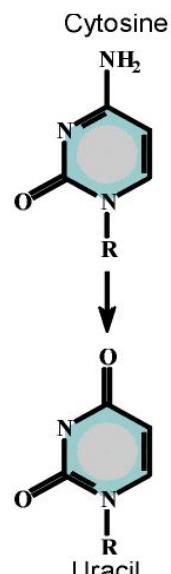
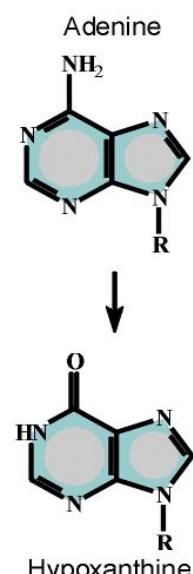


## Typical base lesions

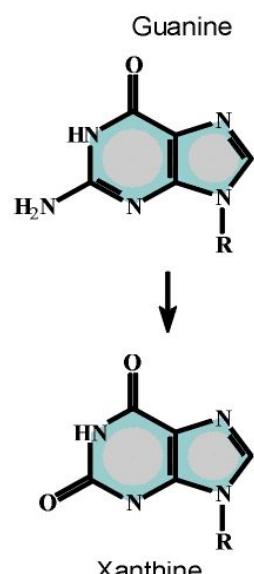
1.



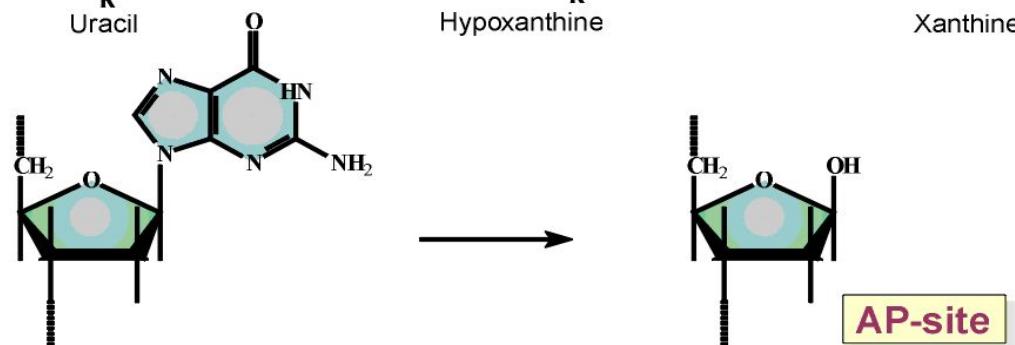
Adenine



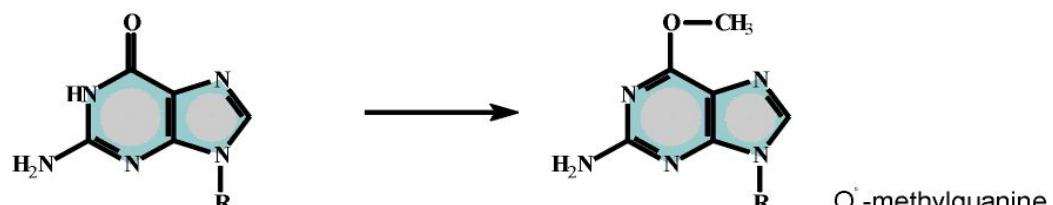
Guanine



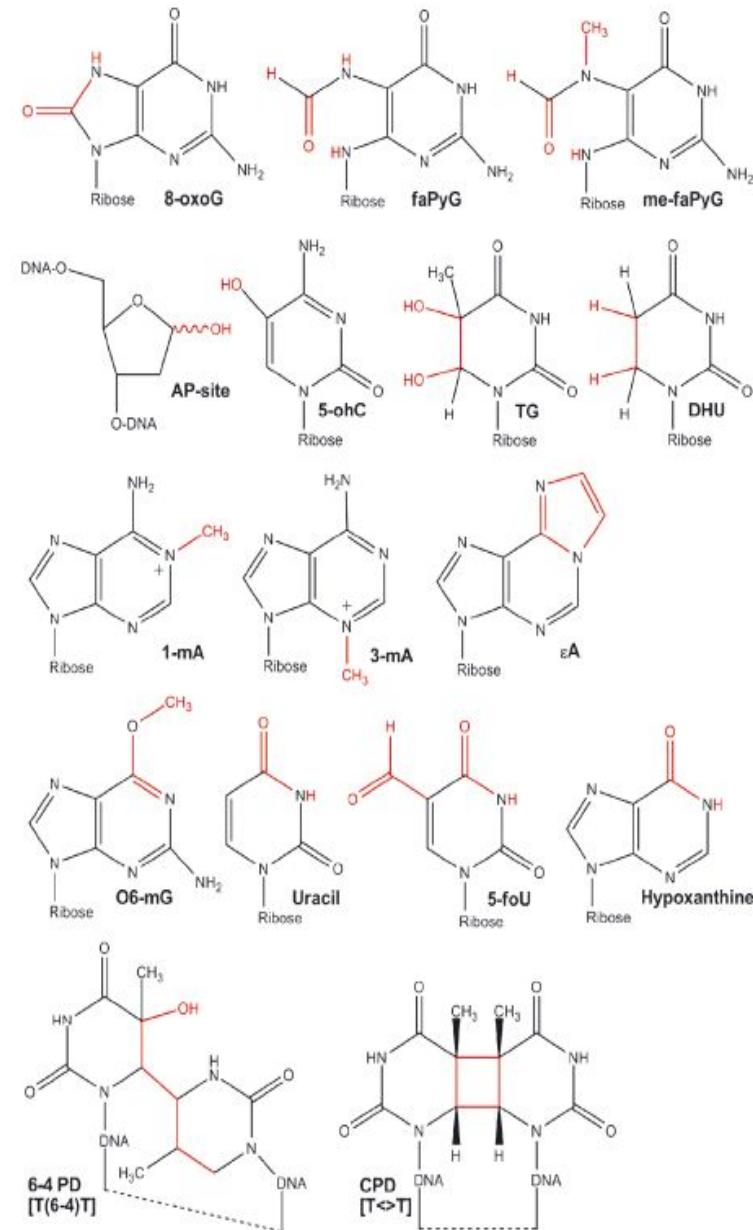
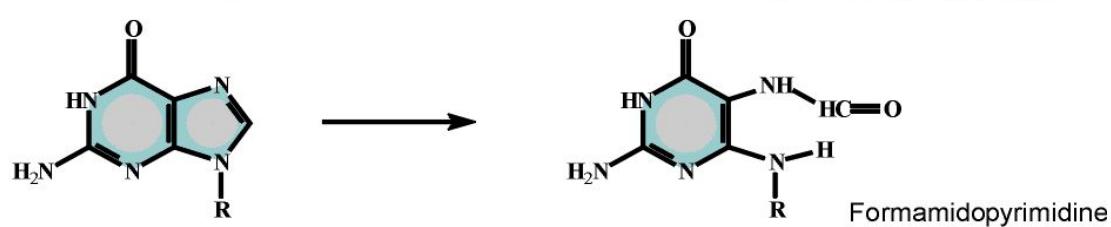
2.



3.



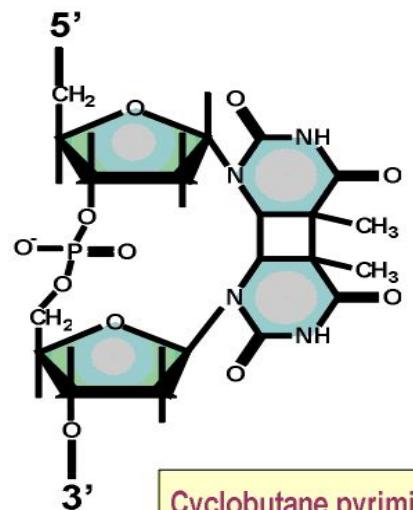
4.



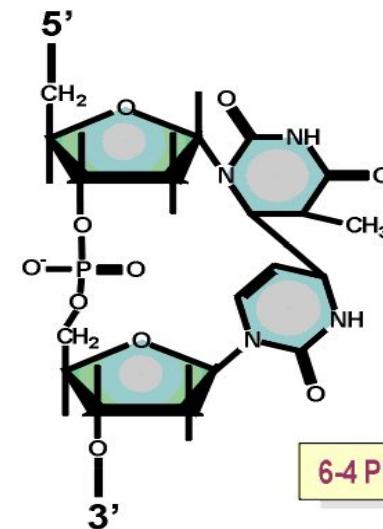
Damaging agent	Prototypical lesions	Major repair mechanism	Prototypical repair enzymes ( <i>E. coli</i> /human)
Alkylating agents	O6-mG	DR	Transferases: Ogt/Agt
	1-mA	DR	Oxidoreductases: AlkB/Abh2
	3-mA, 3-mG, 7-mA, 7-mG	BER	Glycosylases: AlkA/Aag
Hydrolysis	Abasic sites	BER	Endonucleases: EndoV/Ape1
	Deamination (forming uracil)	BER	Glycosylases: Ung
ROS	Deamination (forming hypoxanthine)	NIR	Endonucleases: EndoV
	8-oxoG, faPyA/G, TG, 5-ohC, DHU, DHT	BER	Glycosylases: Fpg, Nth/Ogg1, Nth1
	DHU, DHT, 5-ohC	NIR	Endonucleases: EndoV/Ape1
Replication errors	(a) Base mismatches	MMR	Mismatch proteins:
	(b) Insertion/deletion loops		MutS, MutL, MutH/MutS $\alpha/\beta$ , MutL $\alpha$
UV radiation	Bulky adducts	NER	XPA–XPF+others
	CPDs, 6-4 PDs	DR	Photolyases: CPD and (6-4) photolyases

BER, base excision repair; DR, direct reversal; MMR, mismatch repair; NER, nucleotide excision repair; NIR, nucleotide incision repair; ROS, reactive oxygen species.

5.



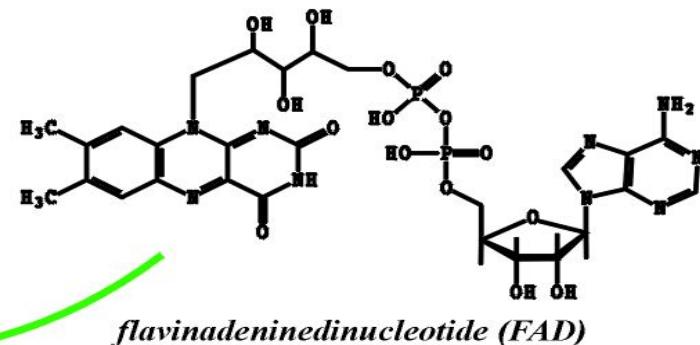
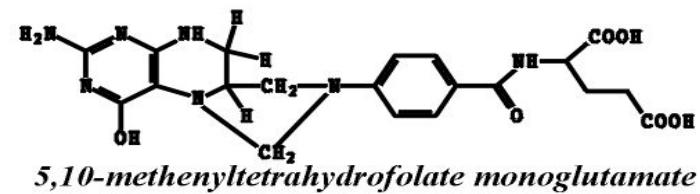
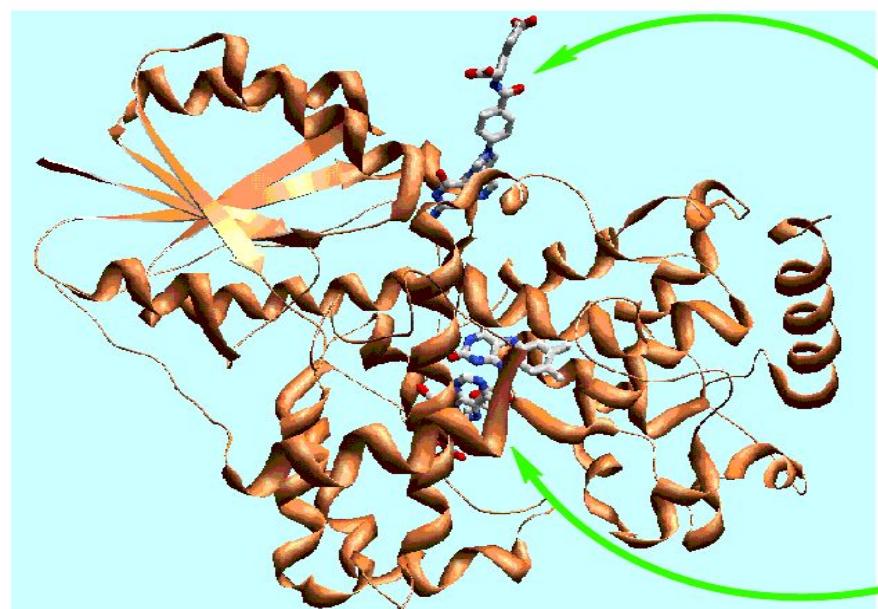
T  
T

