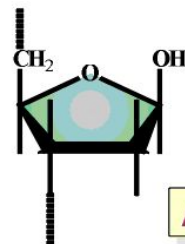
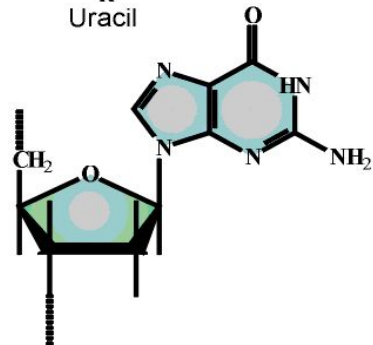
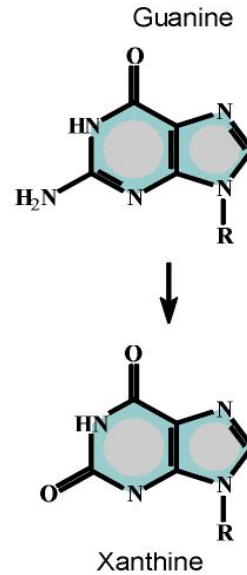
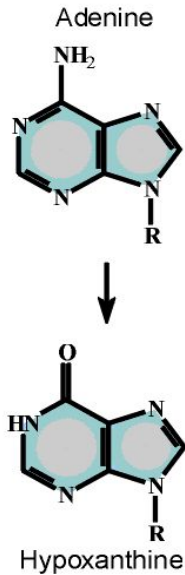
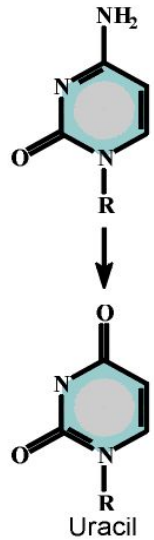
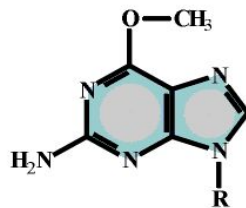
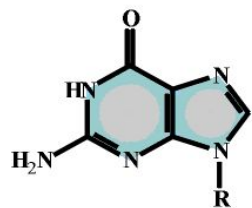


Typical base lesions

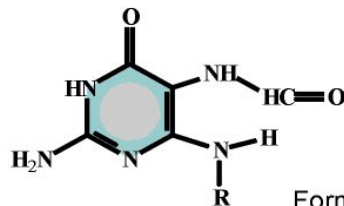
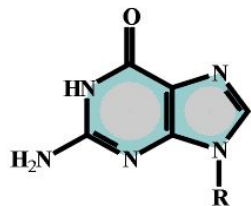
1.



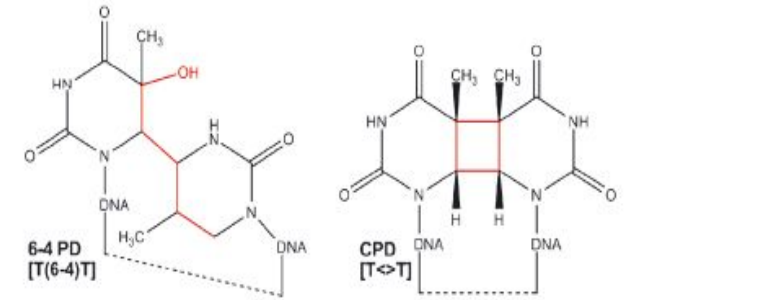
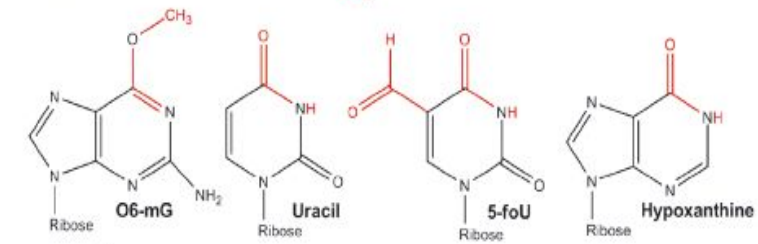
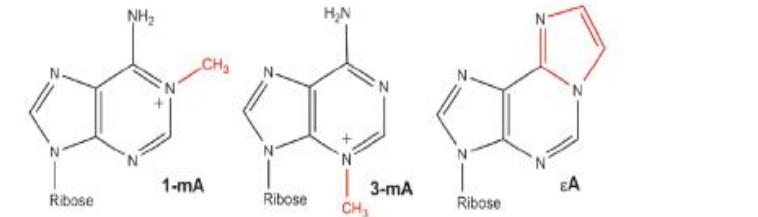
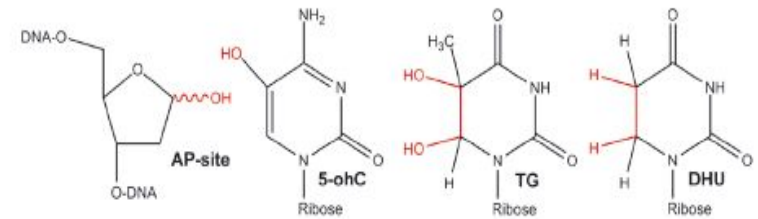
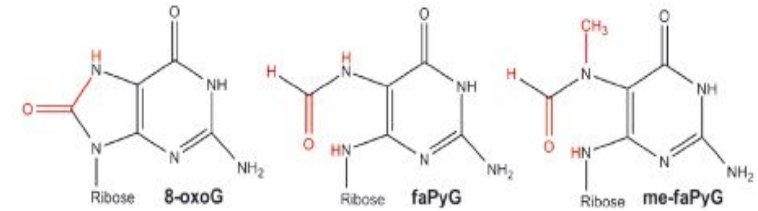
AP-site



O⁶-methylguanine



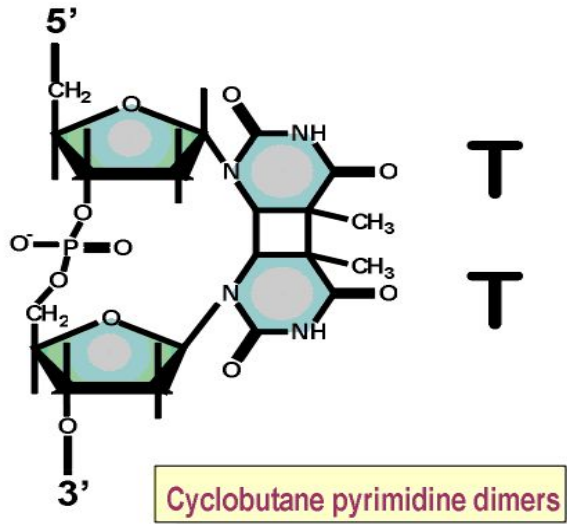
Formamidopyrimidine



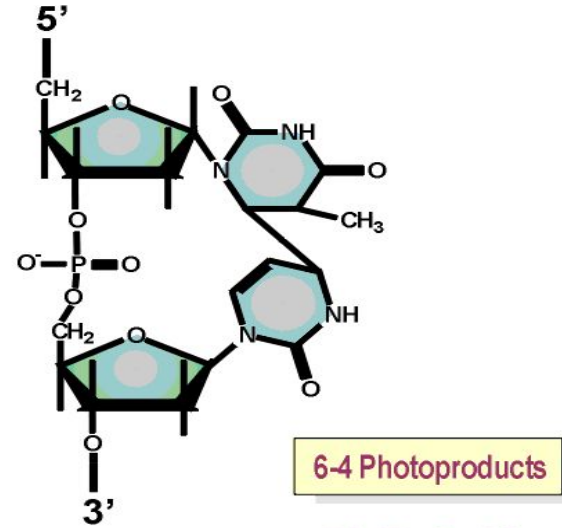
Damaging agent	Prototypical lesions	Major repair mechanism	Prototypical repair enzymes (<i>E. coli</i> /human)
Alkylating agents	O6-mG	DR	Transferases: Ogt/Agt
	1-mA	DR	Oxidoreductases: AlkB/Abh2
	3-mA, 3-mG, 7-mA, 7-mG	BER	Glycosylases: AlkA/Aag
Hydrolysis	Abasic sites	BER	Endonucleases: EndoIV/Ape1
	Deamination (forming uracil)	BER	Glycosylases: Ung
	Deamination (forming hypoxanthine)	NIR	Endonucleases: EndoV
ROS	8-oxoG, faPyA/G, TG, 5-ohC, DHU, DHT	BER	Glycosylases: Fpg, Nth/Ogg1, Nth1
	DHU, DHT, 5-ohC	NIR	Endonucleases: EndoIV/Ape1
Replication errors	(a) Base mismatches	MMR	Mismatch proteins:
	(b) Insertion/deletion loops		MutS, MutL, MutH/MutS α / β , MutL α
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.

