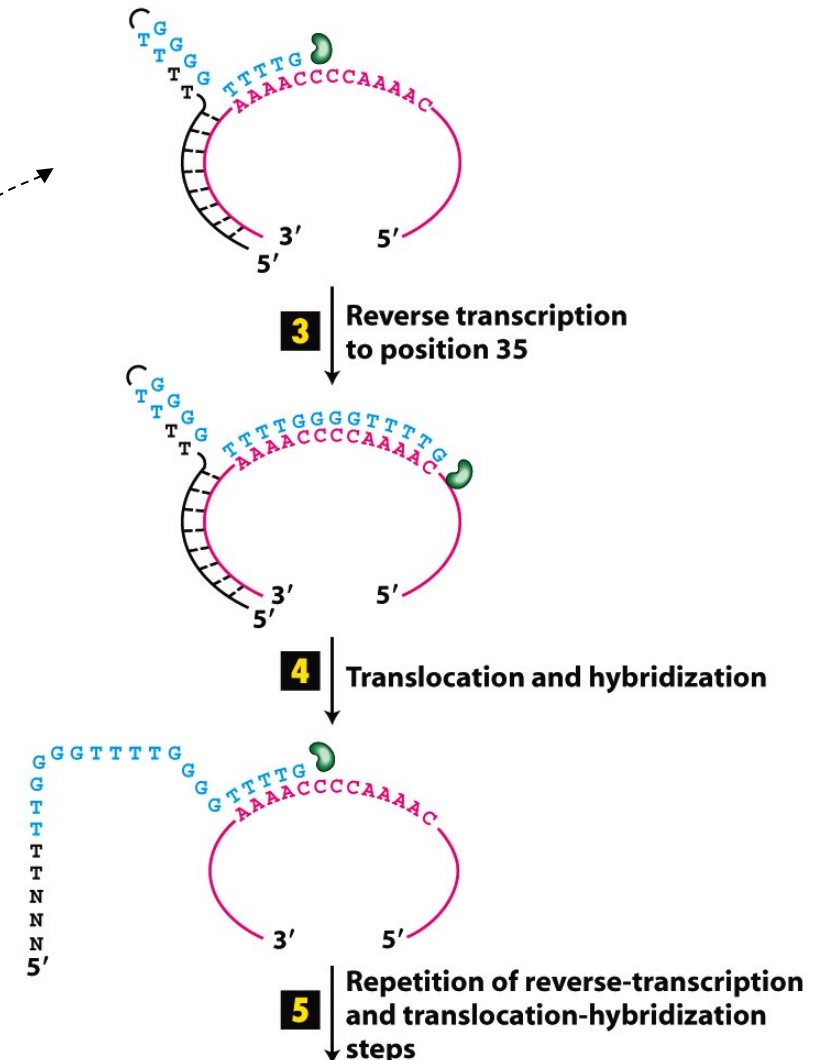
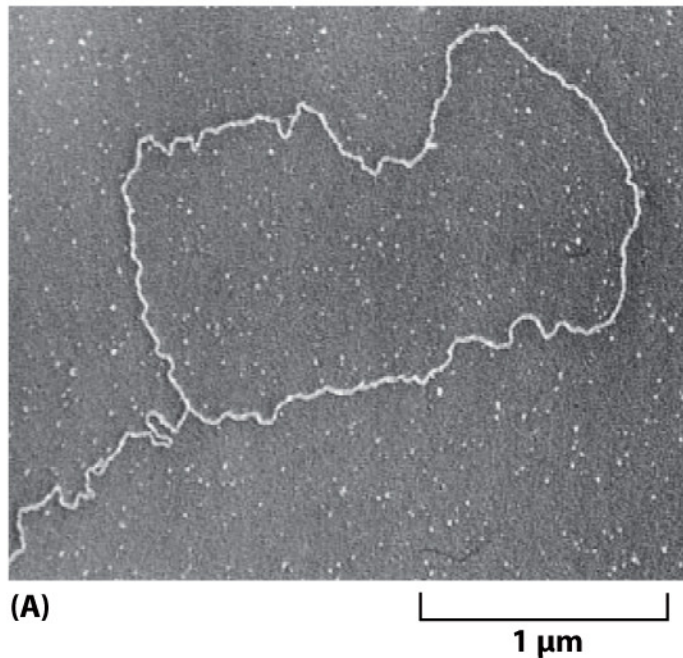


Figure 6-49 part 2
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After extending the telomeres, there's still a ragged end ... but it is then “bundled” into a safe nuclease-resistant loop structure



(Telomerase-mediated end extension might have started way back here)

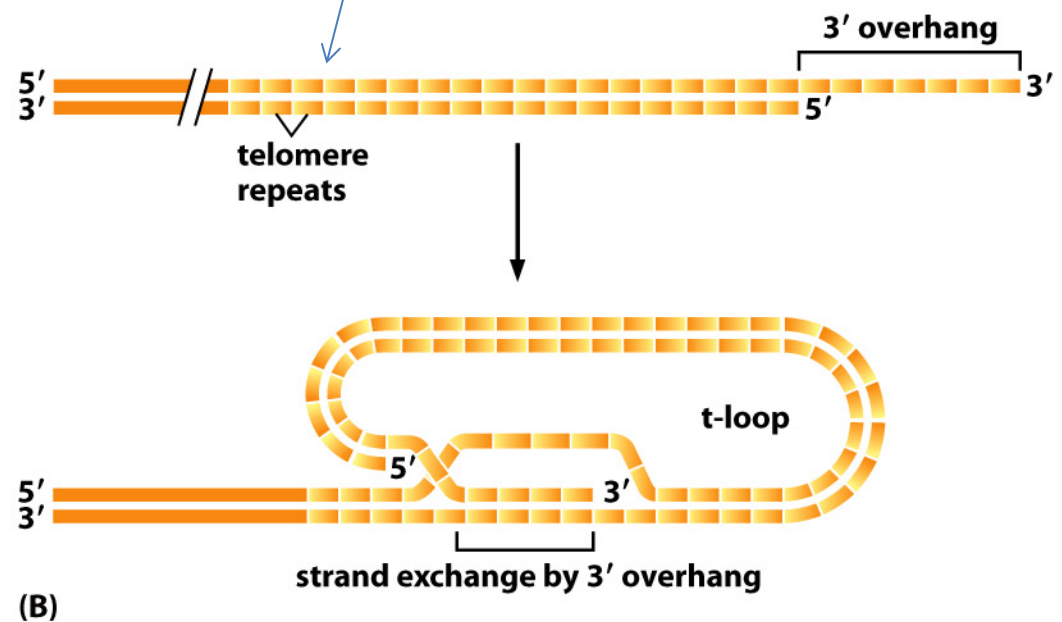


Figure 5-35 Molecular Biology of the Cell 6e (© Garland Science 2015)

Telomerase is expressed specifically by cells that need to self-renew without senescence

- Most cells in our bodies lose telomere repeats slowly with successive rounds of cell division: internal aging clocks
- Stem cells and germ cells are principal sites of telomerase activity in humans
- Some immune cells specialized for retaining “memory” over many years are induced to express telomerase during cell division
- Normally, lack of telomerase protects against cancer... reactivation of expression in tumor cells is a key event in oncogenic transformation

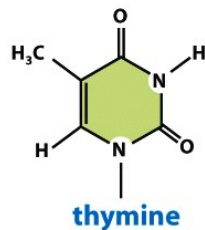
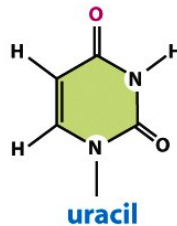
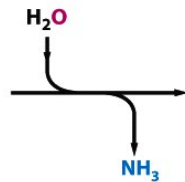
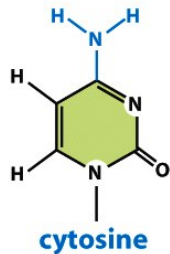
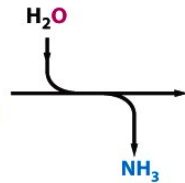
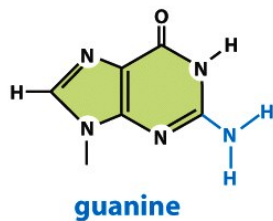
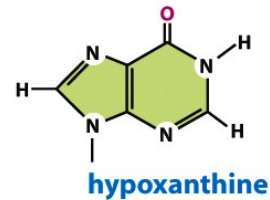
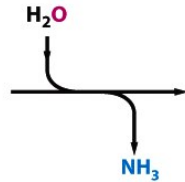
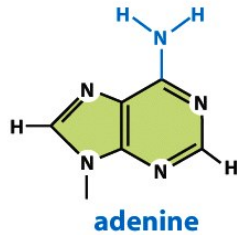
Reasons why DNA needs repair

- DNA breaks (e.g. due to radiation or chemicals)
- Mistakes during replication that escape proofreading
- Single-base damage or pyrimidine dimer formation (UV radiation or chemical damage)

All can result in mutations if not corrected

The problem of damage: even correct bases in DNA can become dysfunctional due to chemical damage