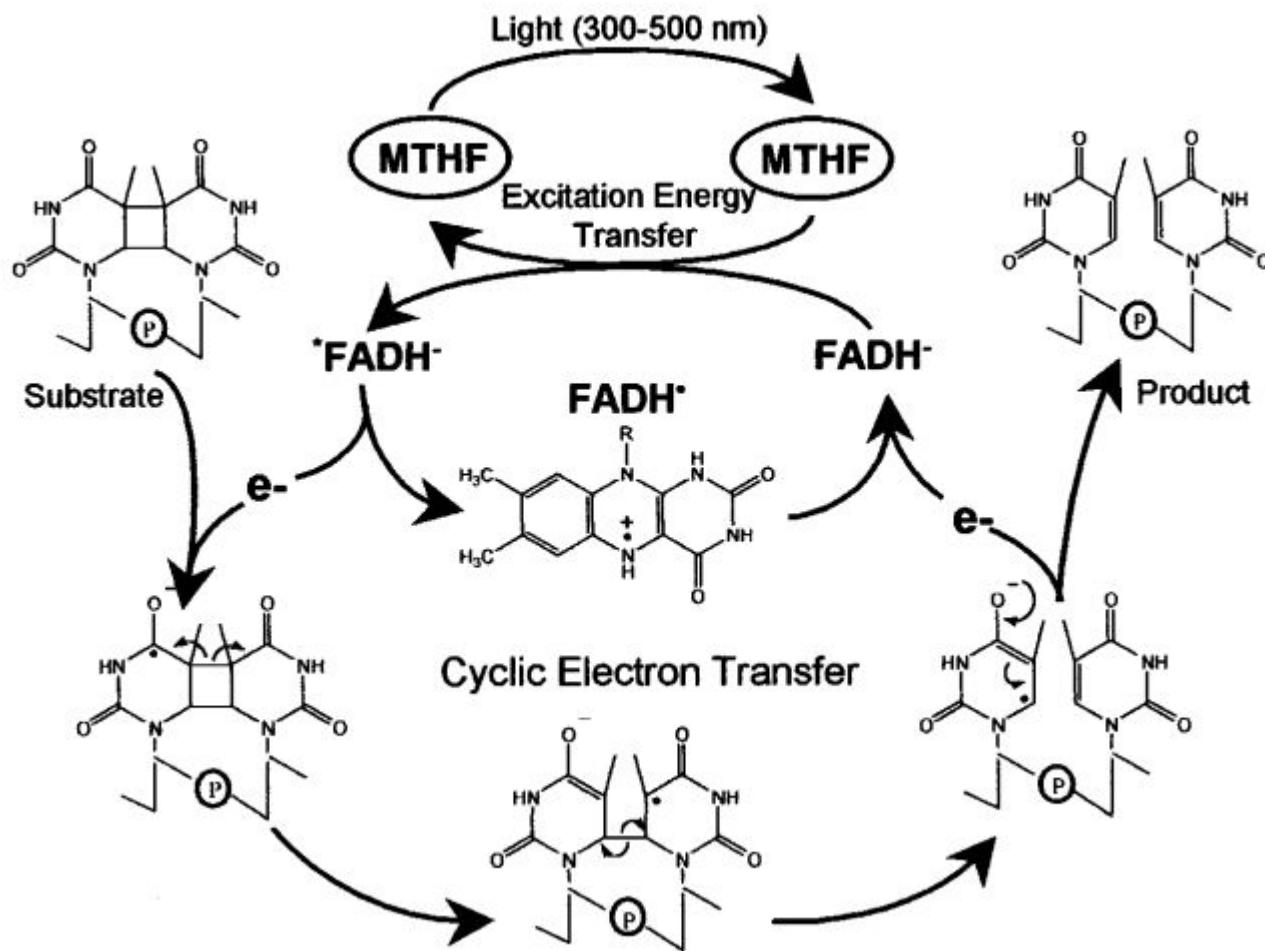


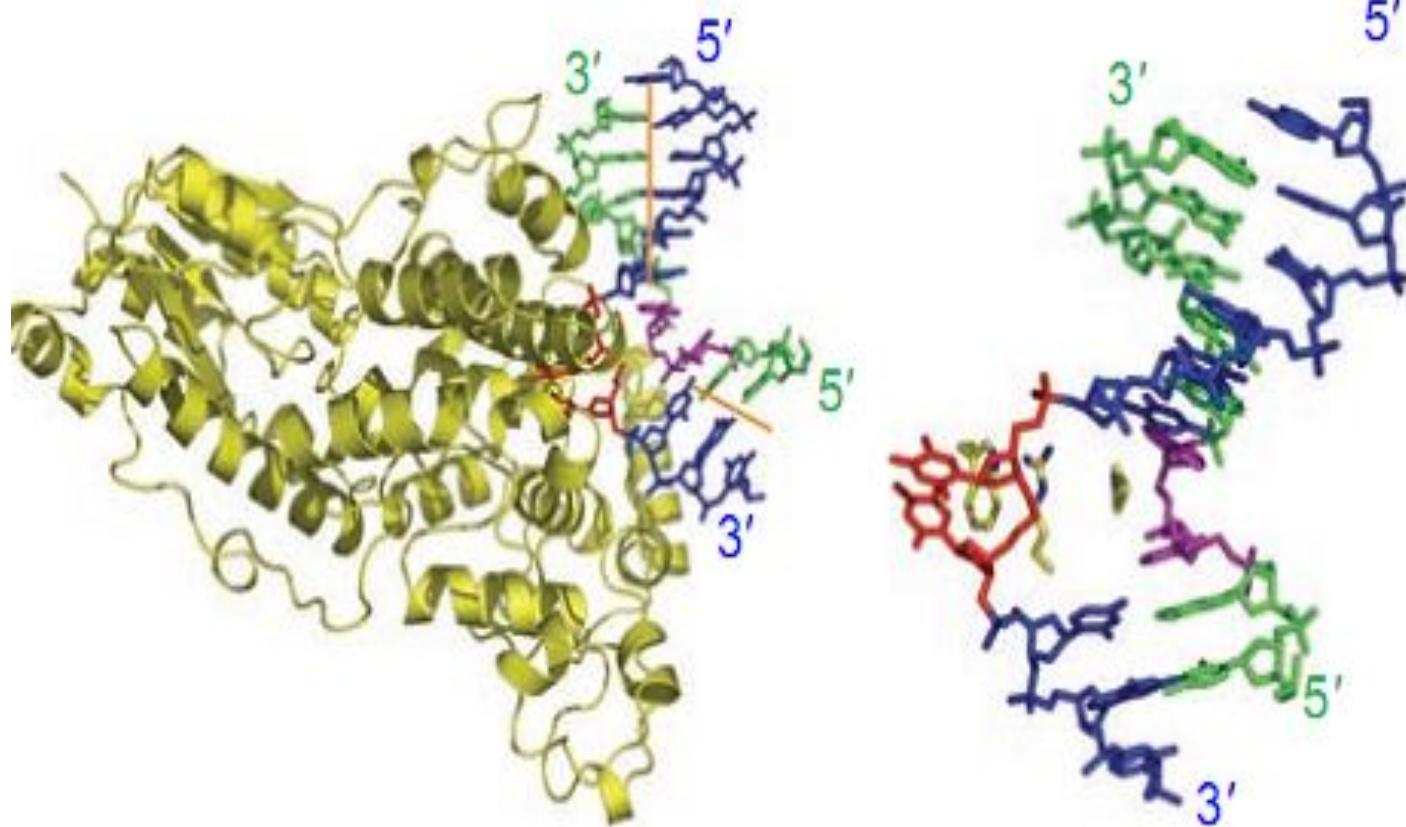
T  
C

5'-T-C-3'  
5'-T-T-3'  
5'-C-C-3'

Any pyrimidine pair

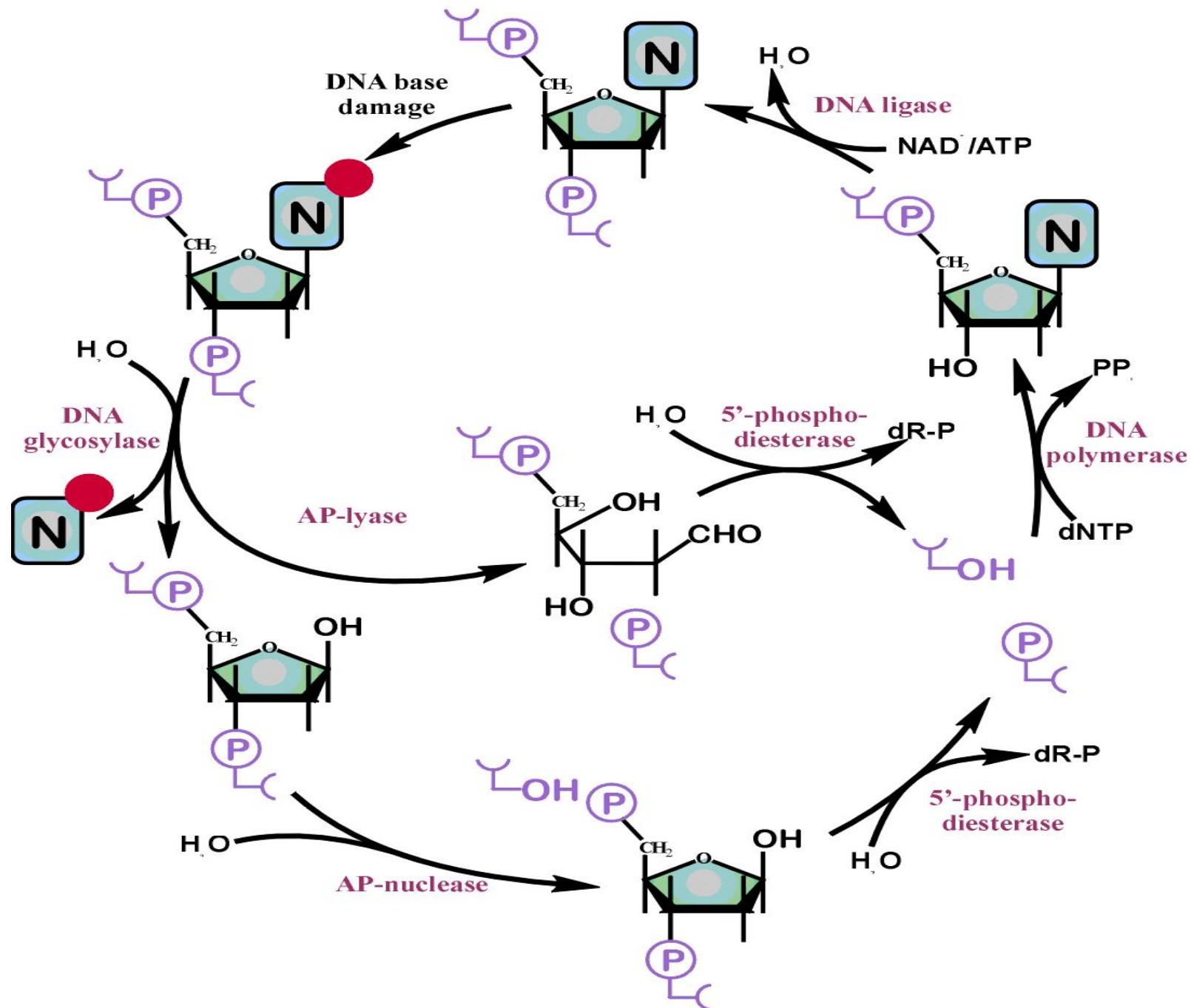


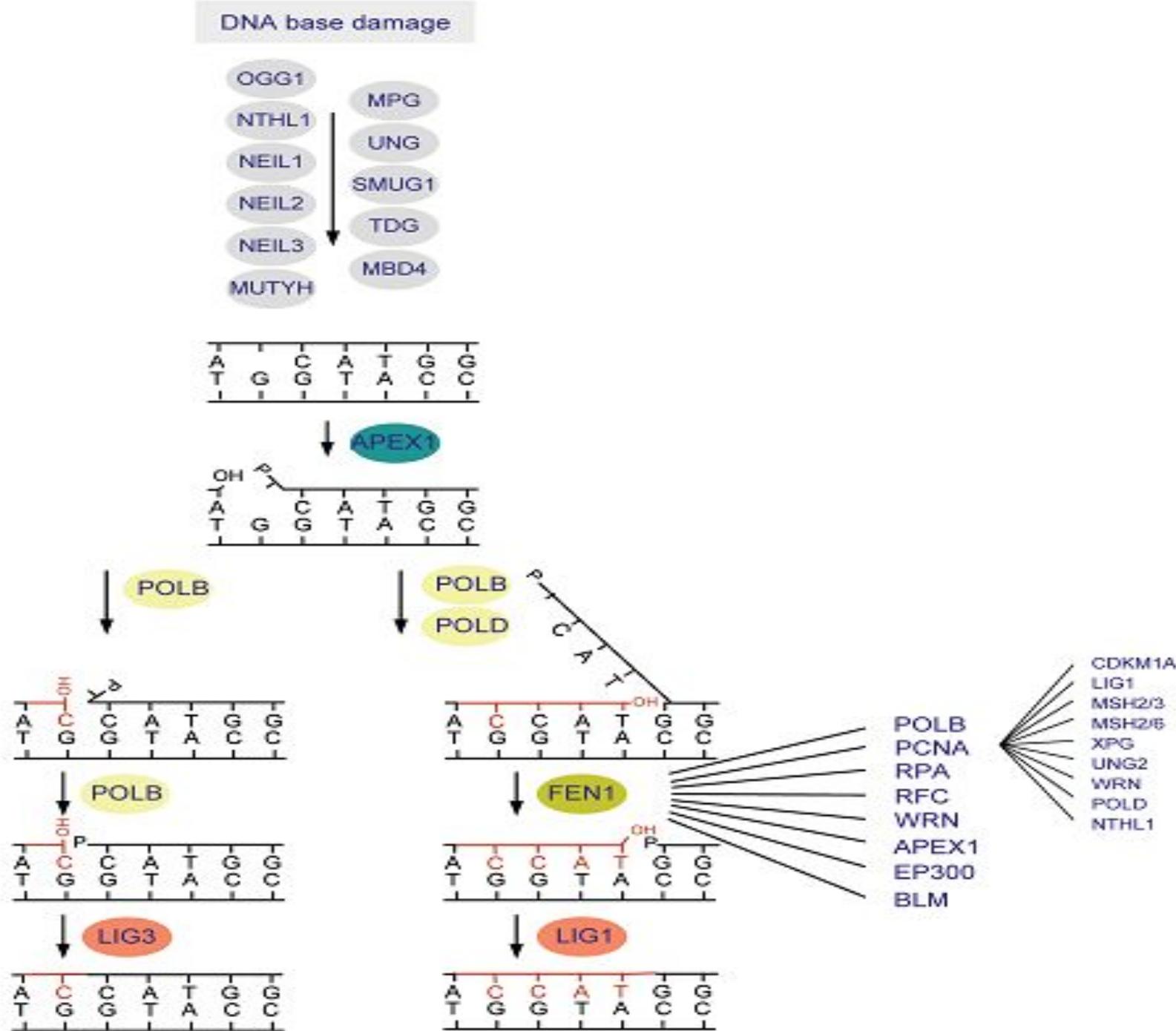
**A**

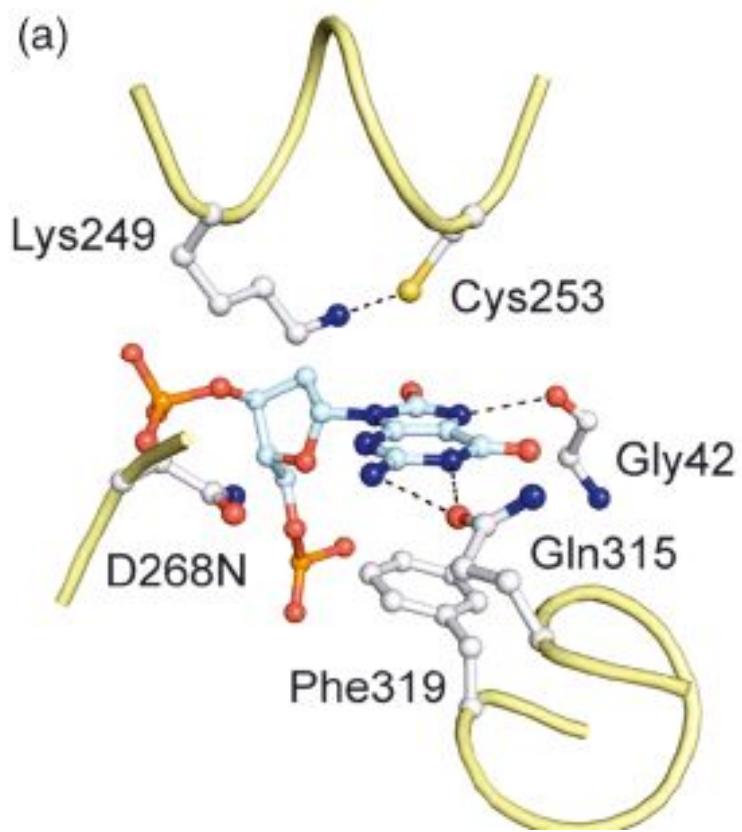
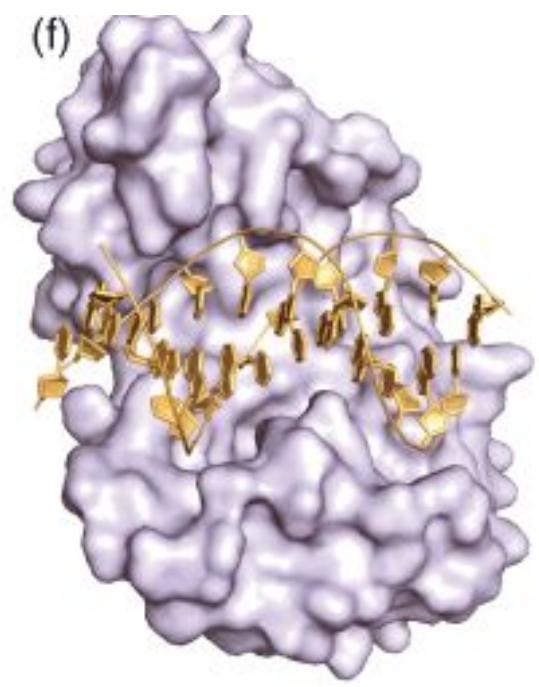


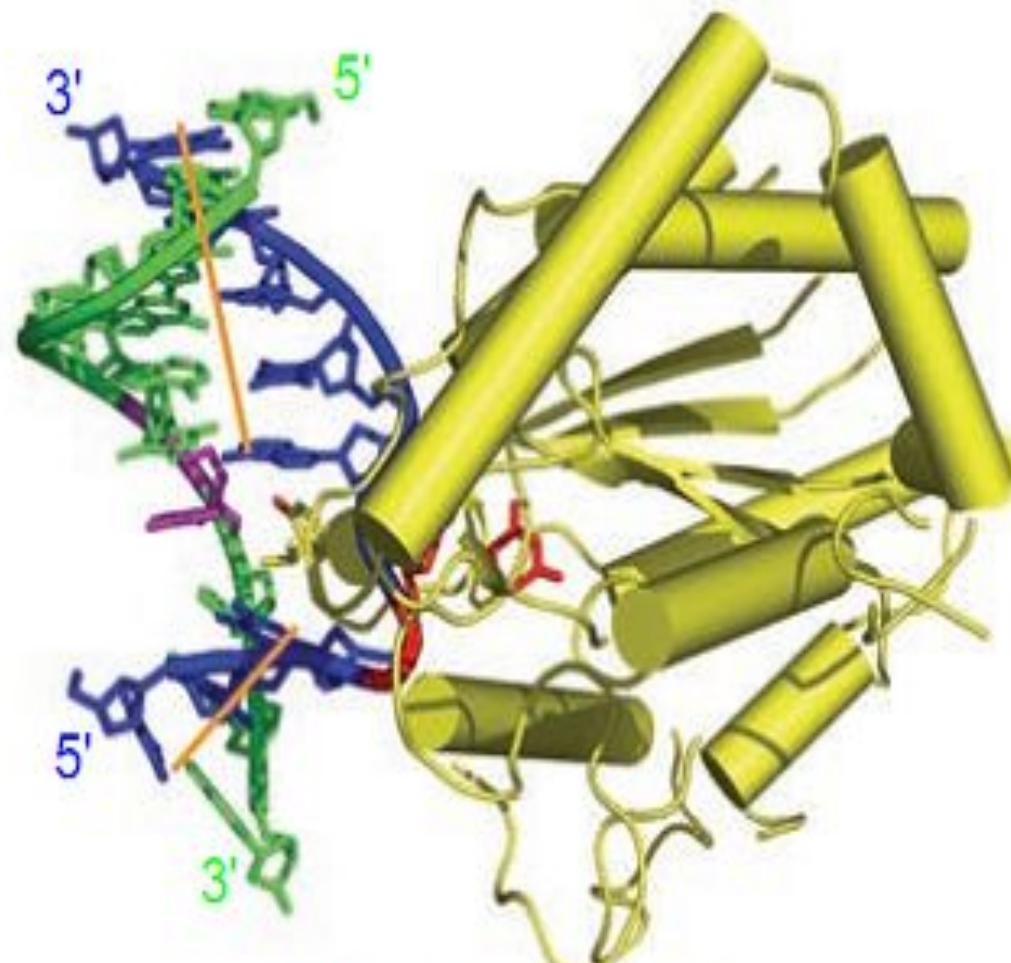
DNA Photolyase - CPD complex (1TEZ)

