

Replication:

Replication of eucaryotic linear chromosomes

Nucleosomes as obstacles during replication

Replication of chromosome ends (telomeres)

DNA repair

Homologous recombination

in DNA repair

for exchange of genetic information

applications

Site specific recombination

applications

## Replication:

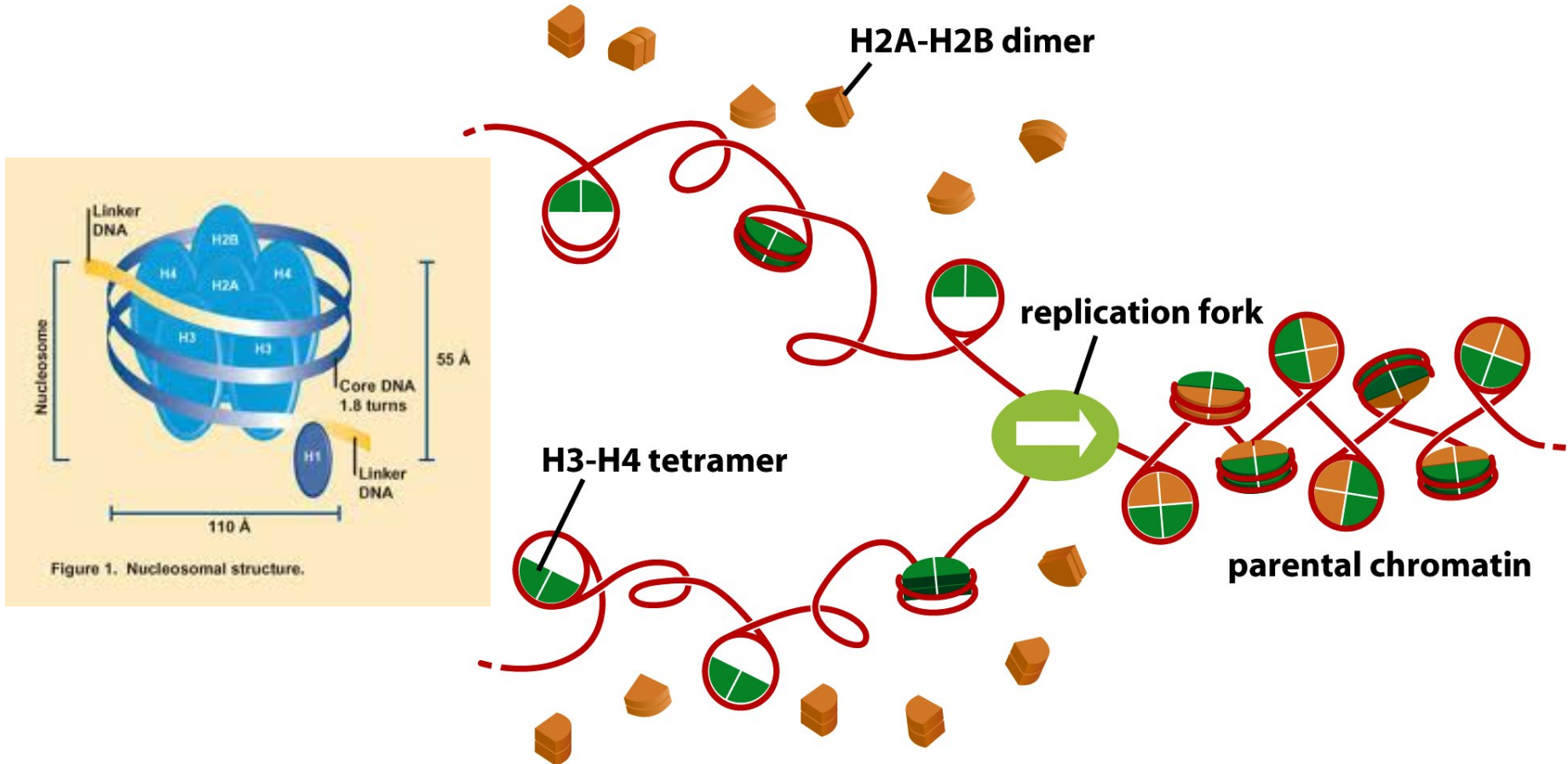
- DNA polymerases synthesize 5'->3' and need a primer (free 3' OH, RNA, Primase)
- Replication fork with leading and lagging strand (Okazaki fragments)
- Helicases, ssDNA binding protein, Topoisomerase, sliding clamp
- Prokaryotic origin of replication
- Eukaryotic ARS: Replication is linked to the cell cycle (S-Phase)
- Eukaryotic chromatin: nucleosomes as fundamental packaging unit  
->nucleosome is histone-octamer (H2A, H2B, H3, H4, synthesized during S-phase unlike most other proteins)

Nucleosome: 2x H2A, H2B, H3, H4 (octamer)

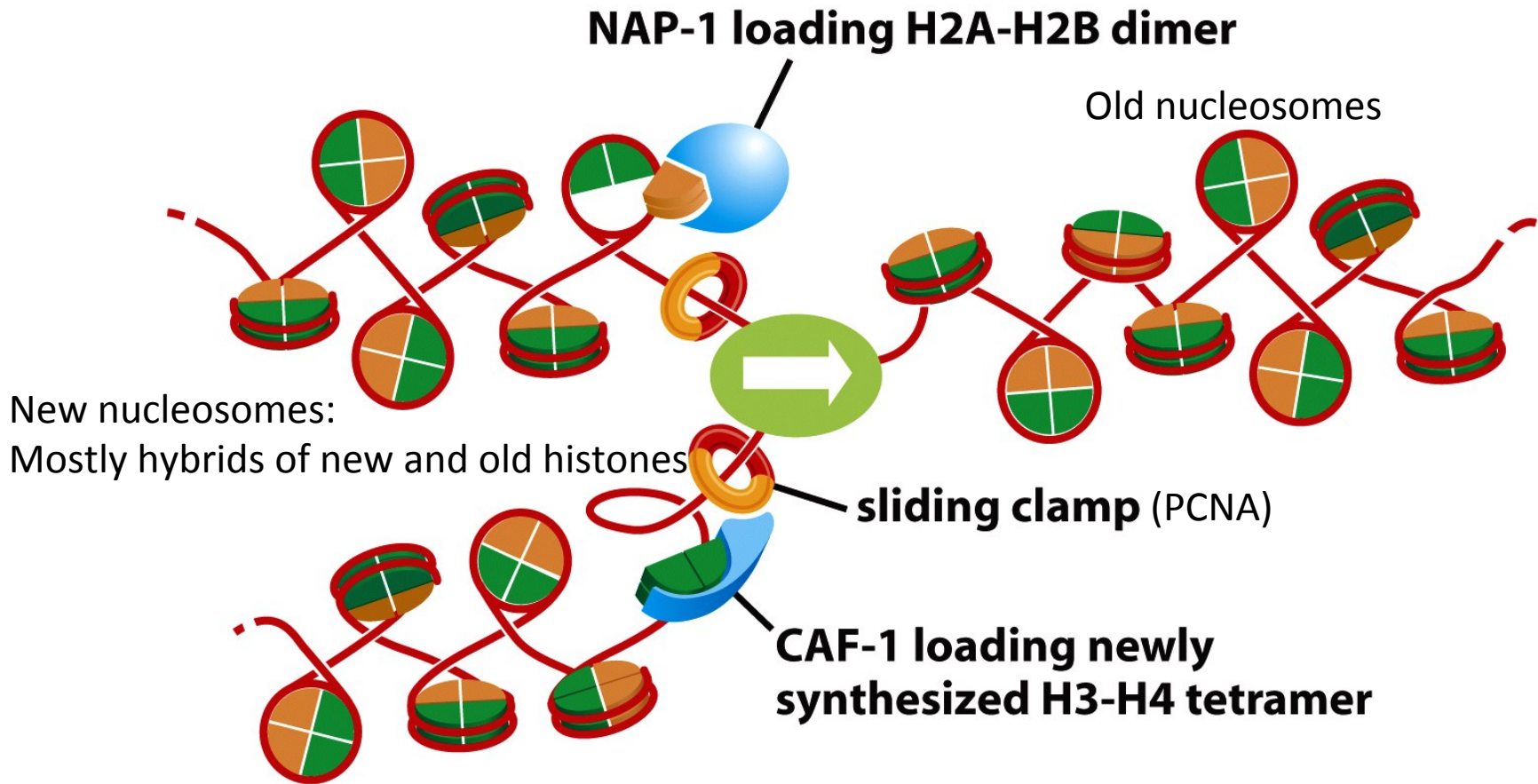
Steric obstacle for the replication fork

Chromatin remodeling proteins destabilize DNA-histone interactions

-> H3-H4 parental tetramers remain DNA associated, randomly segregate to one of the new strands  
H2A-H2B dimers dissociate



New H3-H4 tetramers are added  
Mix of old/new H2AB dimers are added  
NAP/CAF: histone chaperones  
(CAF: chromatin assembly factors)



# Copying of histone modification through H3-H4 tetramer distribution to both DNA strands

This mechanism allows segregation of epigenetic modifications

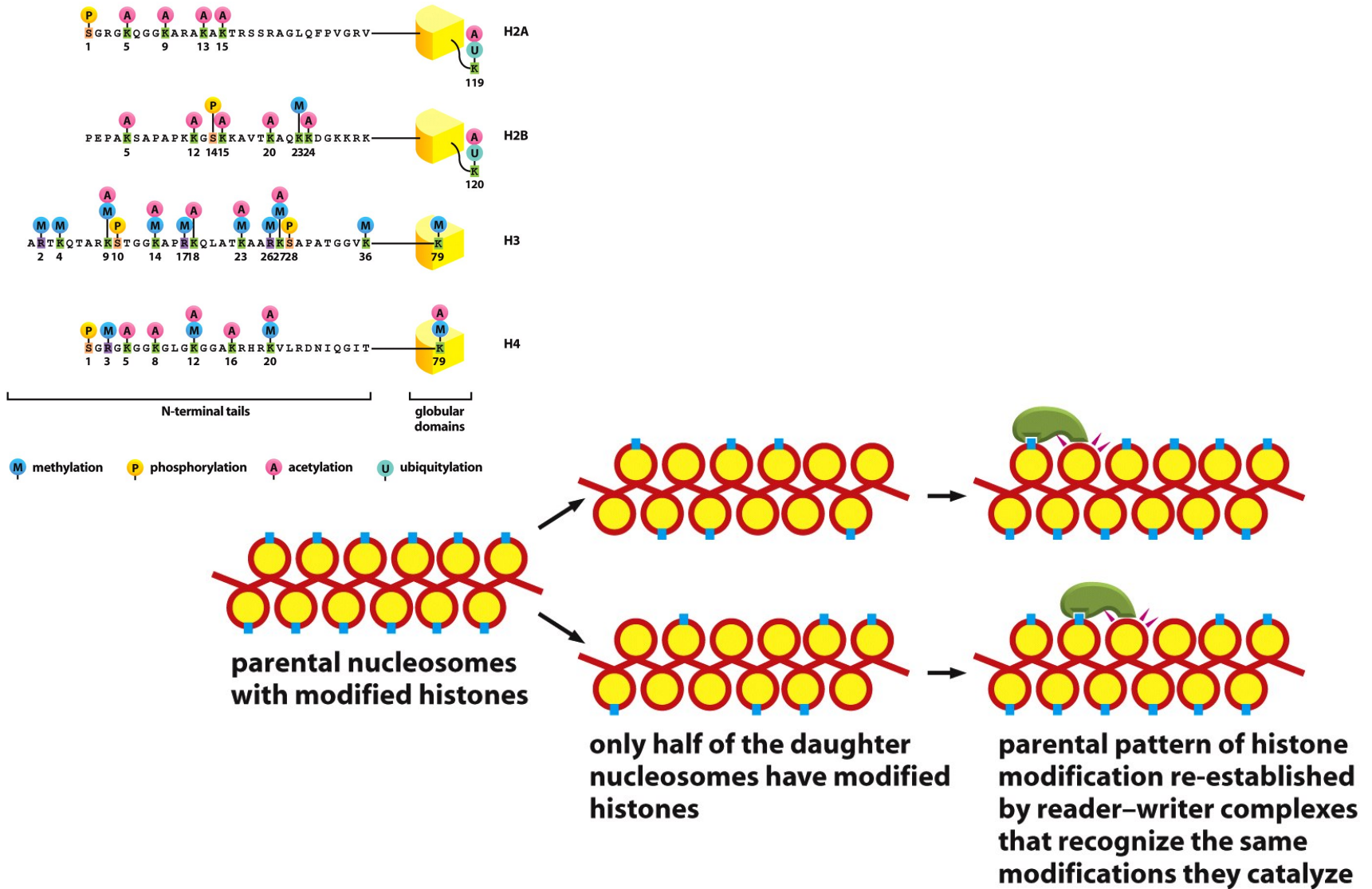
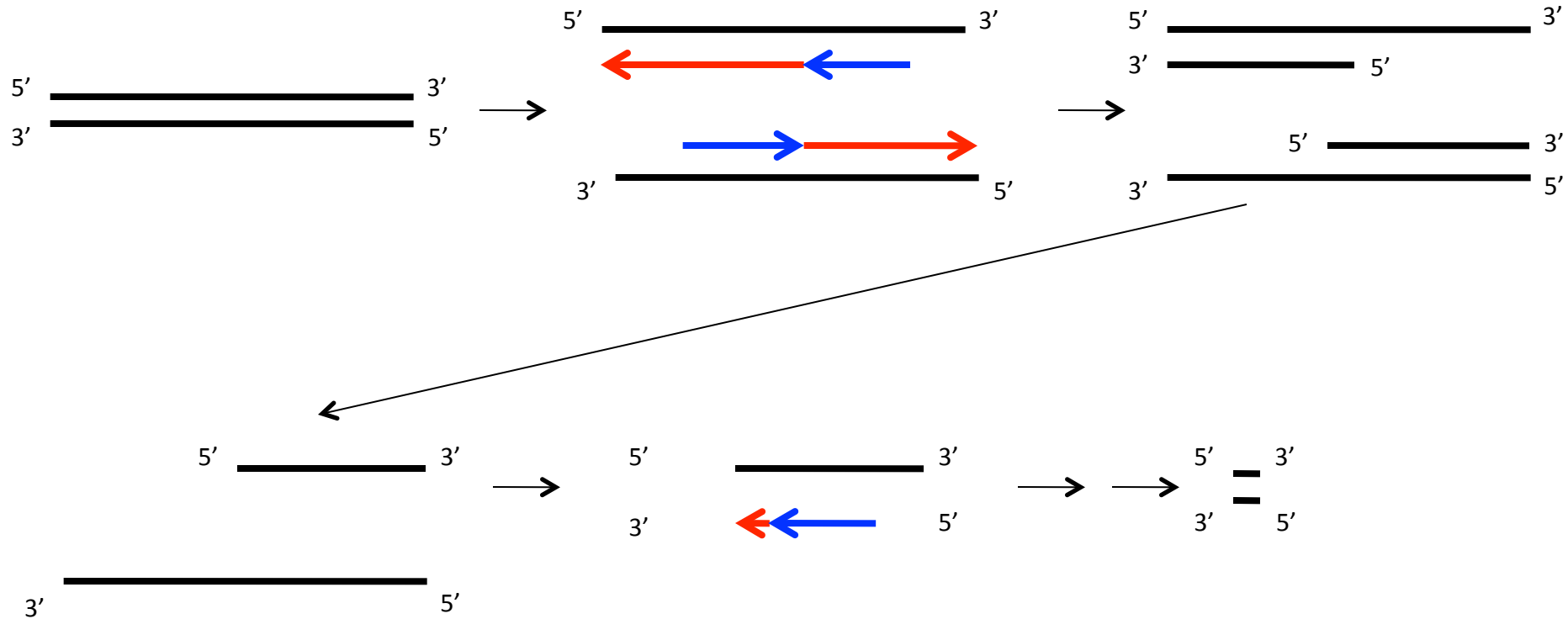