NATURAL DNA BASES

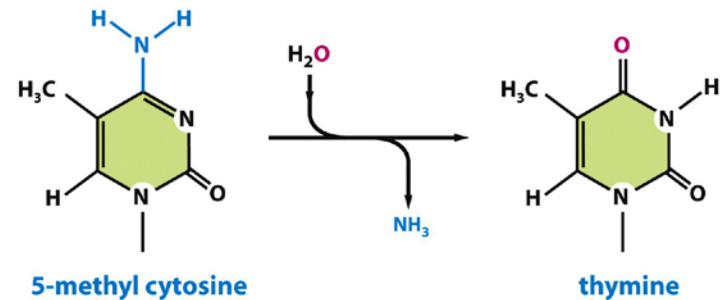


NO DEAMINATION

UNNATURAL DNA BASES

Often by hydrolytic deamination

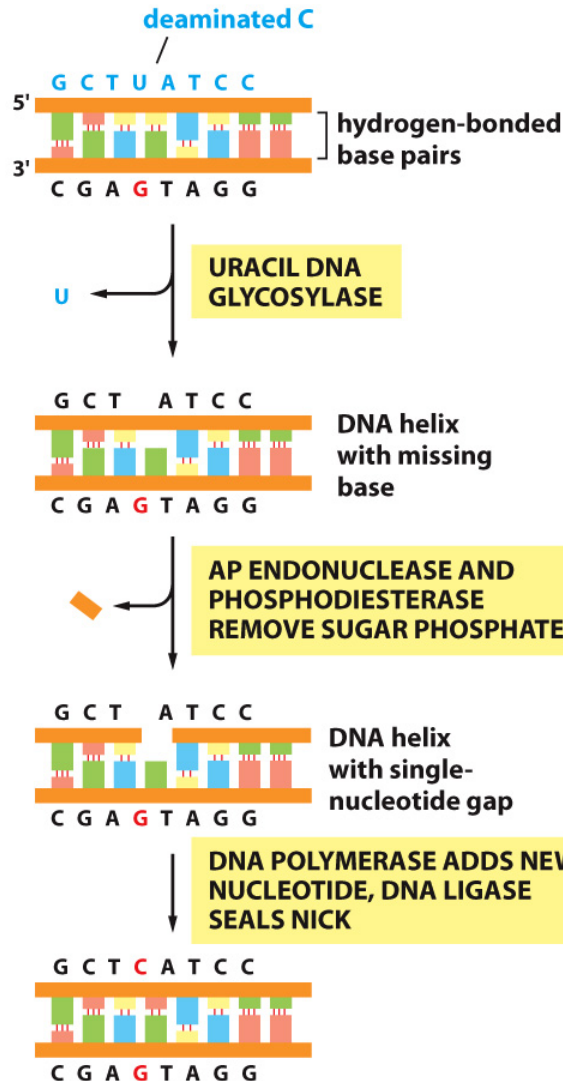
Note: when methylated C is deaminated, there is nothing to show that the base formed is “unnatural”!



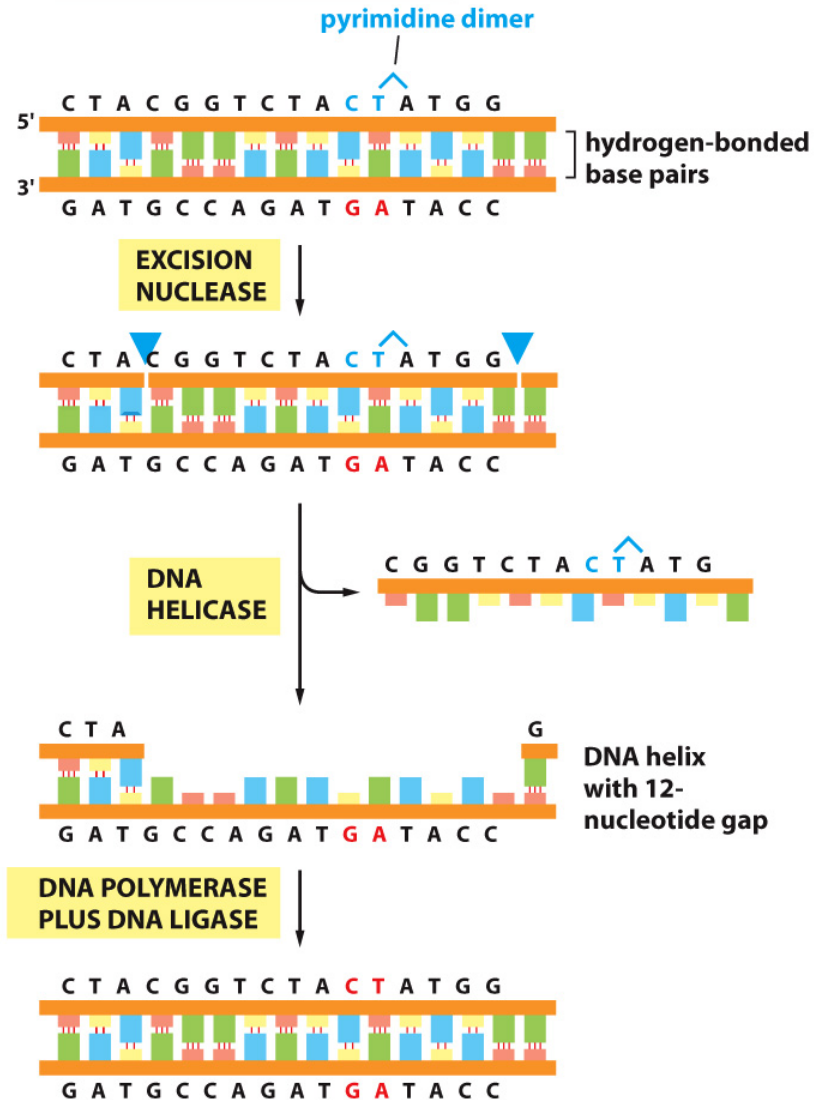
High frequency mutation!

Specialized repair systems excise defective base or region: then DNA is filled in by polymerase, sealed by ligase

(A) BASE EXCISION REPAIR



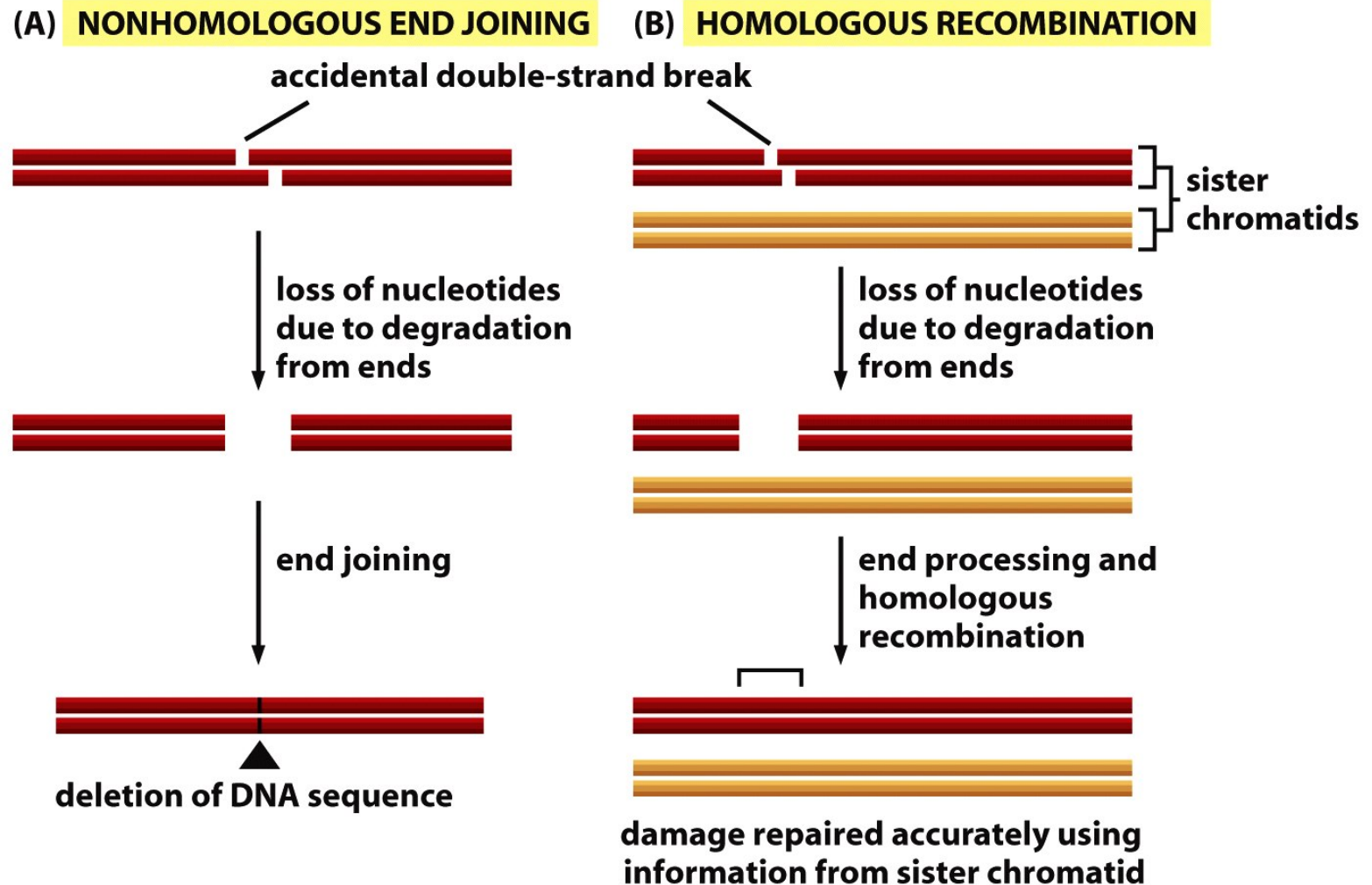
(B) NUCLEOTIDE EXCISION REPAIR



The secret sculptor of genomes: recombination

- Crucial for large-scale lesion repair in DNA
- Creates much evolutionary change in genome size and gene order
- Starts with a DNA break, and “search” of a broken denatured DNA strand for something to anneal to as template for extension/repair
- Different types of possibilities based on how long a hybrid the “searcher” needs to find before being able to be ligated

Two major forms of recombination: different problems to solve, different enzymatic solutions



Key features of homologous recombination

- Requires that broken DNA can find another highly similar, undamaged copy to use as template for repair
- Substantial length of ***sequence identity*** provides the site for the recombination
- Broken DNA is first processed to generate protruding 3' single strand at break: “invader” and primer for repair synthesis
- Conservative mode of recombination: same homologous sequence that was used to target recombination ends up copied faithfully in ***both*** product DNA molecules