# Base excision repair (BER)



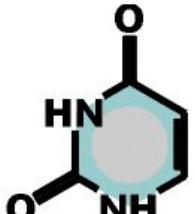




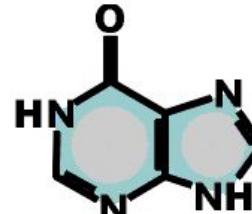


UDG-DNA (1EMJ)

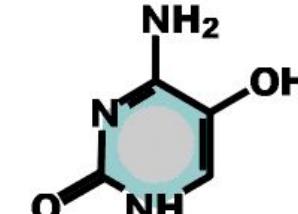
## Typical DNA lesions excited by DNA glycosilases



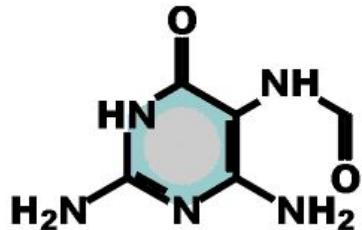
*Uracil*



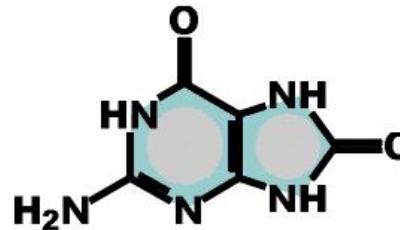
*Hypoxanthine*



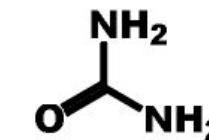
*5-Hydroxycytosine*



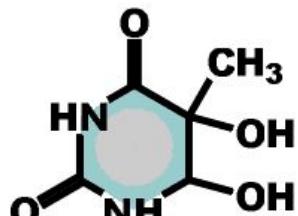
*2,5-Amino-5-formamido-pyrimidine*



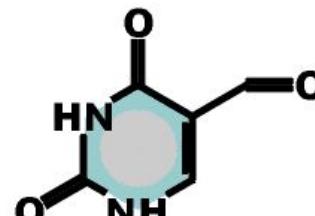
*7,8-Dihidro-8-oxo-guanine*



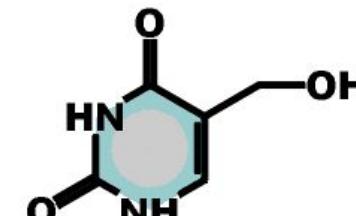
*Urea*



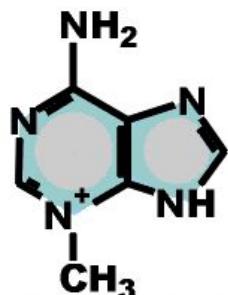
*Thymine glycol*



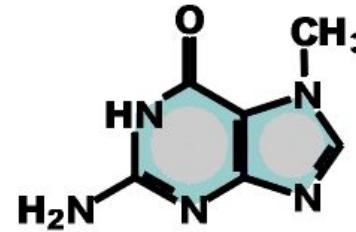
*5-Formyluracil*



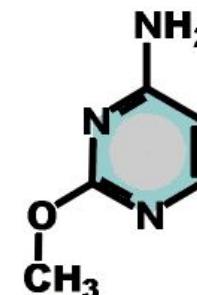
*5-Hydroxymethyluracil*



*3-Methyladenine*

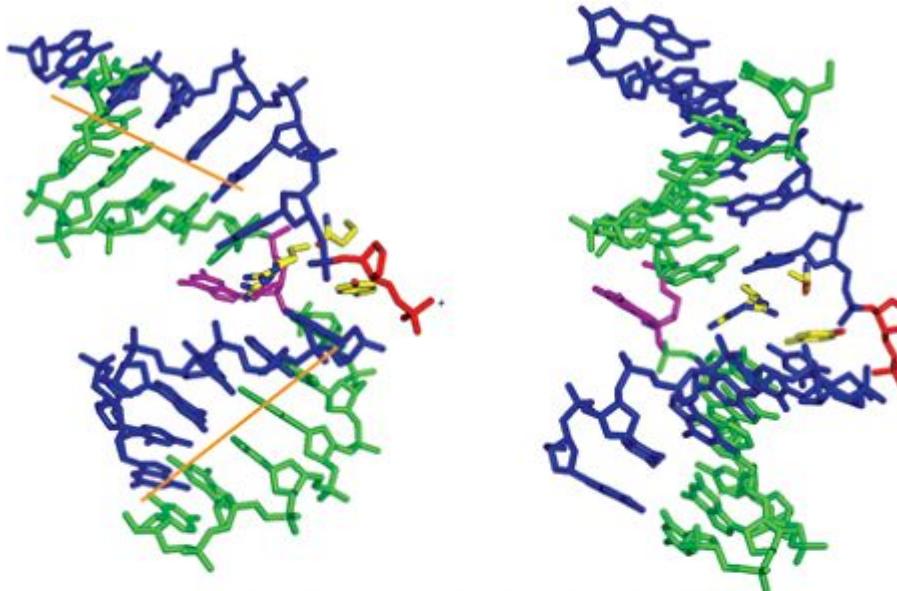


*7-Methylguanine*



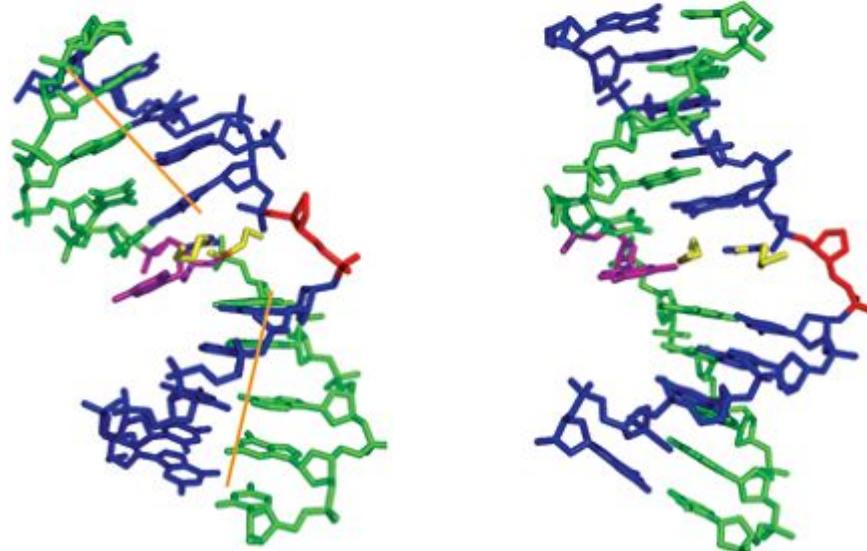
*2-Methylcytosine*

A



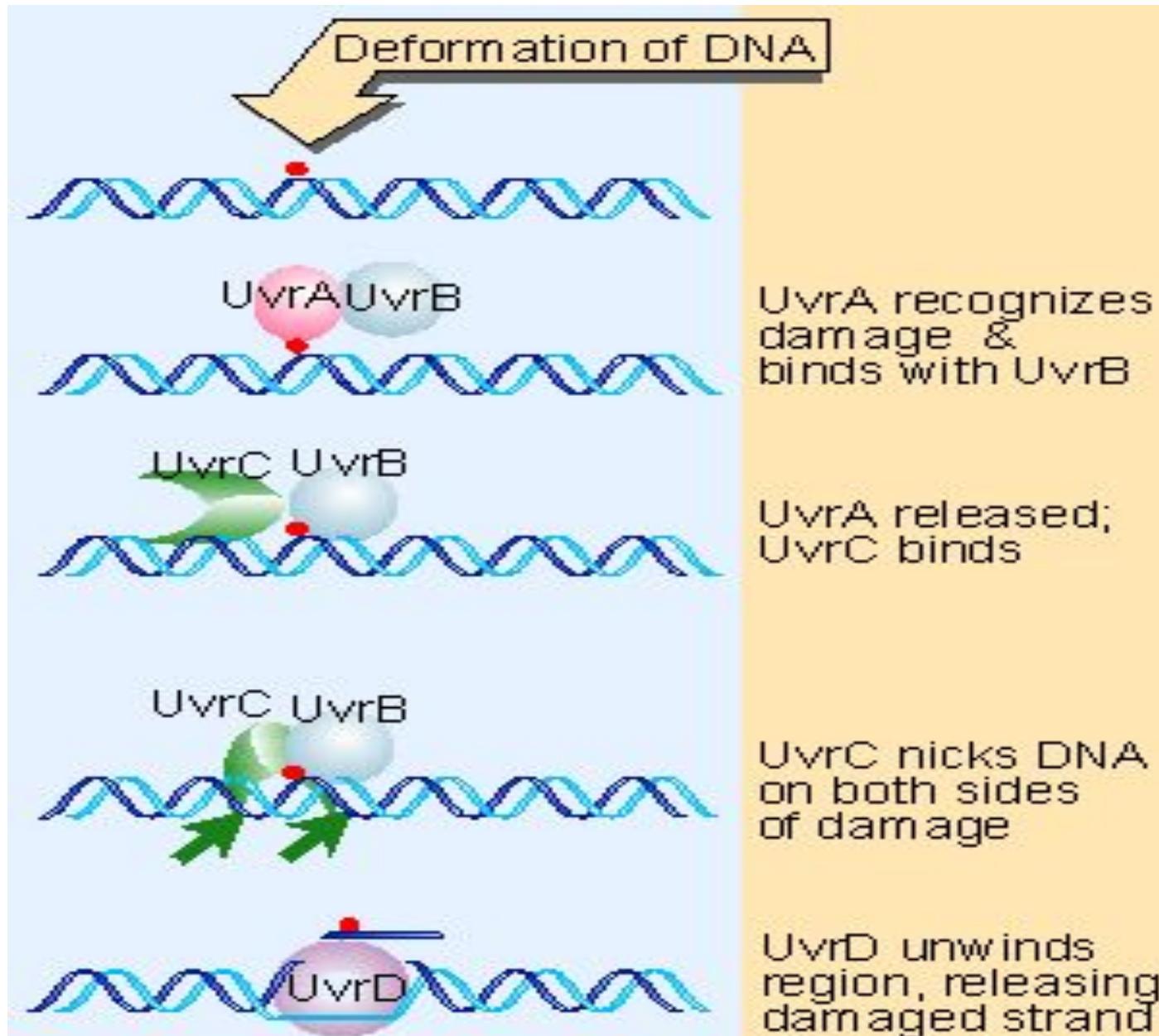
DNA bound to Endo IV (PDB: 1QUM)

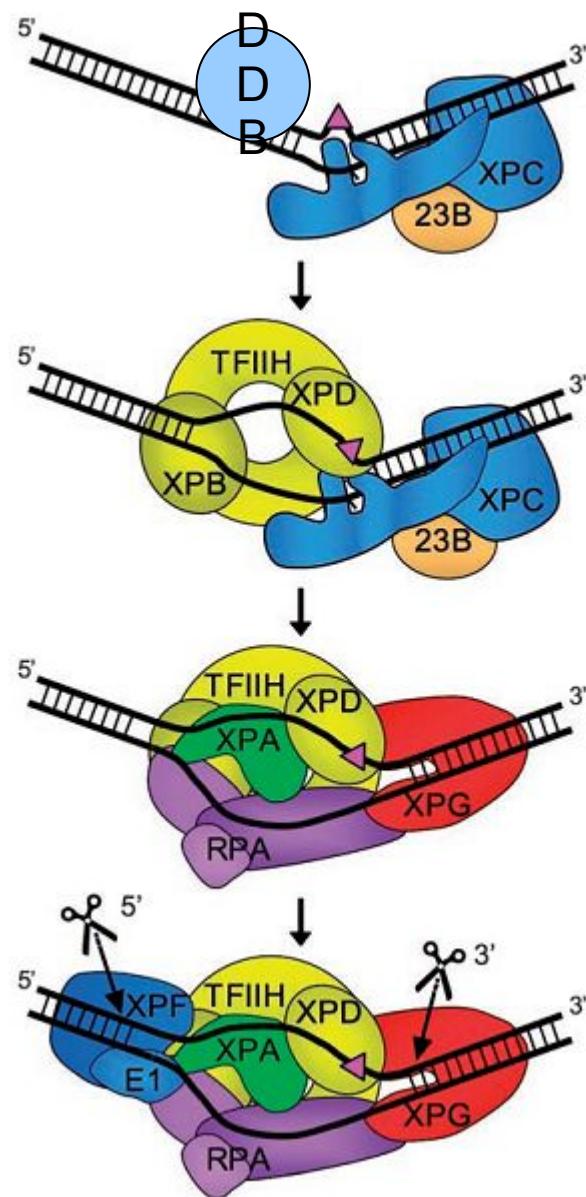
B

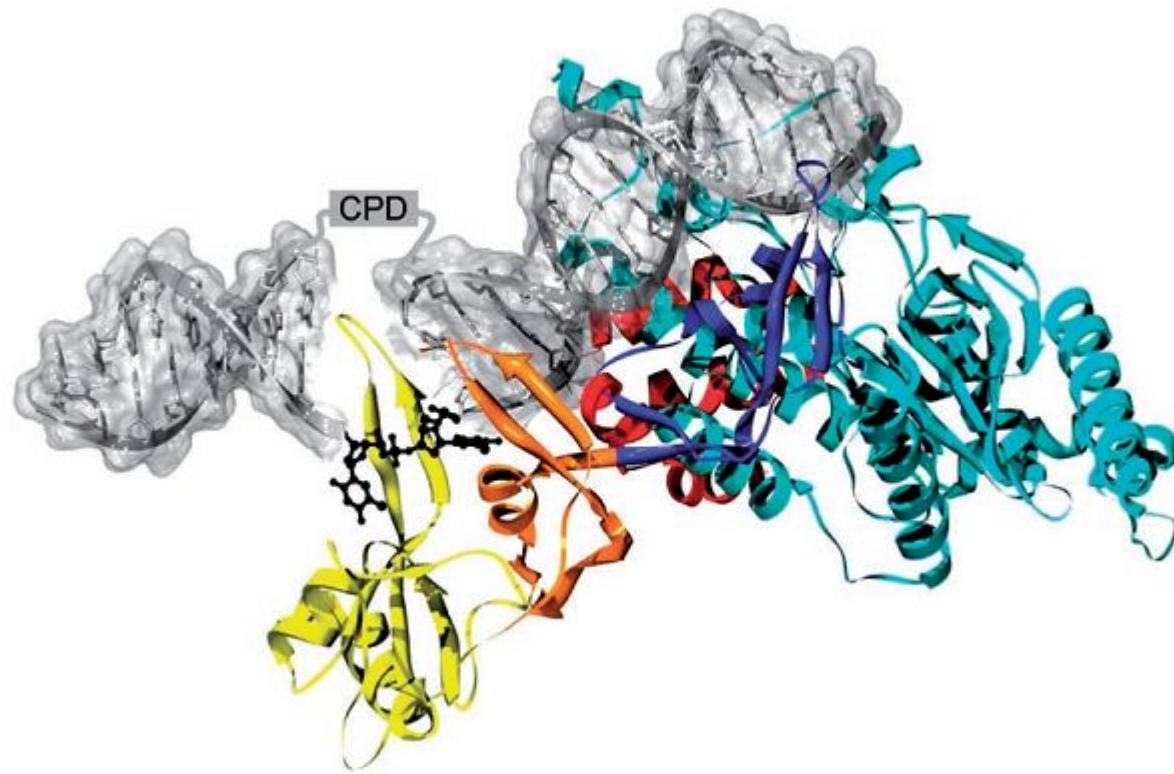


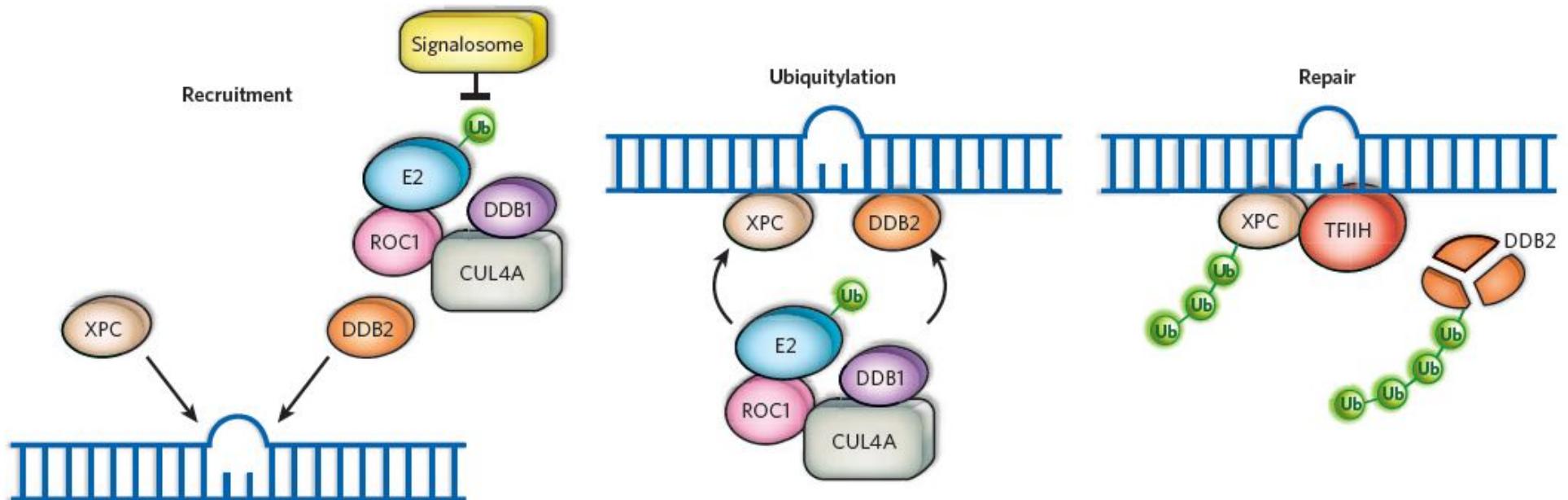
DNA bound to human APF1 (PDB: 1DF8)

# NER









**Figure 2 | Scheme for XPC and DDB2 ubiquitylation.** Helix-distorting lesions are substrates for XPC and DDB2 (left). XPC binds to the undamaged strands of helix-distorted lesions (middle). DDB2 becomes part of a larger, cullin 4a-based E3 ubiquitin ligase complex (CUL4a, DDB1, ROC1 and an E2 ubiquitin-conjugating enzyme). In the absence of DNA damage, the ubiquitylation activity is repressed by the

signalosome (COP9) complex (upper left). Upon DNA damage, the signalosome dissociates, allowing the DDB2-E3 ligase complex to bind to the damaged site. Both XPC and DDB2 are substrates of the ubiquitin ligase; however, whereas DDB2 is degraded, XPC is not (right). The role of XPC ubiquitylation is currently not known, but it may promote specific protein interactions.