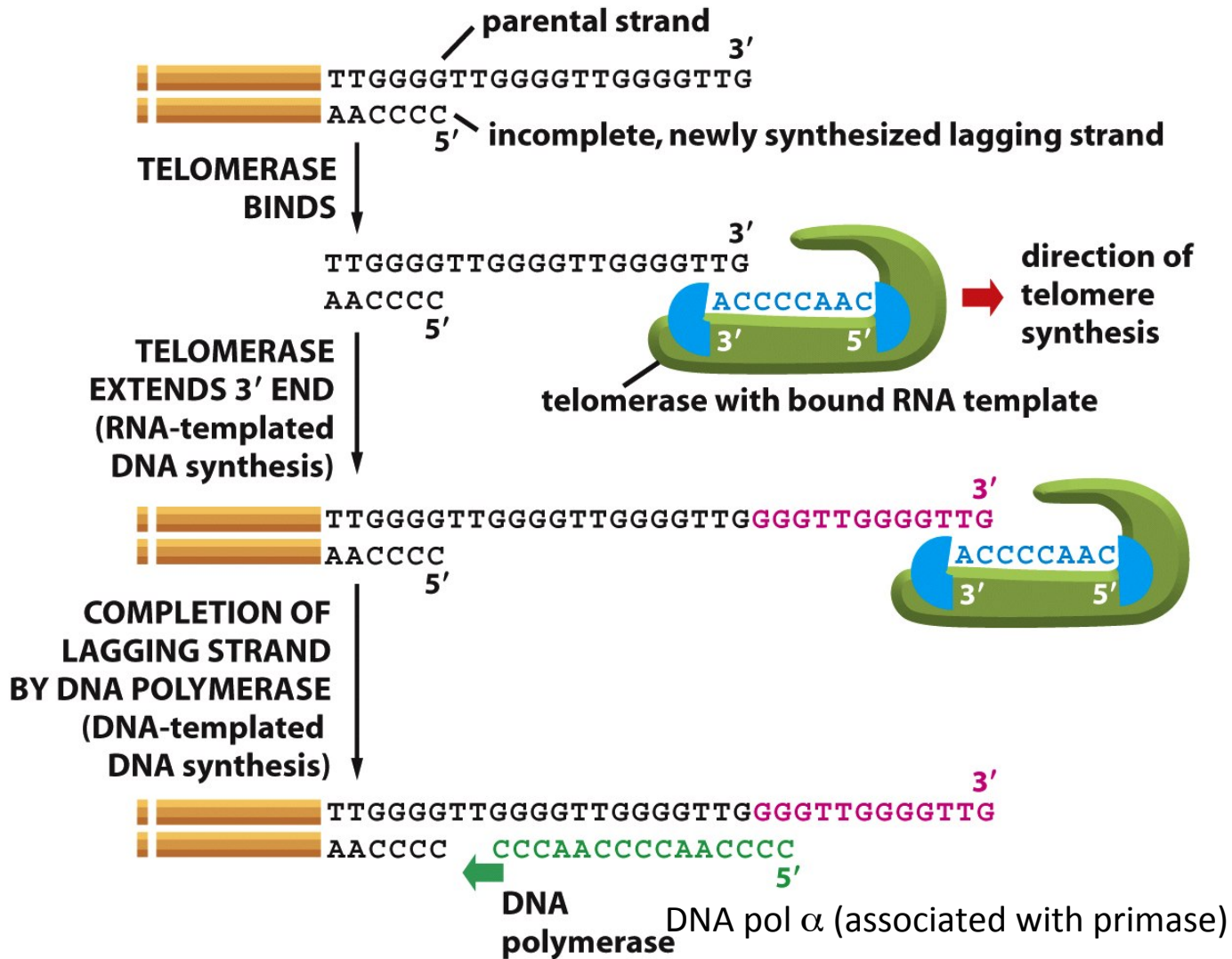
Figure 5-39 *Molecular Biology of the Cell* (© Garland Science 2008)

# Replication of DNA ends (linear chromosomes)



 RNA primer: will be removed

 Newly synthesized DNA strand



Telomerase: Nobel prize 2009 (Blackburn, Greider, Szostak)

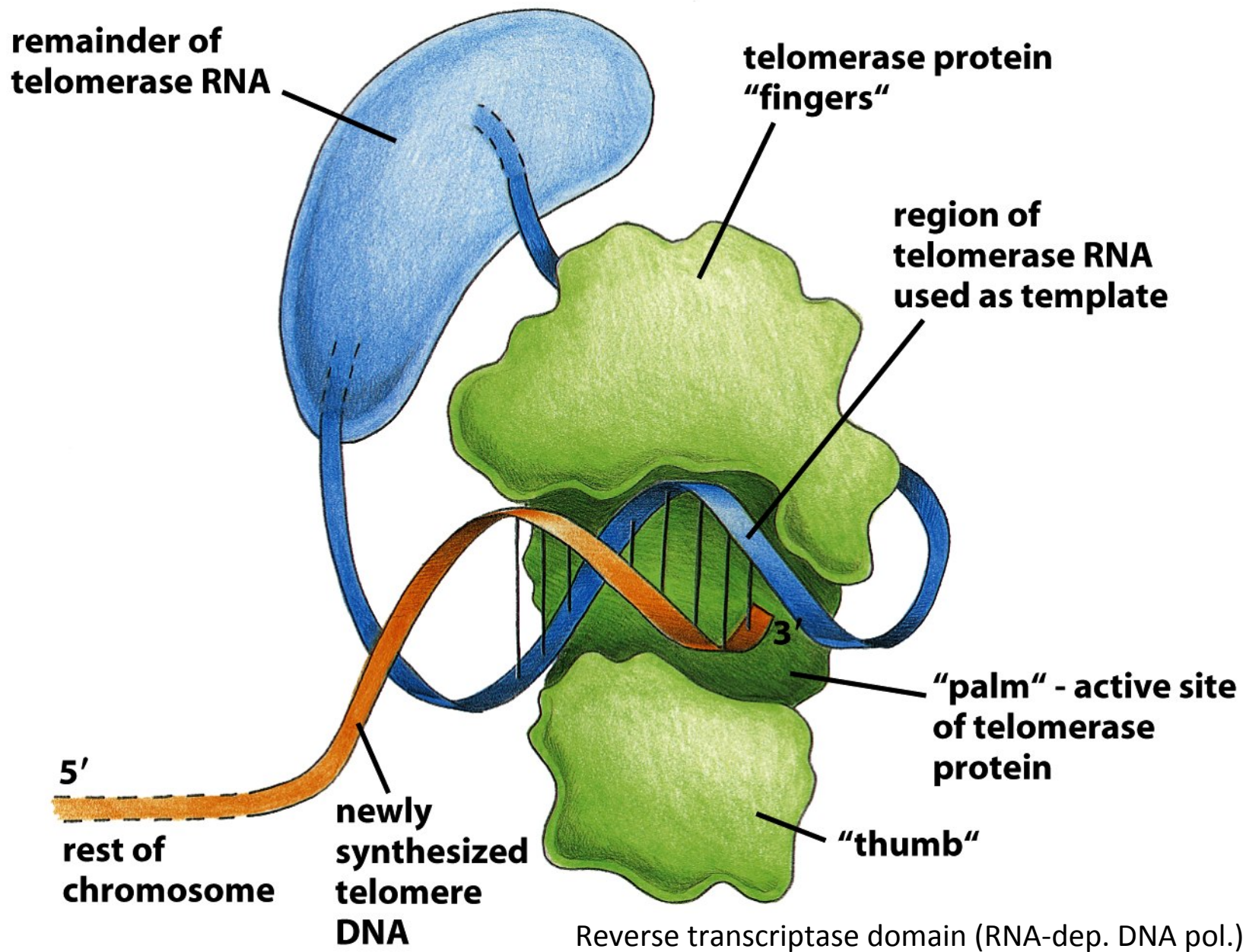


Figure 5-40 *Molecular Biology of the Cell* (© Garland Science 2008)

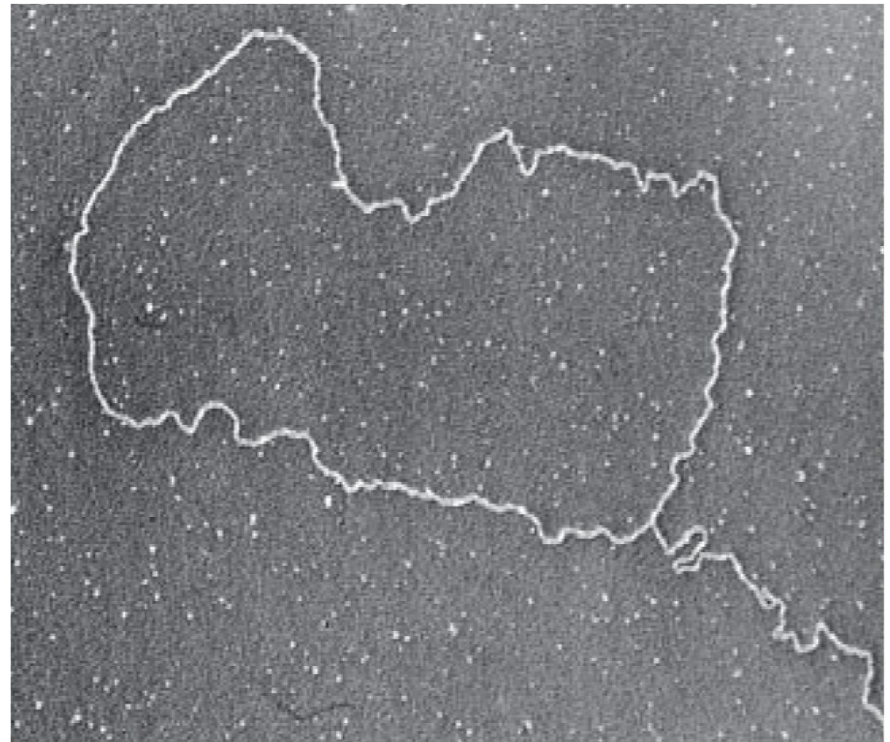
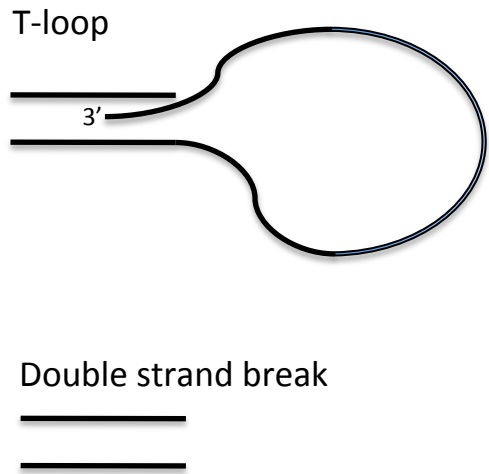


T-loop of protruding 3' end

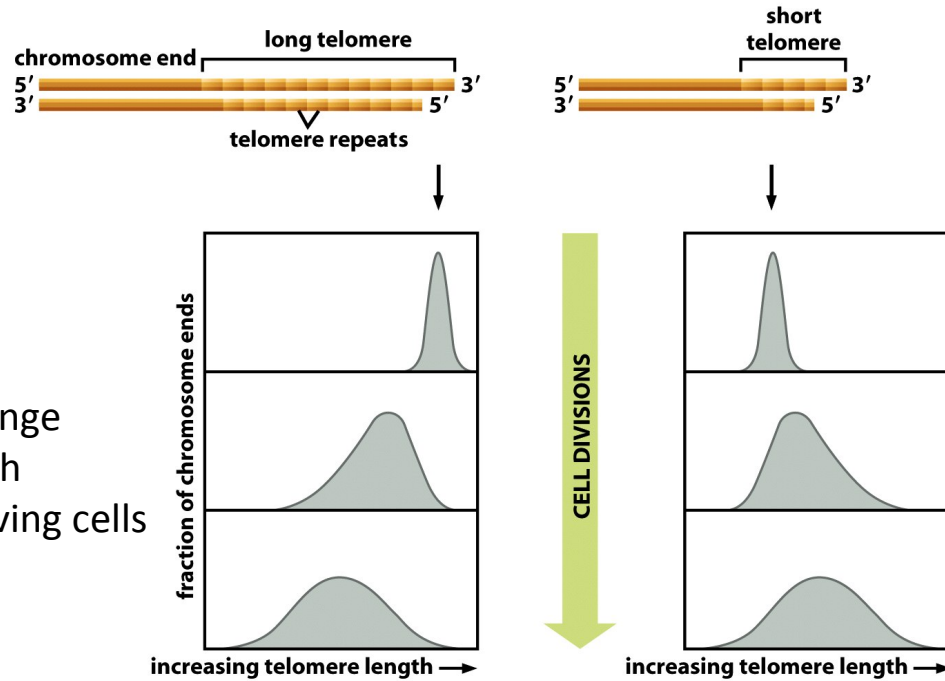
After lagging strand synthesis, 5' end is shortened to produce 3' overhang (to ensure free ss for further elongation by telomerase).

3' overhang loops back and inserts into the double strand

T-loop provides unique structure for DNA ends that distinguishes them from broken DNA molecules -> protection against nucleases



1 μm



Experimental change of telomere length is readjusted in living cells

Telomere length is important

Stem cells: divide often -> high telomerase activity

Somatic less: limited number of divisions -> low telomerase activity

-> Cells cannot proliferate uncontrolled (protection against cancer)

In some cell culture systems increasing telomere length can provide increased potential to divide

Telomerase ko mice develop cancer and age prematurely: cells divide in the absence of telomerase activity which results in disease due to unstable chromosomes

Dolly's telomeres (somatic cells <-> stem cells of germline or adult)

## DNA repair:

Random changes created by environmental influences (heat, radiation, chemicals) and metabolic accidents

Estimate:  $\leq 1/1000$  are fixed in genome, the others are eliminated (repaired)

Mutations that affect DNA repair lead to increased mutation rates and cause disease

->importance of DNA repair systems

**Table 5–2 Some Inherited Syndromes with Defects in DNA Repair**

NAME	PHENOTYPE	ENZYME OR PROCESS AFFECTED
<b>MSH2, 3, 6, MLH1, PMS2</b>	<b>colon cancer</b>	<b>mismatch repair</b>
<b>Xeroderma pigmentosum (XP) groups A–G</b>	<b>skin cancer, UV sensitivity, neurological abnormalities</b>	<b>nucleotide excision–repair</b>
<b>XP variant</b>	<b>UV sensitivity, skin cancer</b>	<b>translesion synthesis by DNA polymerase <math>\eta</math></b>
<b>Ataxia telangiectasia (AT)</b>	<b>leukemia, lymphoma, <math>\gamma</math>-ray sensitivity, genome instability</b>	<b>ATM protein, a protein kinase activated by double-strand breaks</b>
<b>BRCA2</b>	<b>breast, ovarian, and prostate cancer</b>	<b>repair by homologous recombination</b>
<b>Werner syndrome</b>	<b>premature aging, cancer at several sites, genome instability</b>	<b>accessory 3'-exonuclease and DNA helicase</b>
<b>Bloom syndrome</b>	<b>cancer at several sites, stunted growth, genome instability</b>	<b>accessory DNA helicase for replication</b>
<b>Fanconi anemia groups A–G</b>	<b>congenital abnormalities, leukemia, genome instability</b>	<b>DNA interstrand cross-link repair</b>
<b>46 BR patient</b>	<b>hypersensitivity to DNA-damaging agents, genome instability</b>	<b>DNA ligase I</b>