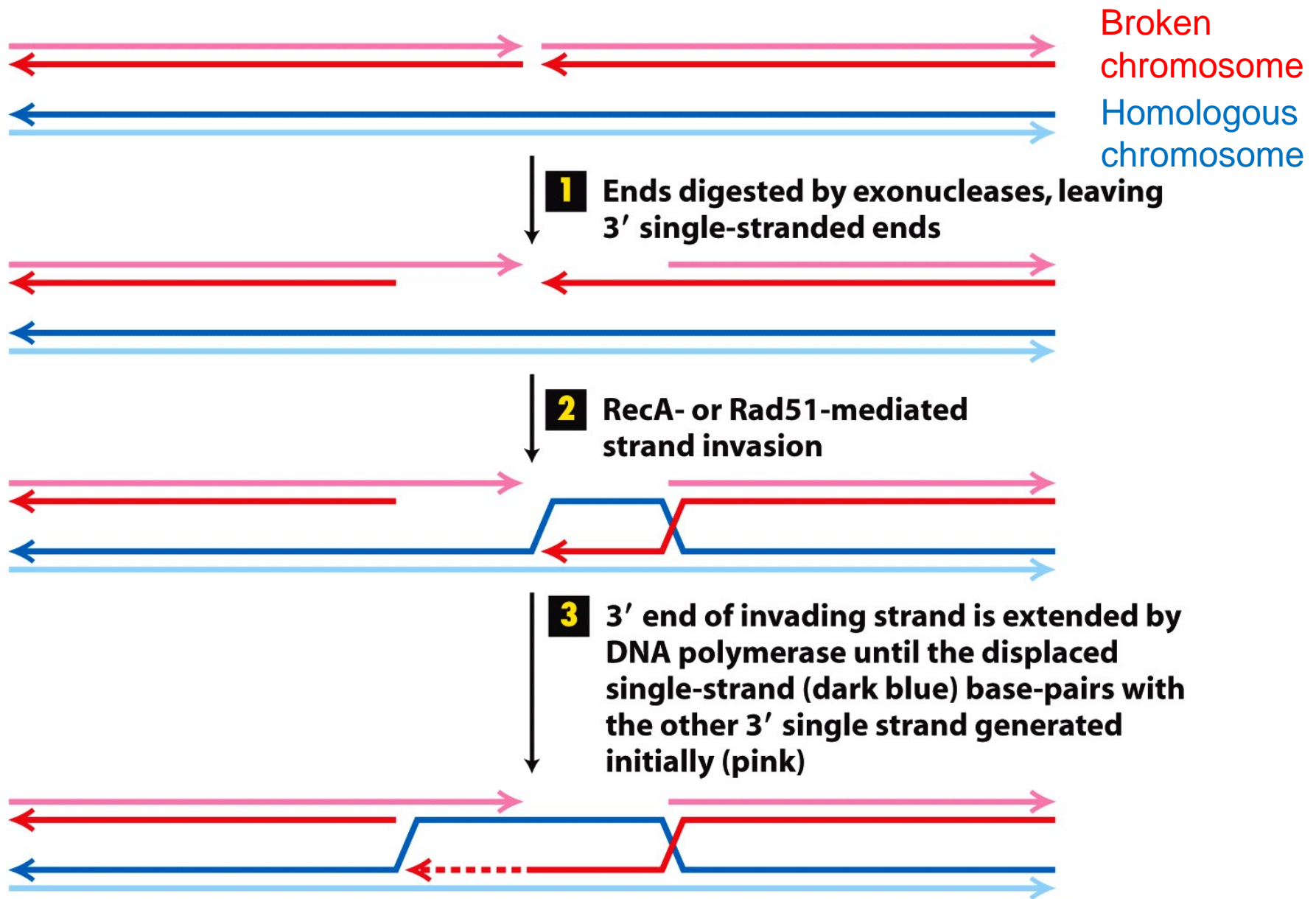


Figure 4-42 part 1
Molecular Cell Biology, Sixth Edition
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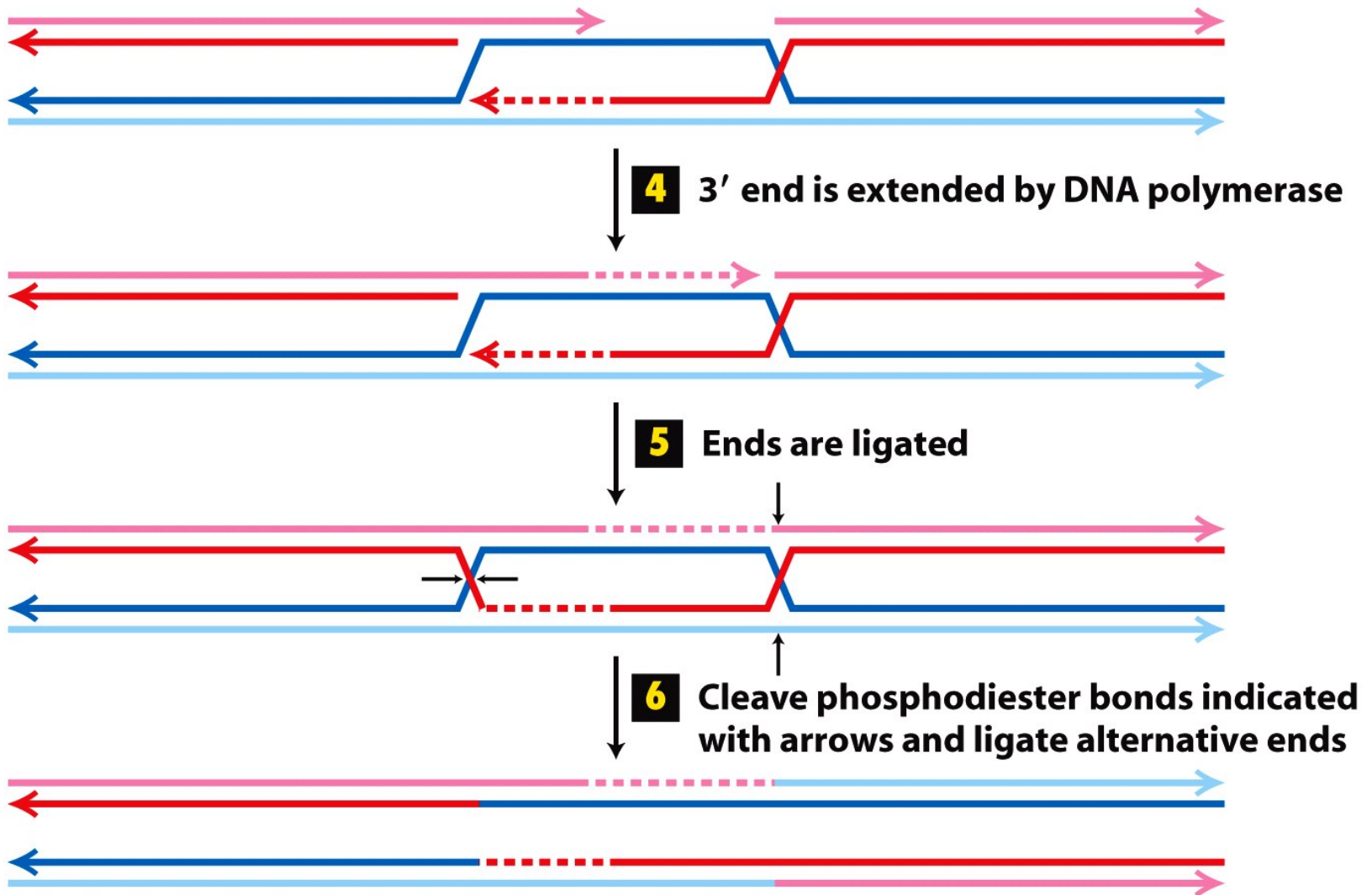
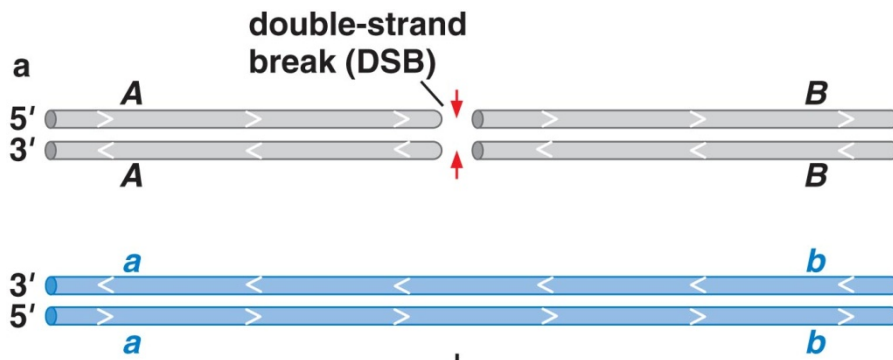
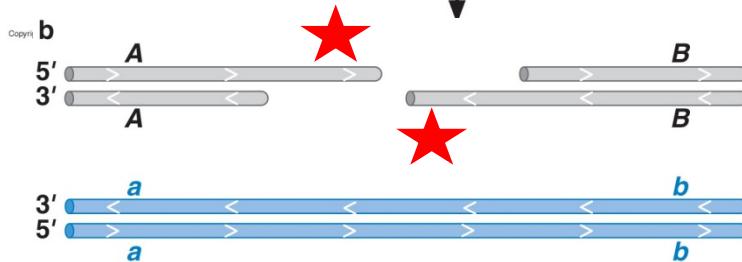


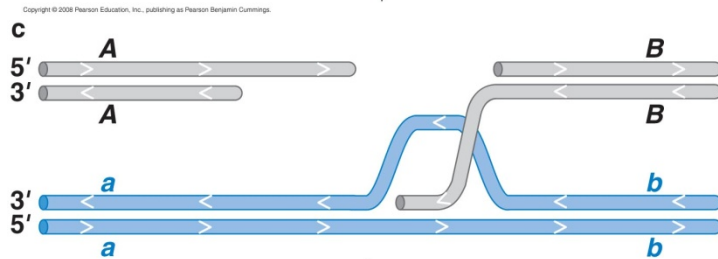
Figure 4-42 part 2
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processing to
generate gapped
DNA with 3' ss tails