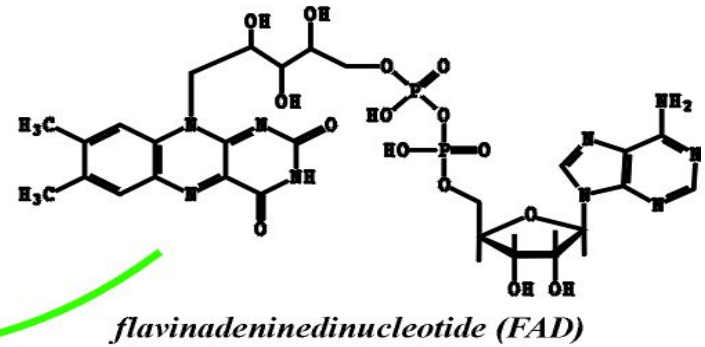
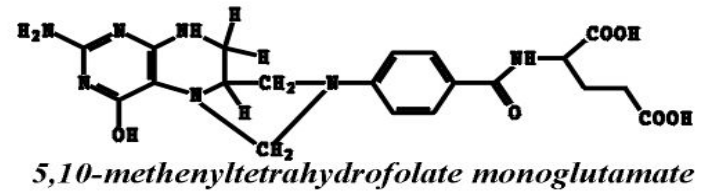
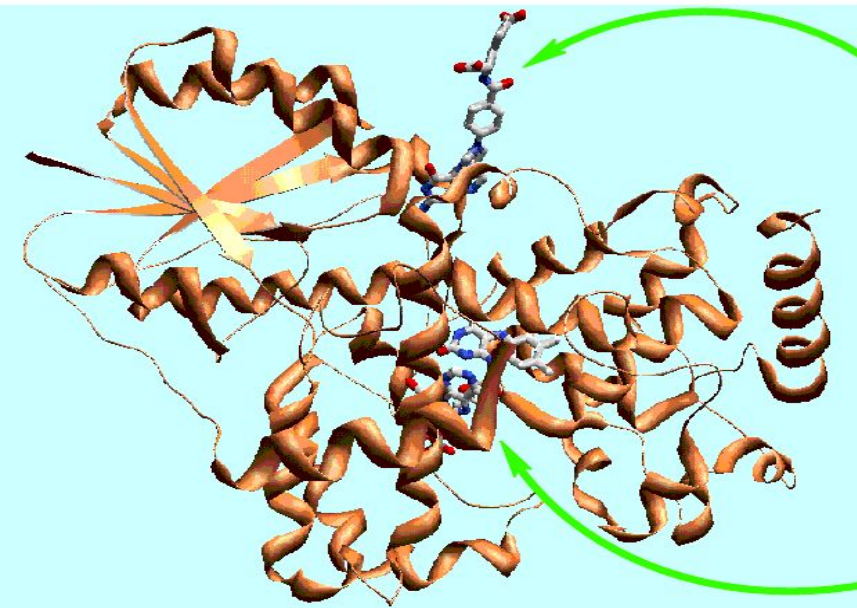
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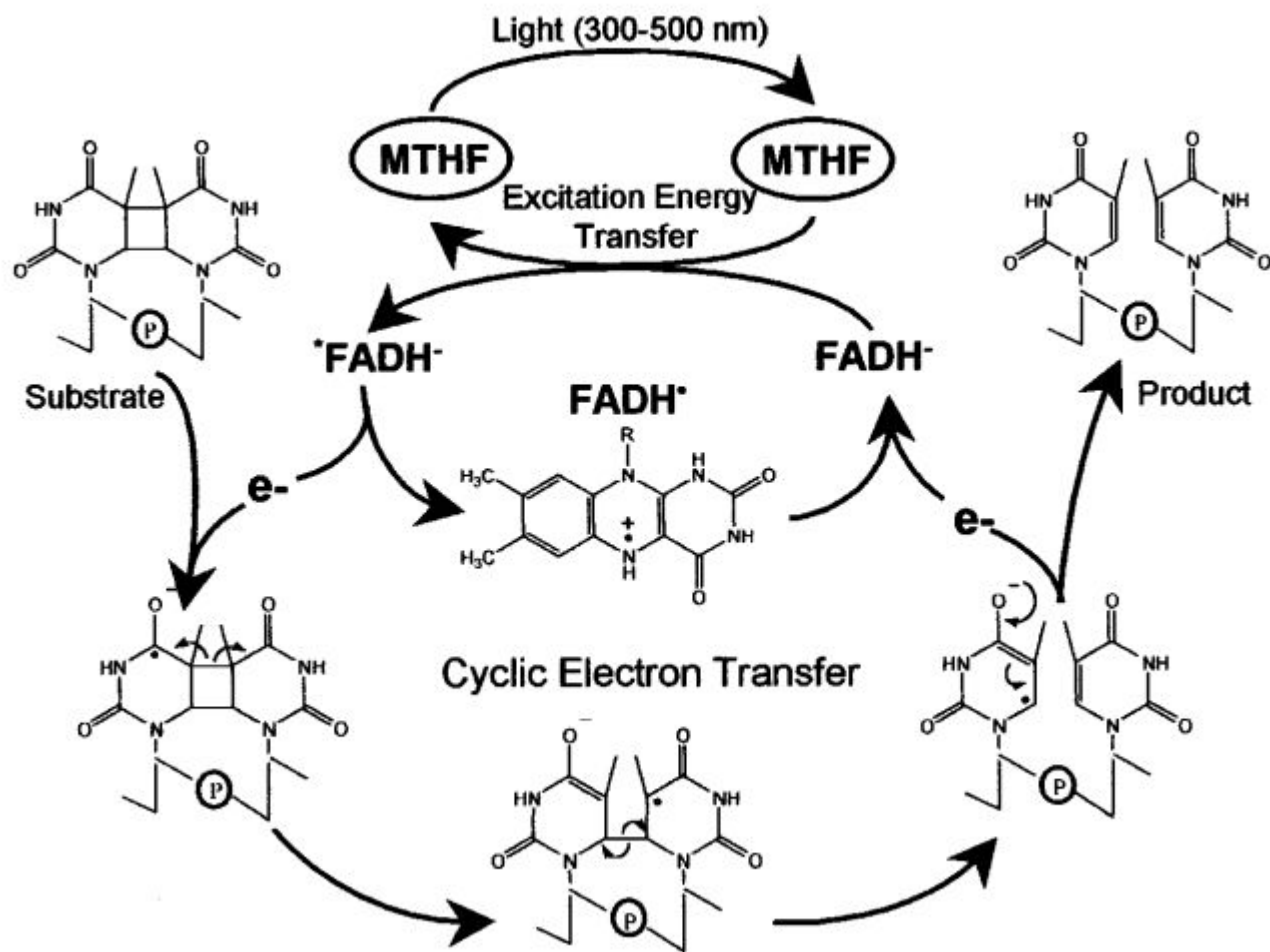