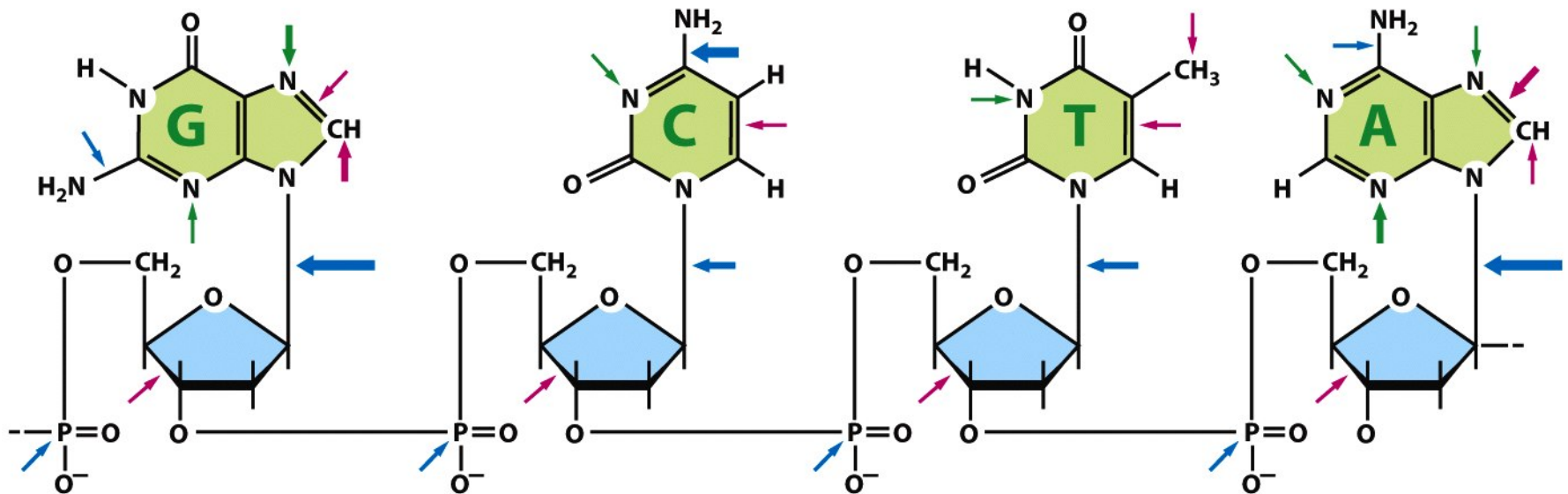
## Spontaneous changes in DNA

Depurination: loss of G, A base due to hydrolysis; 5000/cell/day

Deamination of C (->U); 100/cell/day

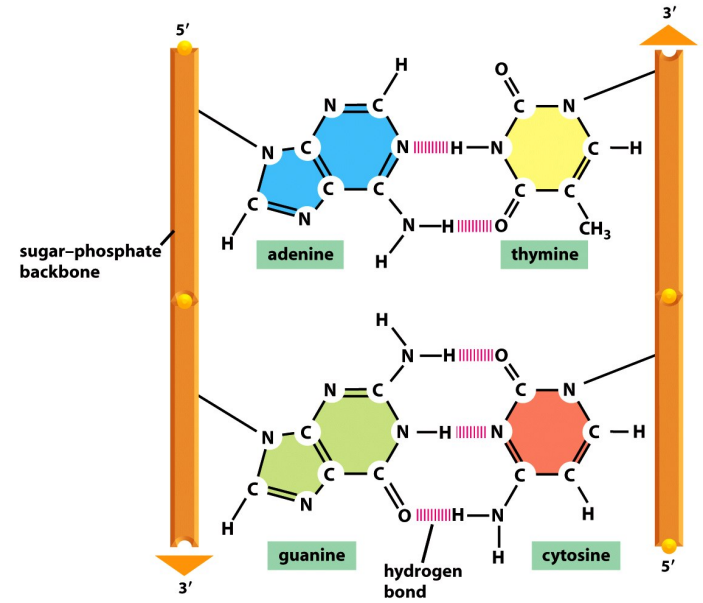
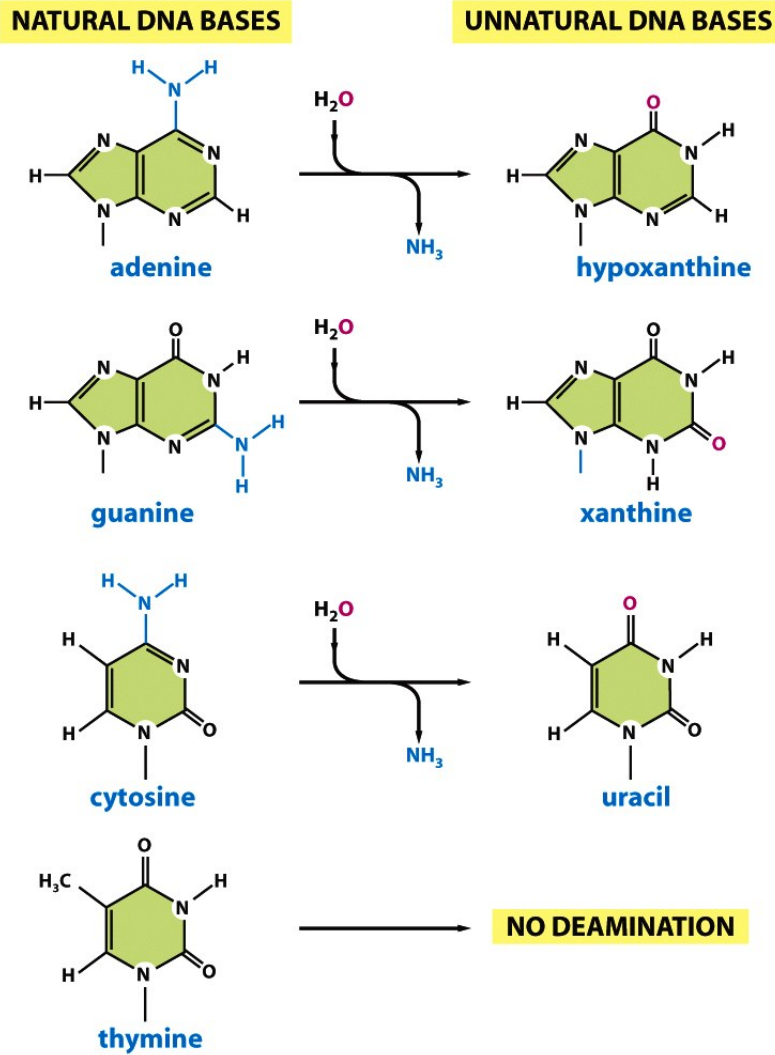
Oxidation (red arrows)

Uncontrolled methylation (green arrows)



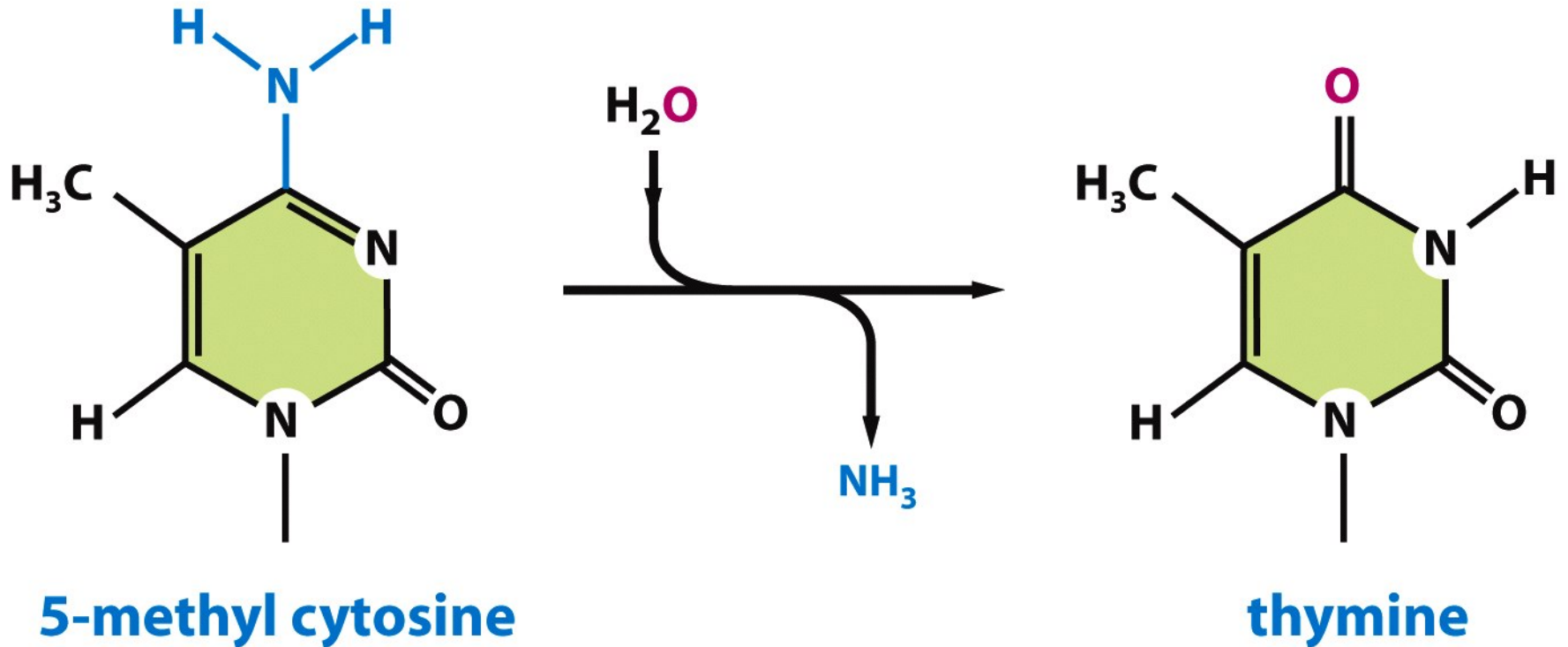
Uncorrected changes may result in mutations (deletions, base-pair substitutions)

# Deamination results in unnatural bases that can be recognized in DNA



Uracil is not used in DNA  
 Therefore C→U deamination  
 can be detected

Deamination of methylated C results in T, mis-pairing of T-G can be detected by the repair systems  
The repair of T-G mismatches is biased to exchanging T for C and thus restoring the correct sequence

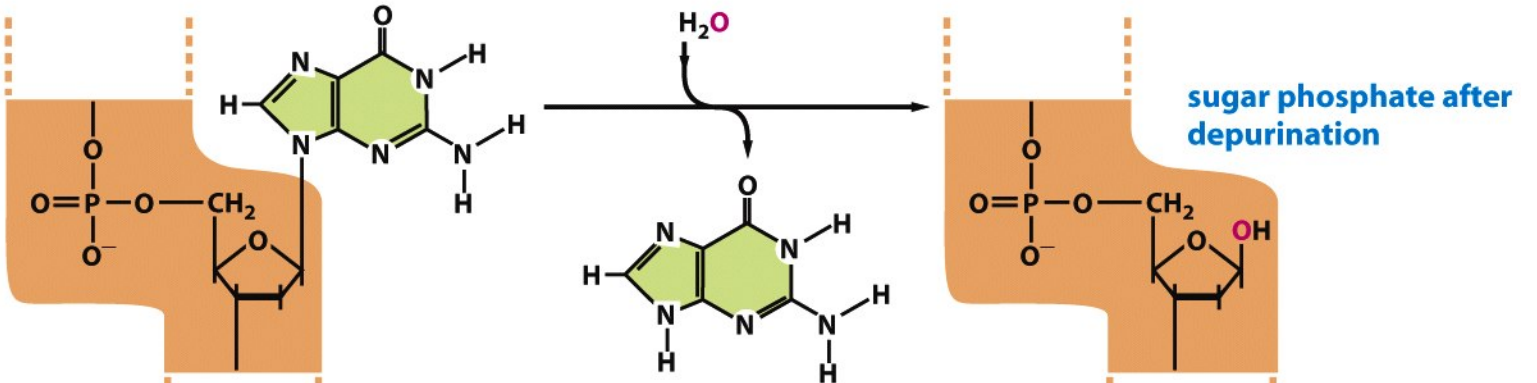


Ineffective repair: about 3% of C are methylated, mutations in these nucleotides account for about 30% of single-base mutations in inherited human disease.

# The most frequent DNA damages/changes

**GUANINE**

**DEPURINATION**



**CYTOSINE**

**DEAMINATION**

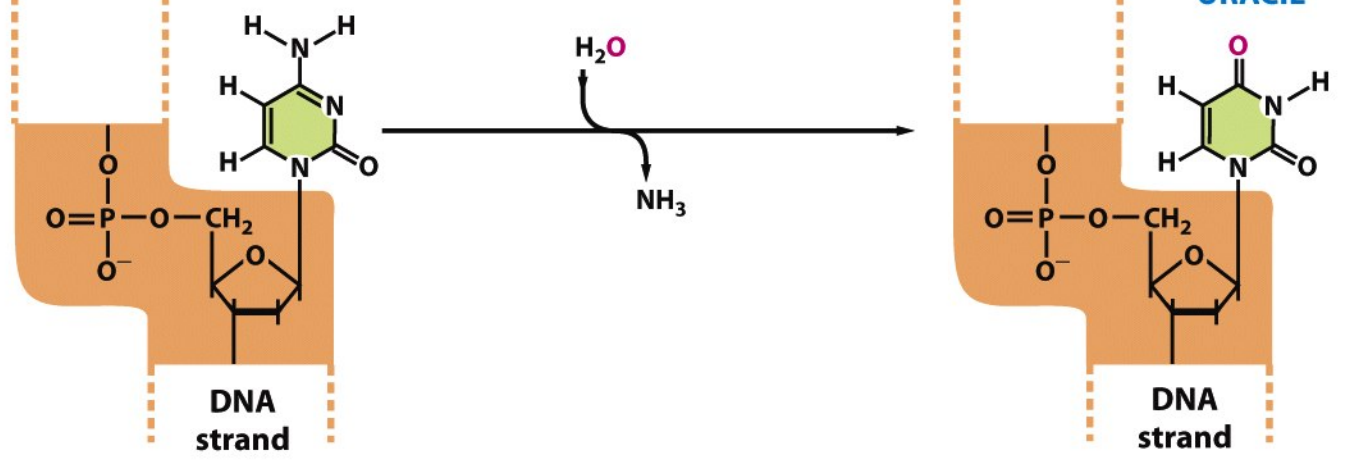
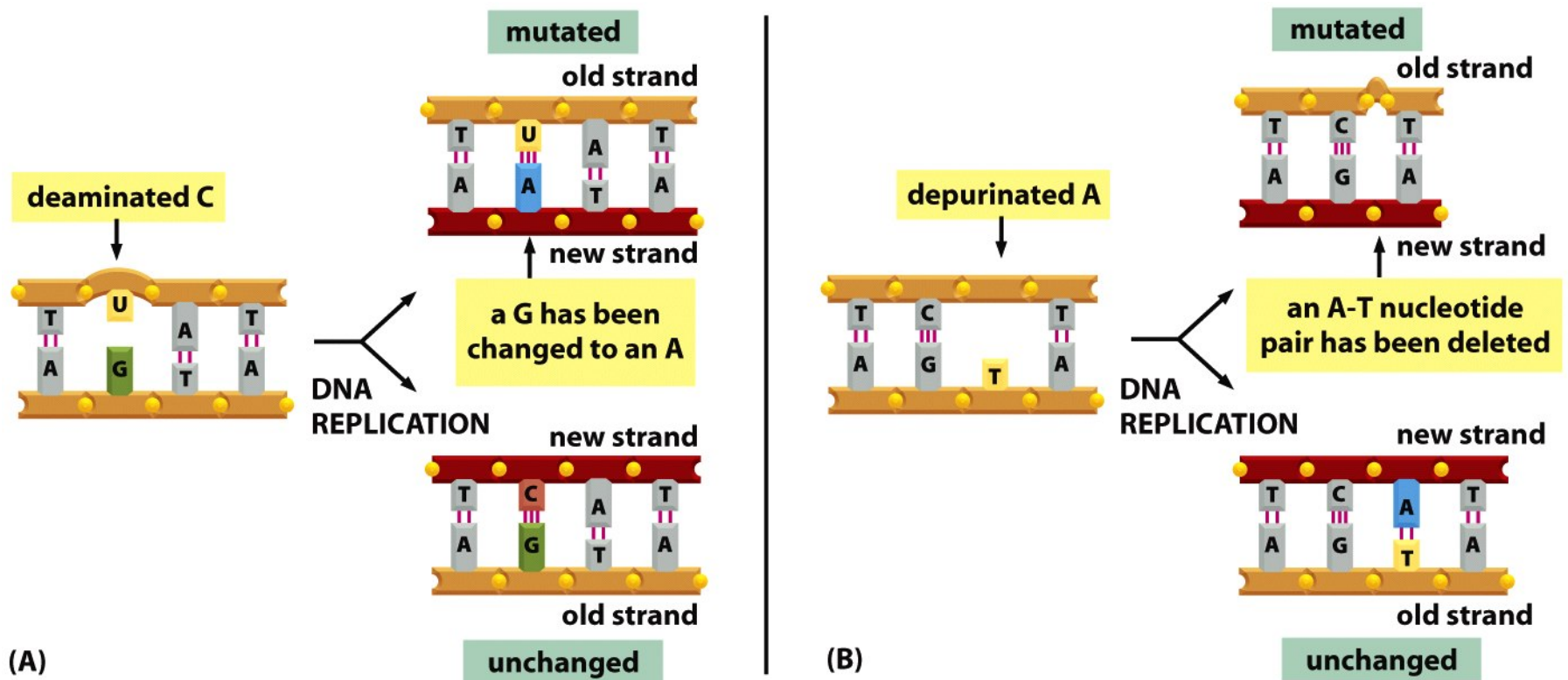


Figure 5-45 *Molecular Biology of the Cell* (© Garland Science 2008)



Advantage of DNA double helix for repair:

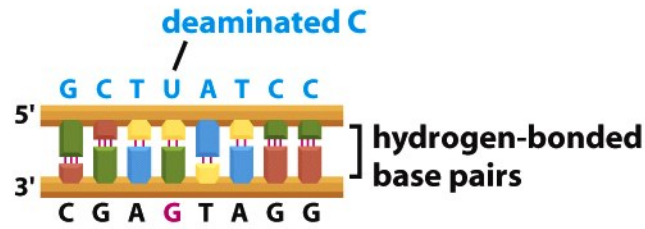
Double-helical structure of DNA allows repair as long as only one strand is affected

The complementary strand provides the template for the repair.