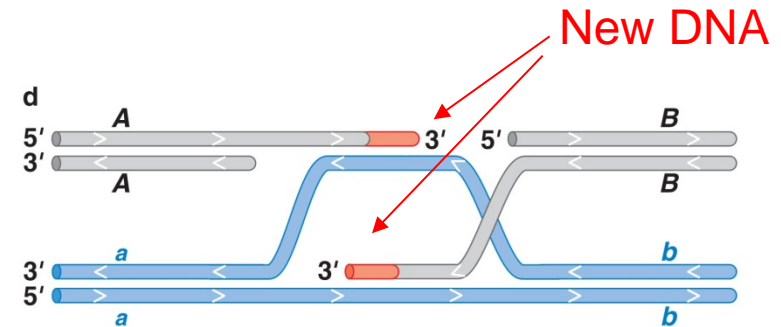


strand invasion
of 3' end

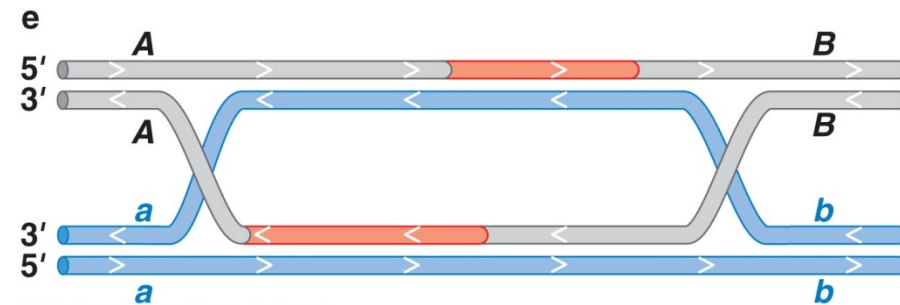


second strand
invasion and DNA
repair synthesis
from 3' ends

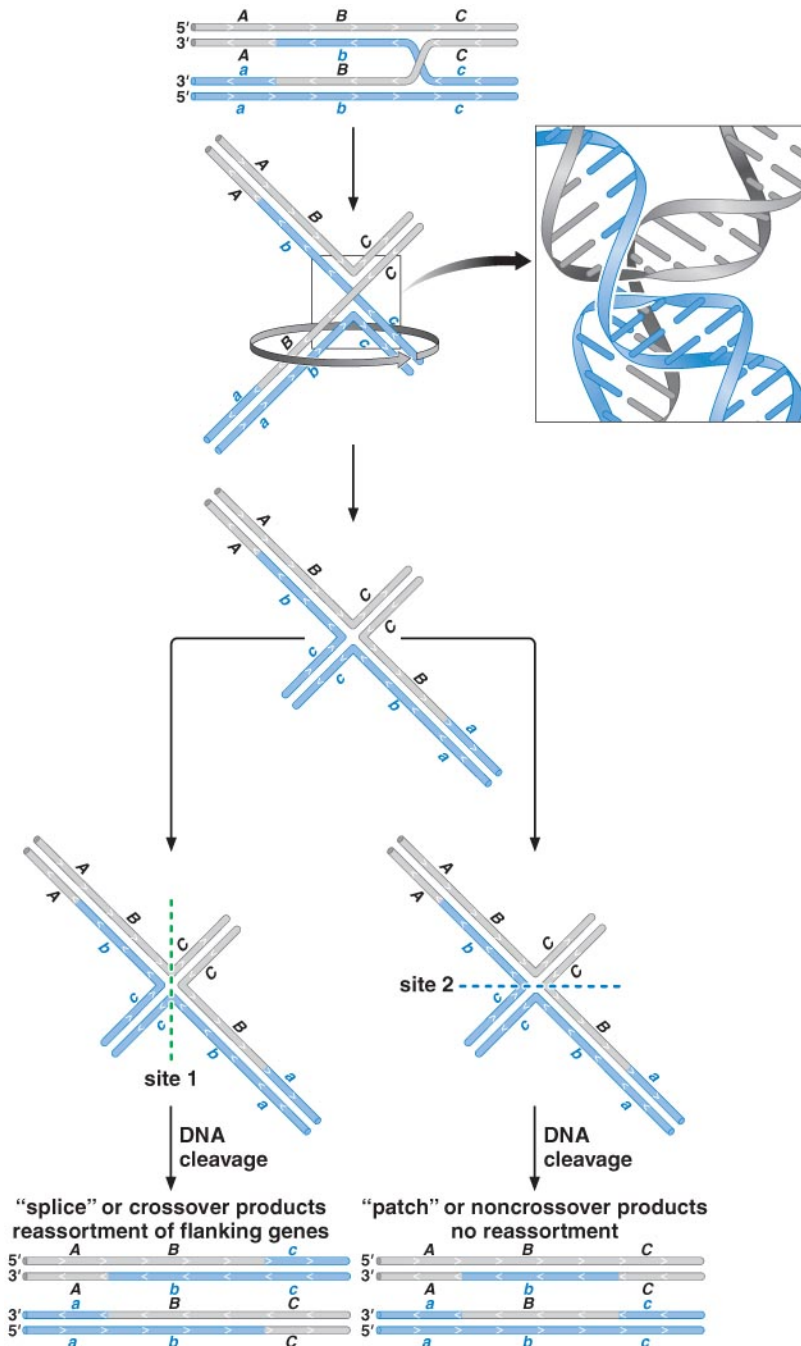
A broken chromosome can be
repaired by homologous
recombination with related
sequences on another
chromosome



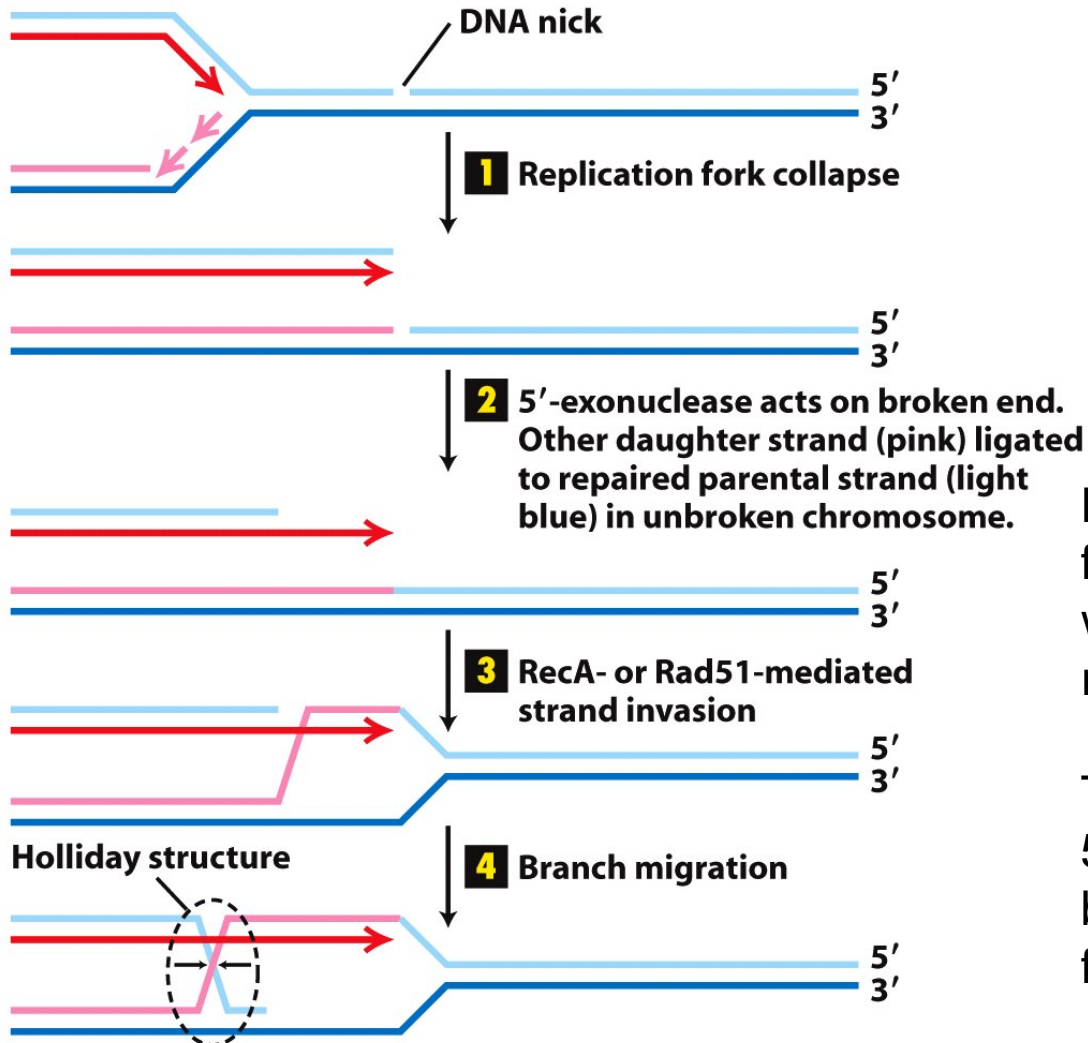
branch migration
and formation of
an intermediate with
two Holliday junctions



No privileged
strands in
Holliday
junction: can
resolve by
cleaving
“outer” pair as
well as “inner”
(strand
invaded) pair



Homologous recombination is especially valuable to rescue replication from a nick



Need to generate a free ss 3'OH end... which can now invade repaired part of duplex

This gives “orphaned” 5' end behind the break a new chance for a partner

Crossed-over complex now has primers and templates enough for completing all strands:
cut, extend, and ligate