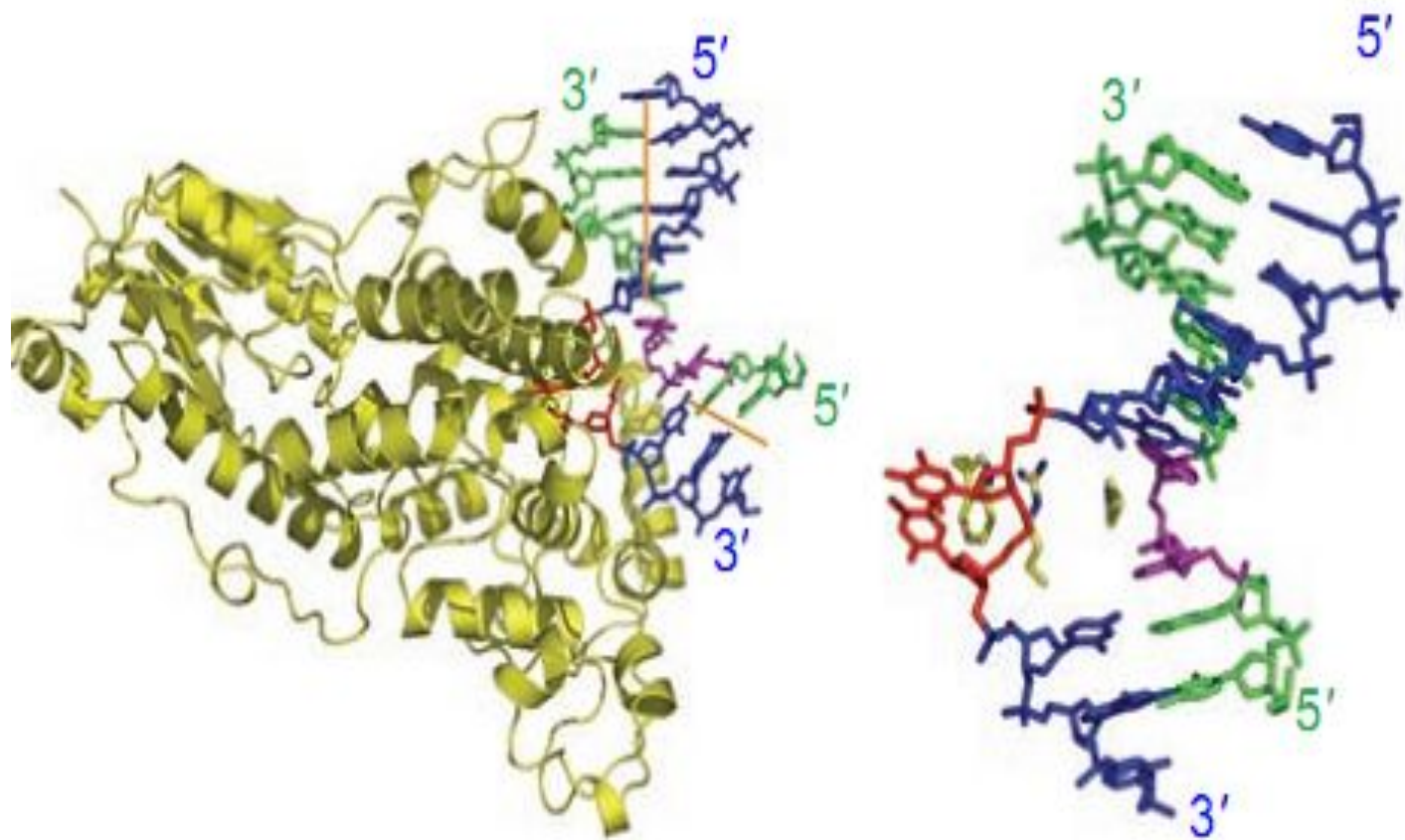
Any pyrimidine pair



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

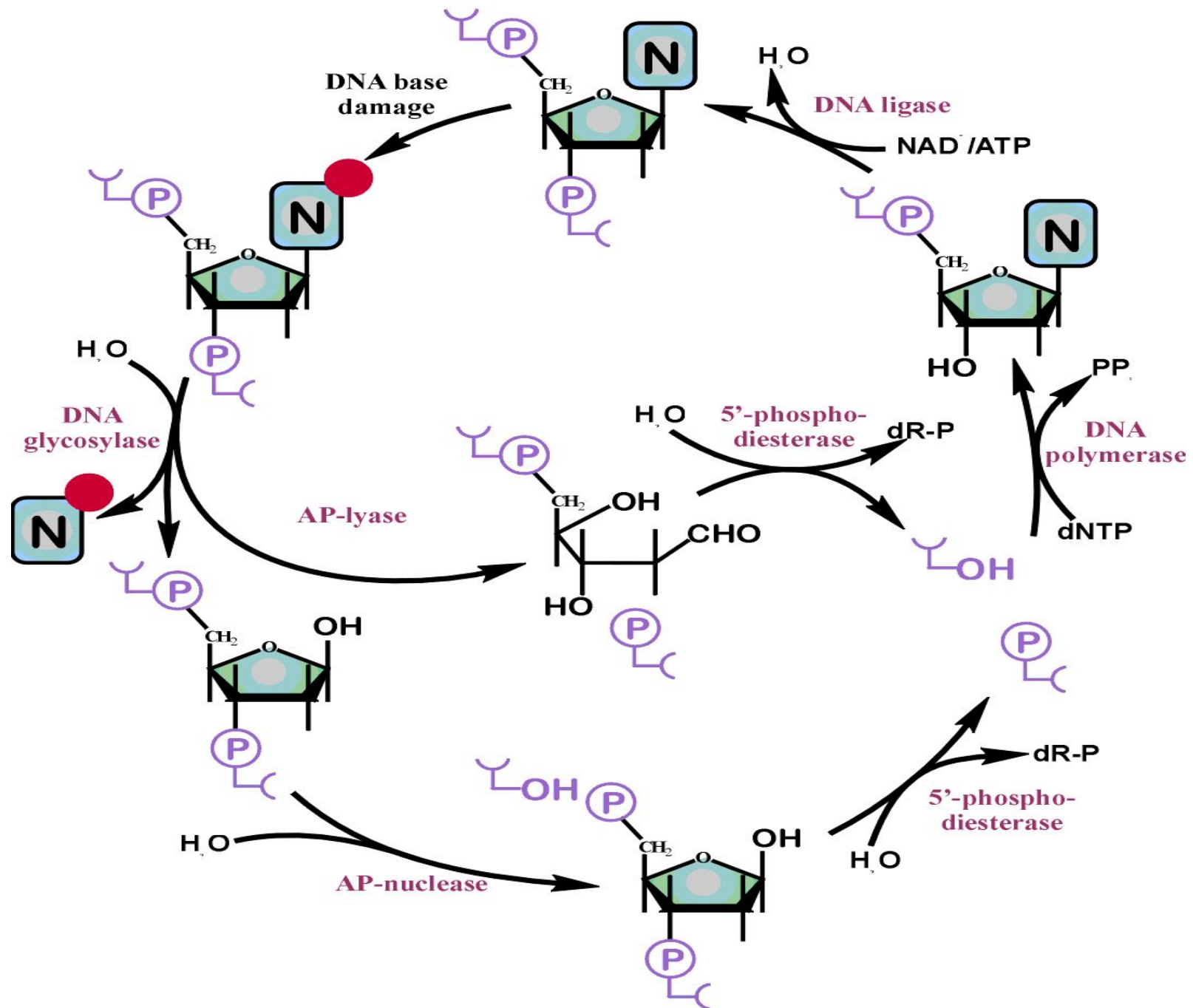


A

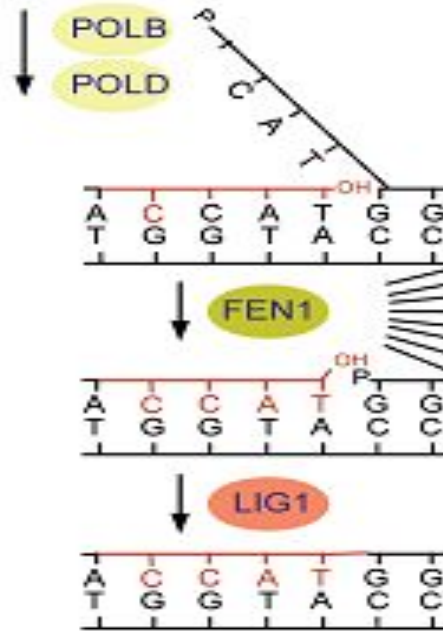
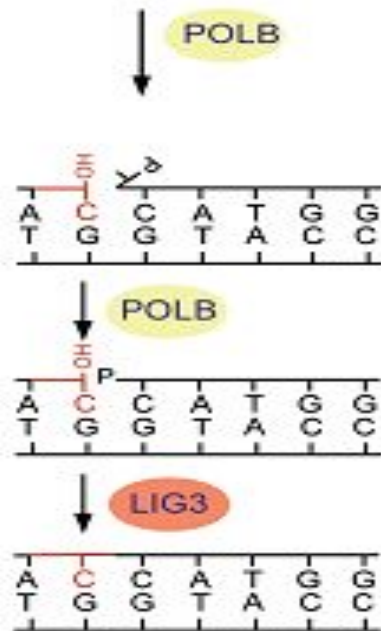
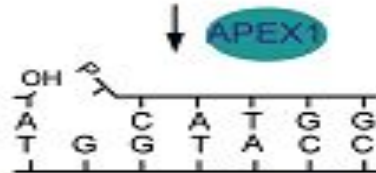
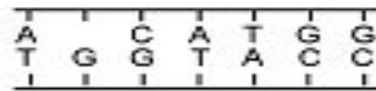


DNA Photolyase - CPD complex (1TEZ)

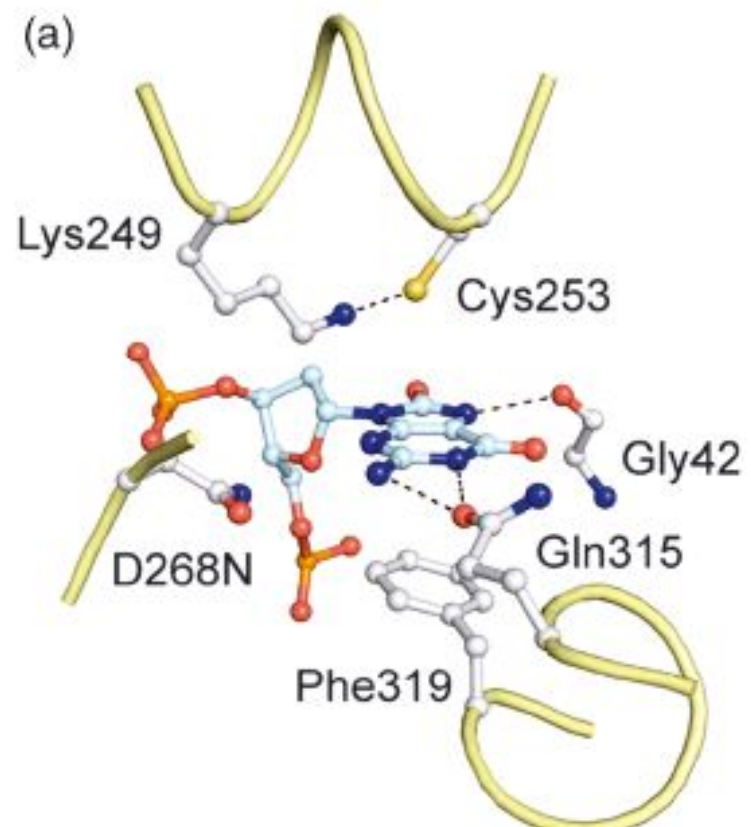
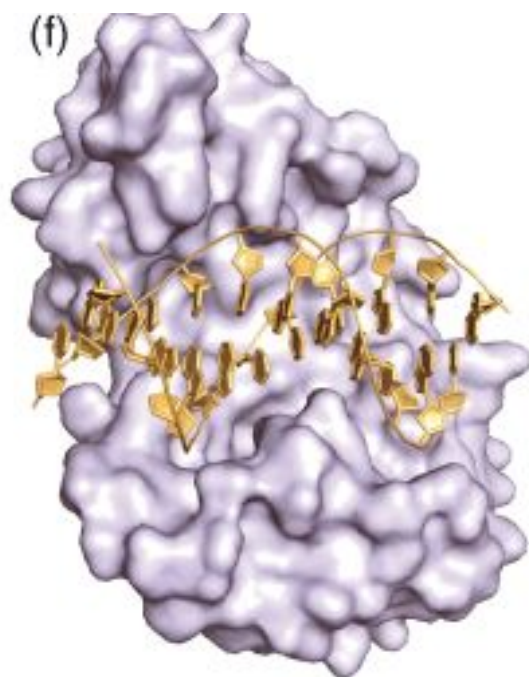
Base excision repair (BER)

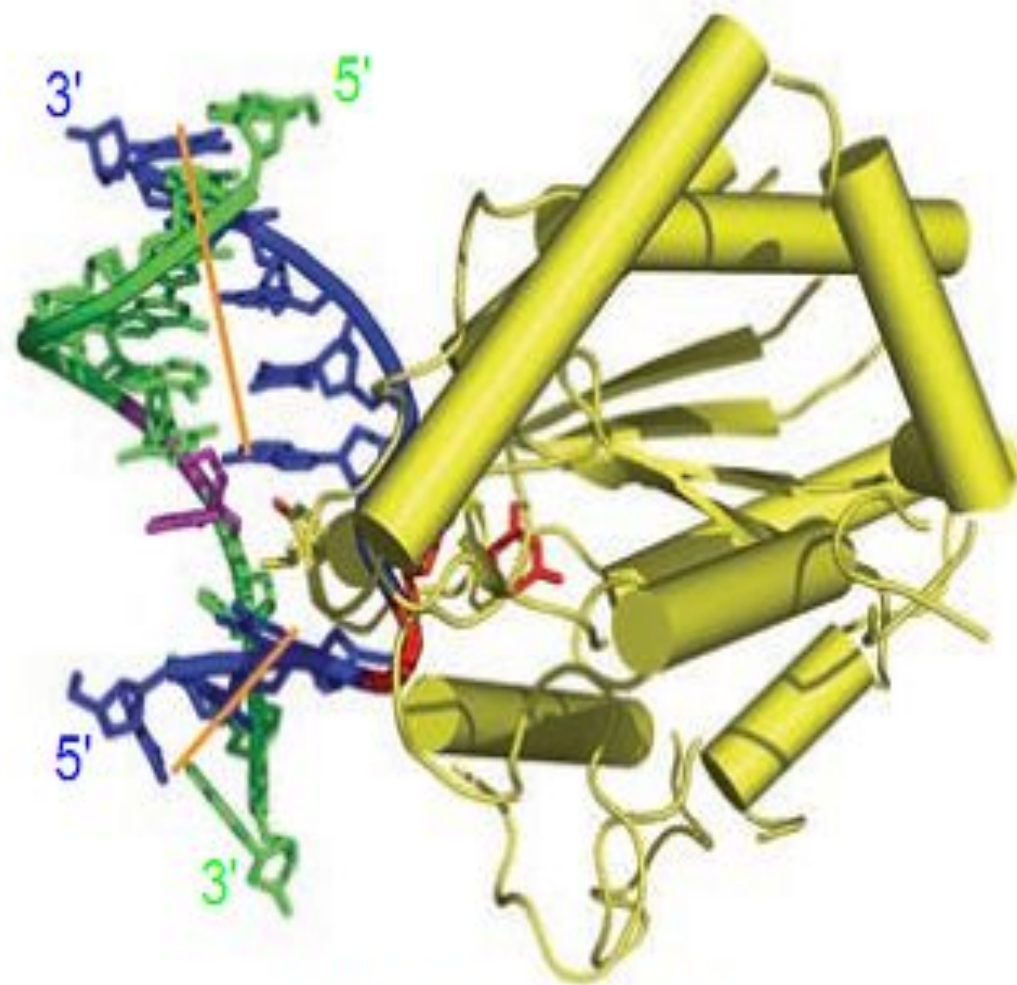


DNA base damage



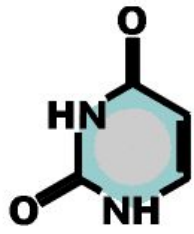
- CDKM1A
 - LIG1
 - MSH2/3
 - MSH2/6
 - XPG
 - UNG2
 - WRN
 - POLD
 - NTHL1
- POLB
PCNA
RPA
RFC
WRN
APEX1
EP300
BLM



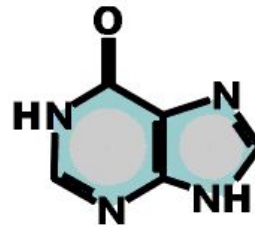


UDG-DNA (1EMJ)

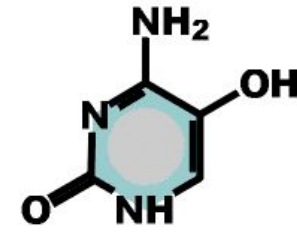
Typical DNA lesions excited by DNA glycosilases