All genomes are ds, except some small viral genomes (ssDNA or ssRNA)



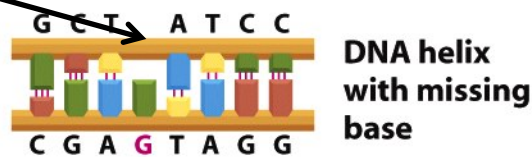
# BASE EXCISION REPAIR



U

URACIL DNA GLYCOSYLASE

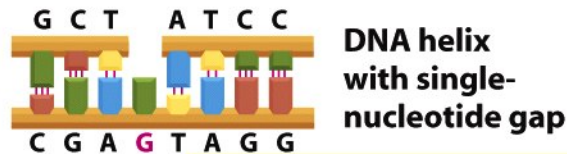
Depyrimidated DNA  
Missing base



Depurinated DNA  
-> missing A or G

AP ENDONUCLEASE AND PHOSPHODIESTERASE REMOVE SUGAR PHOSPHATE

AP: apurinic or apyrimidinic  
Endonuclease: cleaves within the DNA  
(not at the end such as an exonuclease)

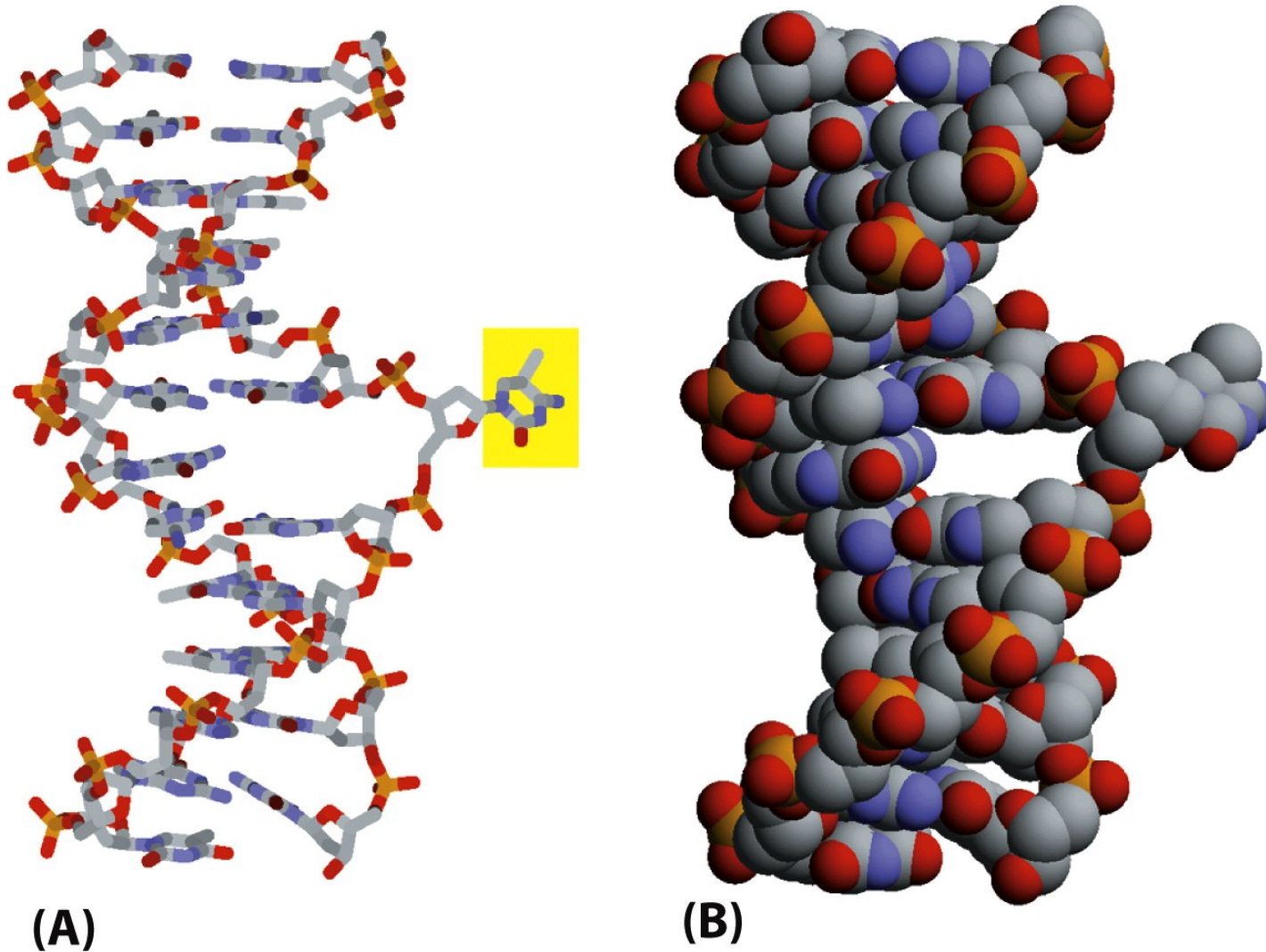


DNA POLYMERASE ADDS NEW NUCLEOTIDES, DNA LIGASE SEALS NICK

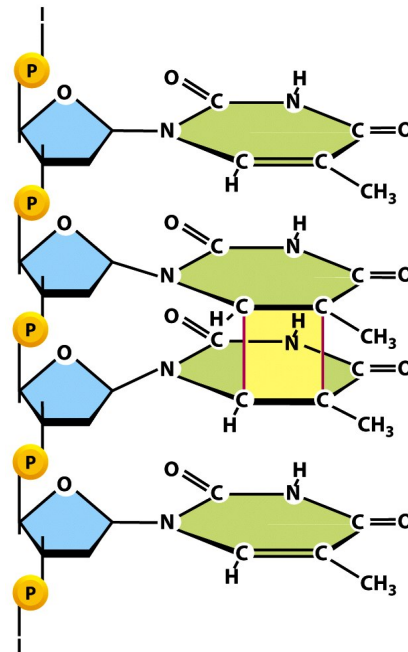
DNA pol  $\beta$



Glycosylase mediated base-flipping to probe individual bases for alterations  
Altered (unnatural) bases are then removed by hydrolysatation



Thymin dimer caused by UV-irradiation



# NUCLEOTIDE EXCISION REPAIR

Removes bulky lesions

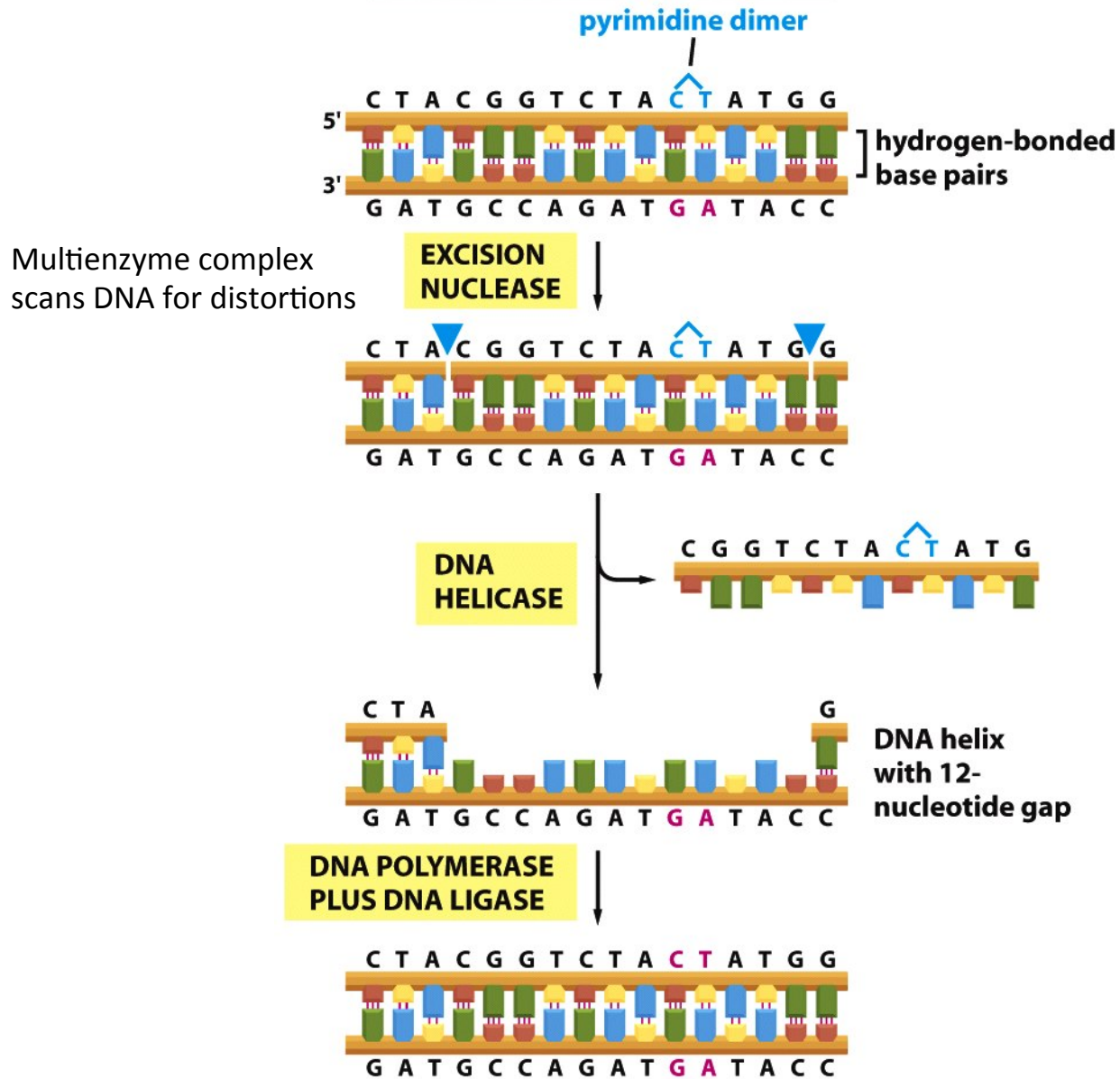


Figure 5-48b *Molecular Biology of the Cell* (© Garland Science 2008)

Error prone repair:

Heavily damaged DNA (stalled DNA replication) may activate 'rough and ready' DNA repair systems (E.coli: SOS repair system), where special DNA polymerases insert nucleotides with less stringency (no 3'→5' exonuclease activity, insertion of random nucleotides) . This results in increased mutation rates.

-> aim is to revert the damaged DNA into a replicable state at all cost.

Controlling the direction of mismatch repair:

In E.coli the parental strand only is methylated. Thus in hemimethylated DNA the unmethylated (i.e. new) strand is corrected.

Nicks rather than methylation are used in eukaryotes to identify the parental strand.

Transcription and DNA repair are coupled:

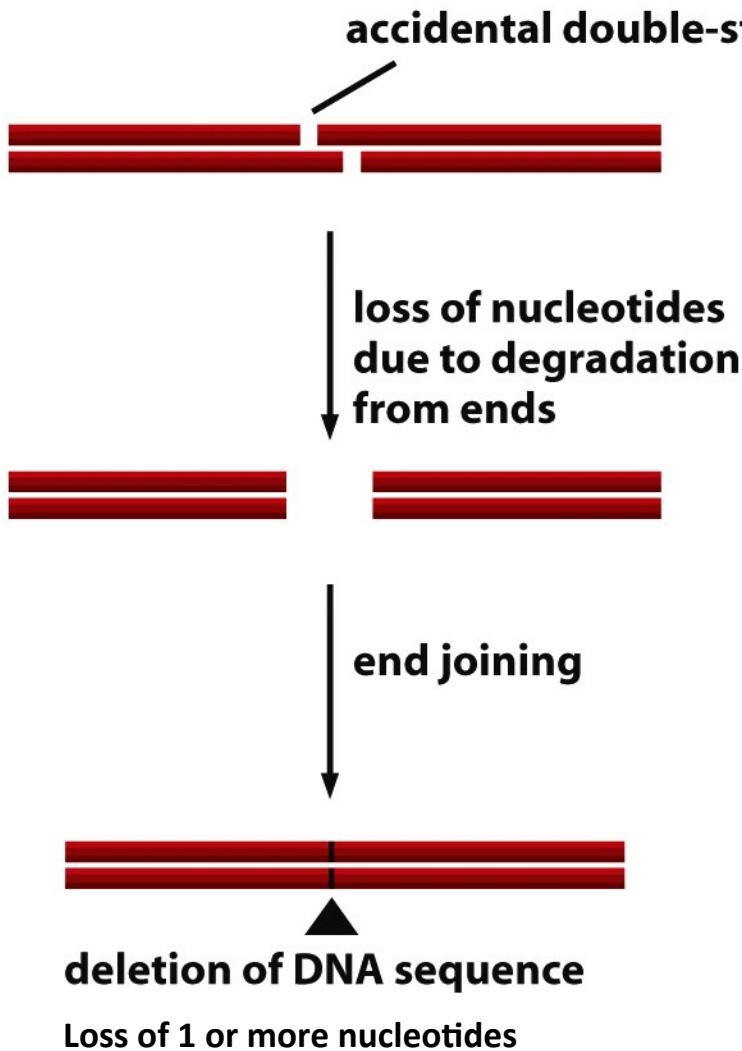
Transcription-coupled repair (TCR): when RNAPol is stalled, specific repair proteins are attracted to the transcription bubble, repair the template strand (without displacing the RNAPol) and let transcription resume. The other strand is not repaired by TCR.

DNA repair and progression of the cell cycle are coupled:

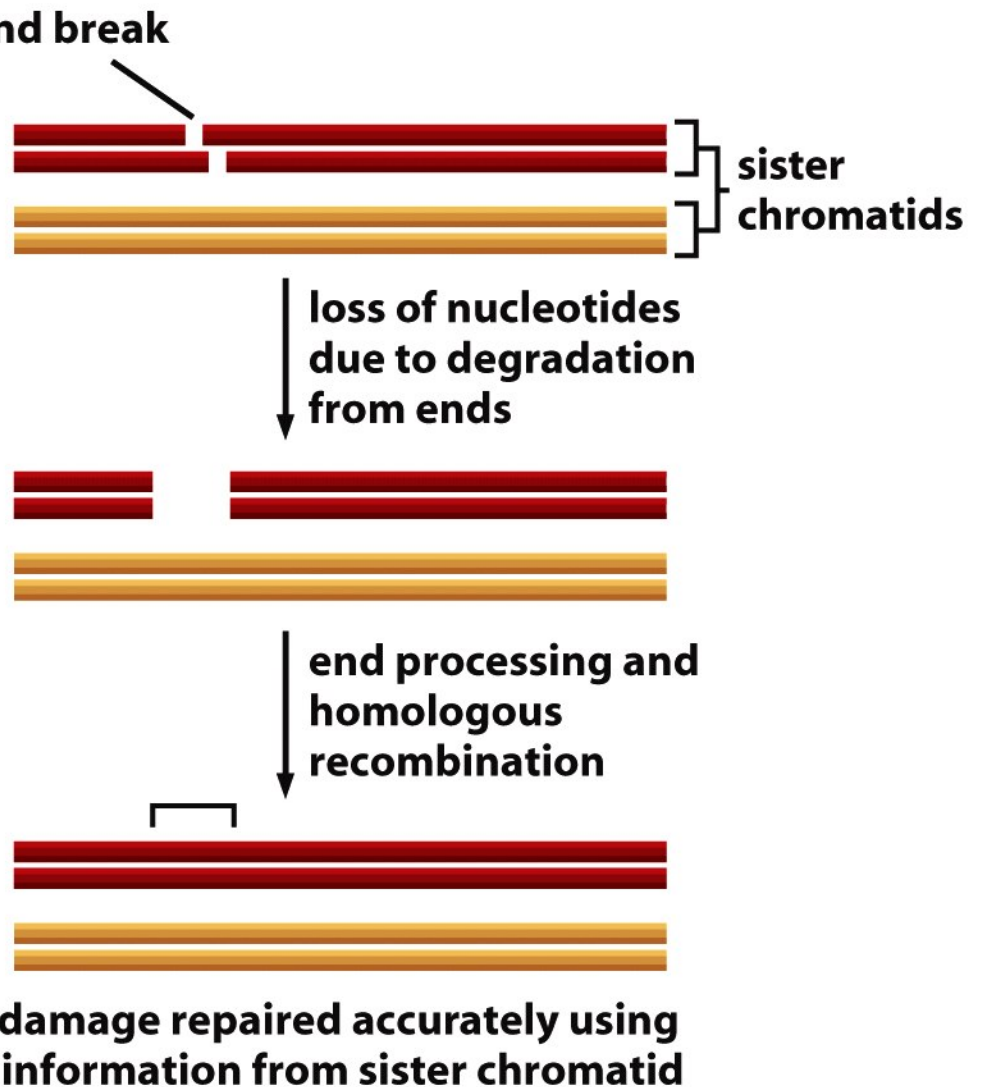
DNA damage can block entry from G<sub>1</sub> into S phase, slow S phase and block transition from S into M phase (check points for cell cycle progression). This gives the cell time to repair the DNA and prevent segregation of damages to daughter cells.