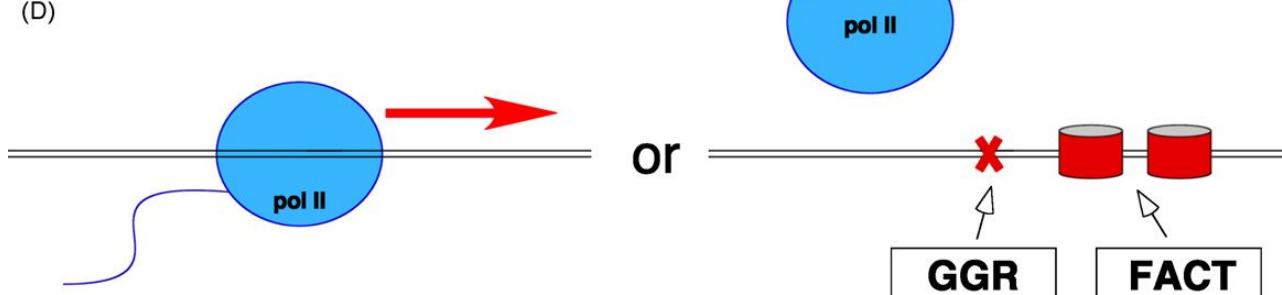
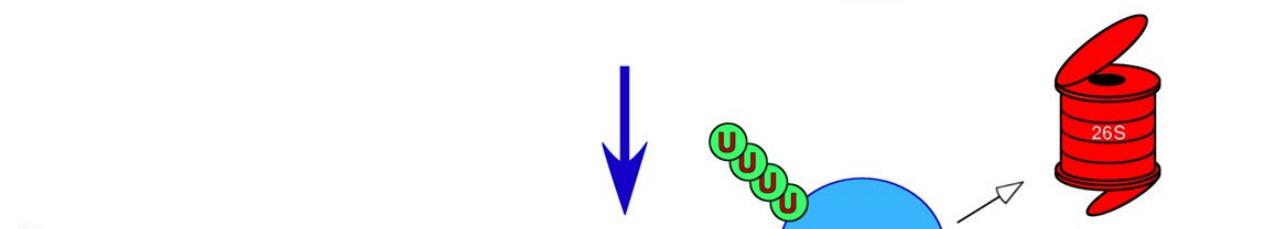
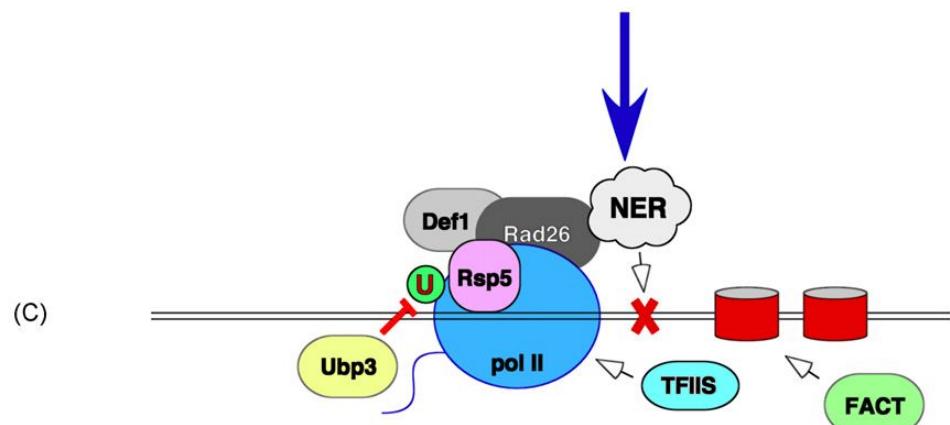
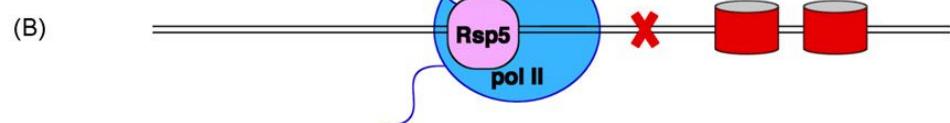
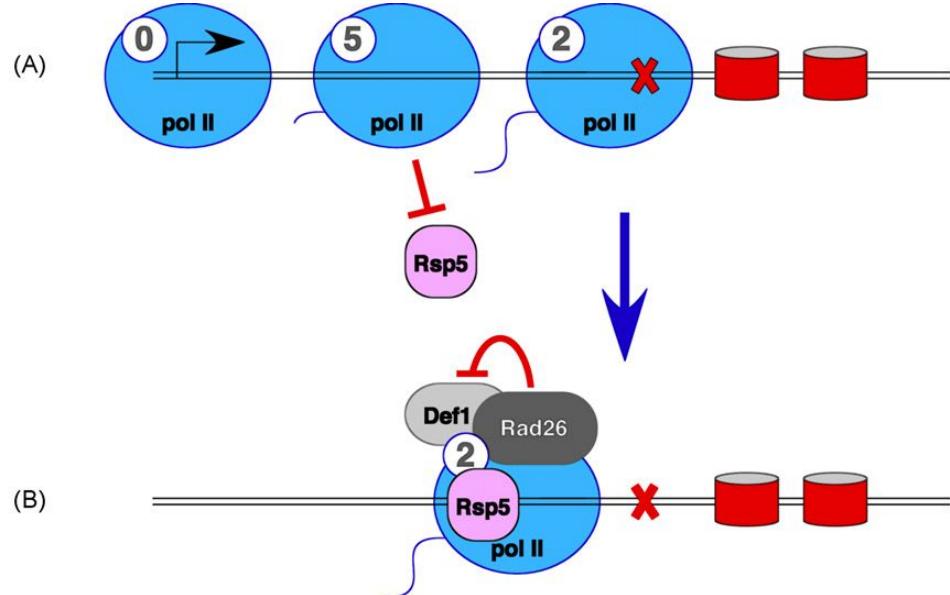
**GG-NER**