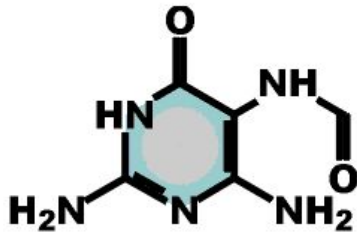
Uracil



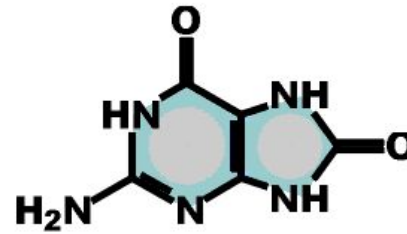
Hypoxanthine



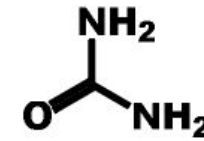
5-Hydroxycytosine



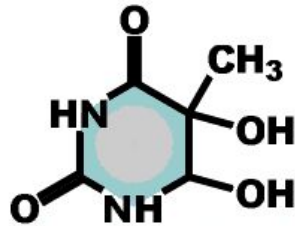
2,5-Amino-5-formamido-pyrimidine



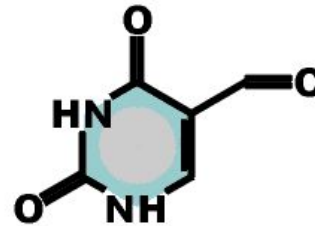
7,8-Dihydro-8-oxo-guanine



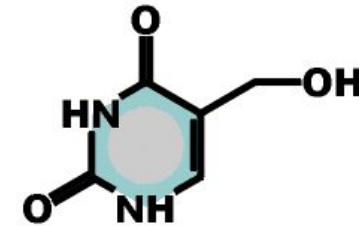
Urea



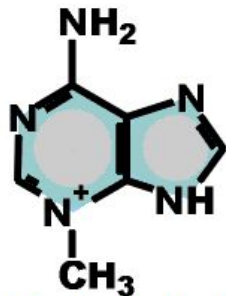
Thymine glycol



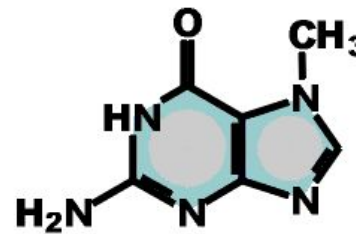
5-Formyluracil



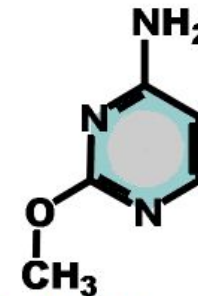
5-Hydroxymethyluracil



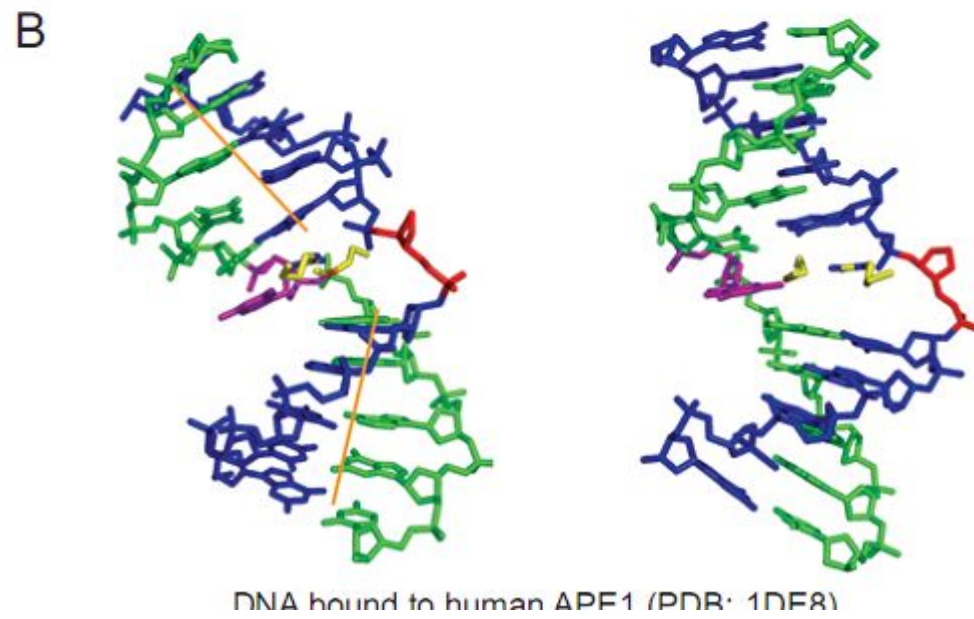
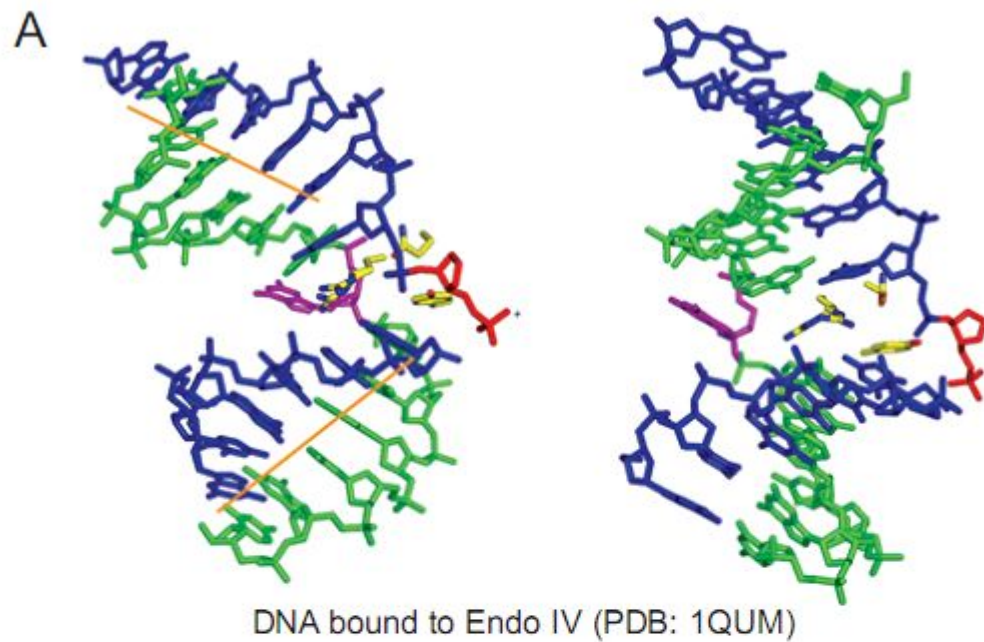
3-Methyladenine