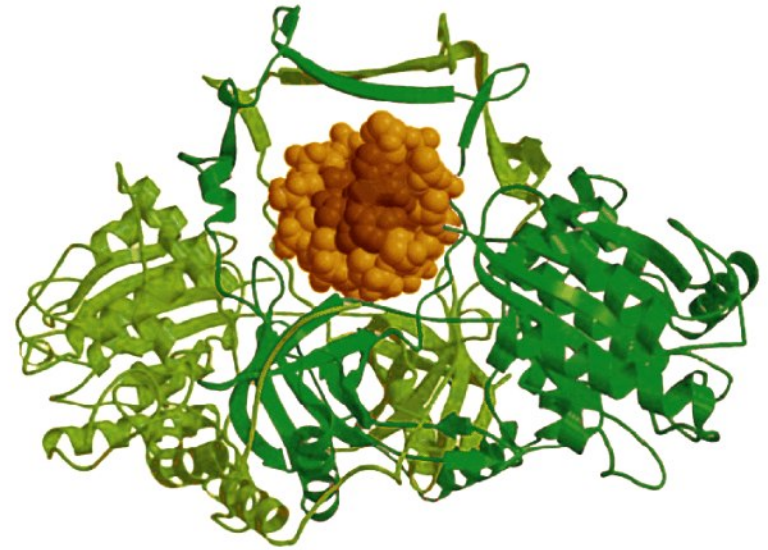
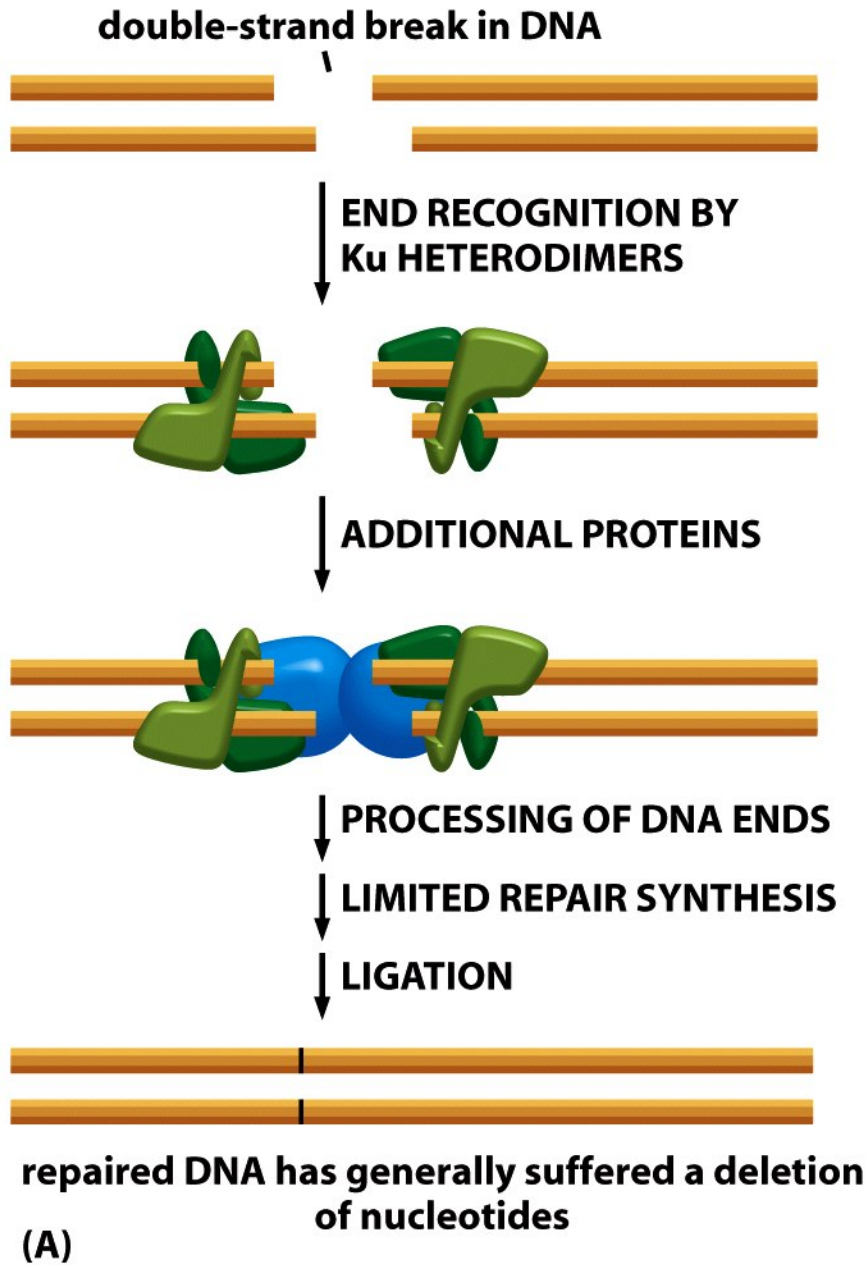
# Repair of double strand breaks

## (A) NONHOMOLOGOUS END JOINING



## (B) HOMOLOGOUS RECOMBINATION





**(B)**

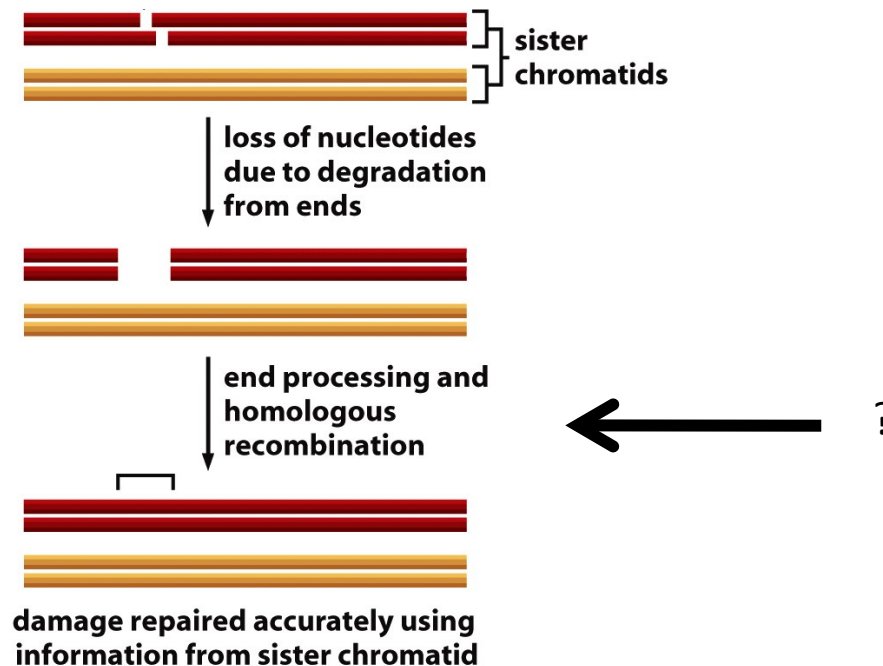
Common repair for somatic cells  
 Most of the genome is non-coding  
 -> Small errors do not matter in most cases

## Homologous recombination:

Exchange between (very) similar DNA molecules

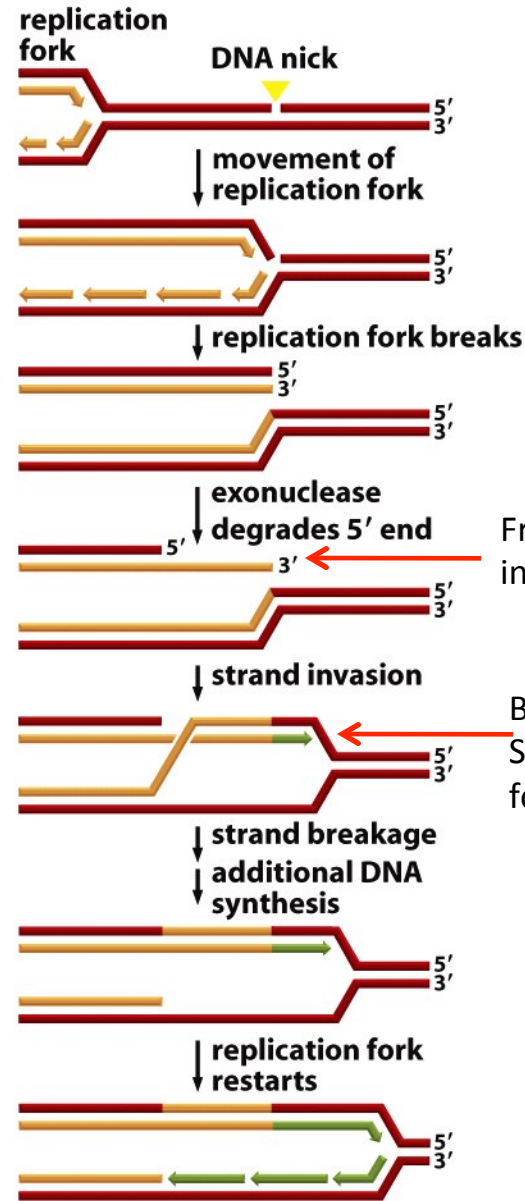
- Repair of ds breaks
  - Exchange of genetic information between chromosomes
- > creating new genetic combinations (genotypes)

Evolutionary conserved mechanism: also present in bacteria





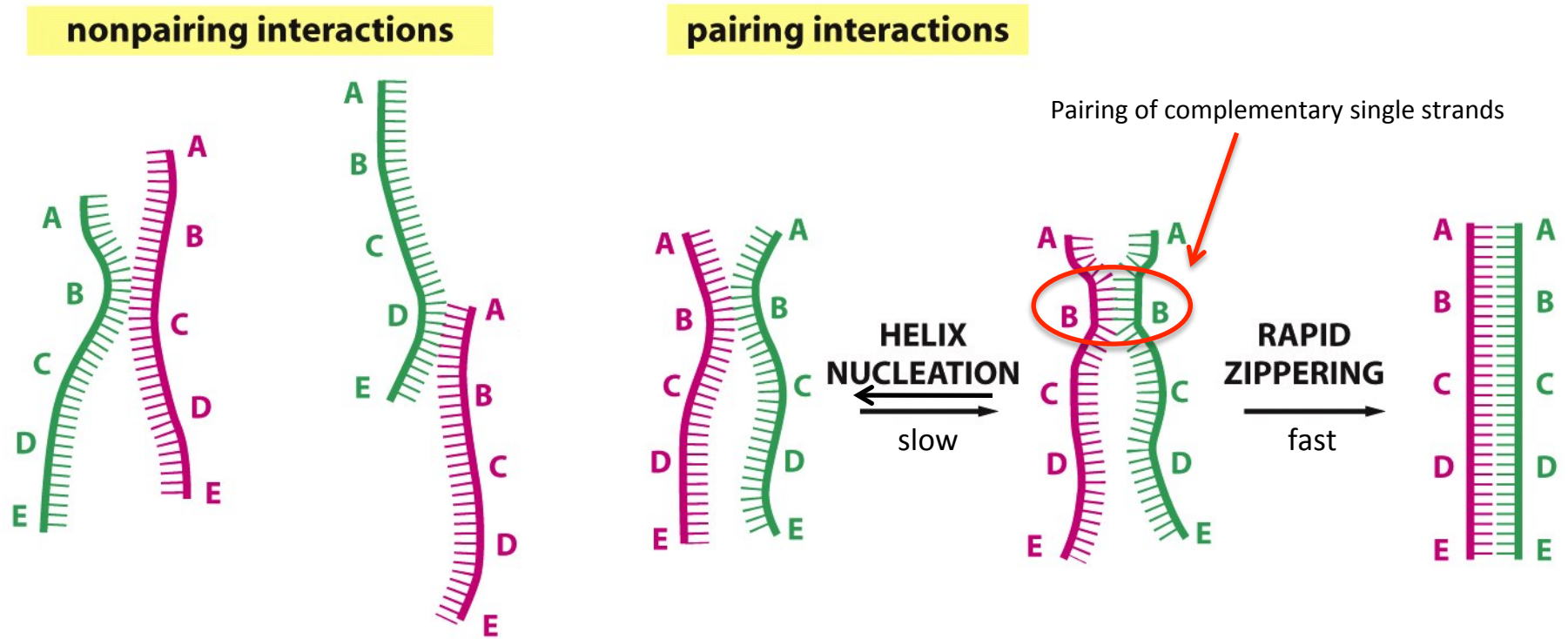
# Repair of a broken replication fork by homologous recombination



**BLOCK TO REPLICATION OVERCOME**

Figure 5-53 *Molecular Biology of the Cell* (© Garland Science 2008)

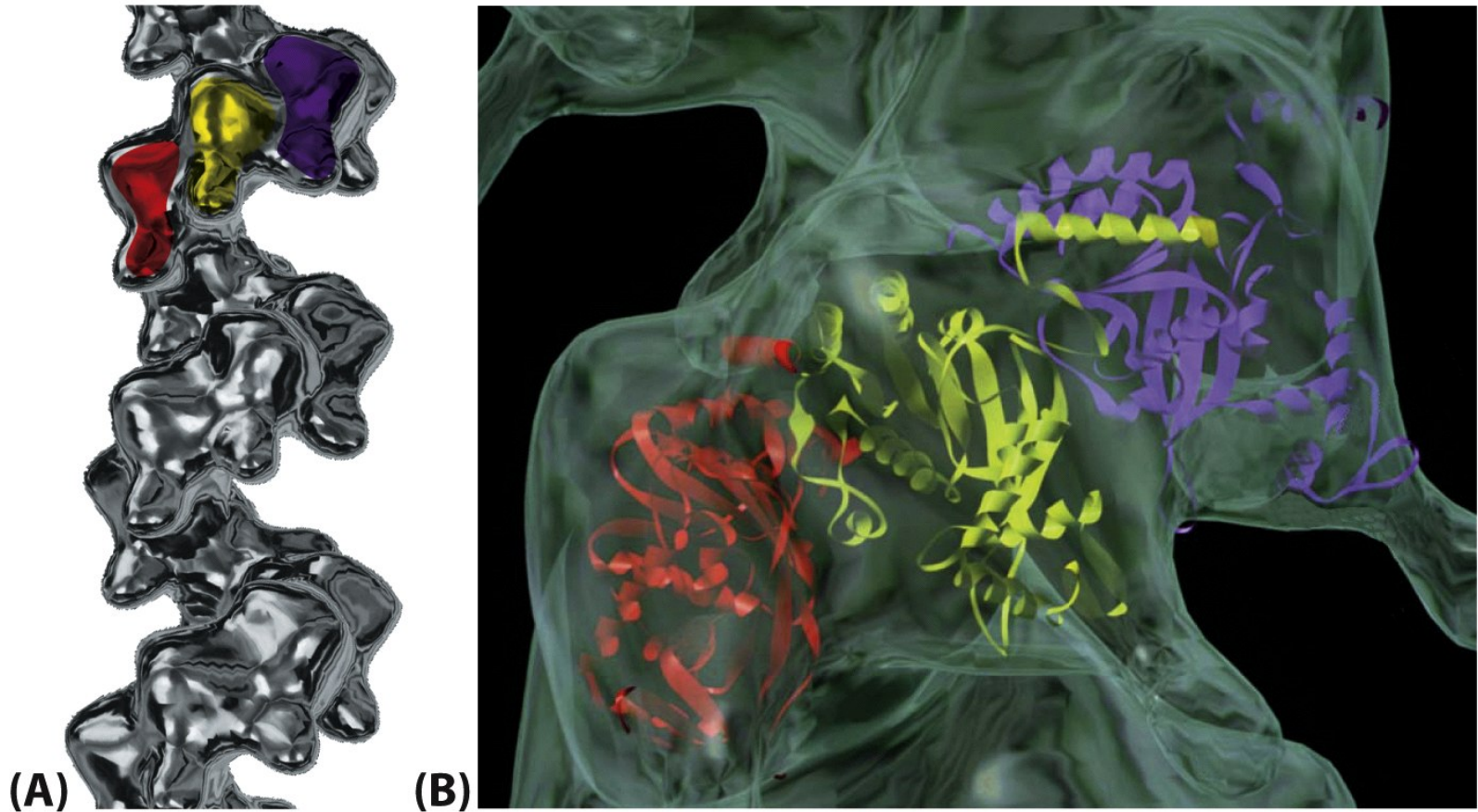
Homologous recombination requires base pairing of complementary, similar ssDNA. Base pairing of ssDNA (denatured) in the test tube: **hybridization** (DNA renaturation) of complementary strands. No enzymes are required! Driving force are A-T and G-C base pairing that lead to stable double helix formation.