**XPC**

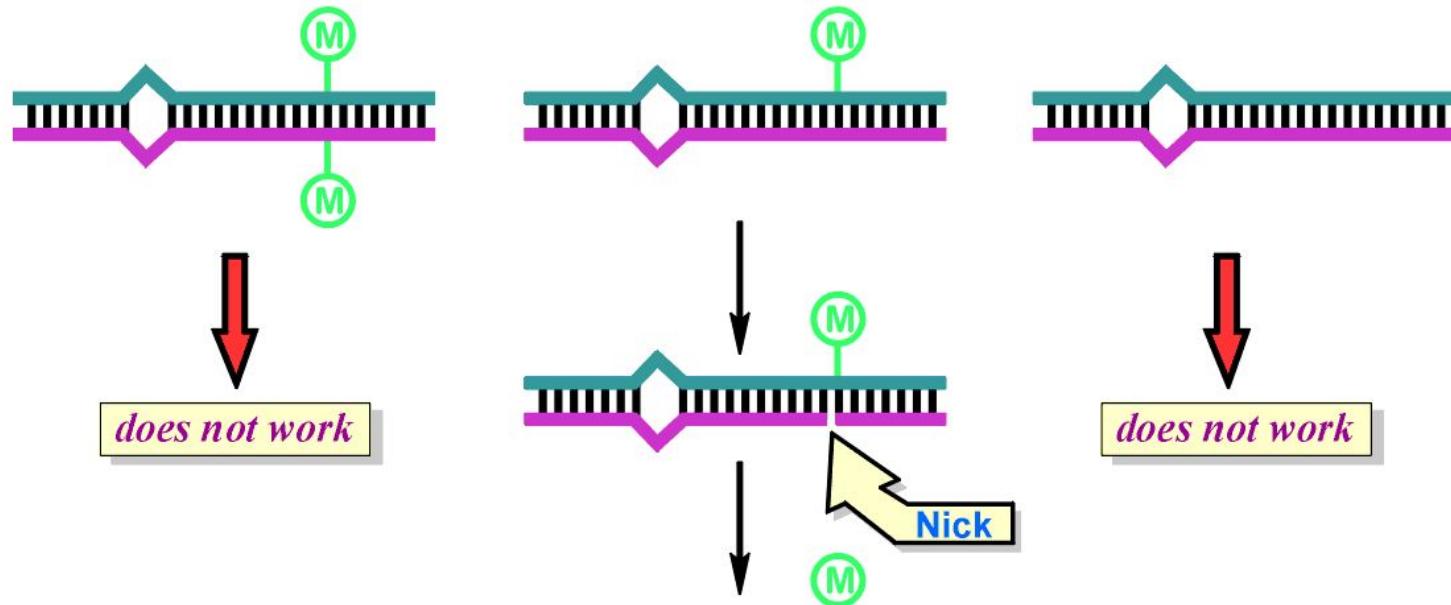
**UV-DDB**

**TC-NER**

**CSA, CSB  
DCAF family  
and ???**

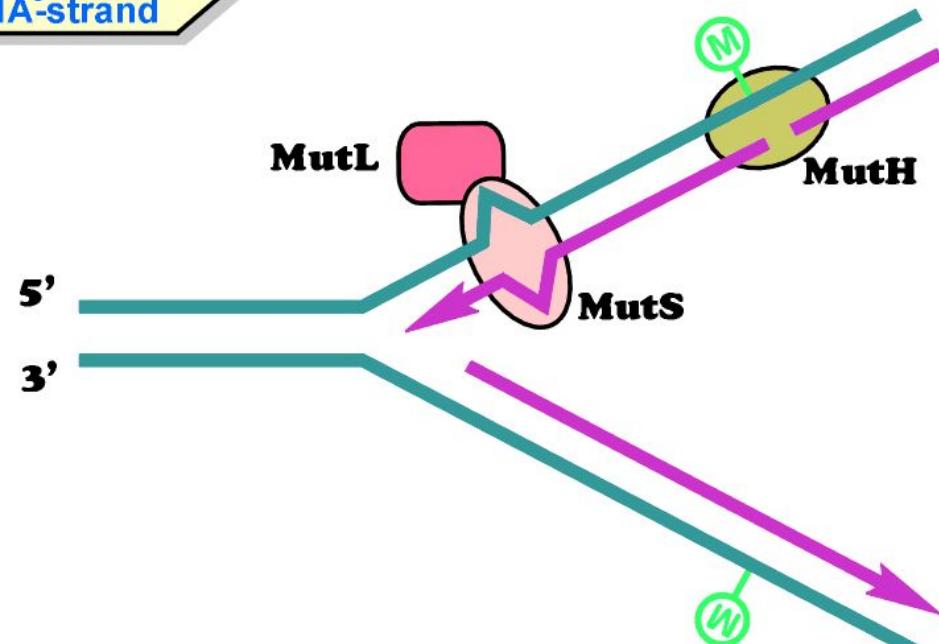


# Mismatch repair

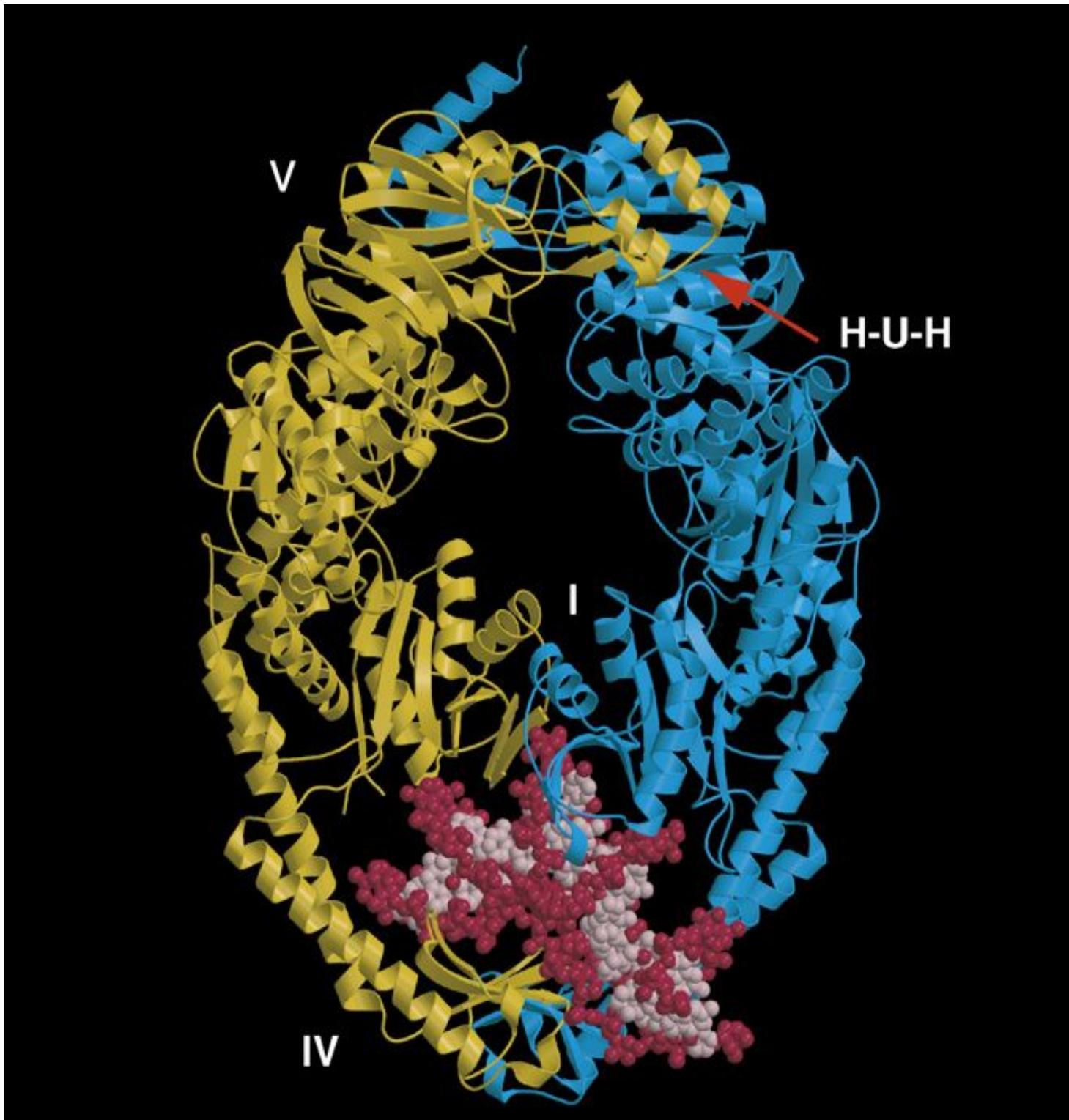


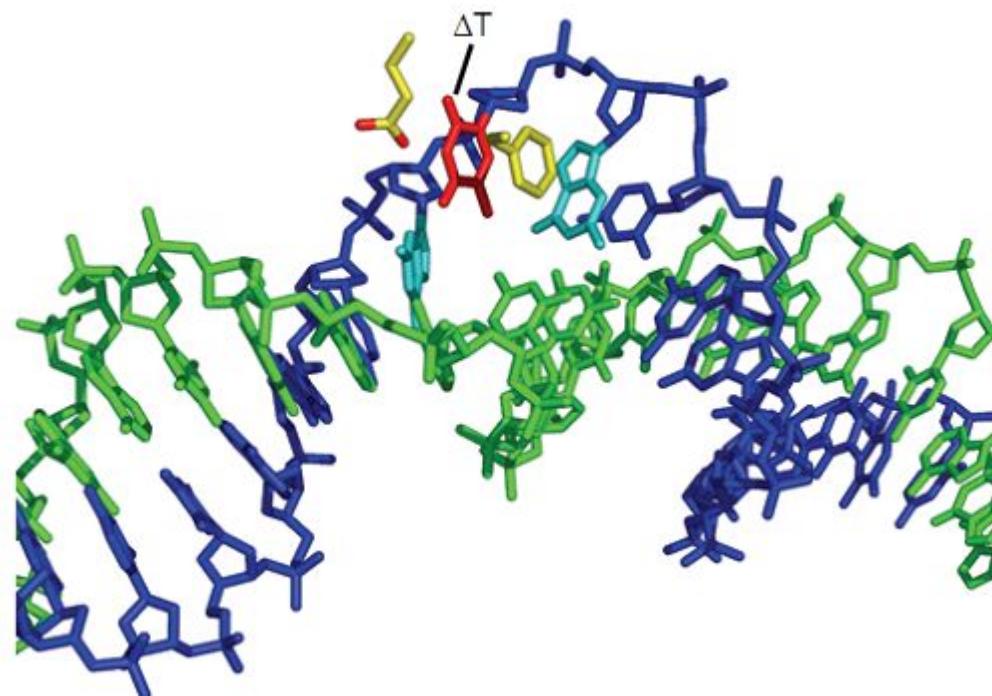
## Excision / resynthesis

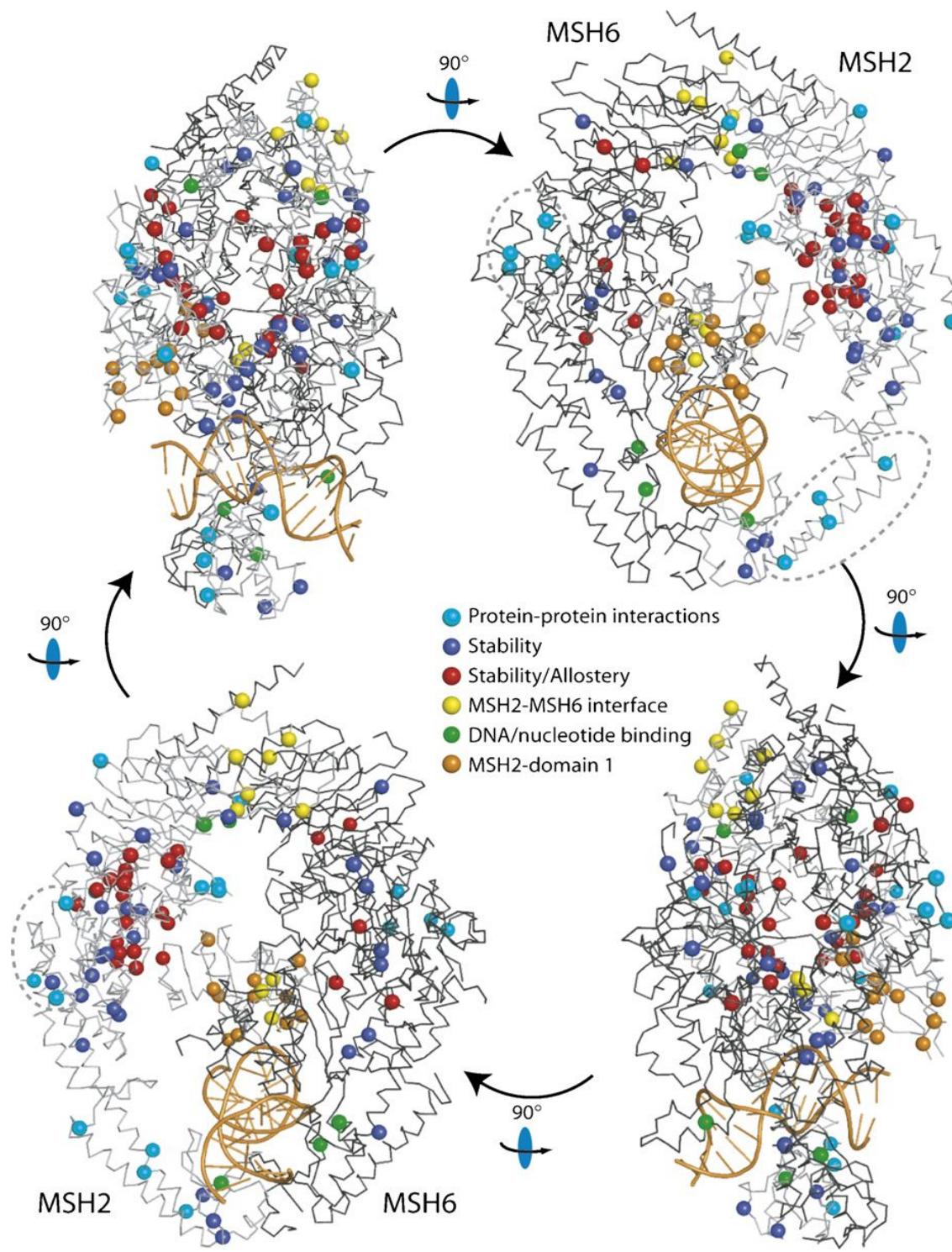
Exo I, Exo VII or RecJ,  
Helicase II,  
DNA pol III, SSB and  
DNA ligase

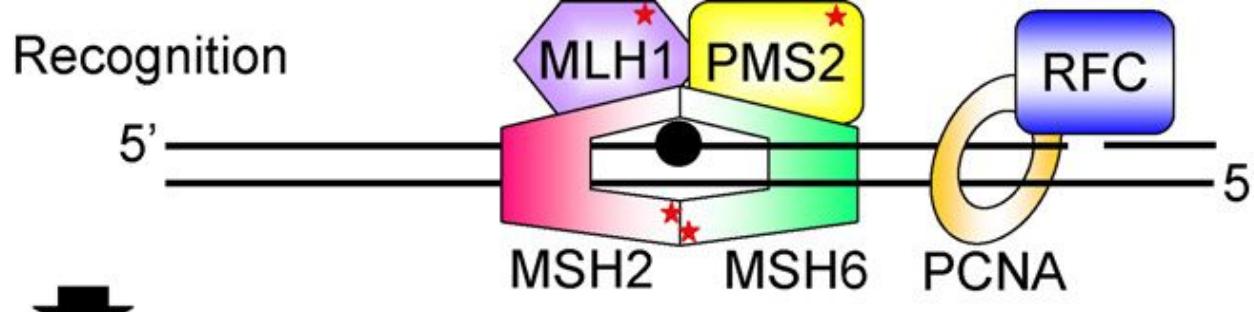


# MutS

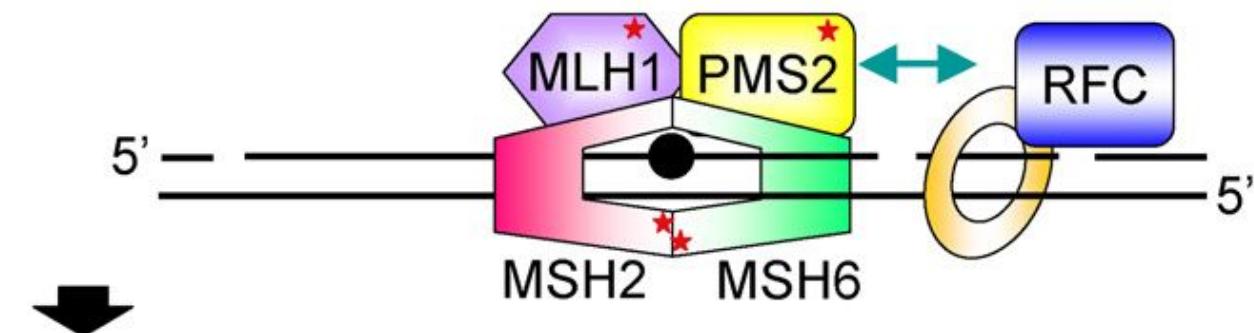




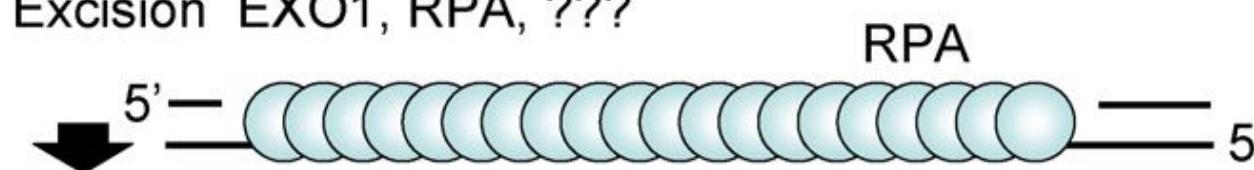




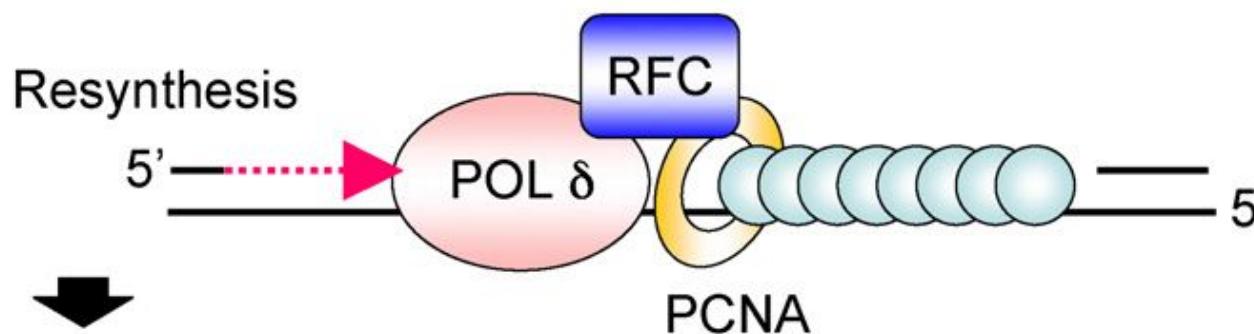
Nicking    ATP → ADP + Pi



Excision EXO1, RPA, ???



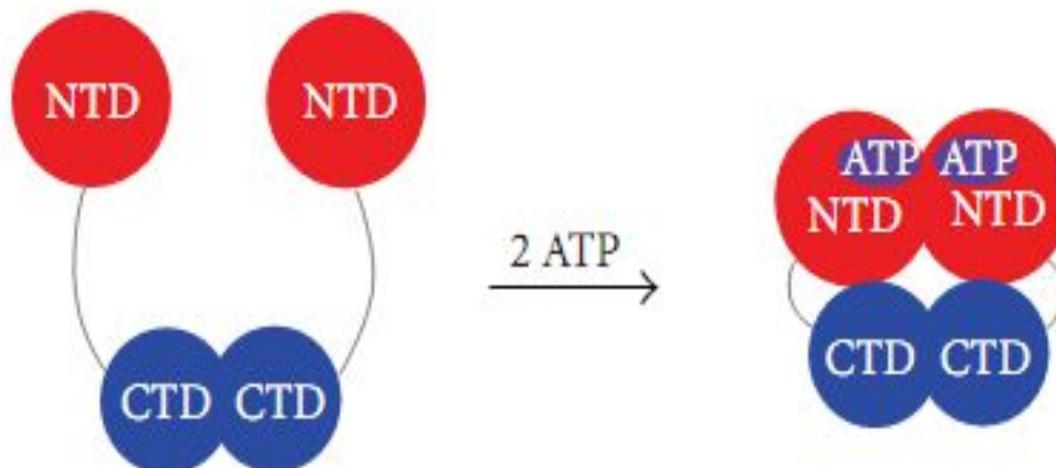
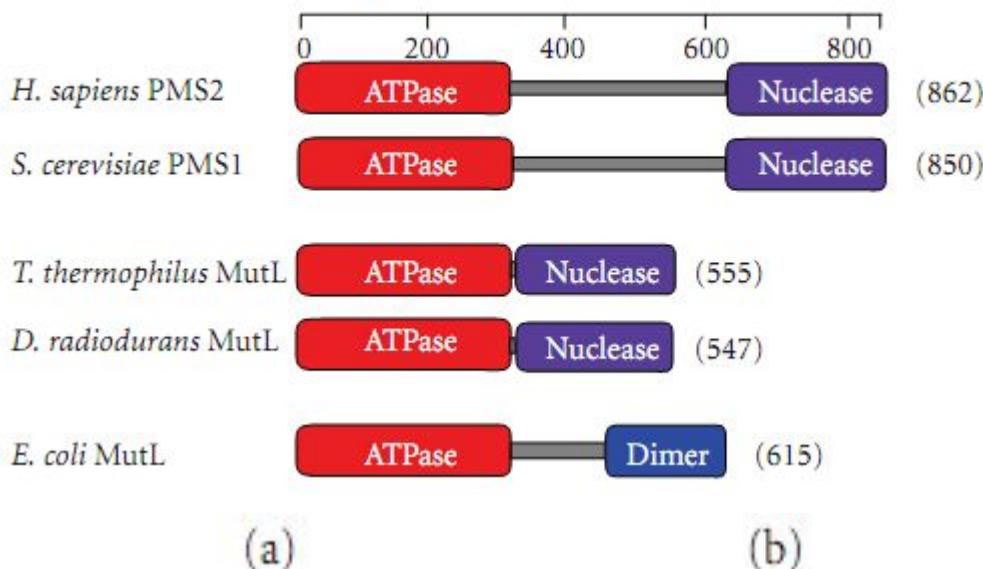
Resynthesis



Ligation

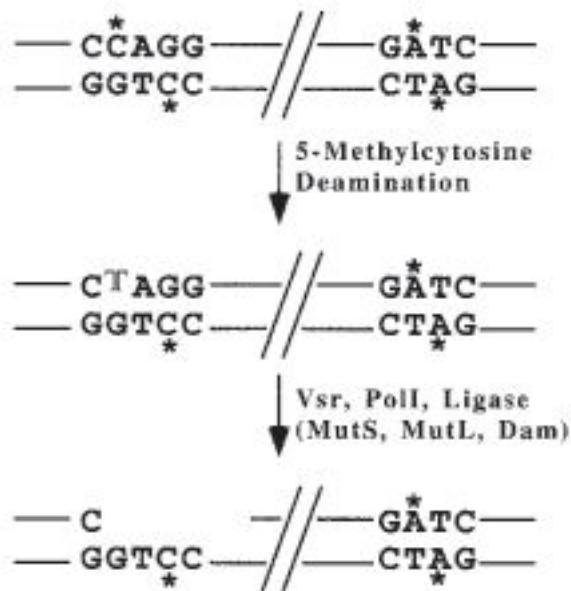


# MutLa

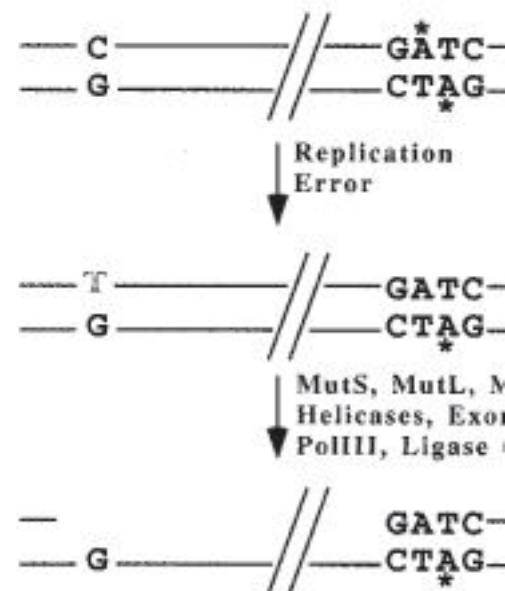


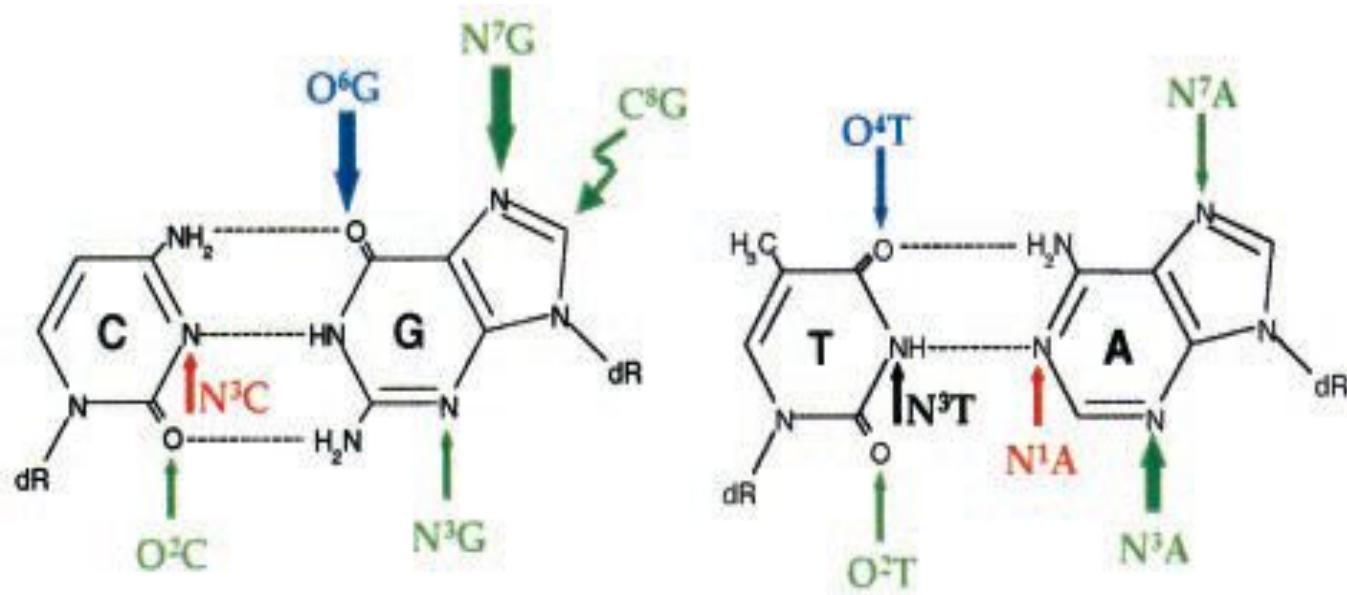
of MutLa, the PMS2 and MLH1 subunits dimerize via their C-terminal domains. ATP binding induces the dimerization of the N-terminal domain and condensation of the molecule.