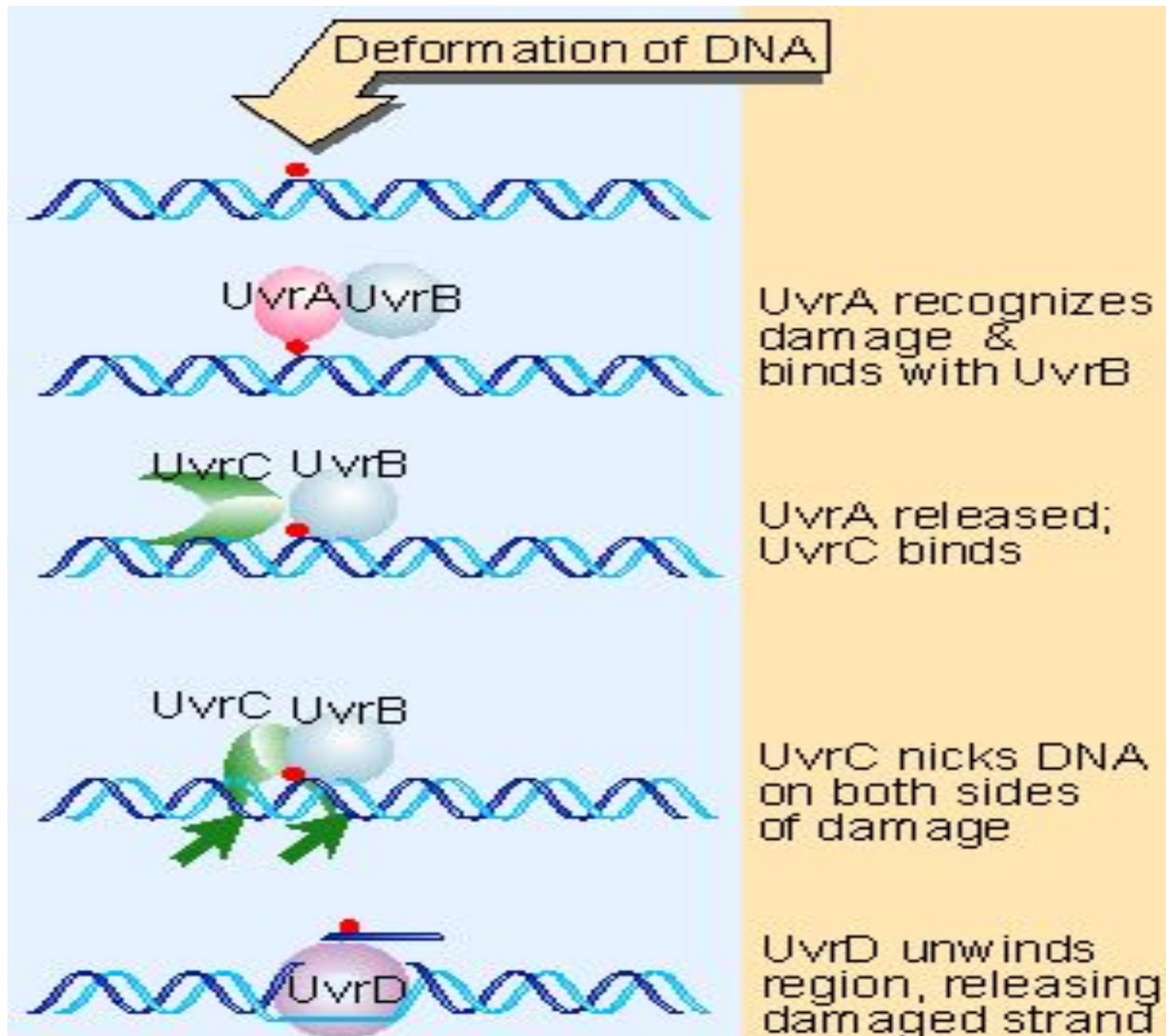
7-Methylguanine

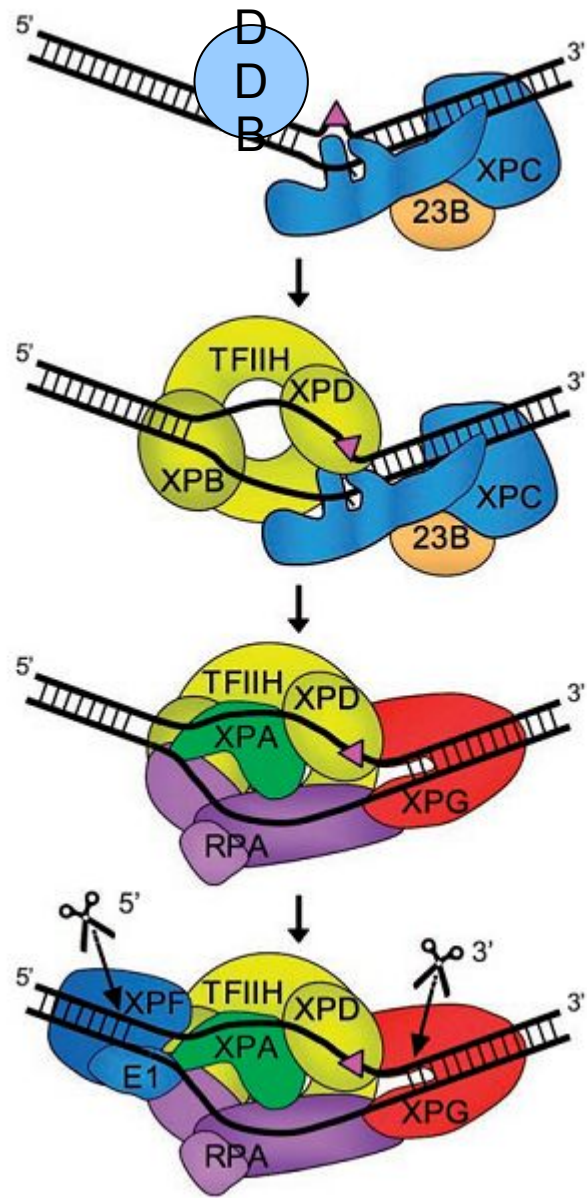


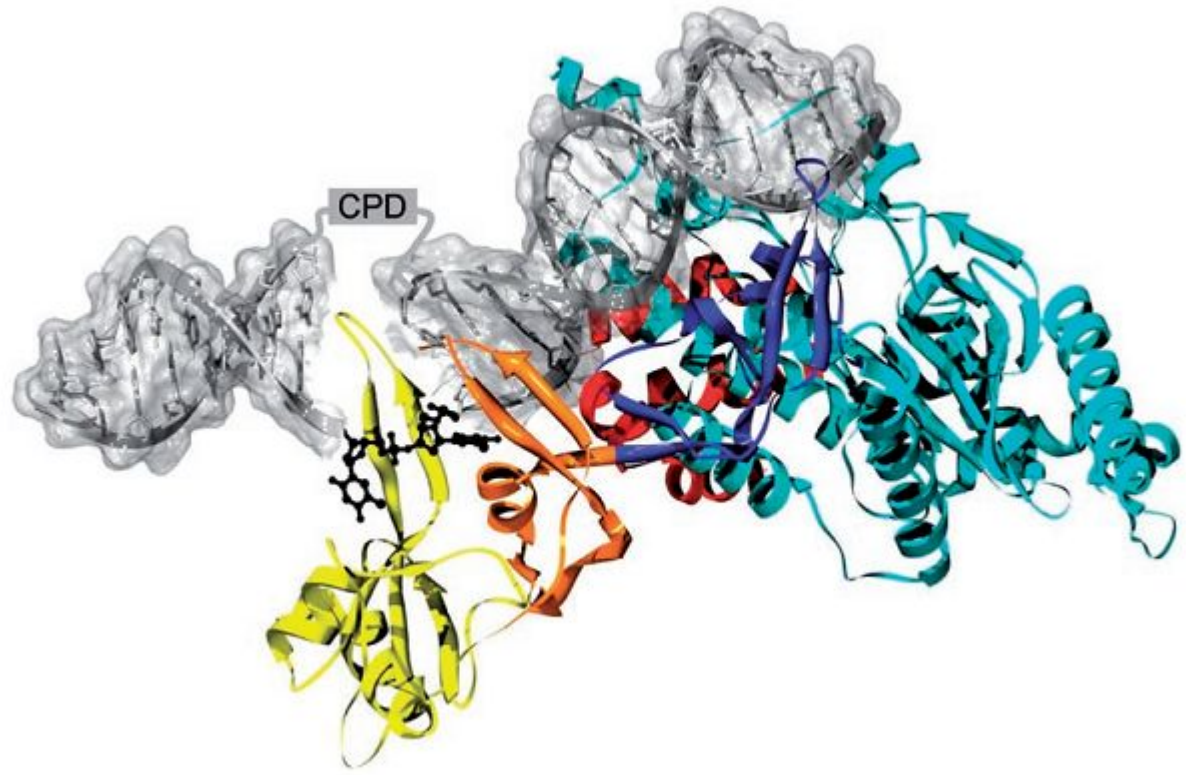
2-Methylcytosine



NER







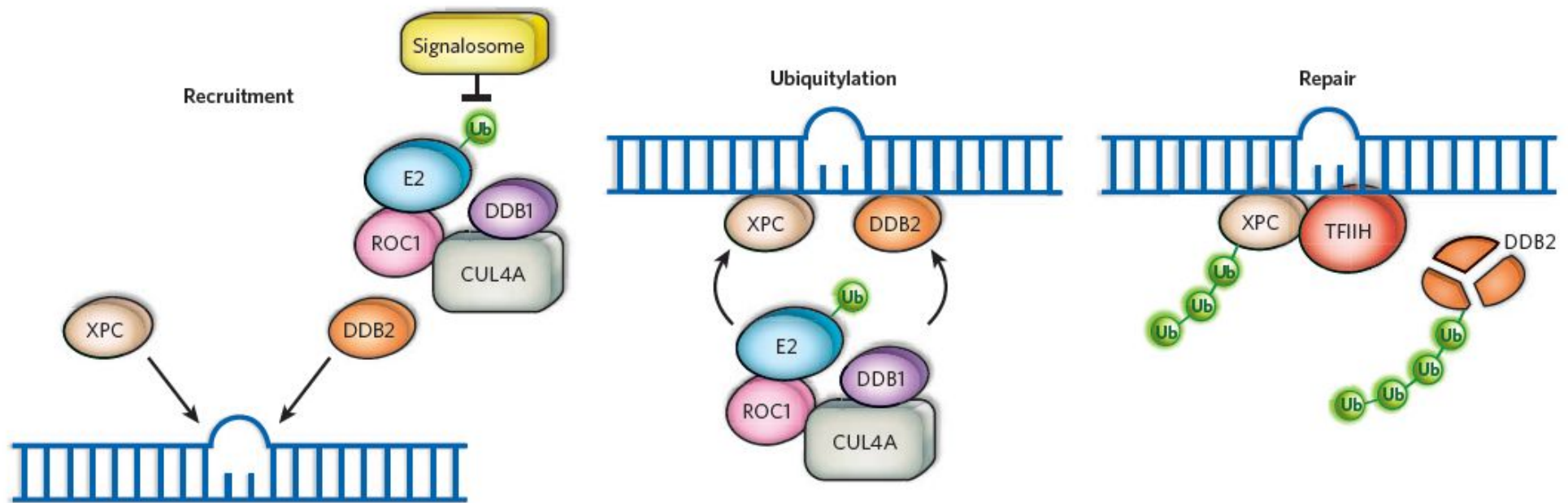


Figure 2 | Scheme for XPC and DDB2 ubiquitylation. Helix-distorting lesions are substrates for XPC and DDB2 (left). XPC binds to the undamaged strands of helix-distorted lesions (middle). DDB2 becomes part of a larger, cullin 4a-based E3 ubiquitin ligase complex (CUL4a, DDB1, ROC1 and an E2 ubiquitin-conjugating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