DNA hybridization in the lab:

Microarrays, hybridization of probes to DNA immobilized on membranes

*In vivo*: ssDNA have to be stabilized for base pairing of homologous strands  
RecA/Rad51: binds in long cooperative clusters to ssDNA  
-> nucleoprotein filament  
can at the same time interact with a dsDNA molecule



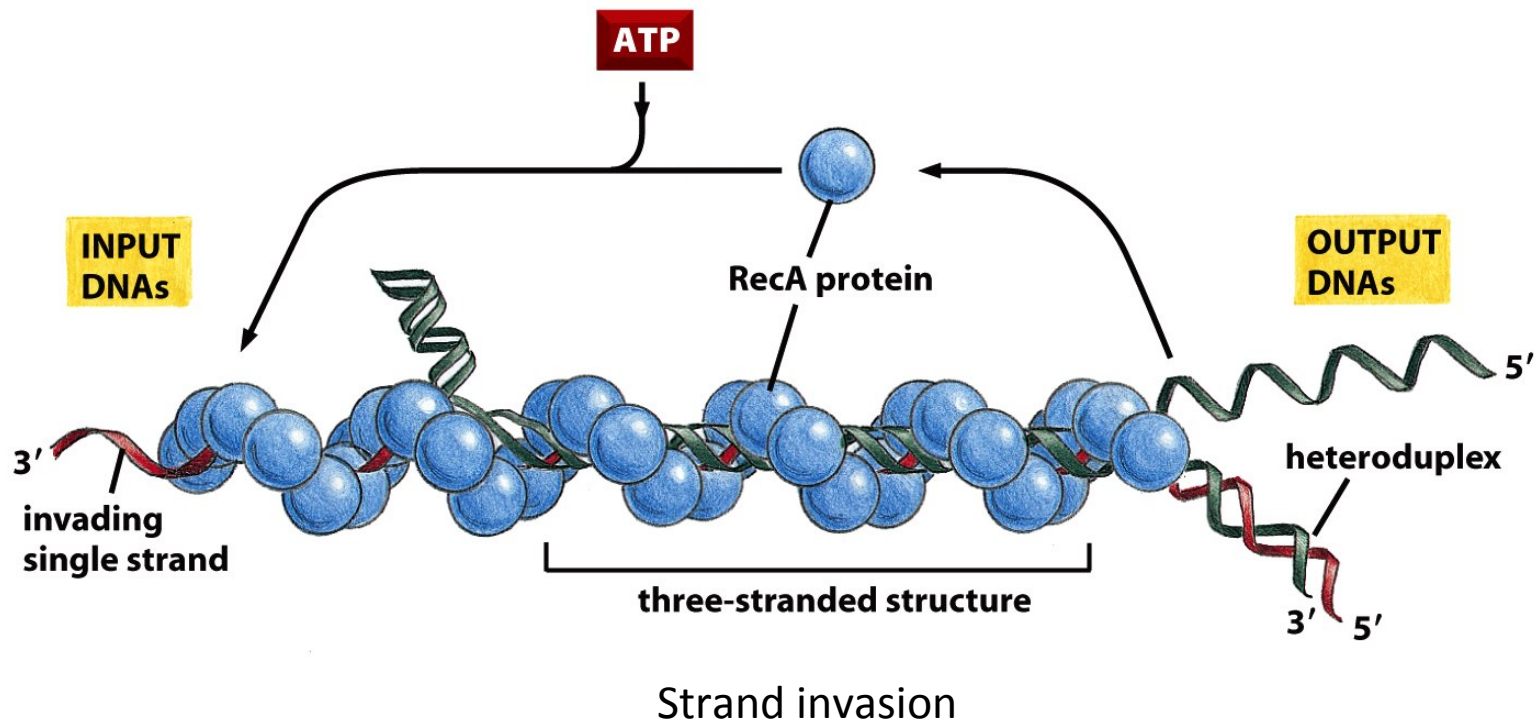
Multistep DNA synapsis reaction:

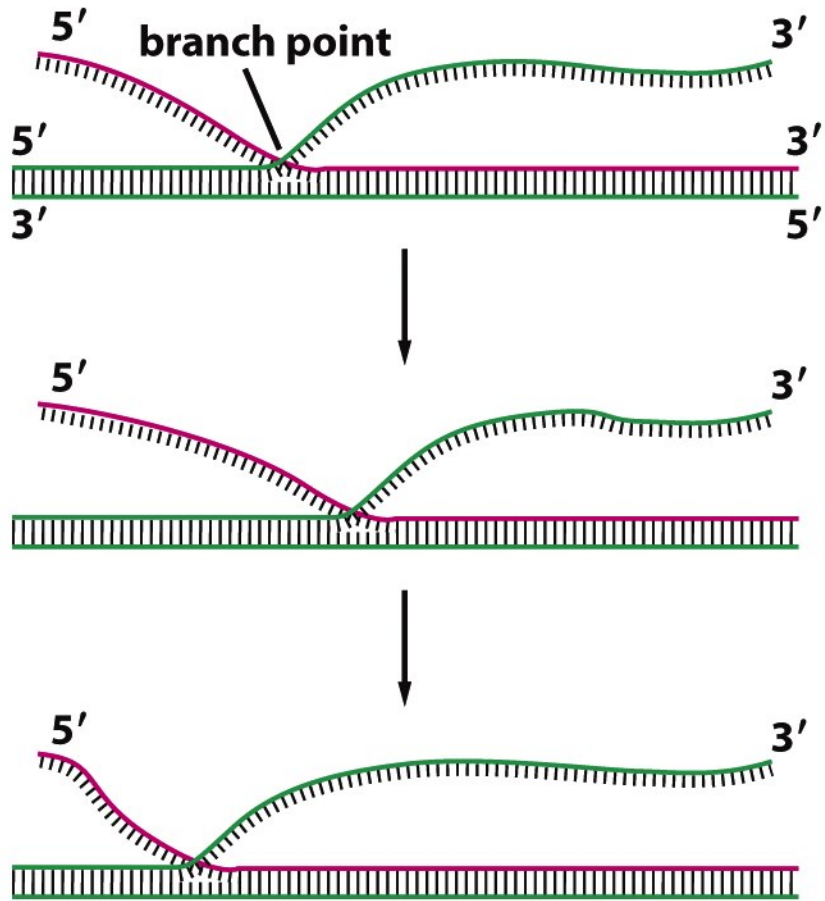
RecA intertwines ssDNA with dsDNA molecules (sequence independent)

ssDNA 'searches' for homology (transient base-pairing by 'flipped-out' bases?)

Strand invasion: ssDNA displaces the respective strand of the double helix

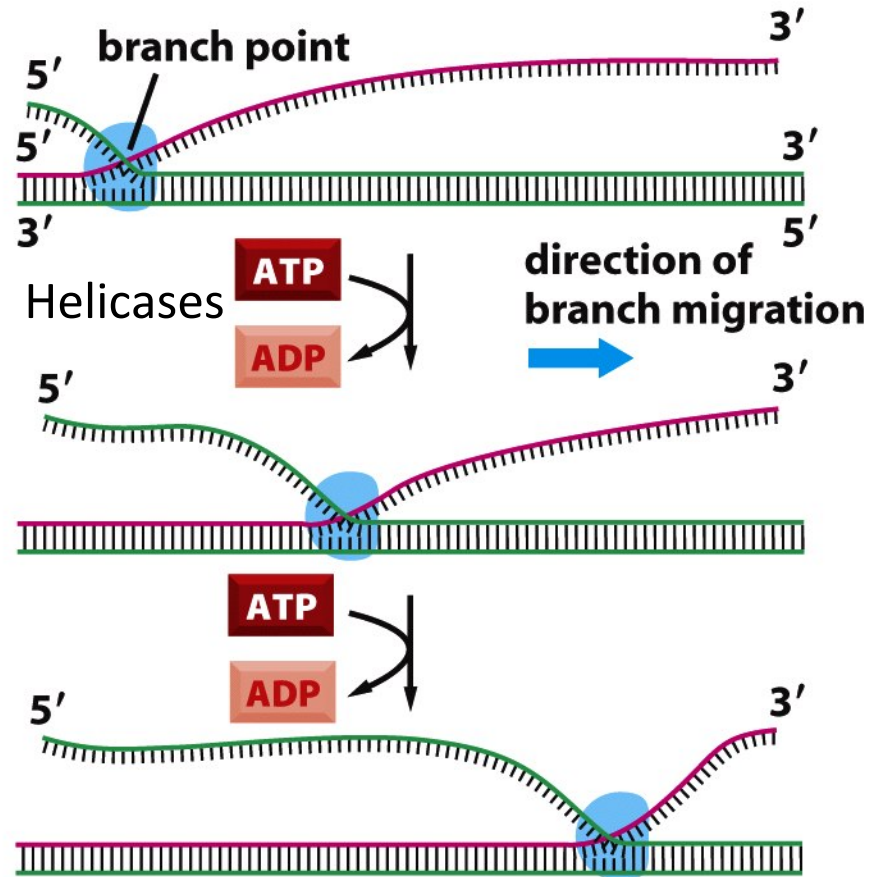
-> hetero-duplex formation





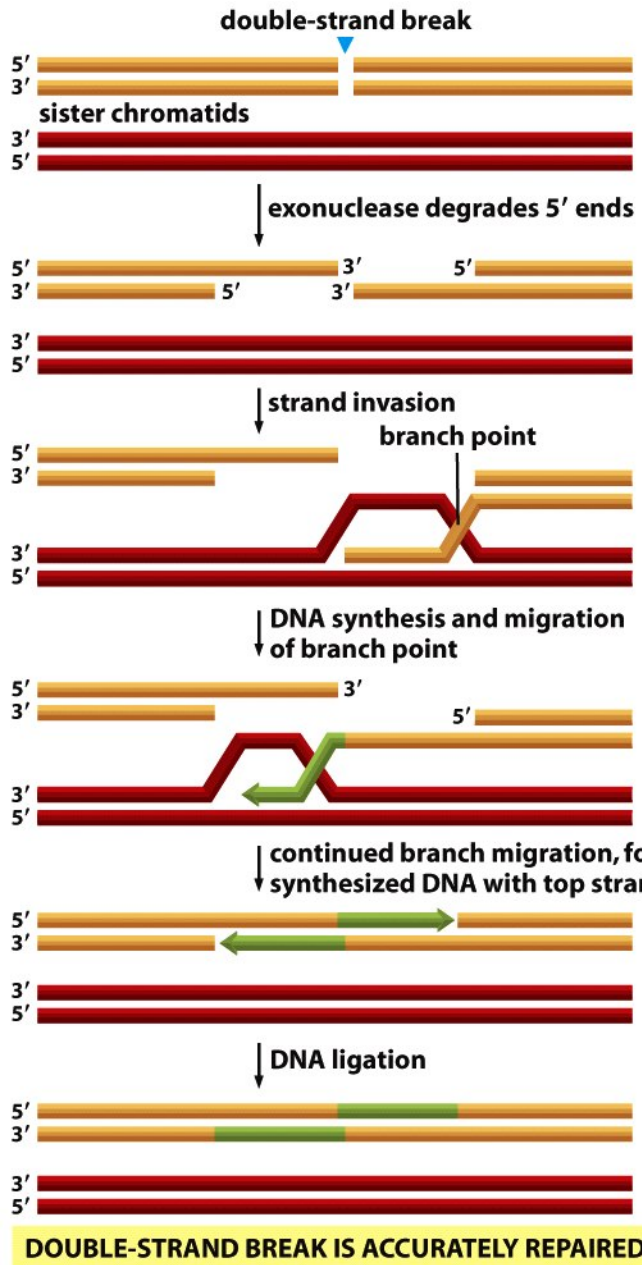
**(A) SPONTANEOUS BRANCH MIGRATION**

Not directional



**(B) PROTEIN-DIRECTED BRANCH MIGRATION**

Specific direction  
-> enlarged hetero-duplex



## Repair of double strand brake

-> recombinogenic ssDNA

RecA/Rad51

Helicase, DNA polymerase

Gene conversion: template mediated repair using the homologous dsDNA: repaired region corresponds to template  
 -> loss of heterozygosity: assuming red and yellow were different, after the repair both strands are the same (same as red)