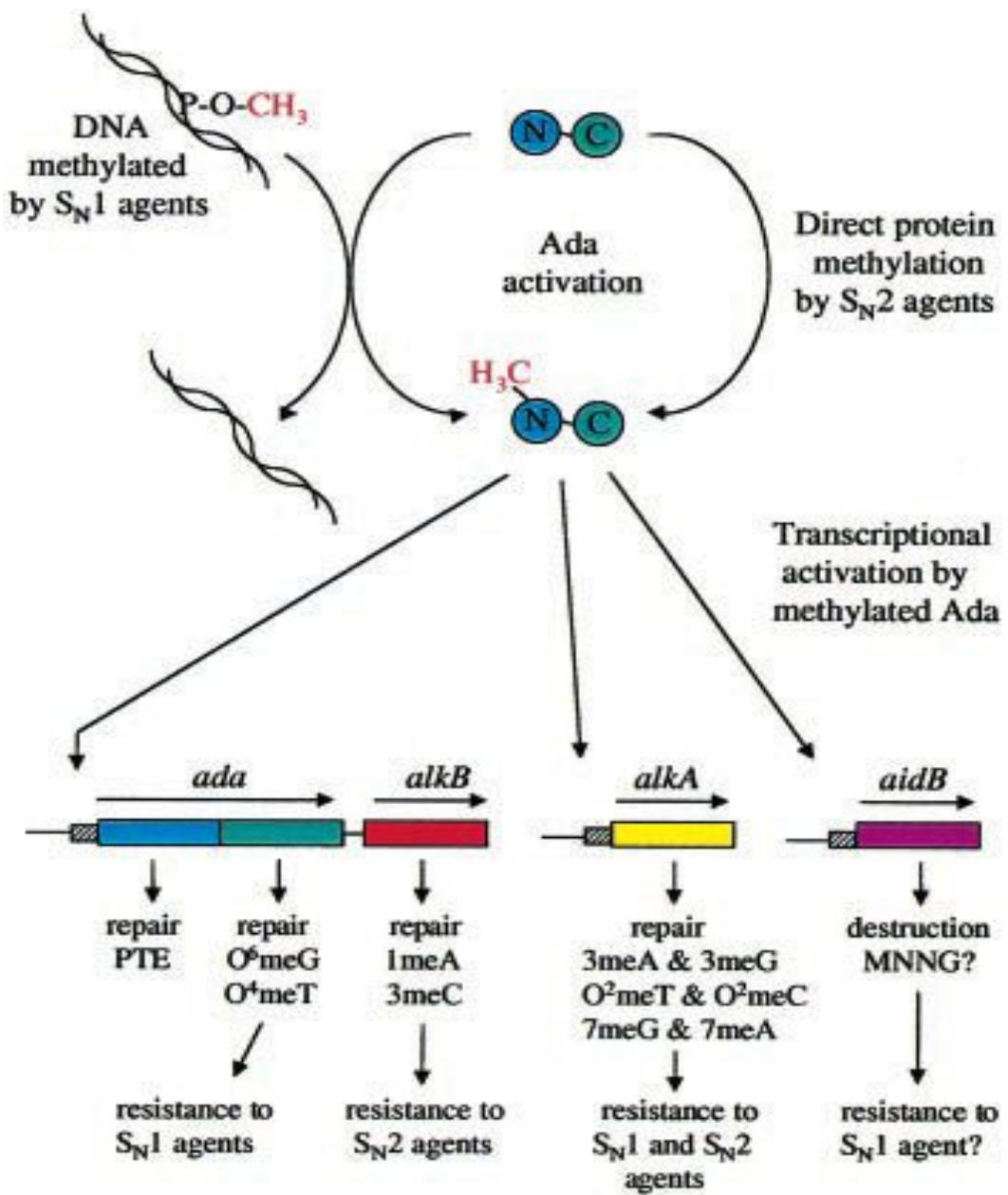
## VSP REPAIR



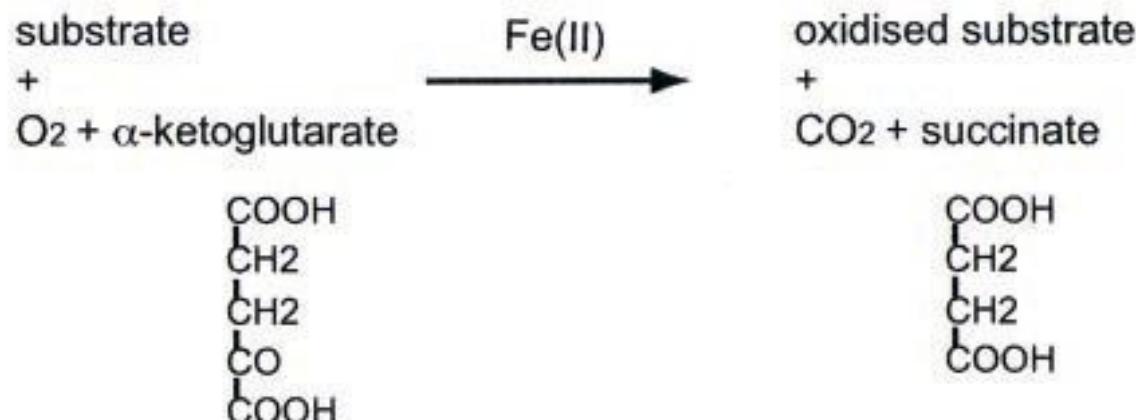
## MMR



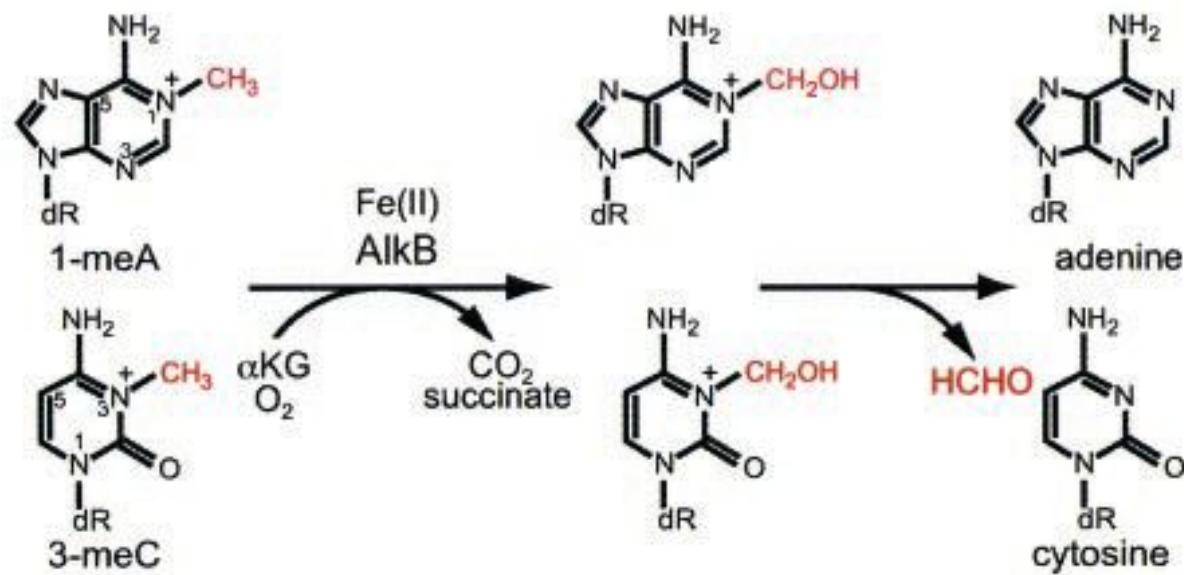


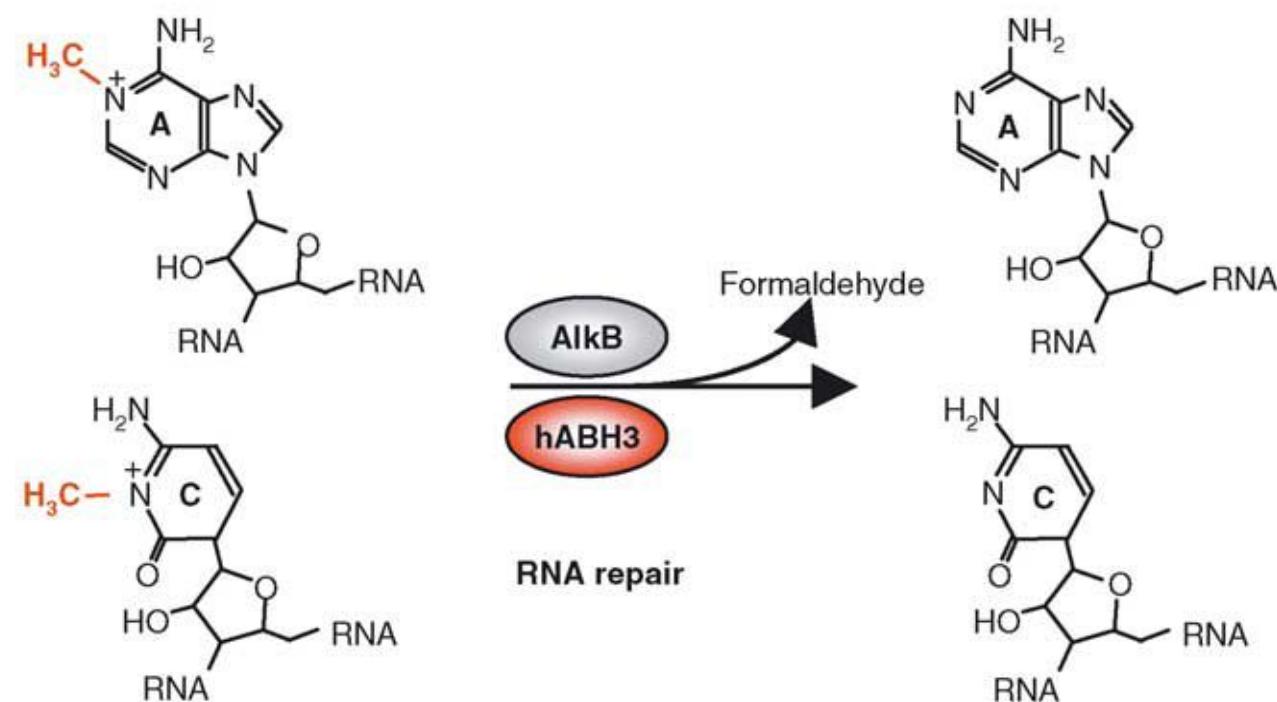
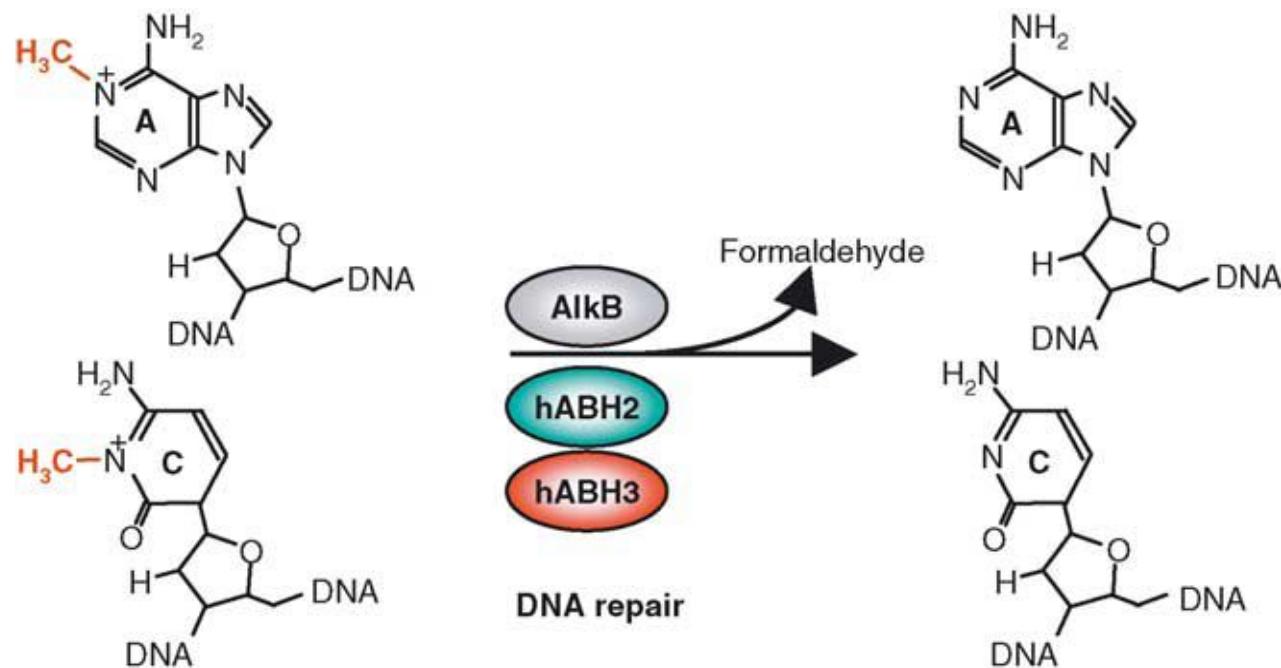