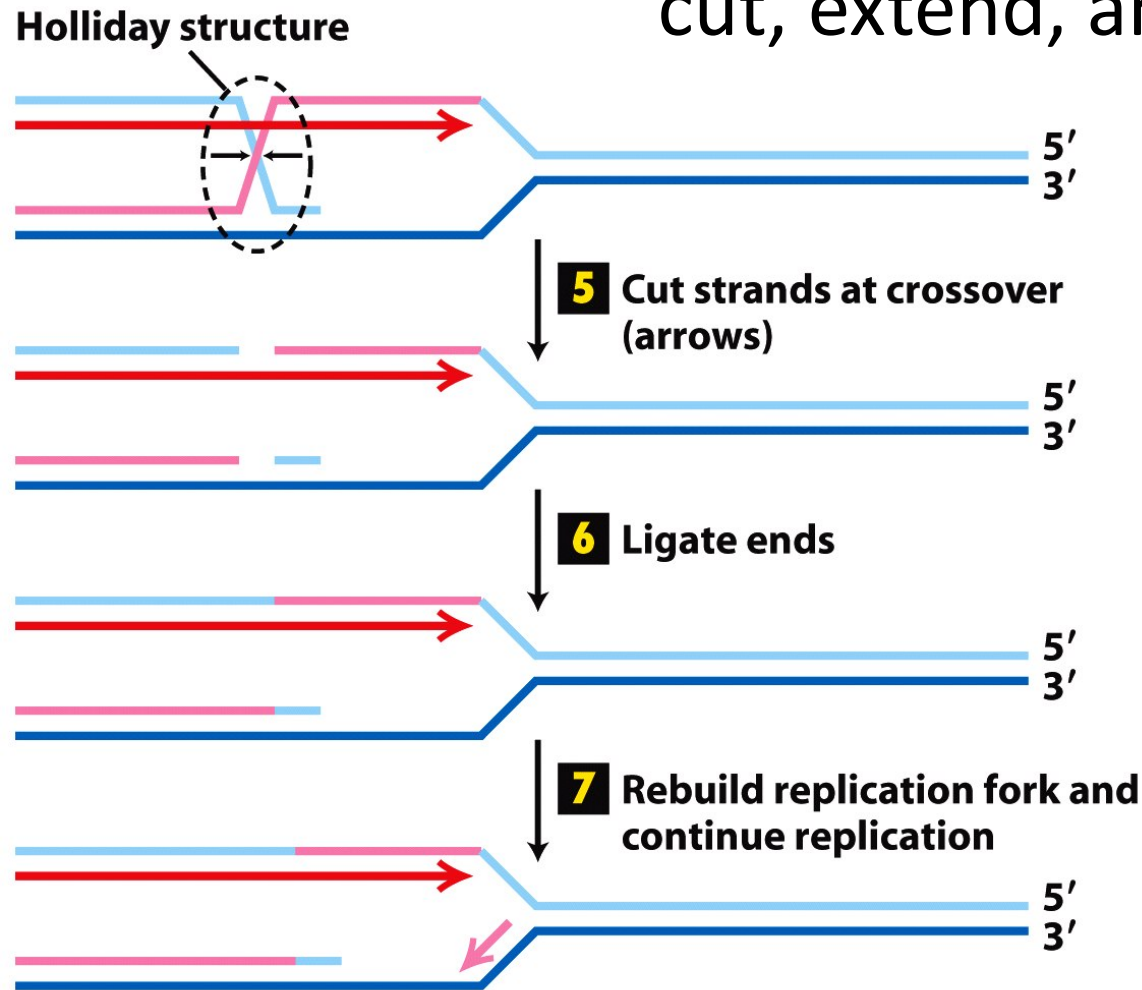


Figure 4-41 part 2
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Recombination
between
homologous
chromosomes,
initiated by a DNA
ds break, is
programmed into
meiosis

(to form germ cells)

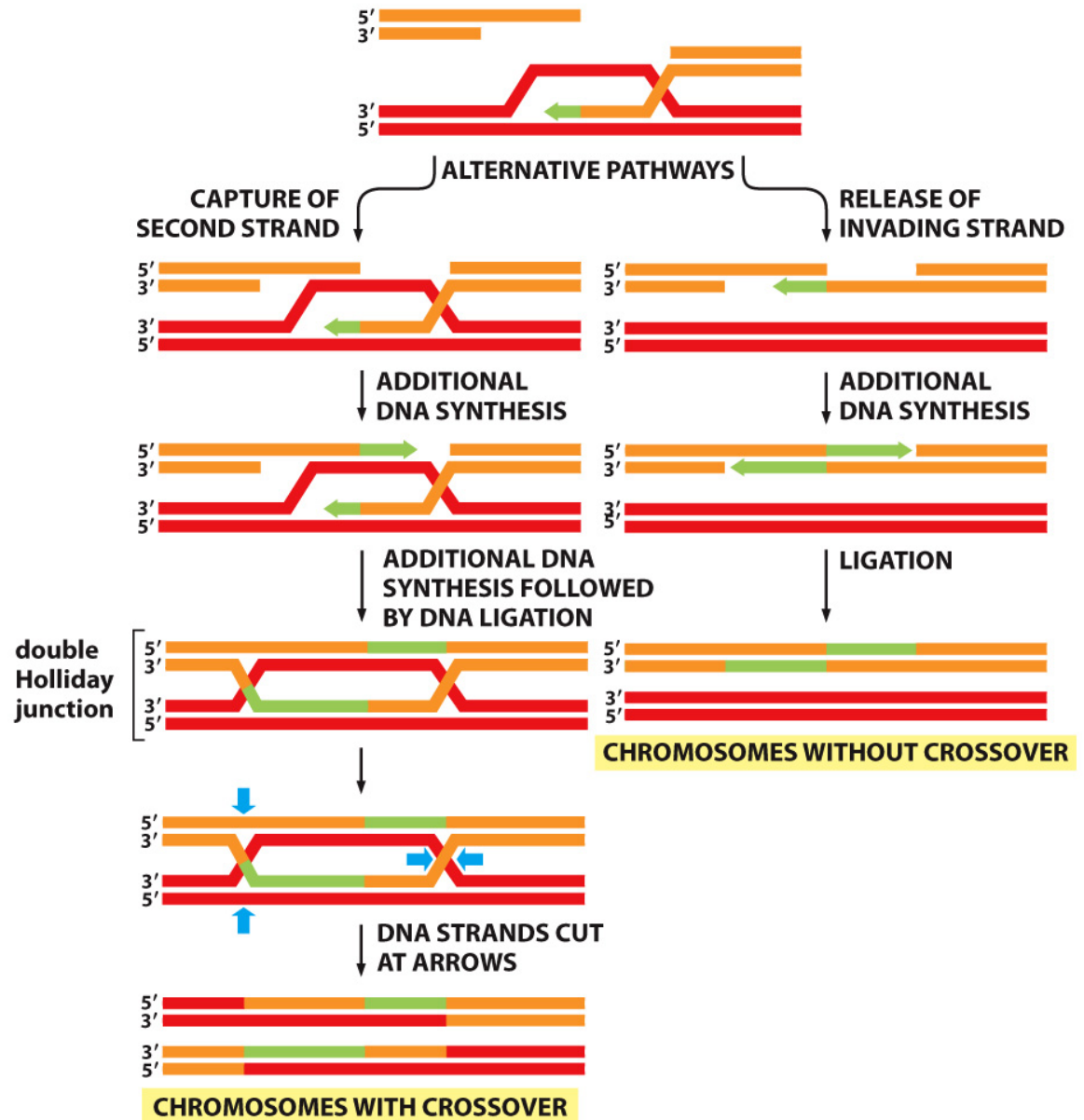
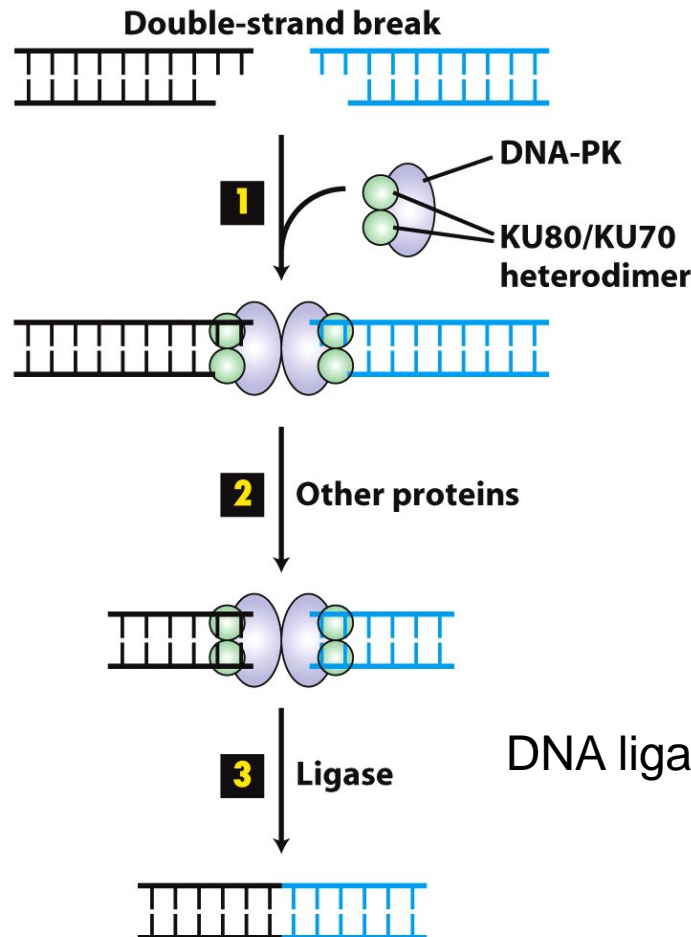


Figure 5-54 (part 2 of 2) Molecular Biology of the Cell 6e (© Garland Science 2015)

Nonhomologous end joining: when the homologous DNA is not easy to find

often imprecise, but a lot better than a broken chromosome



Key: protect broken ends so that they cannot do harm!