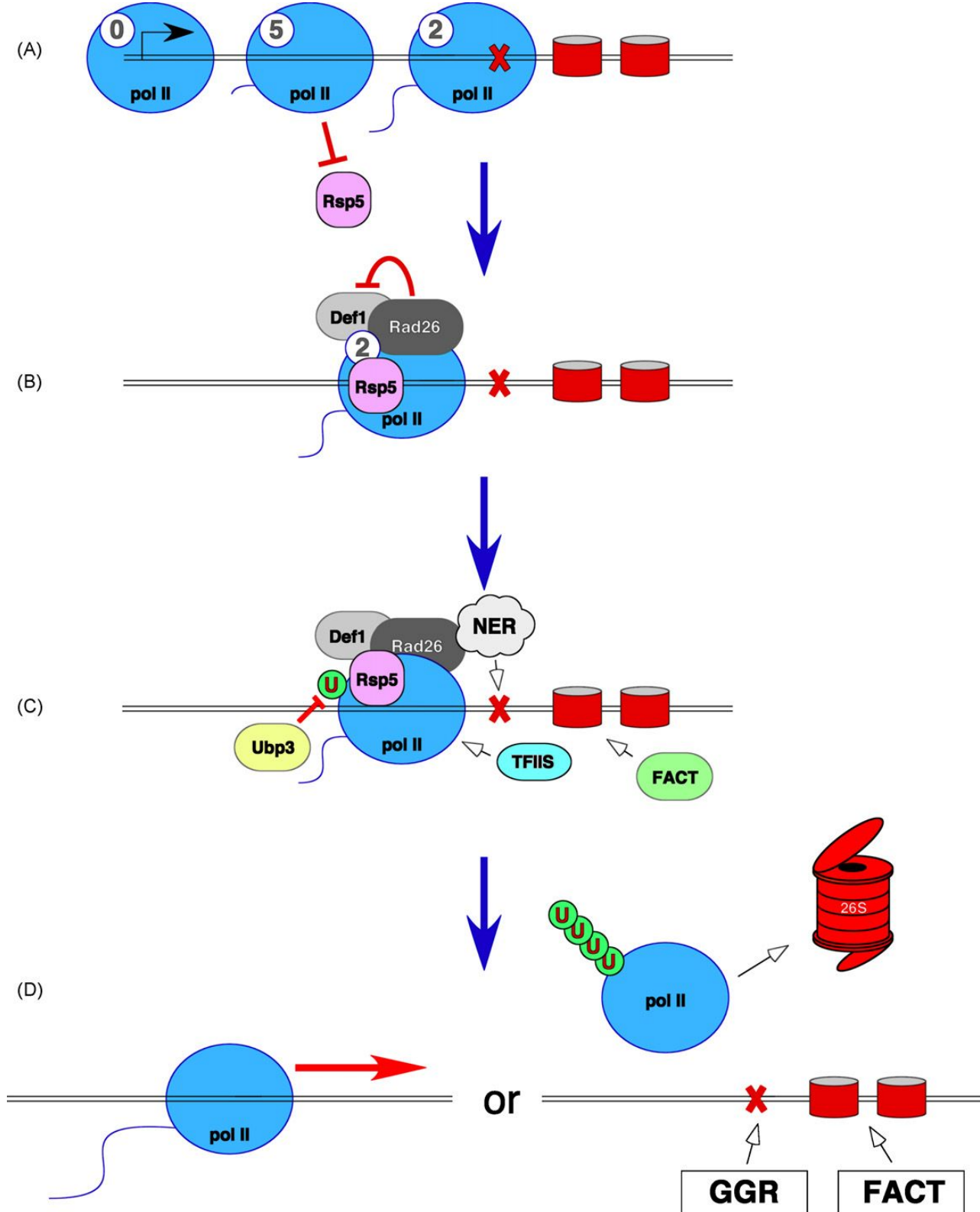
UV-DDB

TC-NER

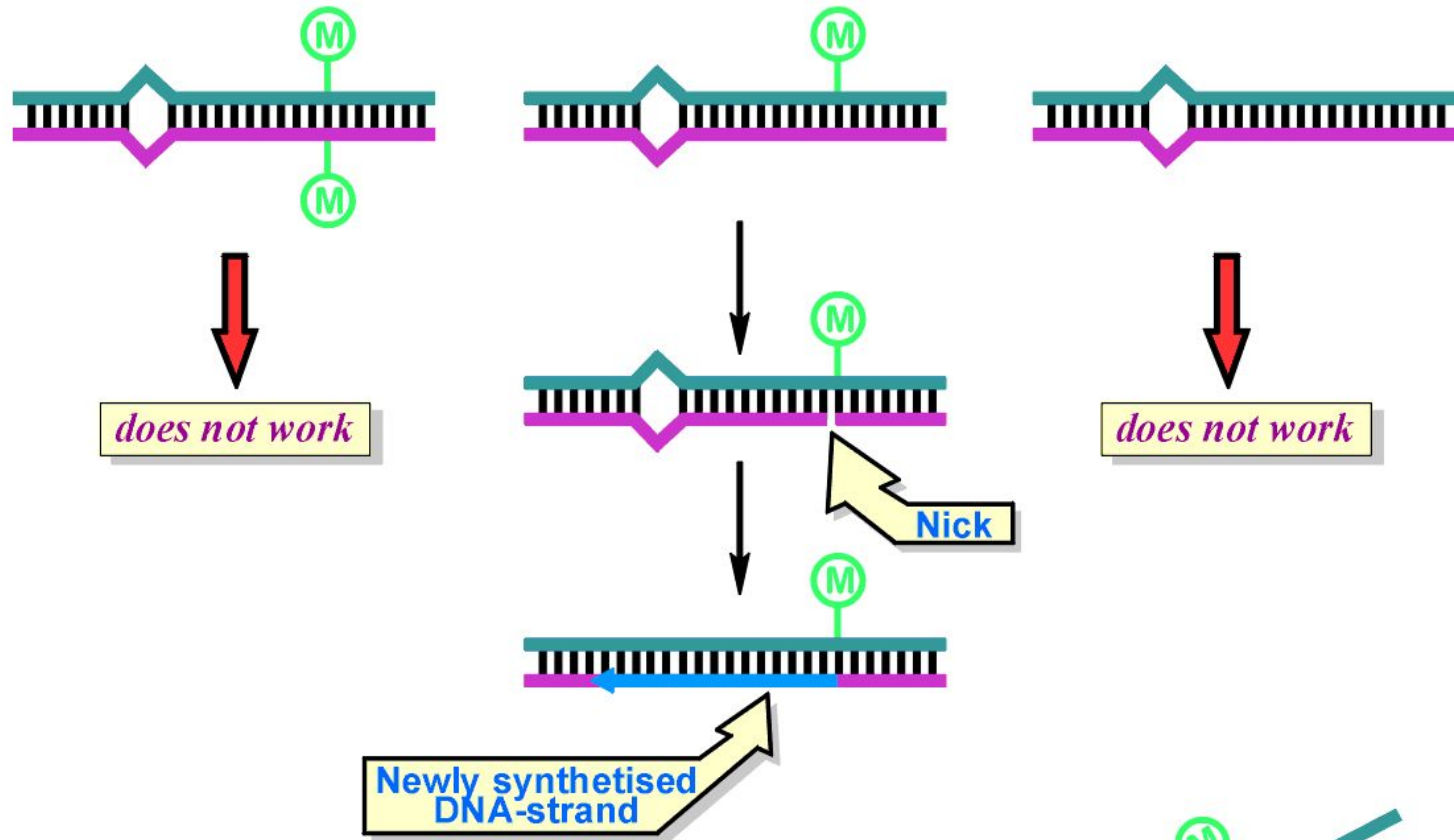
CSA, CSB

DCAF family

and ???