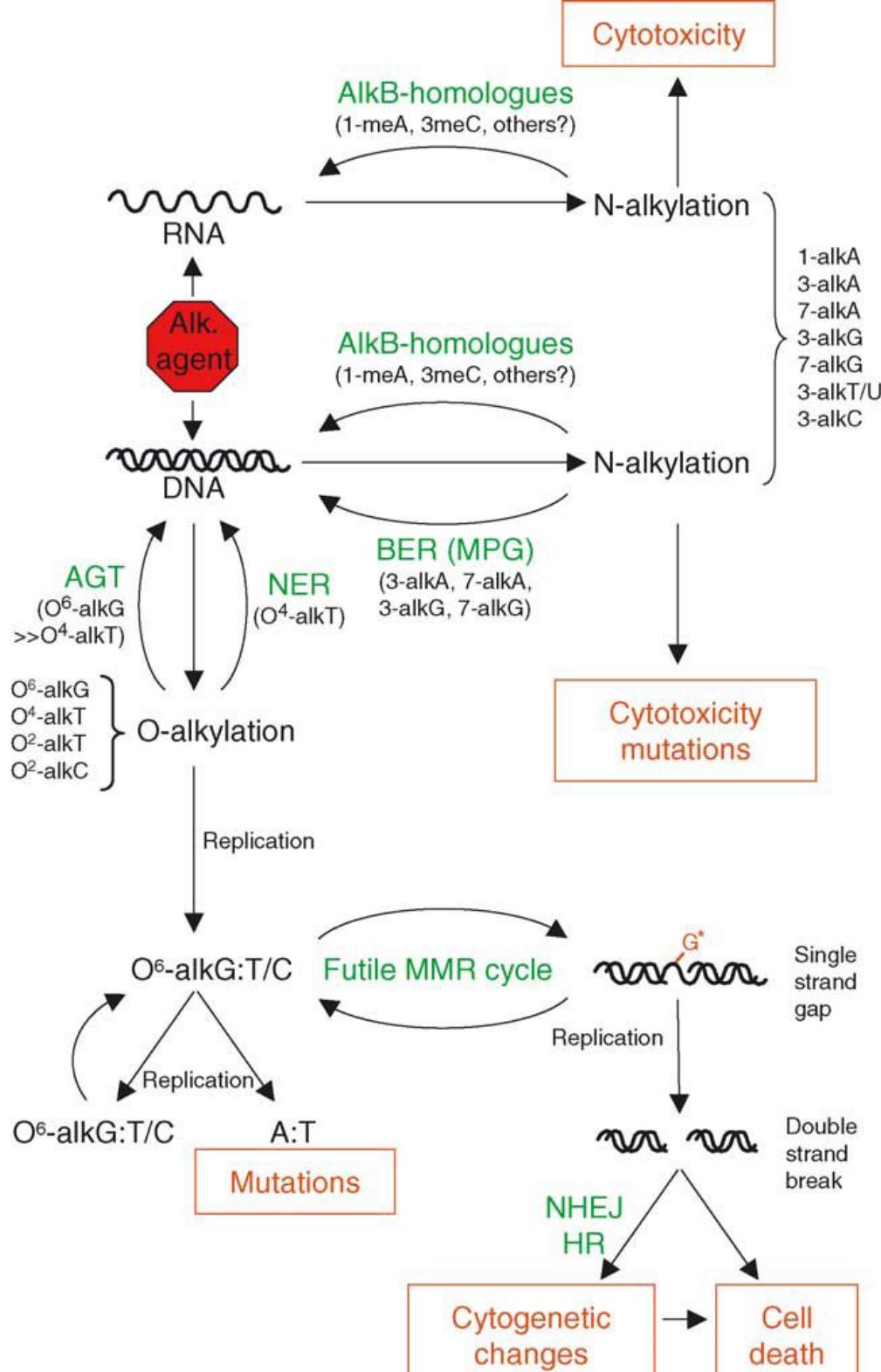
**A.**



**B.**

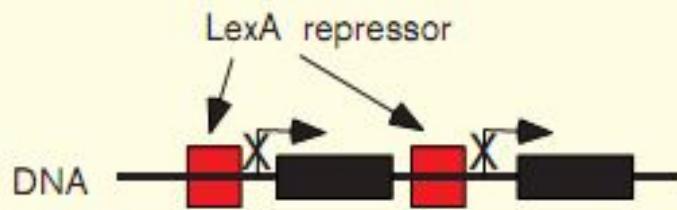






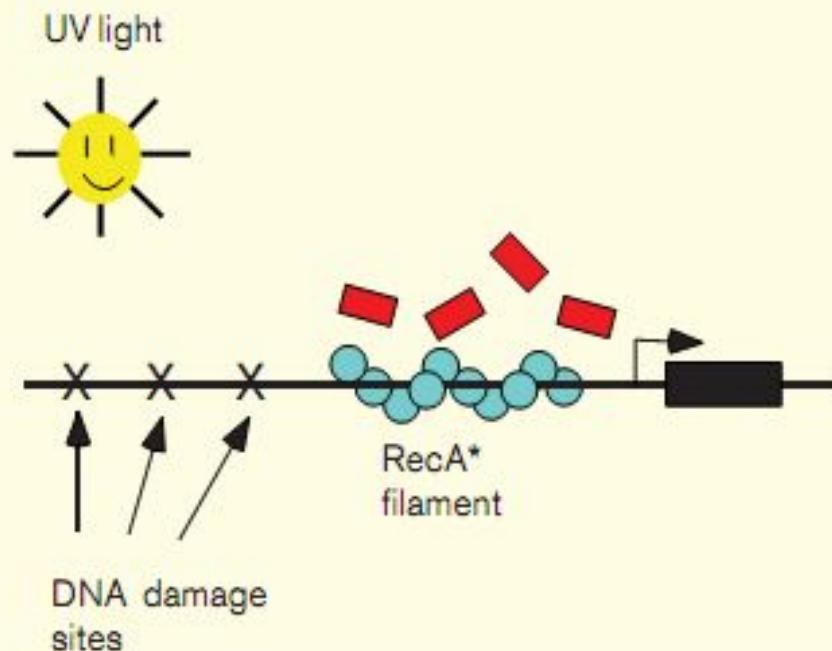
# SOS

(a) SOS System off

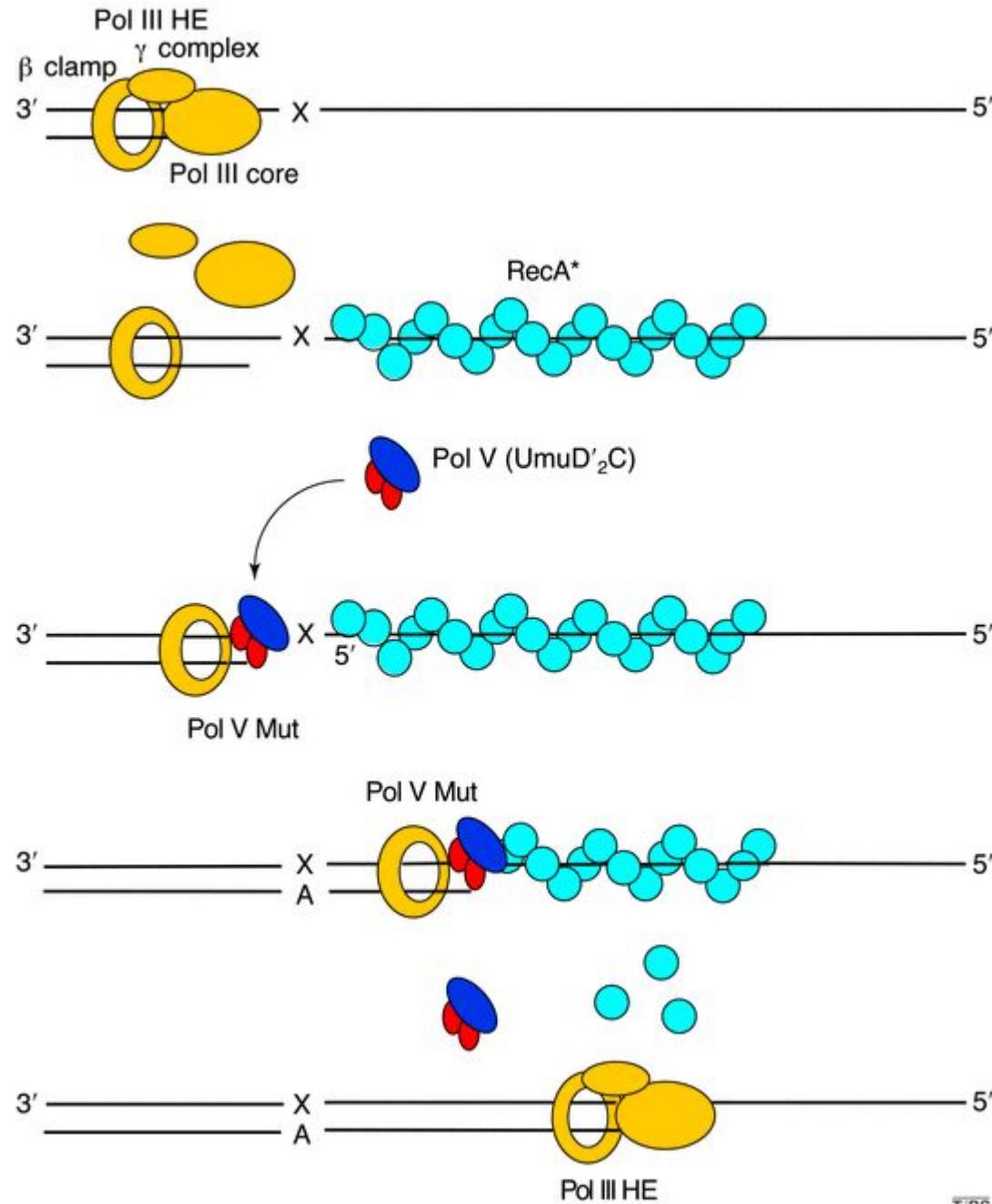


SOS genes repressed by LexA protein

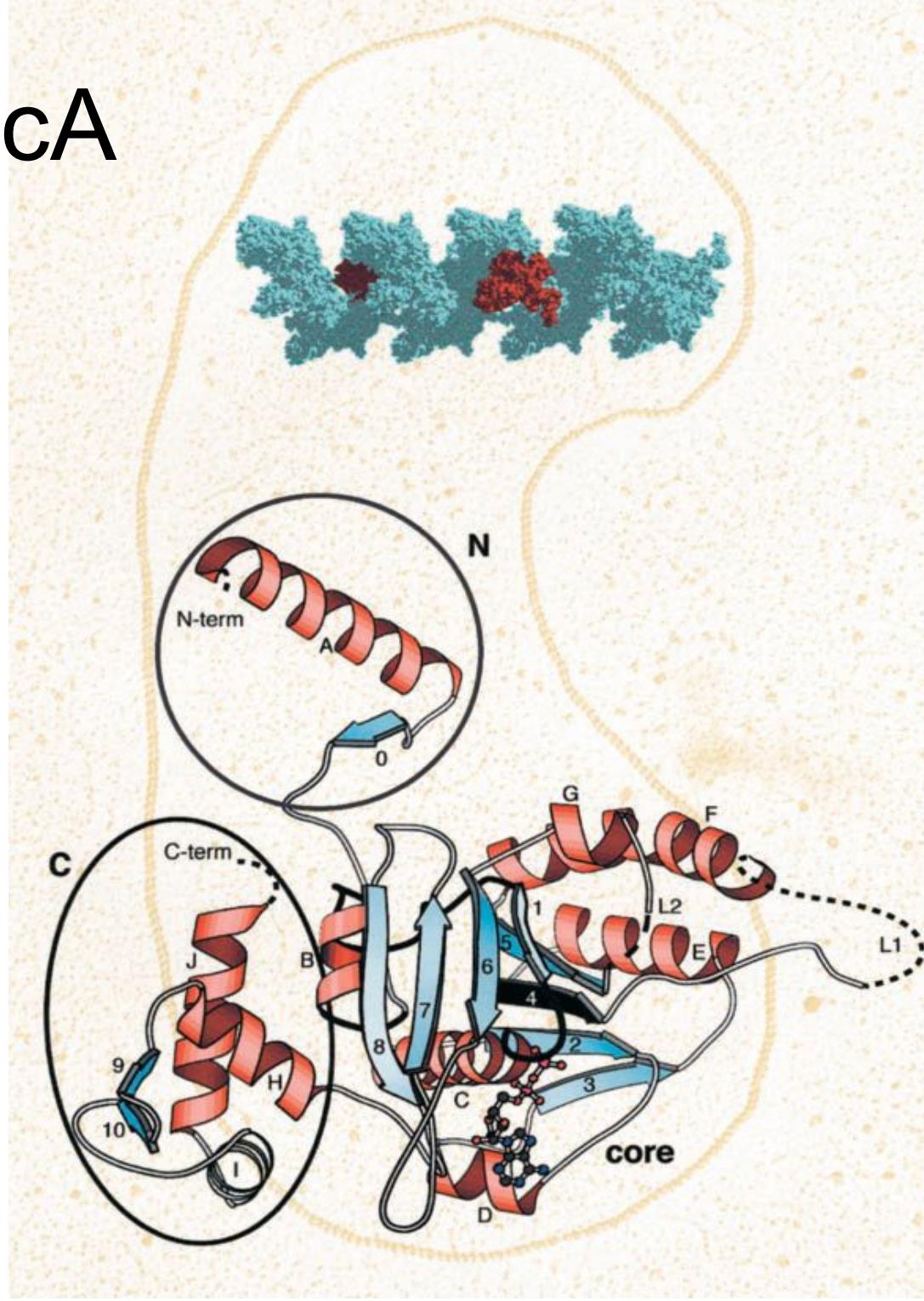
(b) SOS System On



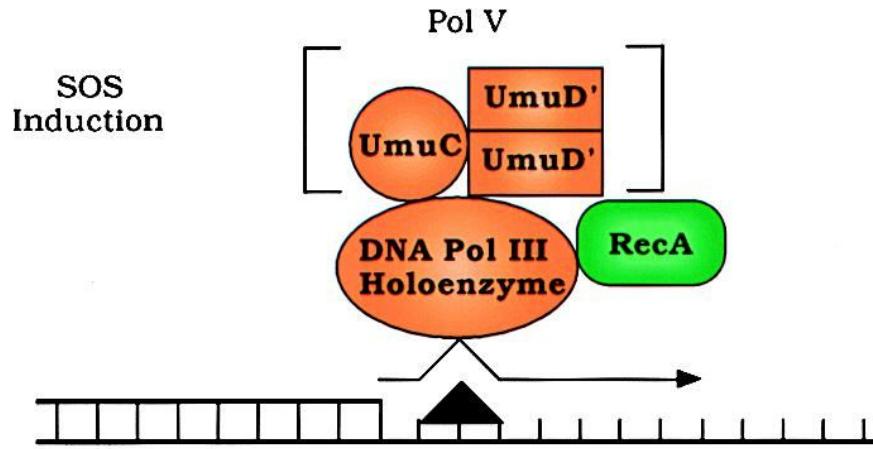
RecA\* promotes autocatalytic cleavage of LexA repressor  
SOS genes turned on



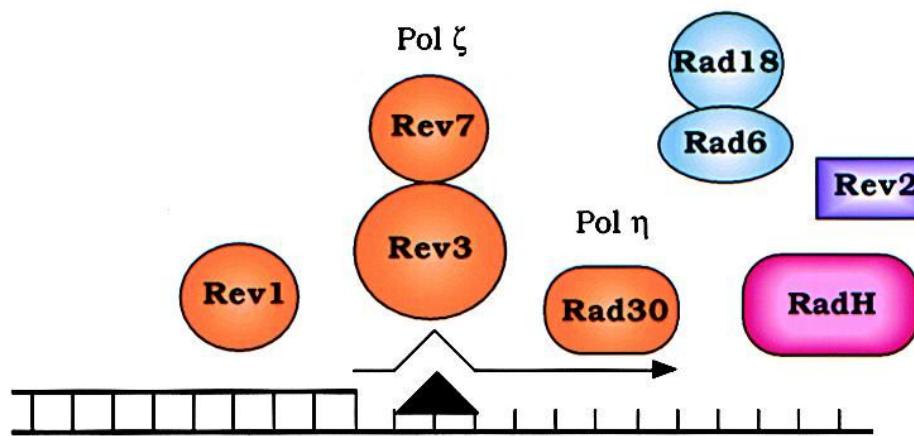
# RecA



A.



B.

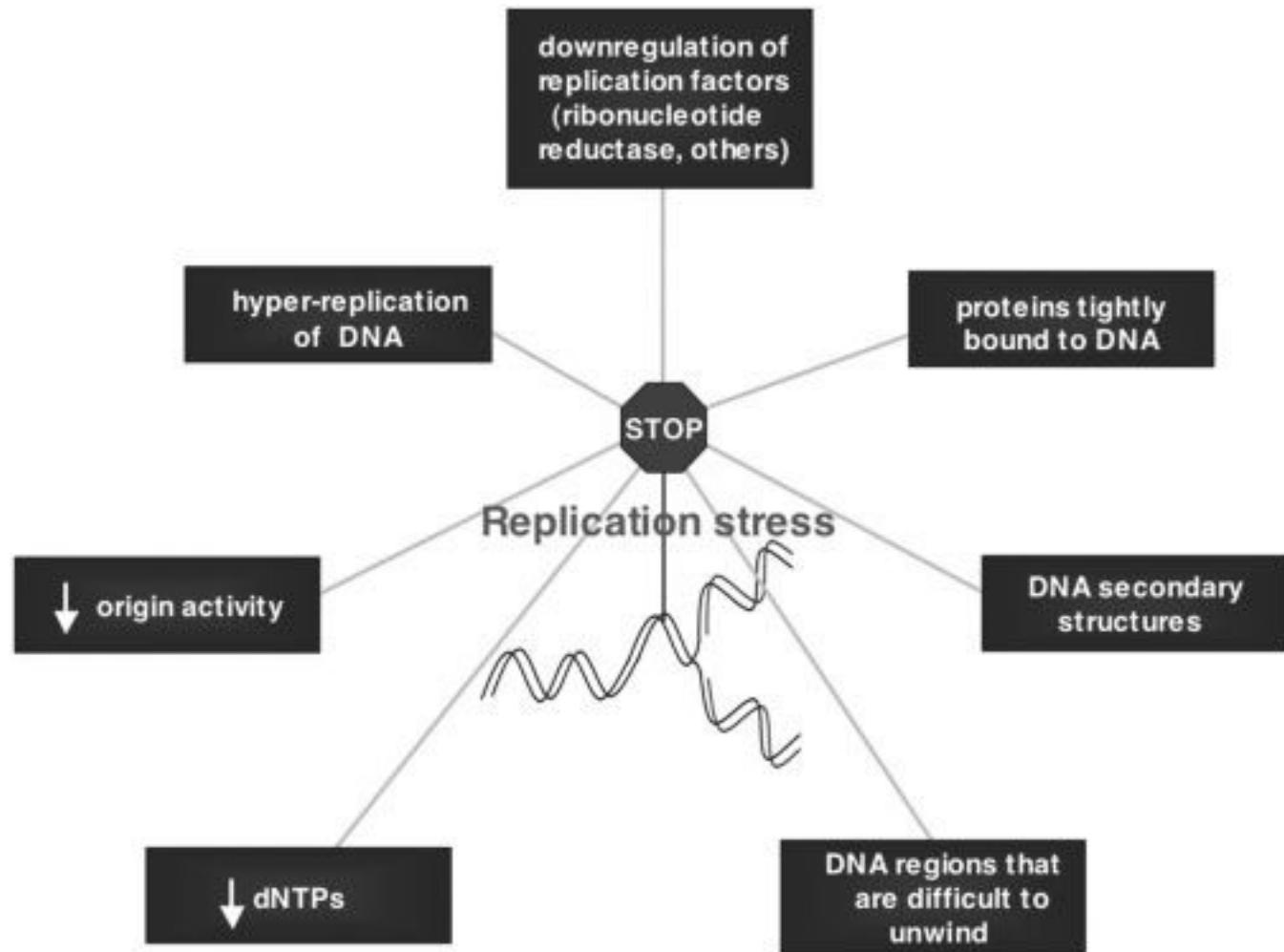


C.