But missing bases are not added back

DNA ligase IV, Xrcc4, Artemis, etc

Recombination as a way of life: meiosis and transposable elements

- Formation of gametes – sperm and eggs – involves a step of cell division where recombination between maternal and paternal alleles is specifically enhanced
 - Resorting of mother's/father's alleles among resulting chromosomes offers more chances for new combinations
 - Preserves completely normal chromosome gene order, DNA length for both resulting types of chromosome
- “Selfish DNA” – transposable elements – recombine to exist
 - Passengers in host chromosomal DNA
 - Addition or subtraction of sequence to host chromosomes
 - Often imprecise in insertion, excision → genetic instability
 - Many copies inserted can damage chromosomes (increased recombination among homologous patches on nonhomologous chromosomes)

Typical DNA insertion element in its integrated location

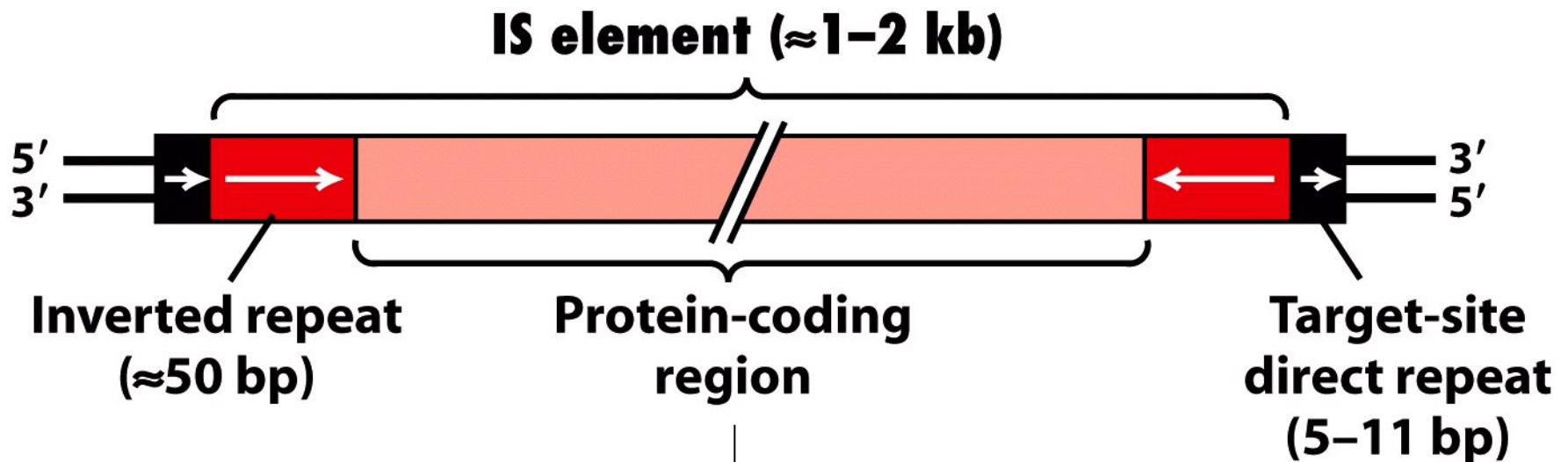


Figure 6-9
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Encodes specific transposase enzyme that promotes recombination & integration: recognizes inverted repeat sequences of insertion element and **cuts** IS element, target DNA

Staggering success
of “selfishness”:

Our genomes are
full of transposable
elements that have
greatly increased in
copy number
... just since mice
and humans
diverged

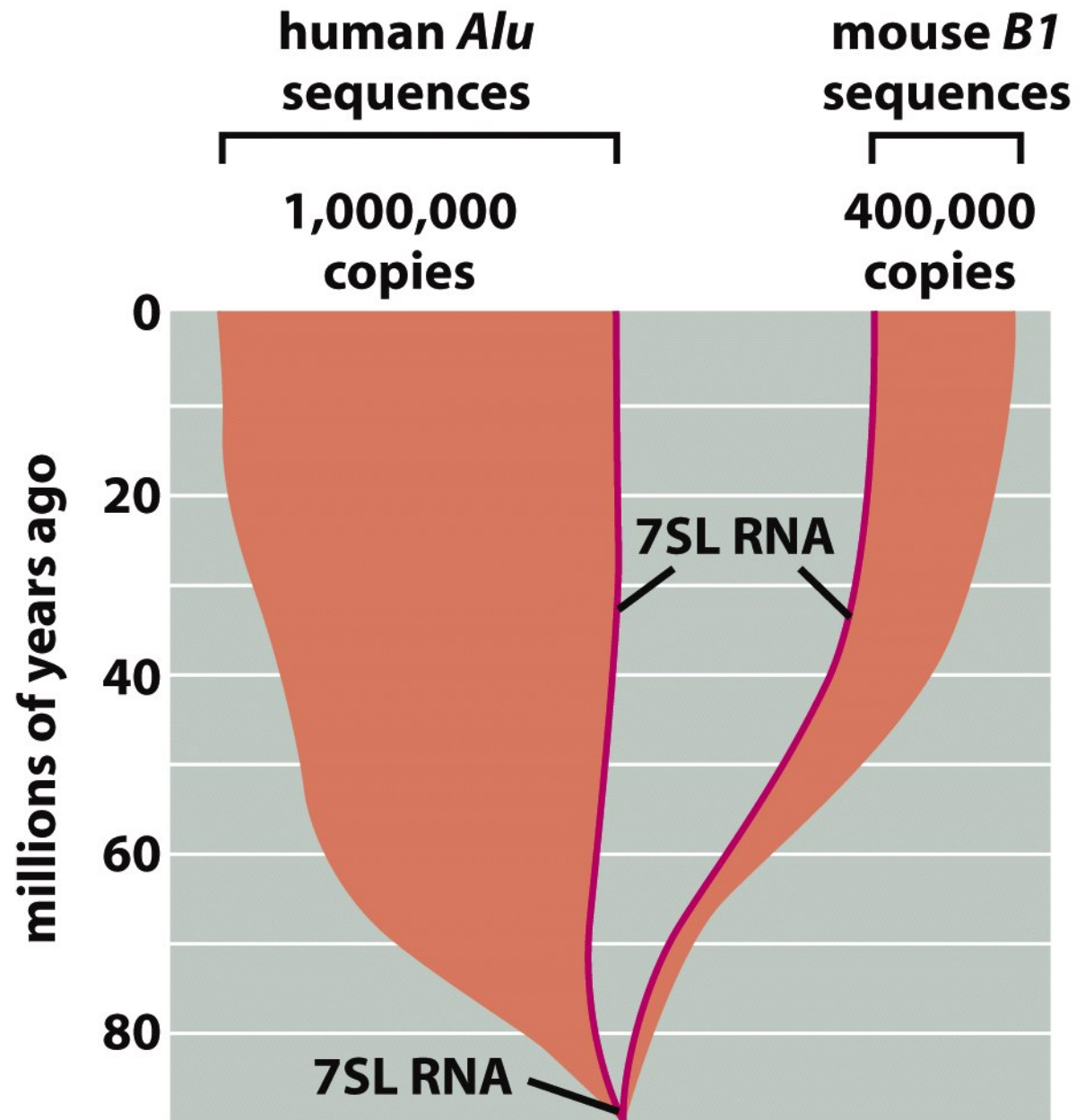


Figure 5-75 *Molecular Biology of the Cell* (© Garland Science 2008)

Randomly
inserting
transposable
elements use
blunt-end DNA
ligation without
homology for
inserting into new
DNA sites

Note: don't allow target DNA sites to have 3' overhangs so that the target DNA cannot "invade" the transposon's sequence...

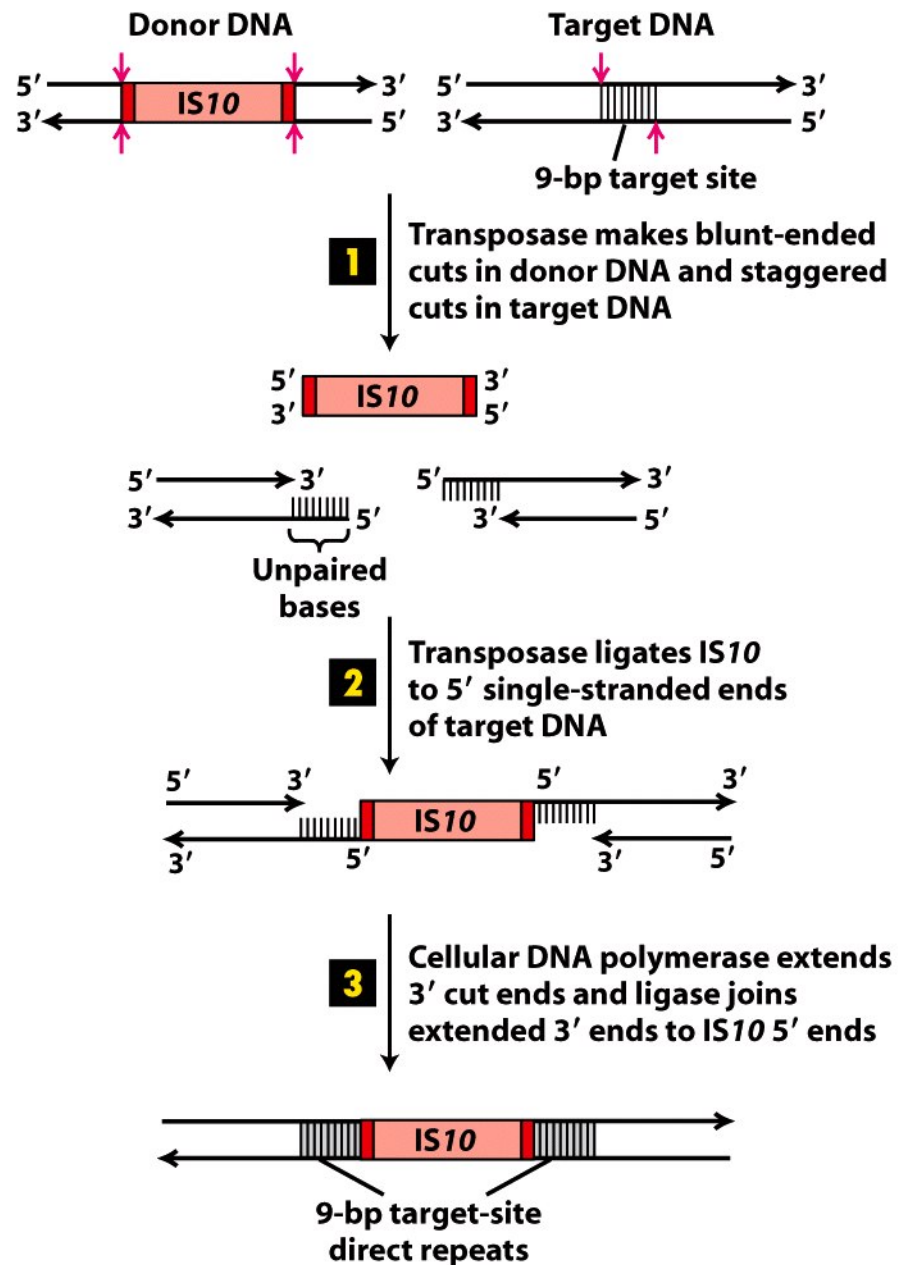
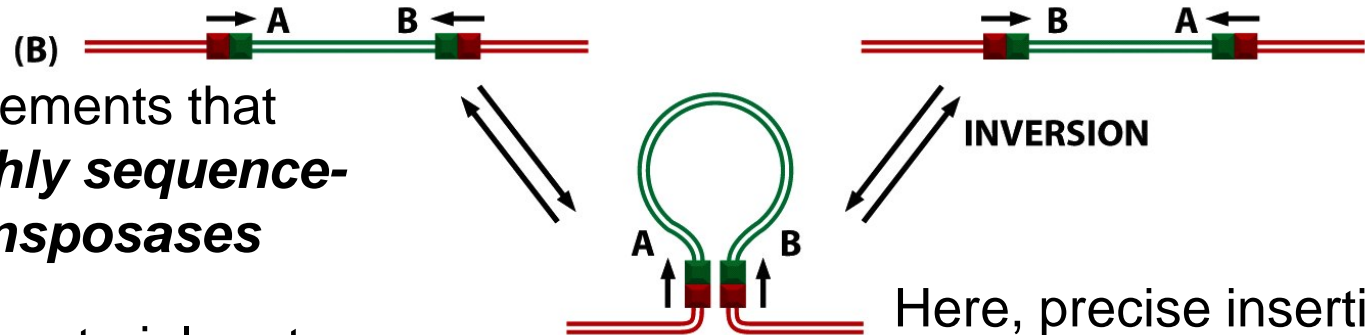
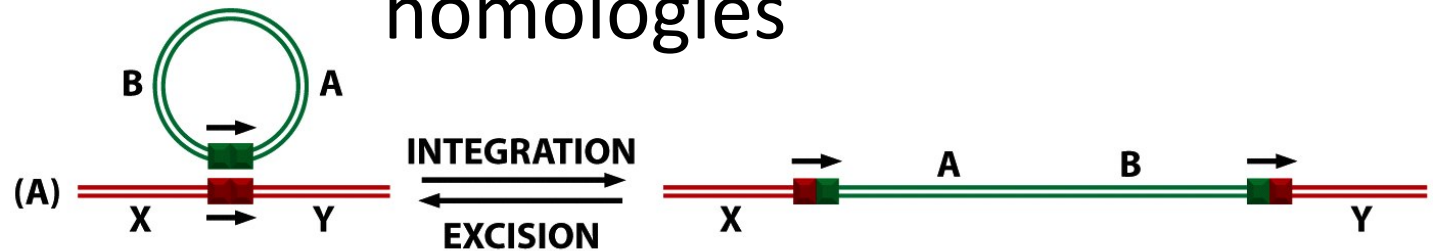