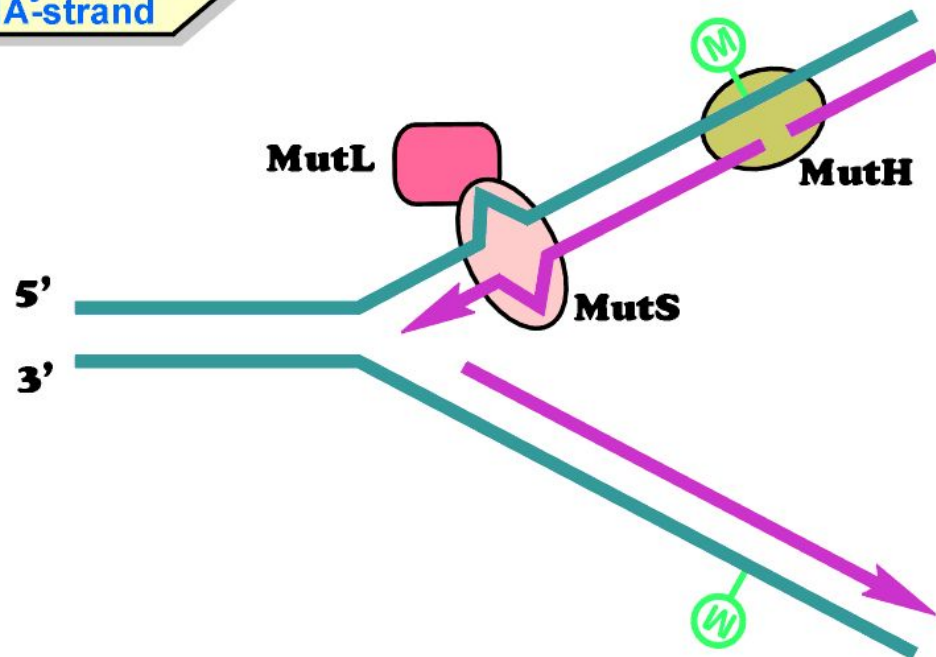


Mismatch repair

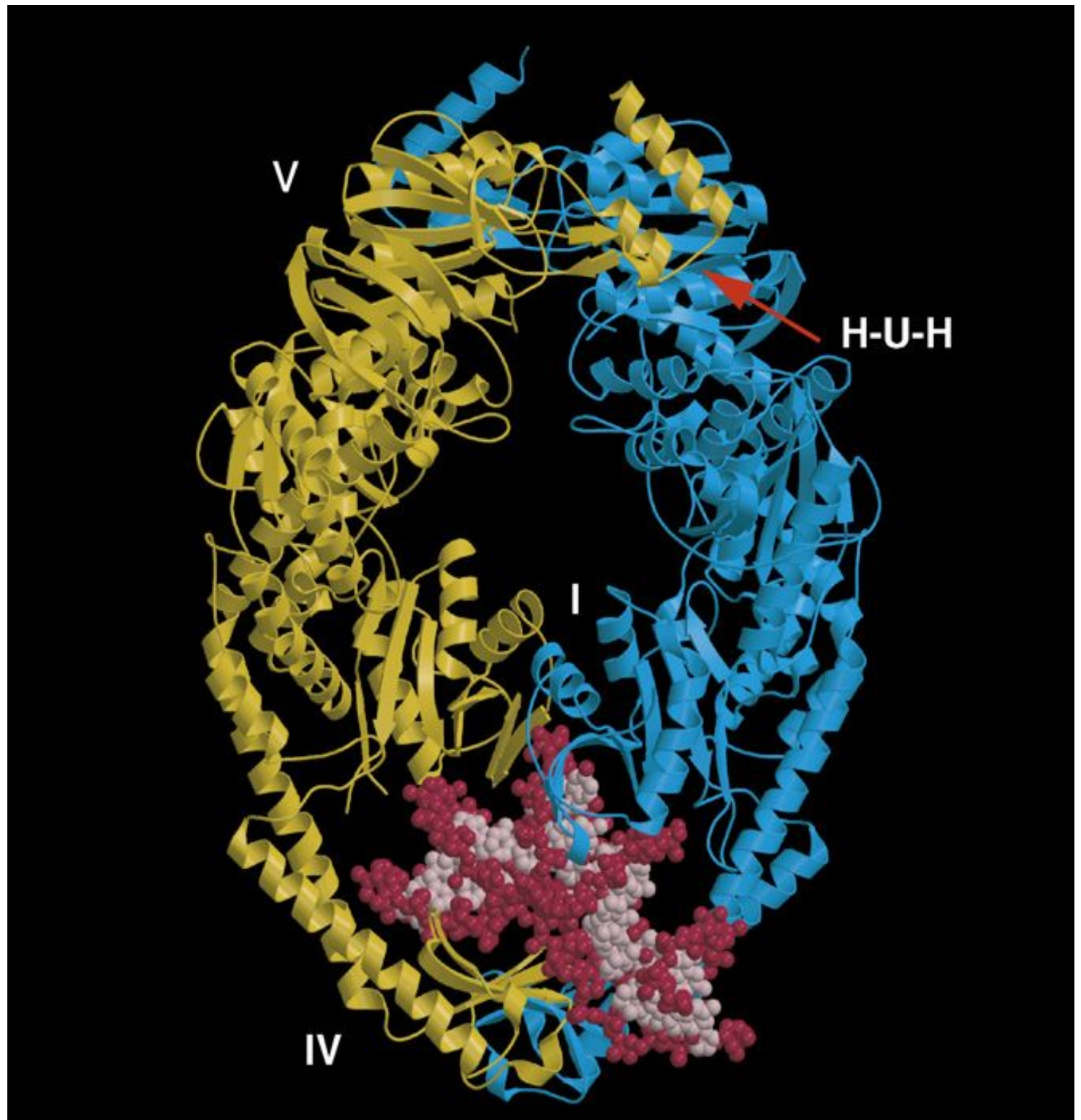


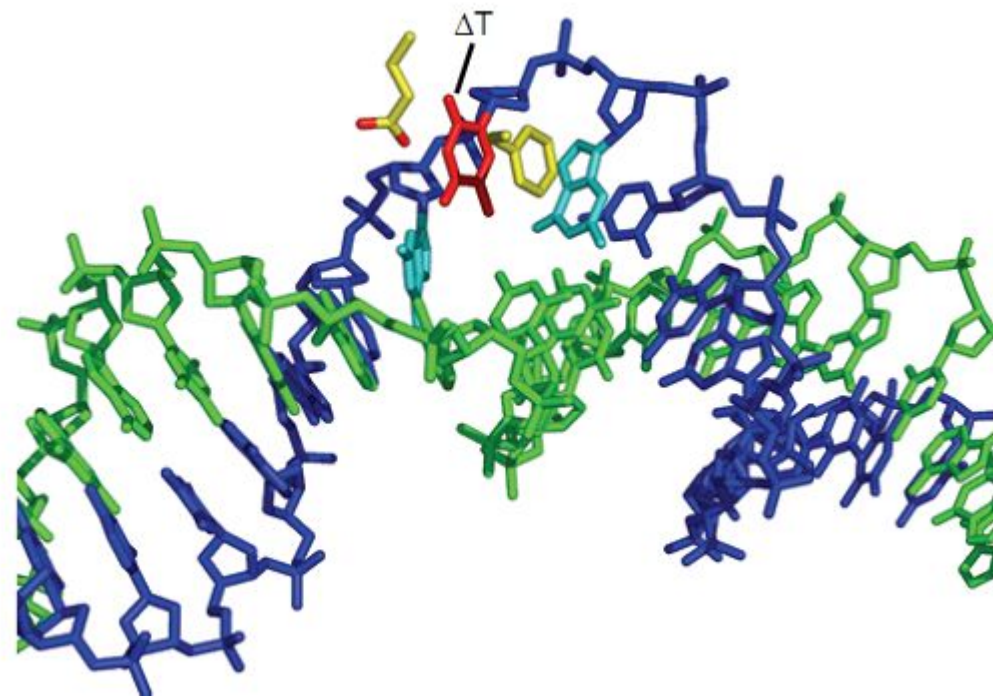
Excision / resynthesis

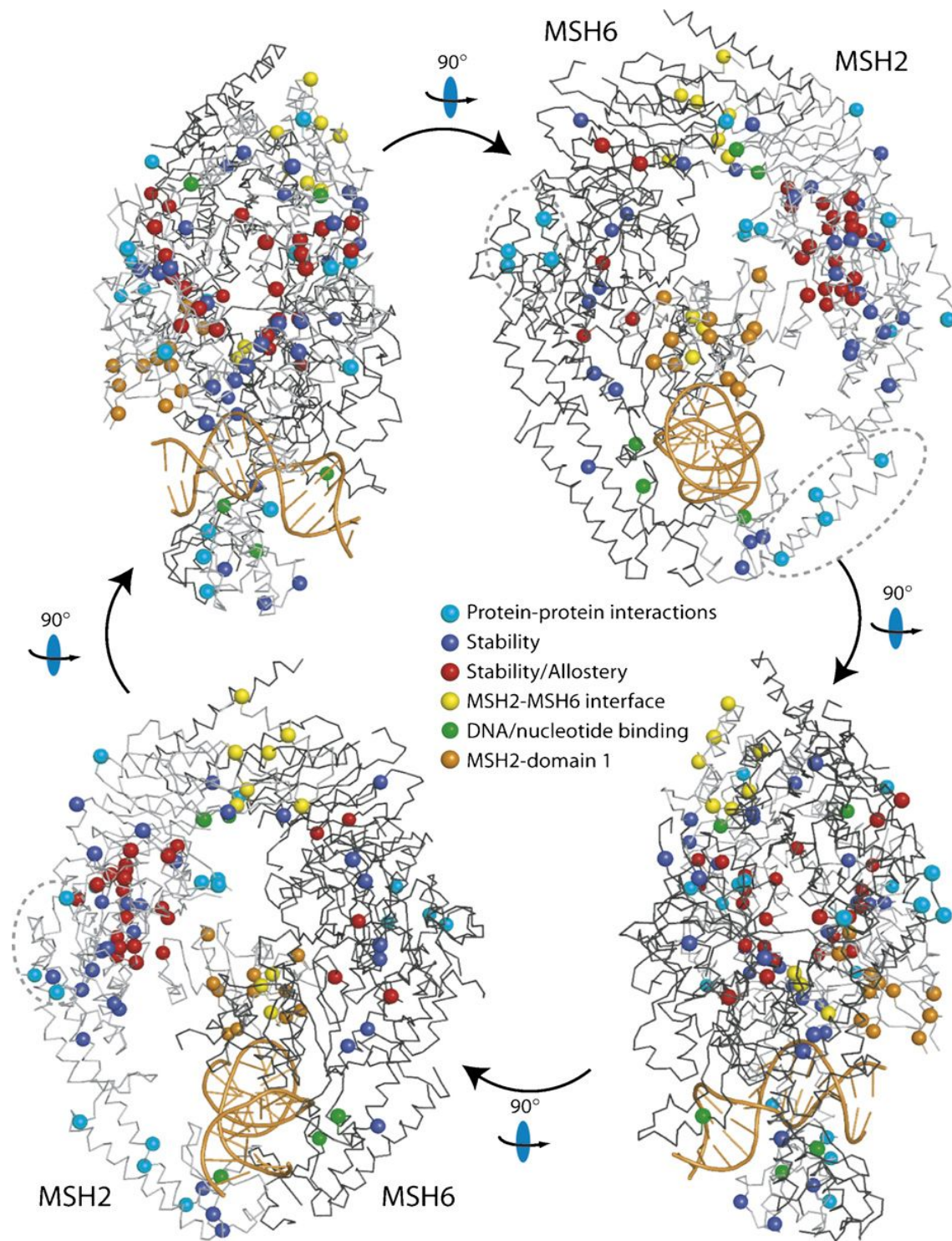
Exo I, Exo VII or RecJ,
Helicase II,
DNA pol III, SSB and
DNA ligase

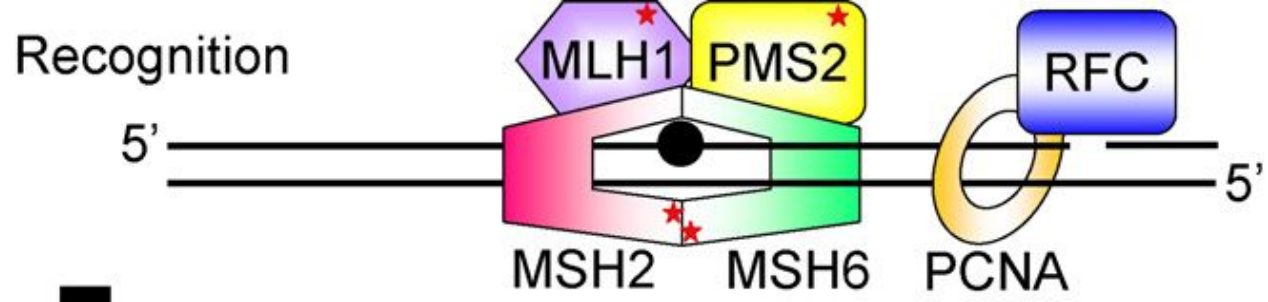


MutS



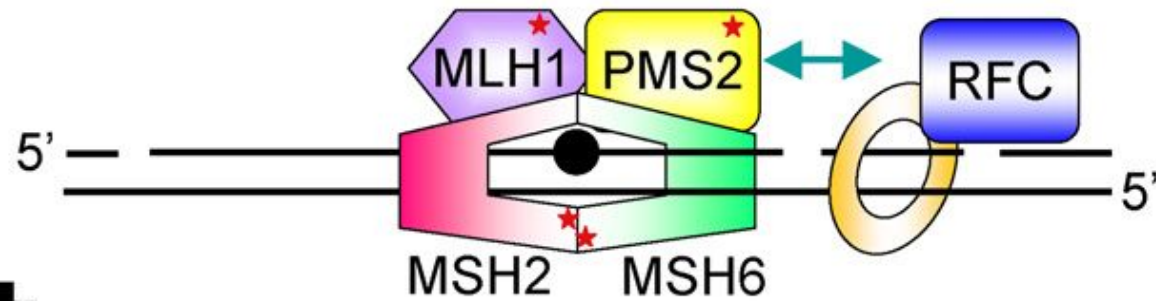






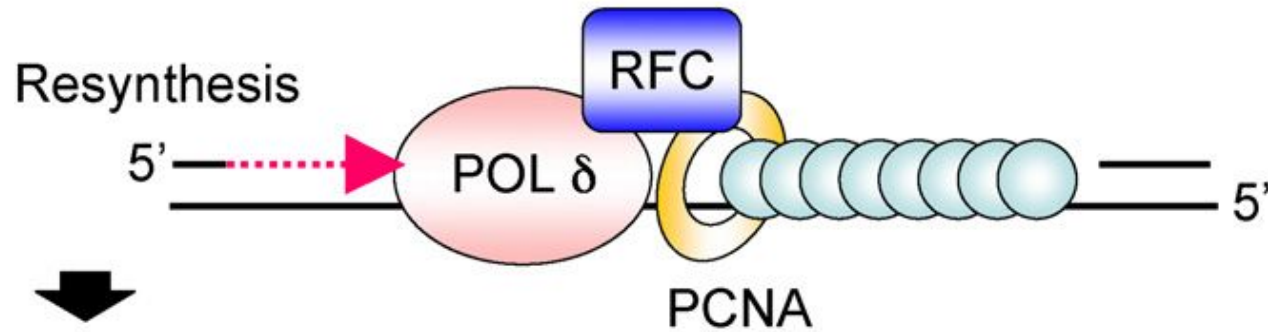
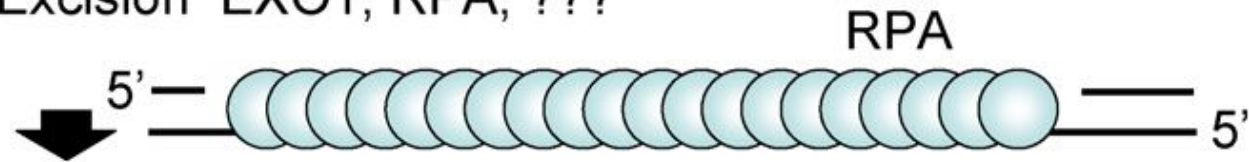
↓

Nicking $\text{ATP} \rightarrow \text{ADP} + \text{P}_i$



↓

Excision EXO1, RPA, ???