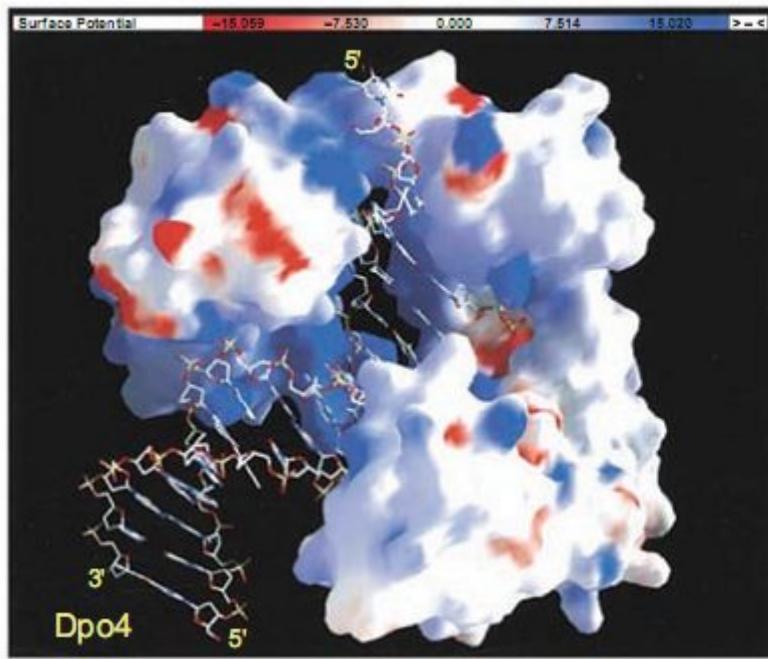
SOS  
Induction

Pol IV

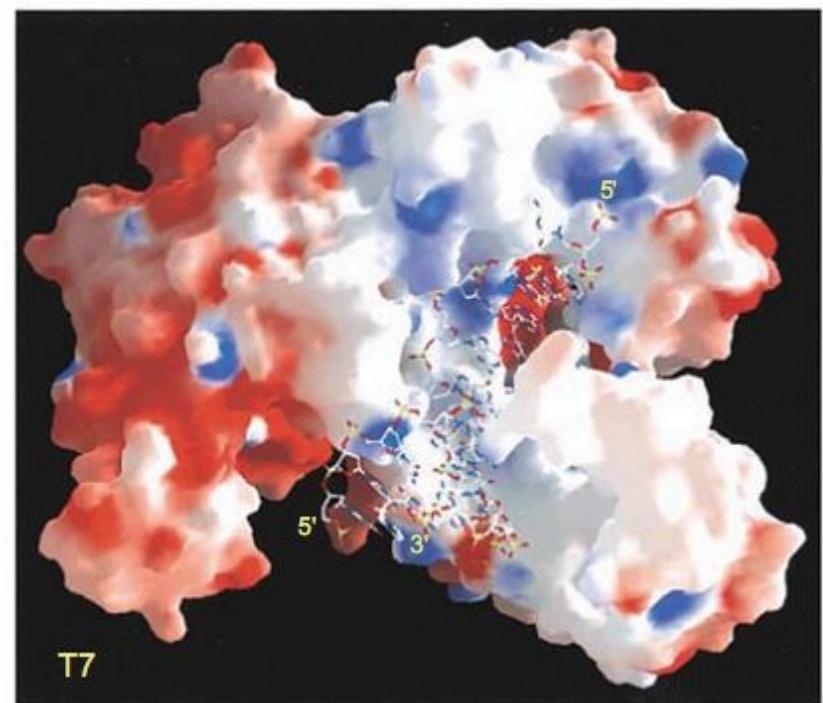


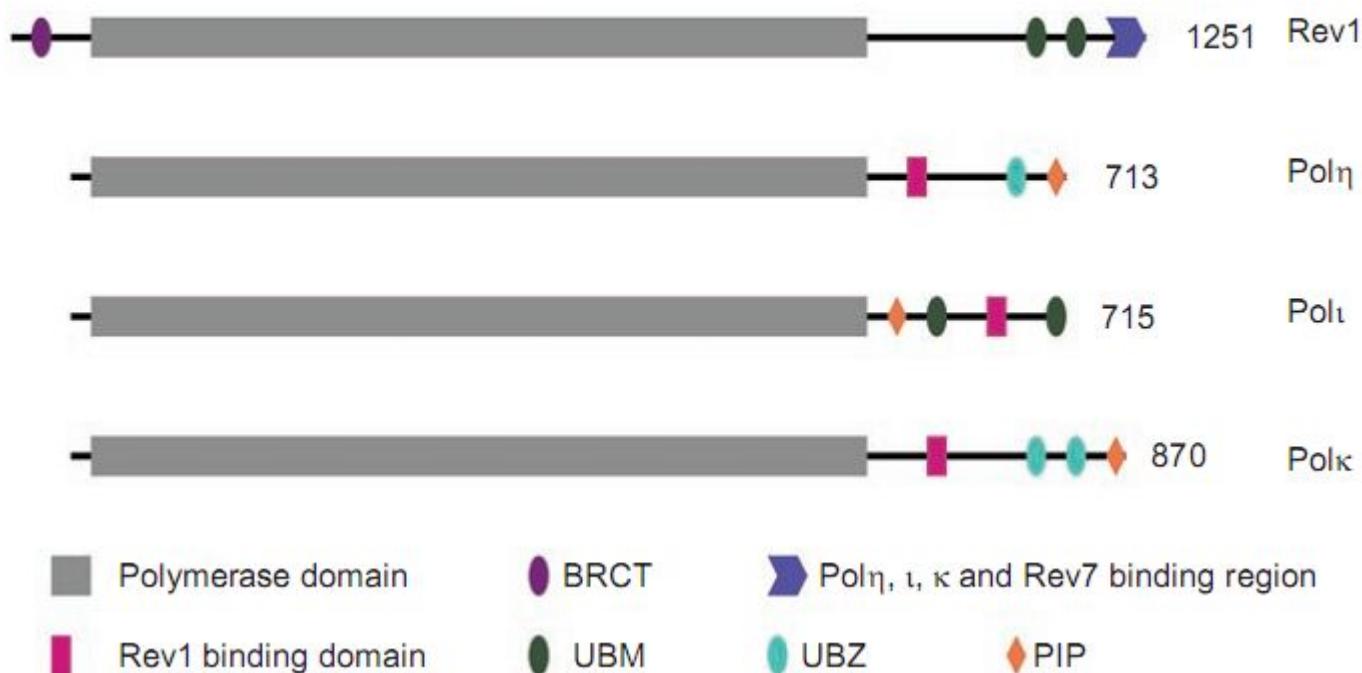


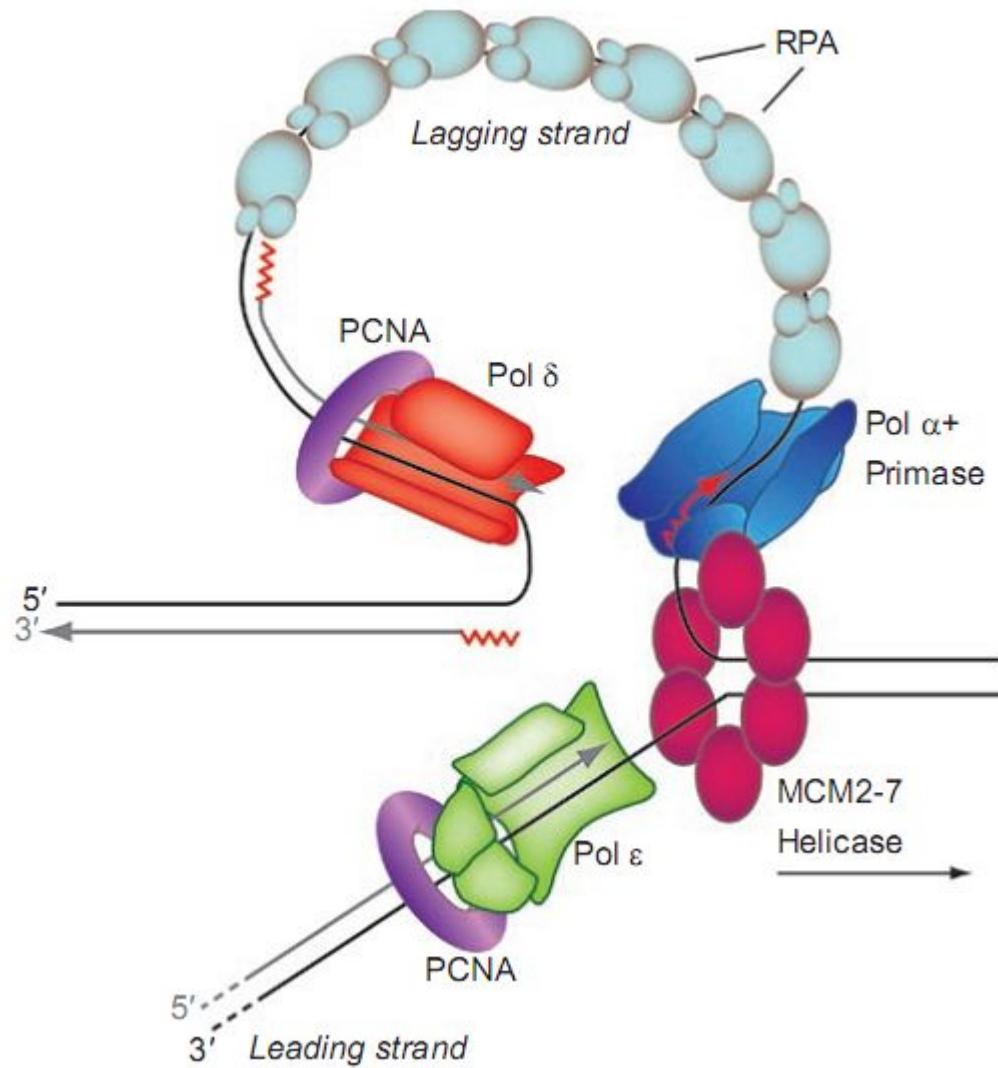
A

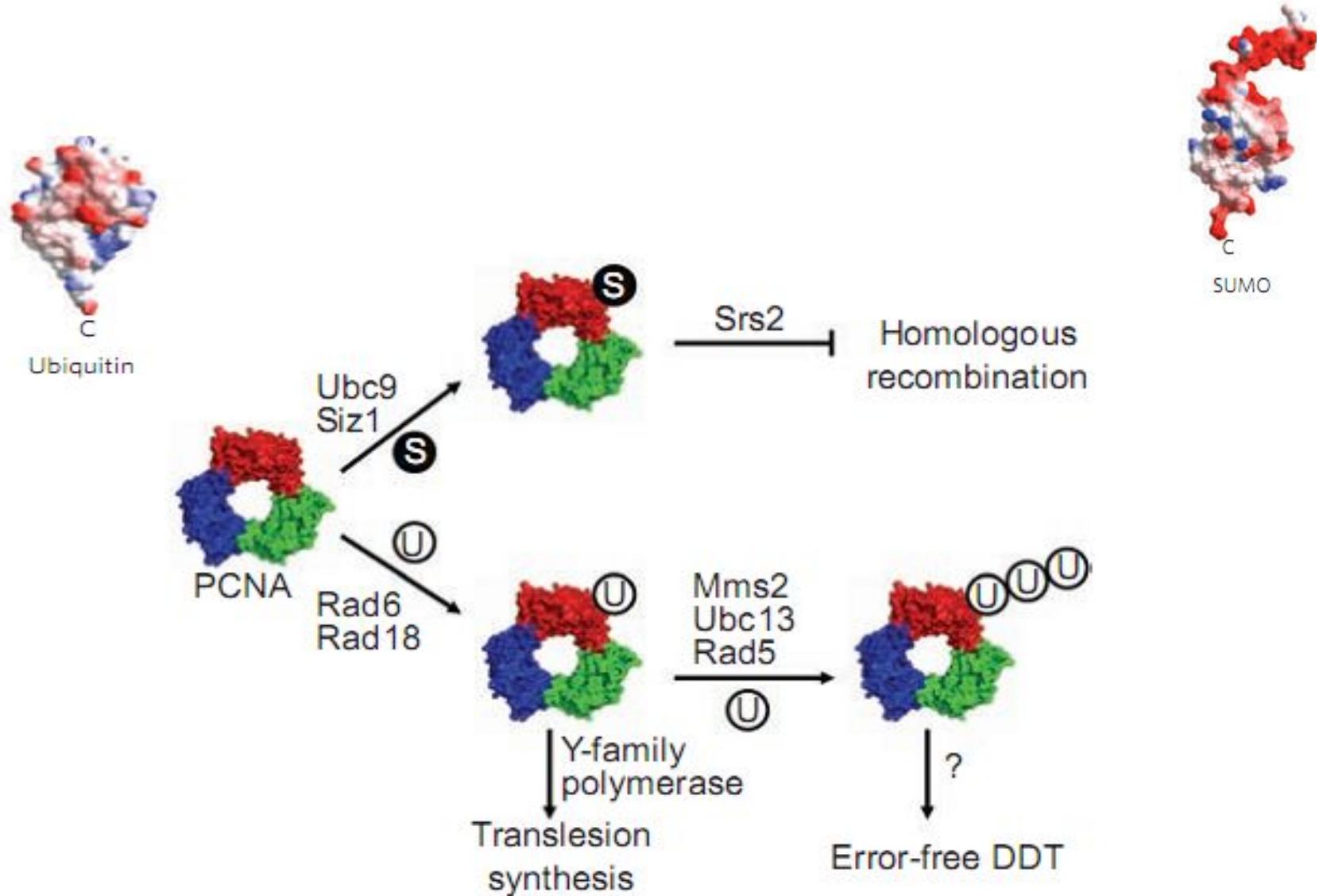


B

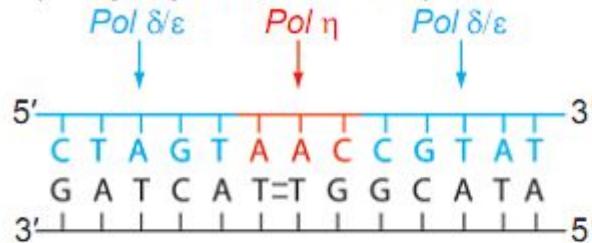




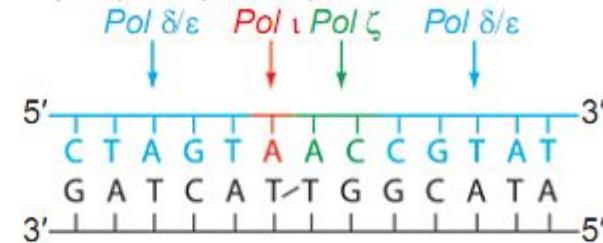




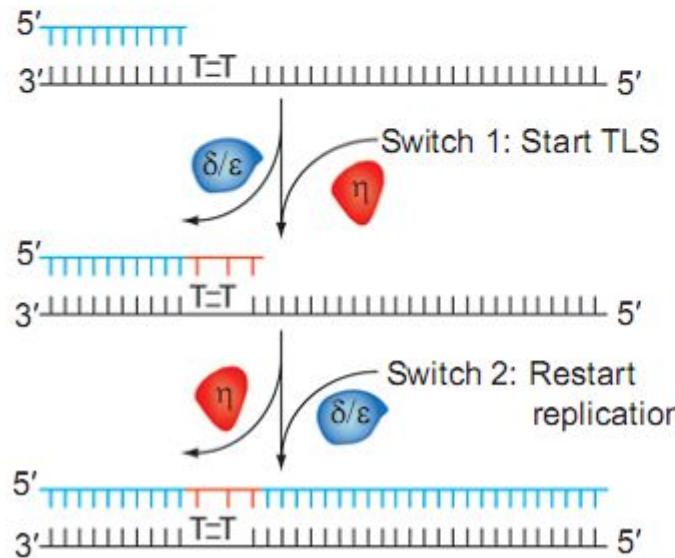
**A** 1-Polymerase model of TLS  
(*cis-syn* cyclobutane dimer)



**B** 2-Polymerase model of TLS  
(6-4 photoproduct)



**C** Co-replication model of TLS



**D** Post-replication or gap filling model of TLS