Figure 6-10
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Some very specific DNA transposons have site-specific modes of integration and excision:
basically homologous recombination with short homologies



These are elements that code for ***highly sequence-specific transposases***

Well known bacterial systems:
Cre/lox, Flp/Frt, and λ phage
integration where specific host target
sequences are recognized

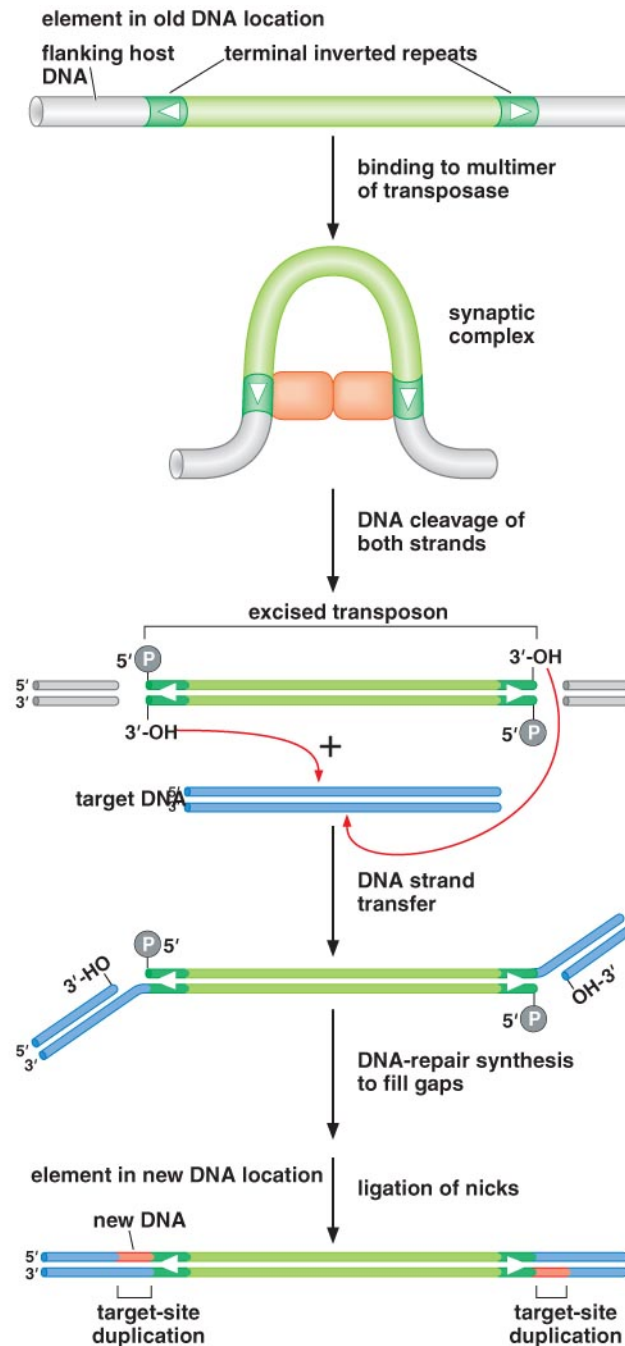
Here, precise insertion
and excision; may
undergo reciprocal
recombination to “invert”

Site-directed recombination as a tool for genetic engineering

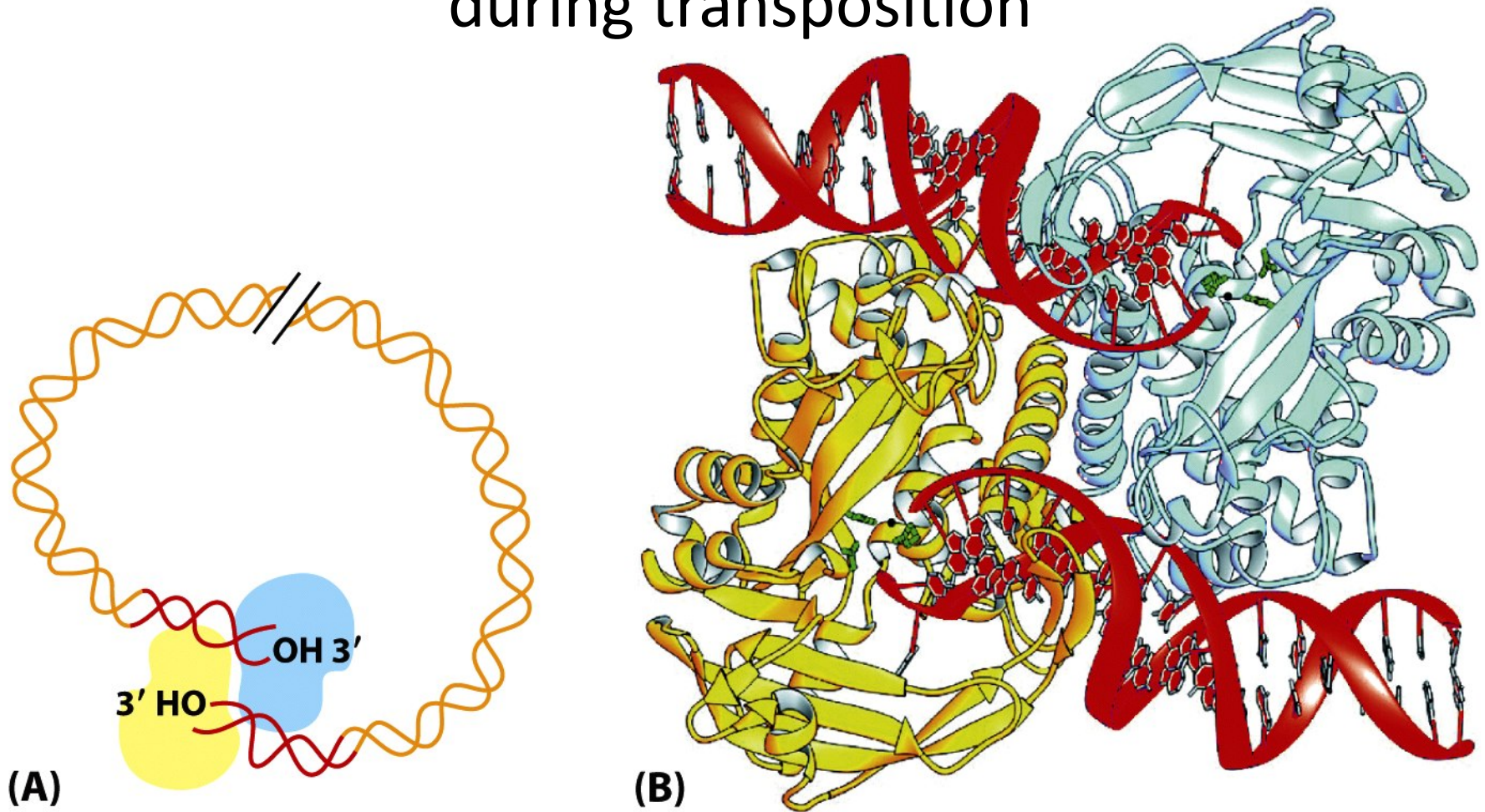
- Highly specific **recombinases** such as Cre, Flp, and λ integrase can be cloned into vectors under control of known promoter/enhancers
- Highly specific recombinational **target recognition sites** (e.g. LoxP, Frt, λ att's; 30 bp) are very rare in genomes normally
- Target recognition sites can be inserted in pairs around a gene of interest without disrupting function (e.g. “floxing” with Cre target LoxP sites)
- Can make double transgenic with floxed target gene plus specifically regulated Cre recombinase vector... then target gene works normally except in tissue or condition in which Cre expression is induced... and then target gene is **deleted**
- Can set up any site in any gene as a **specific target** for Cre (or Flp, or λ integrase)-mediated **insertion** of any DNA of interest, if it is flanked with correct recombination recognition sites