Spo1 induces DSB

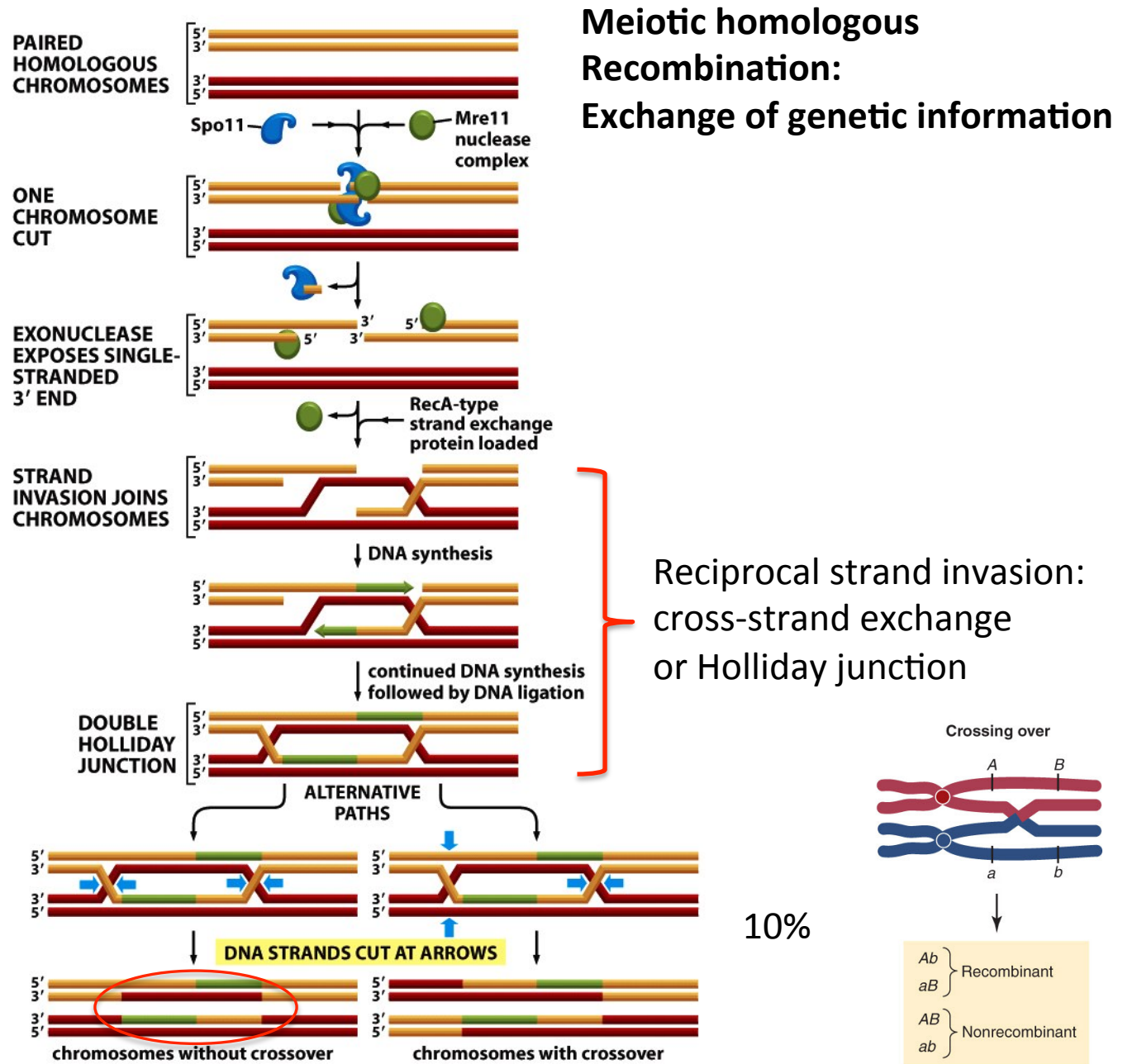
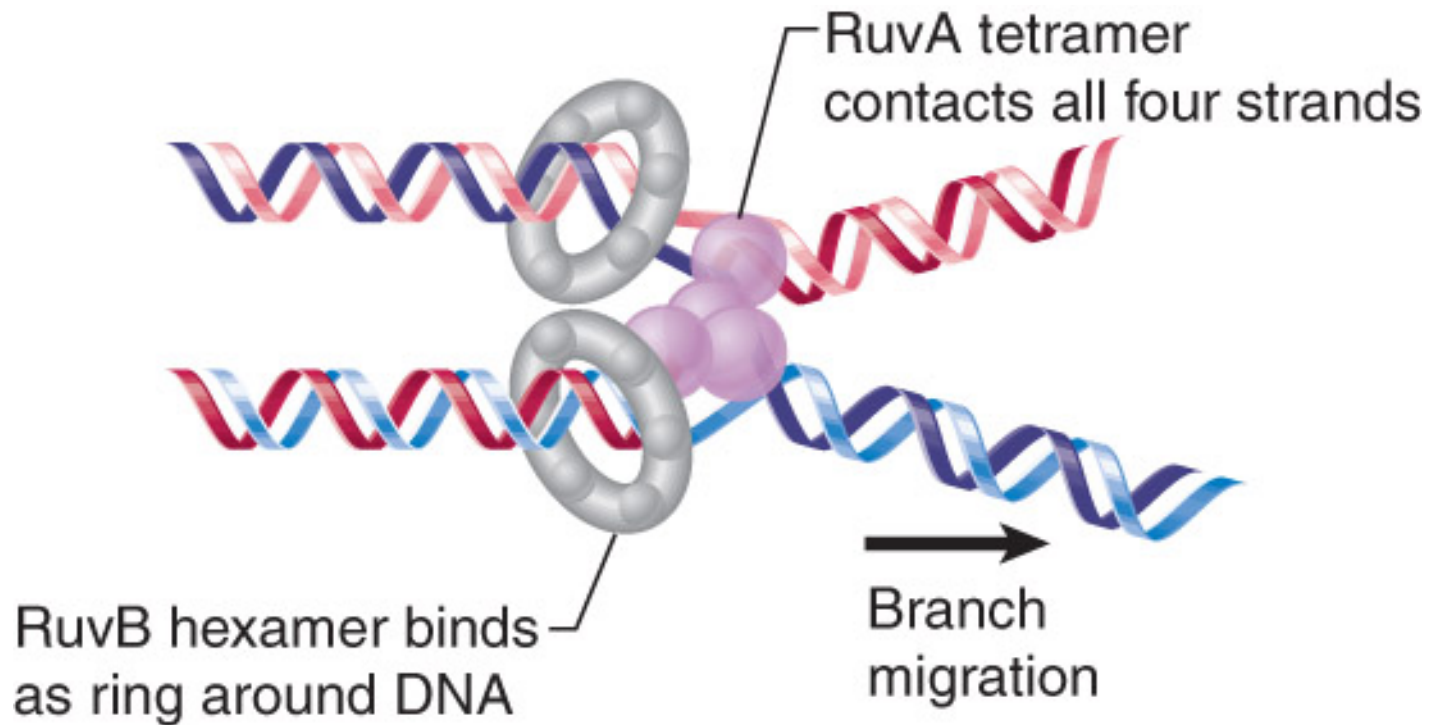


Figure 5-64 *Molecular Biology of the Cell* (© Garland Science 2008)

RuvA and RuvB: promote branch migration of cross over (Holliday junction)  
Endonuclease RuvC cleaves Holliday junction (resolution)





# Heteroduplex repair and gene conversion

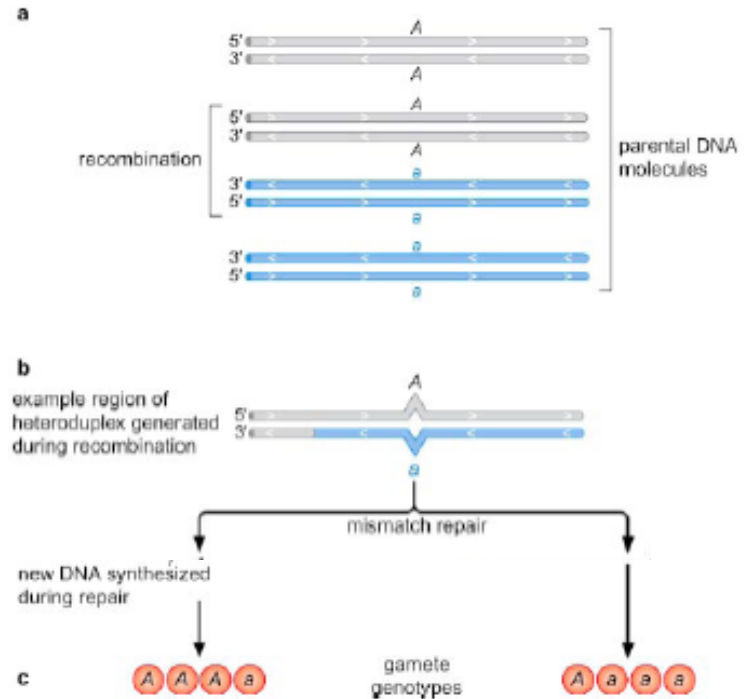
**heteroduplex generated during meiosis covers site in gene X where red and blue alleles differ**



**MISMATCH REPAIR EXCISES PORTION OF BLUE STRAND**



**DNA SYNTHESIS FILLS GAP, CREATING AN EXTRA COPY OF THE RED ALLELE OF GENE X**



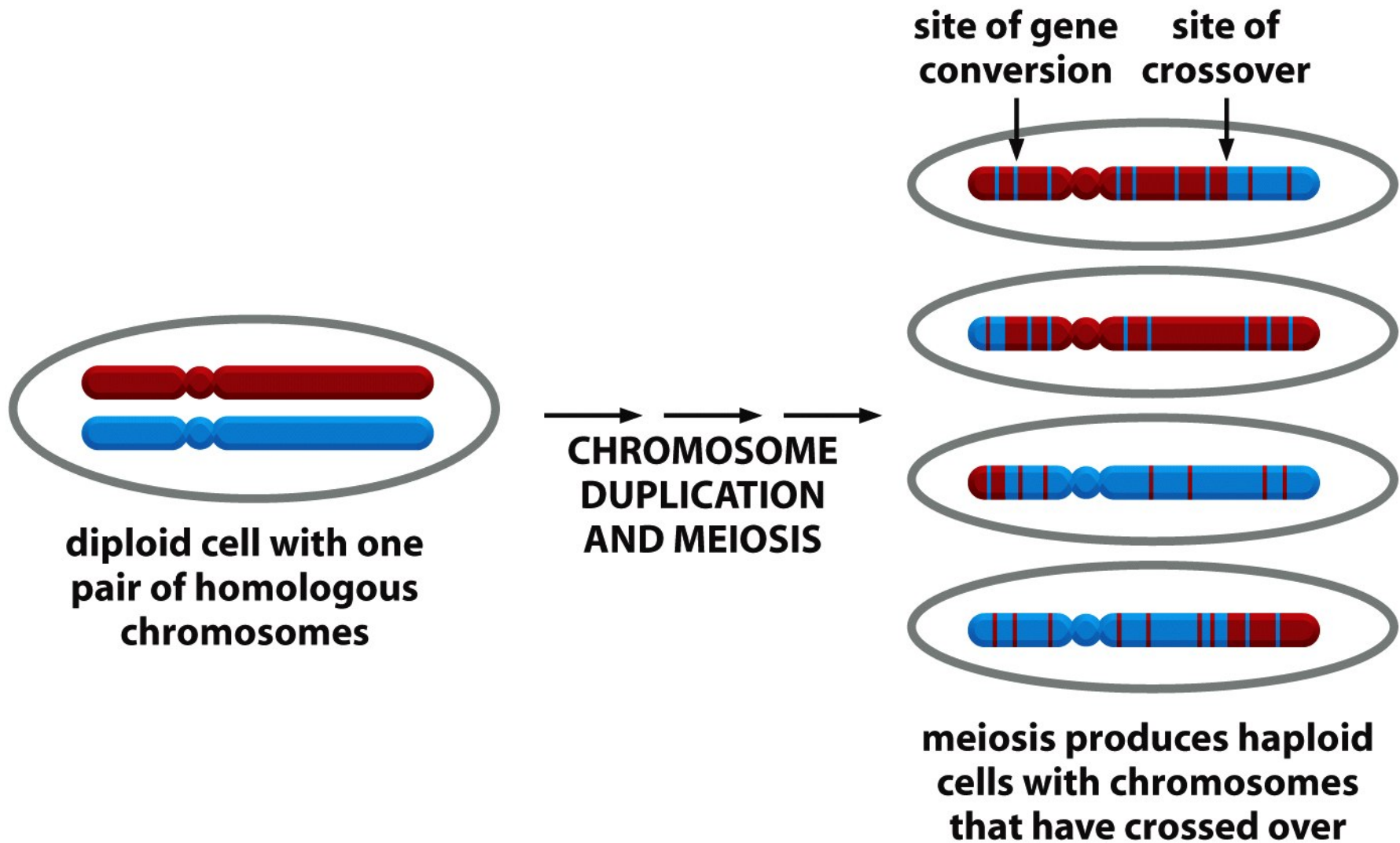
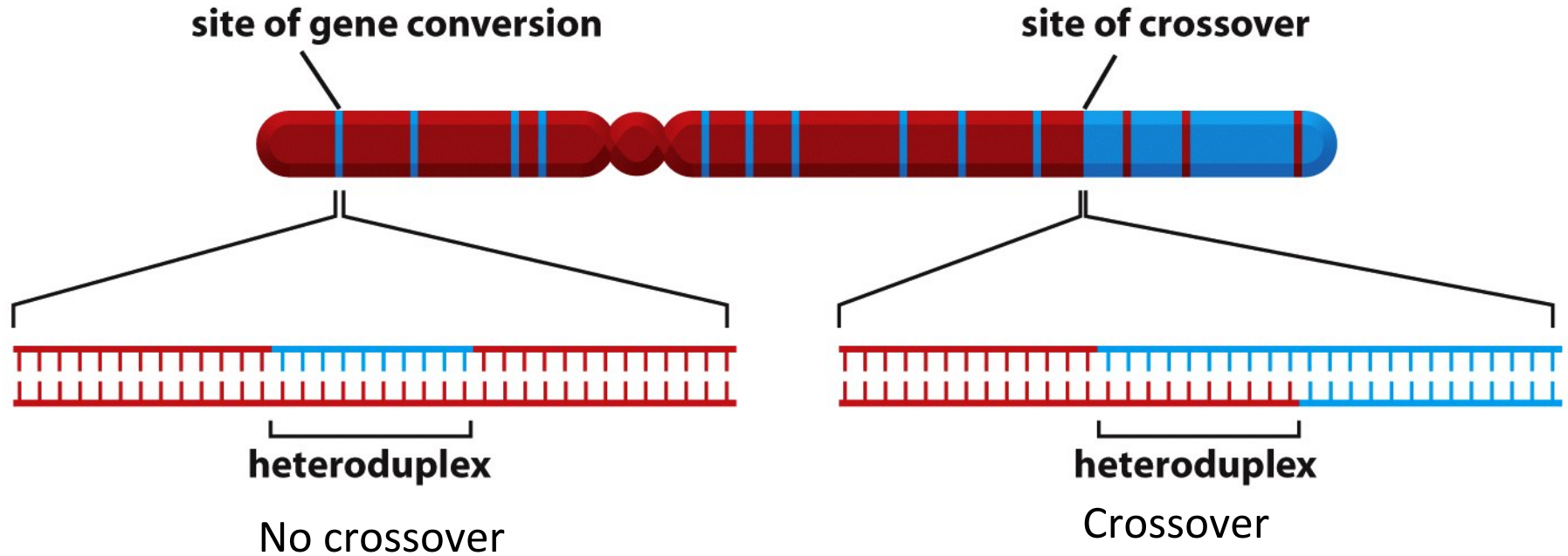


Figure 5-63 *Molecular Biology of the Cell* (© Garland Science 2008)



- Homologous recombination always results in heteroduplex (length is determined by extend of branch migration)
- Resolution of holliday junction determines whether crossover occurs

Components of the mismatch repair system prevent recombination between poorly matched sequences

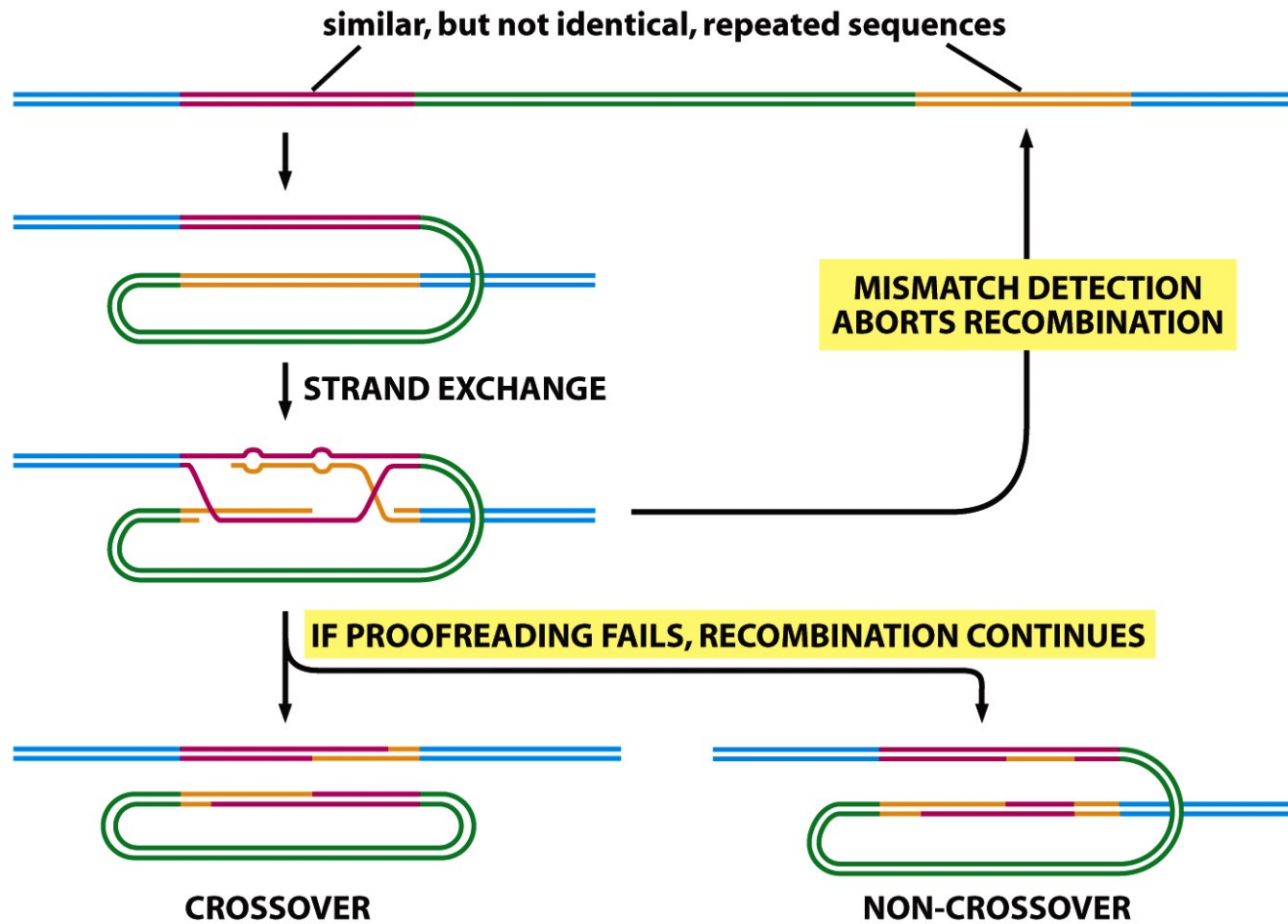
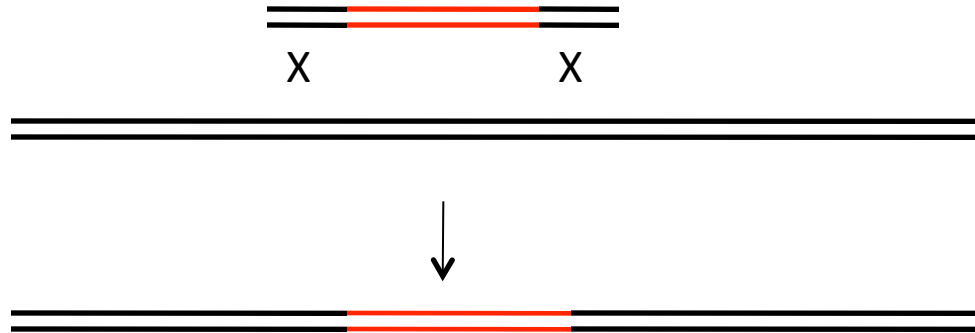