“Cut and paste”:
DNA transposons need
to cut themselves out of
old location to insert in
new one

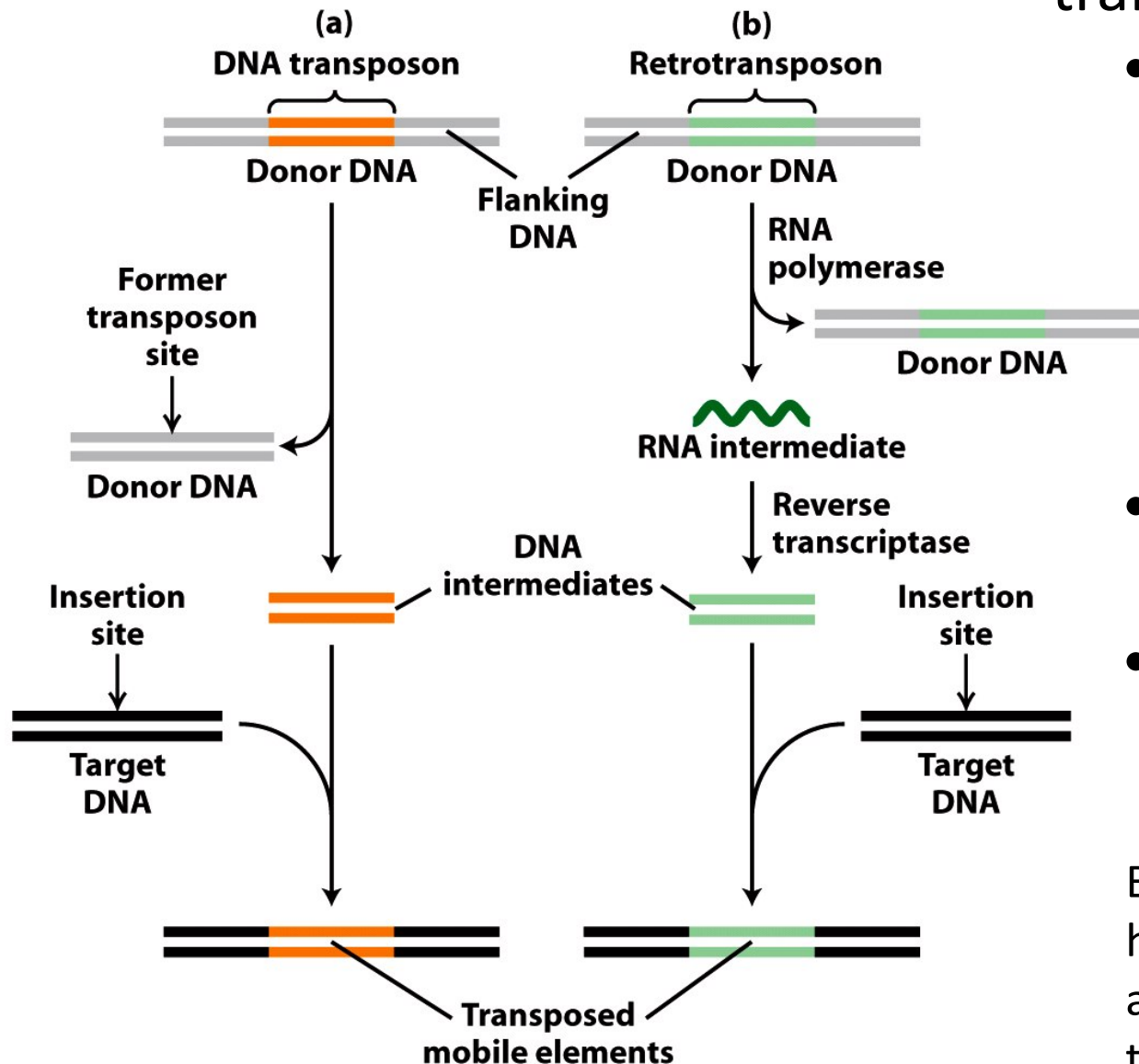
Only way to increase copy
number is for already-
replicated copy behind
replication fork to hop into
another site ahead of
replication fork



A recombinosome complex keeps ends together during transposition



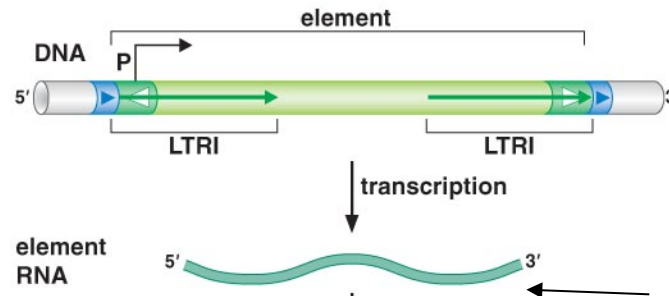
Viruses that integrate in host genomes use a “transposon” strategy



- Viral genome is an element with highly defined, specific sequences at each end recognized by special recombinase
- Two biochemical pathways
- Both invade host DNA by attack on **random** sequence

Both make staggered cuts in host DNA a few bp apart to assist insertion: after repair, telltale micro-duplications

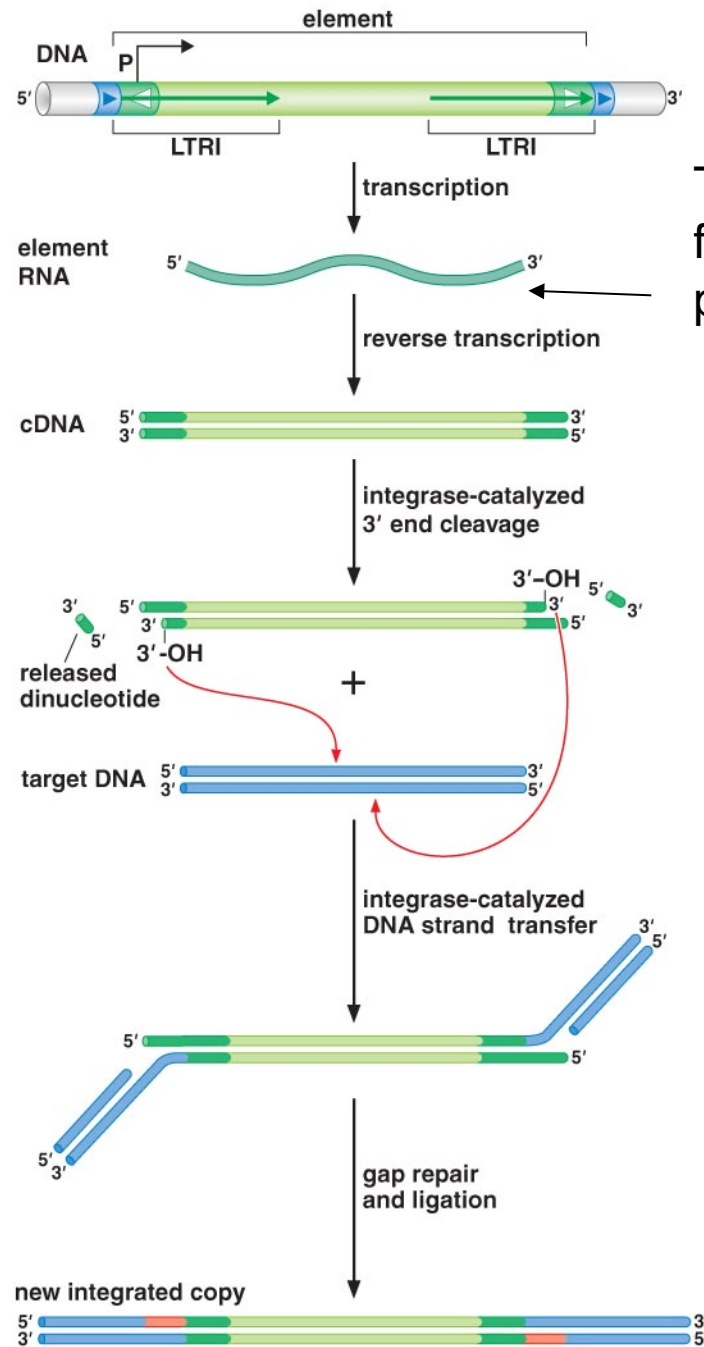
Retroviral
integration &
retrotransposon
integration: use
RNA polymerase
and reverse
transcriptase to
make the insertion
copy – no need to
excise, ever



This RNA is the
form that is
packaged in
virus of
infectious
retroviruses...
with its own
encoded
proteins
coating it

Virus particle itself contains reverse
transcriptase, encoded by viral
RNA. This enables first RNA-DNA
hybrid, then DNA duplex to be
made from same viral RNA when it
re-enters a cell

Retroviral
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integration: use
RNA polymerase
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make the insertion
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excise, ever



This RNA is the
form that is
packaged...

in
nucleus
of the
infected
cell

The irony of the arms race:
Regulated, but transposable element-like
recombination is ***central*** to immune cell development

- Genes that code for T and B cell receptors are not assembled in germline genome
- Clusters of gene elements need to be assembled via DNA recombination in order to create transcription units
 - ***No*** splice donor/acceptor sites
 - Promoters and enhancers can be > 1 Mb apart in germline genome
- Specific recombinases need to rearrange DNA for immune cells to express receptors, and to survive
 - Variable sequences at recombination joints contribute greatly to immune recognition diversity