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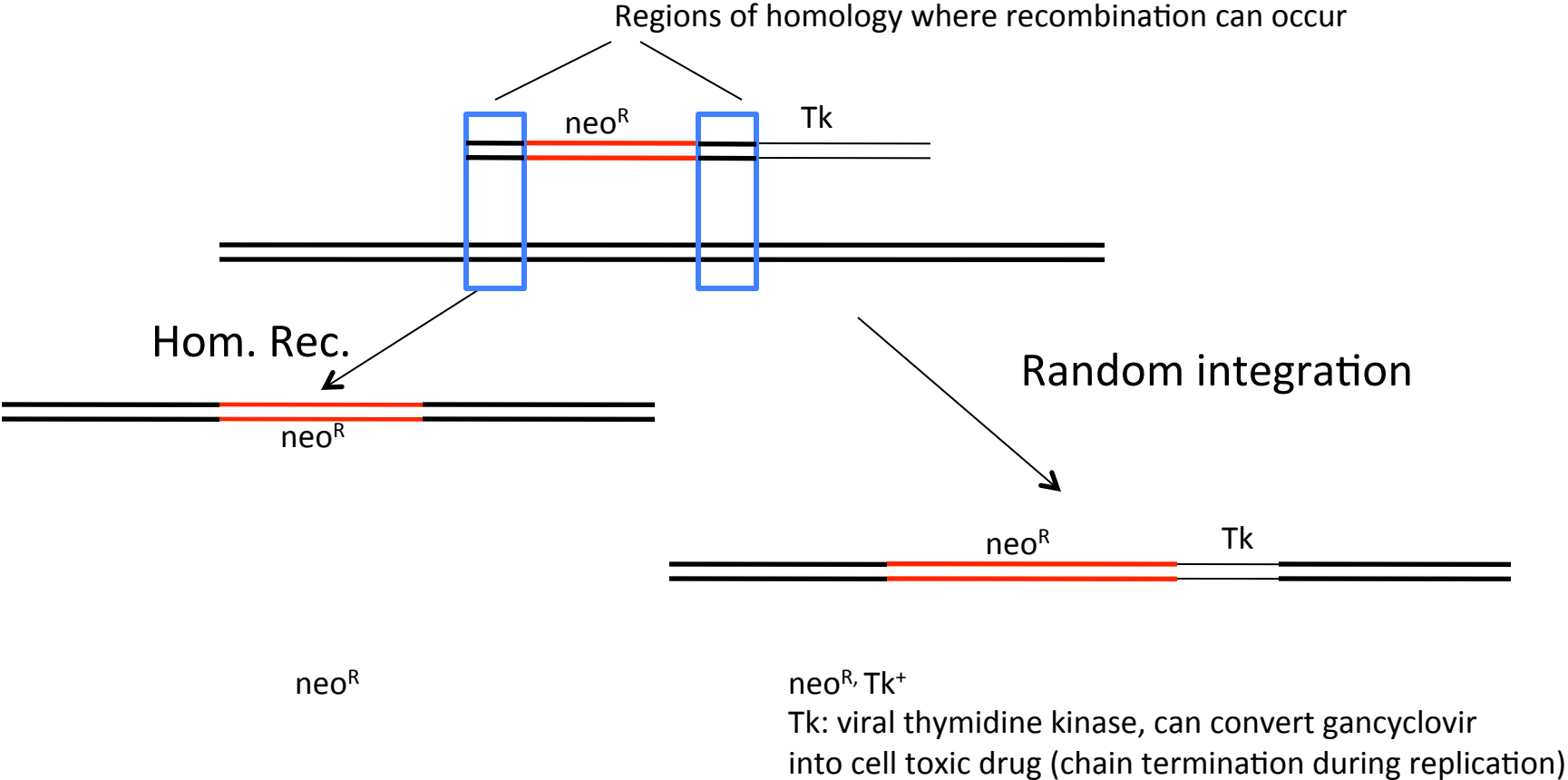
# Homologous recombination as a tool to manipulate genomes



Introduce the DNA into the genome of interest by homologous recombination  
Bring the template DNA into the nucleus (injection, electroporation)  
Select for the cell where homologous recombination took place (selectable marker: antibiotics resistance, fluorescence). Rare event, estimate:  $0.5 \times 10^6$ /cell

Make an organism of the cell with the manipulated genome, -> requires totipotent cells  
-> embryonic stem cells (ES cells)

Positive/negative selection for a homologous recombination event



Selection with neomycin and gancyclovir:

**cell growth**

**cell death**

1 : 500'000

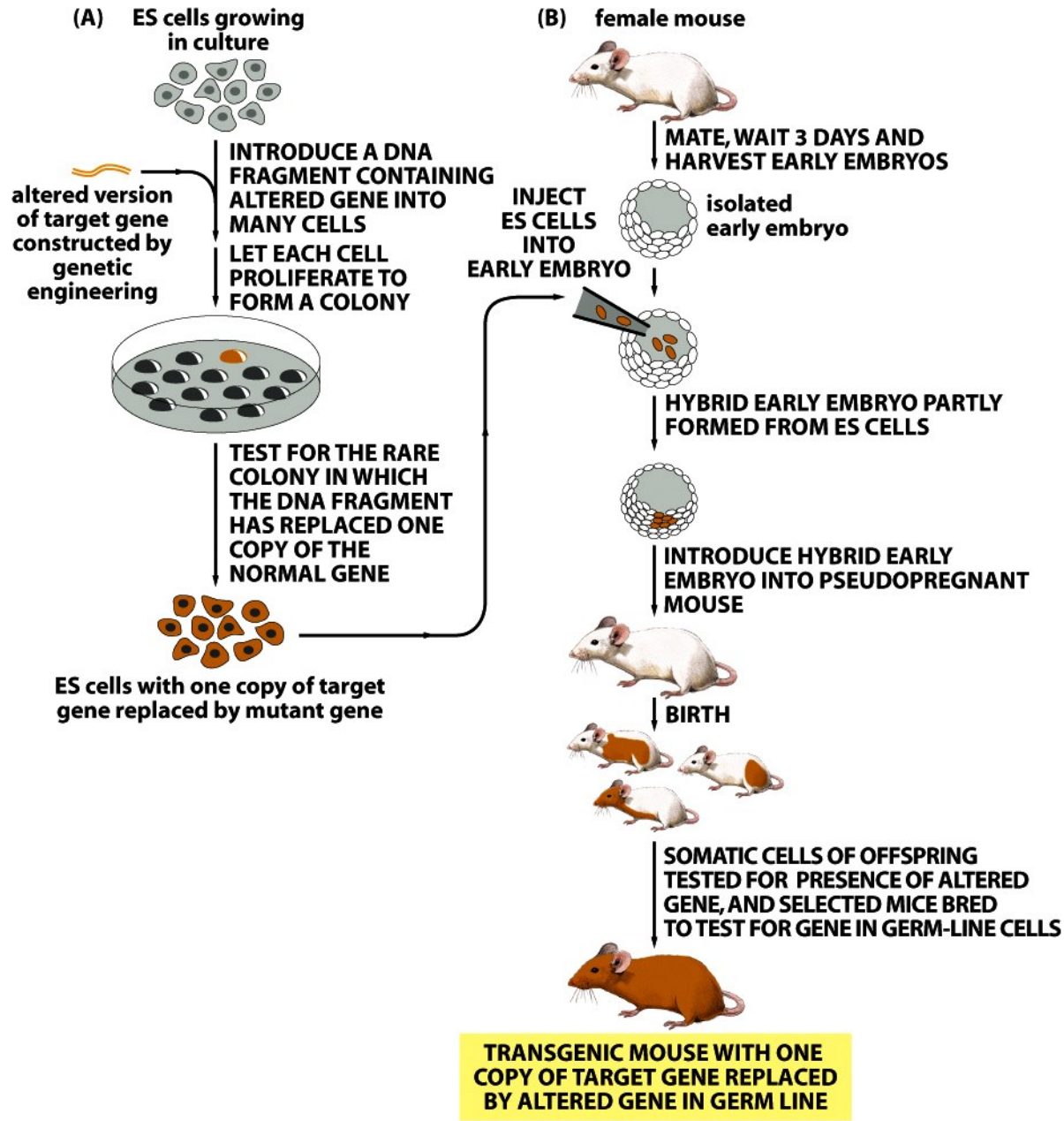
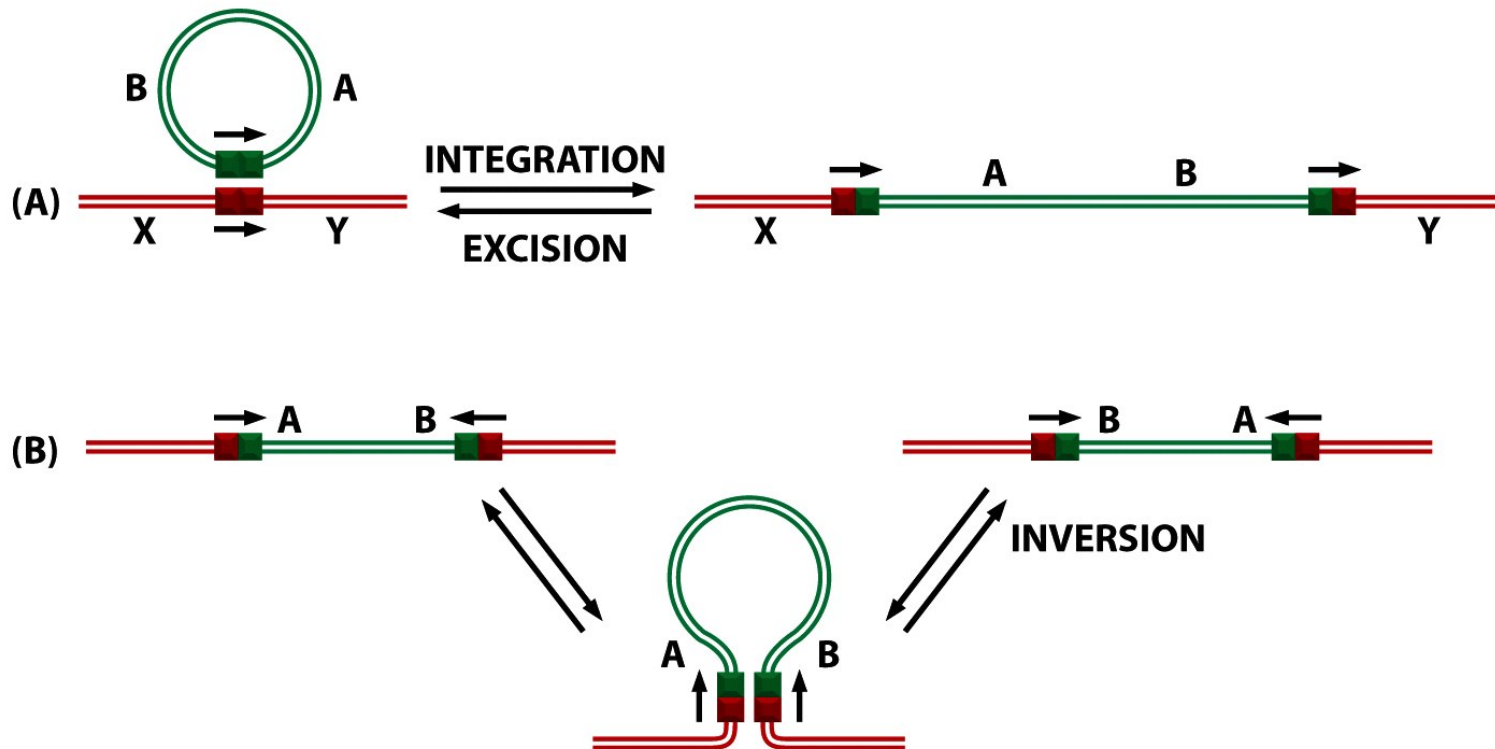


Figure 8-65 *Molecular Biology of the Cell* (© Garland Science 2008)

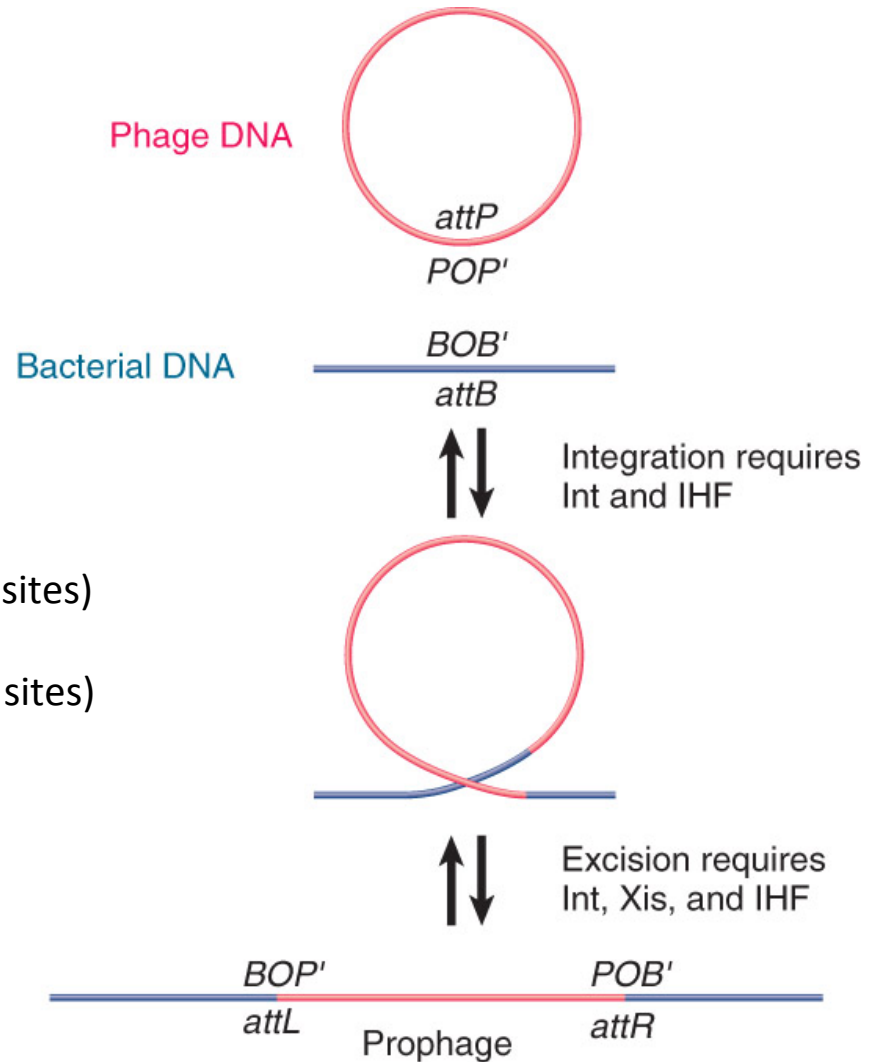
## Conservative site specific recombination

- requires specific sequences (target sites for the recombinases)
- requires specific enzymes (recombinases); resemble topoisomerases I since they form transient covalent bonds with the DNA. Require no energy. Reversal of the integration (excision) restores original sequence (-> conservative).





# Phage $\lambda$ genome integration into the E.coli host genome (lysogenic pathway)



Integration: Int and IHF (*attP*, *attB* rec. sites)

Excision: Int, Xis and IHF (*attL*, *attR* rec. sites)

# Cre/lox system for conditional knockouts in mouse

Phage P1 Cre recombinase recognizes and cleaves lox sites (34bp: 2 x 13 bp inverted repeat with 8bp spacer)