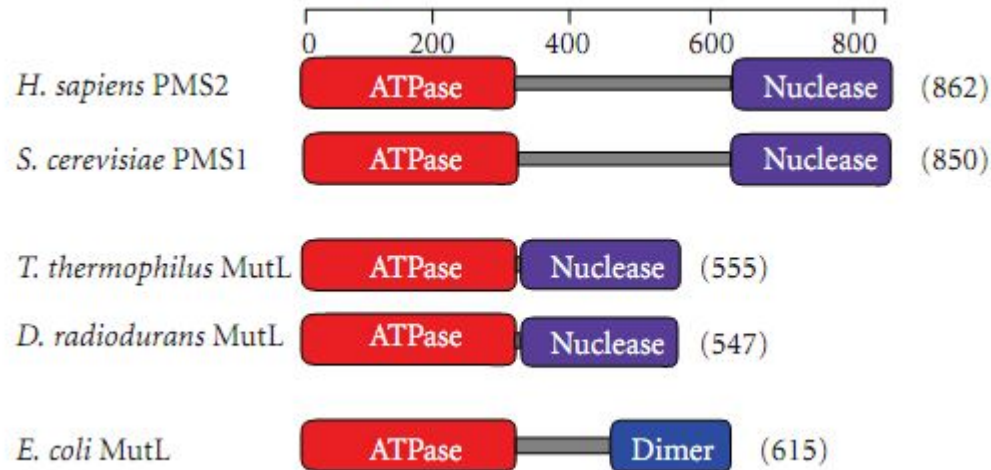


↓

Ligation

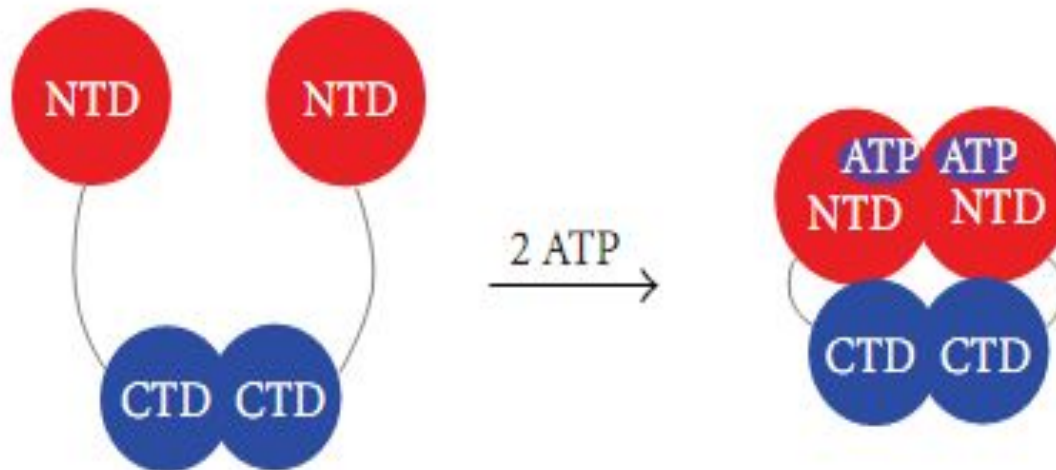


MutL α



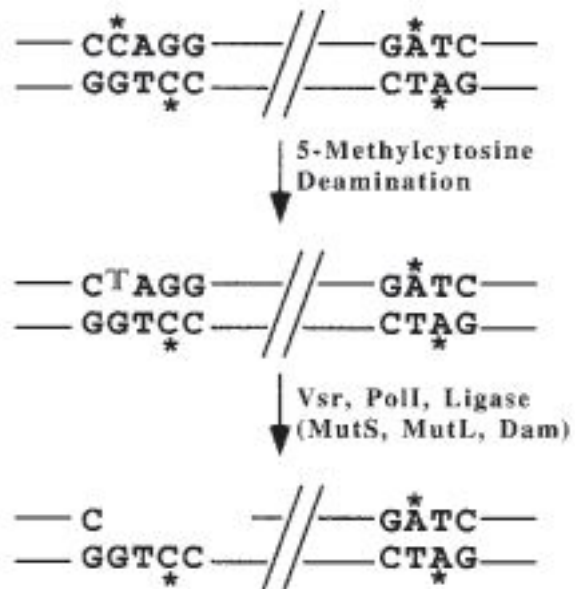
(a)

(b)

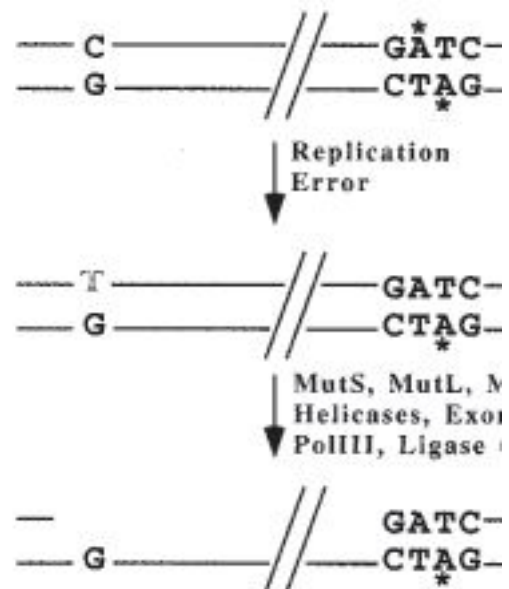


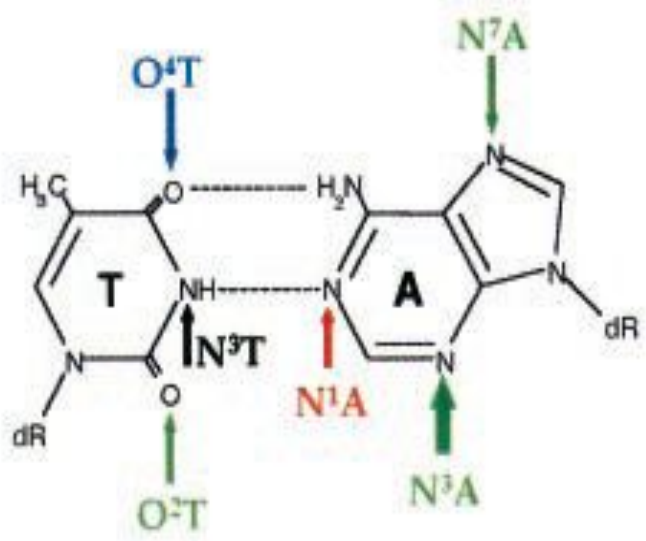
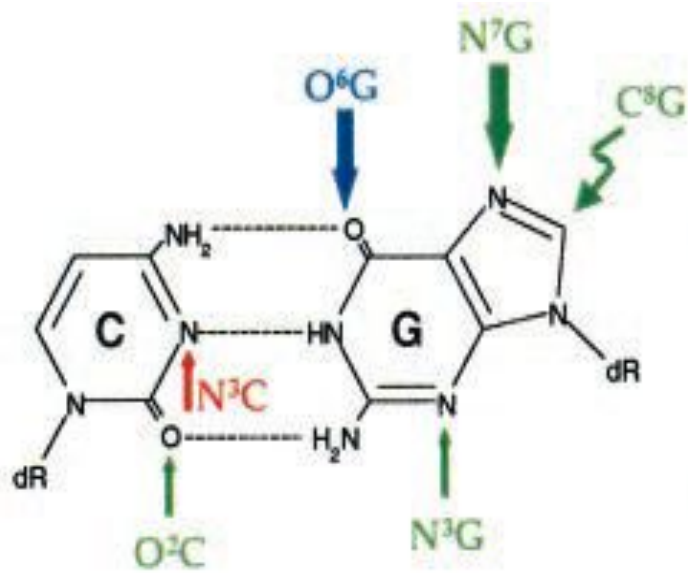
of MutL α , the PMS2 and MLH1 subunits dimerize via their C-terminal domains. ATP binding induces the dimerization of the N-terminal domain and condensation of the molecule.

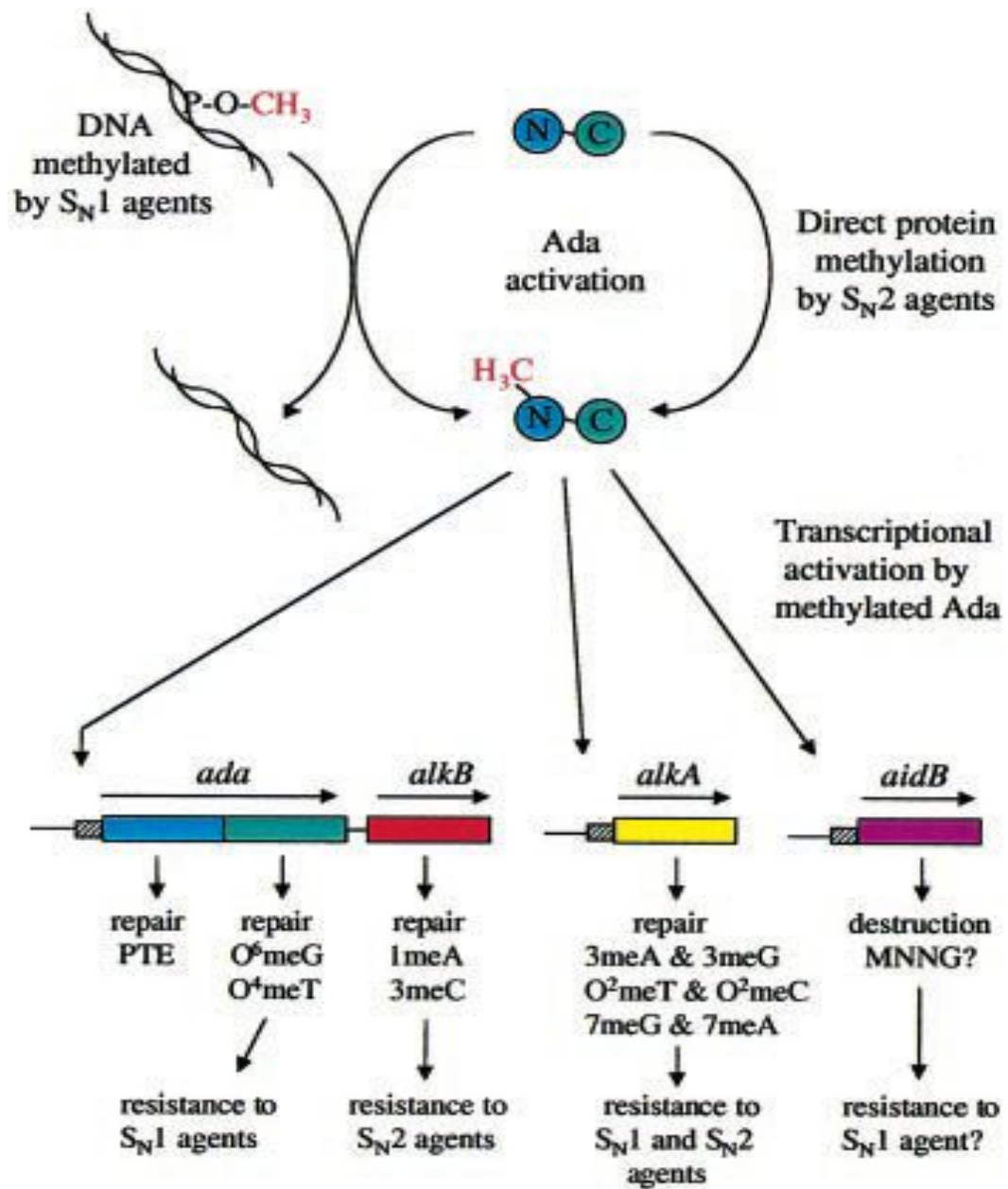
VSP REPAIR

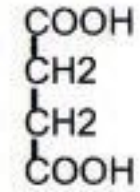
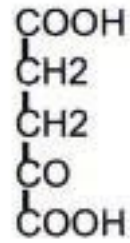
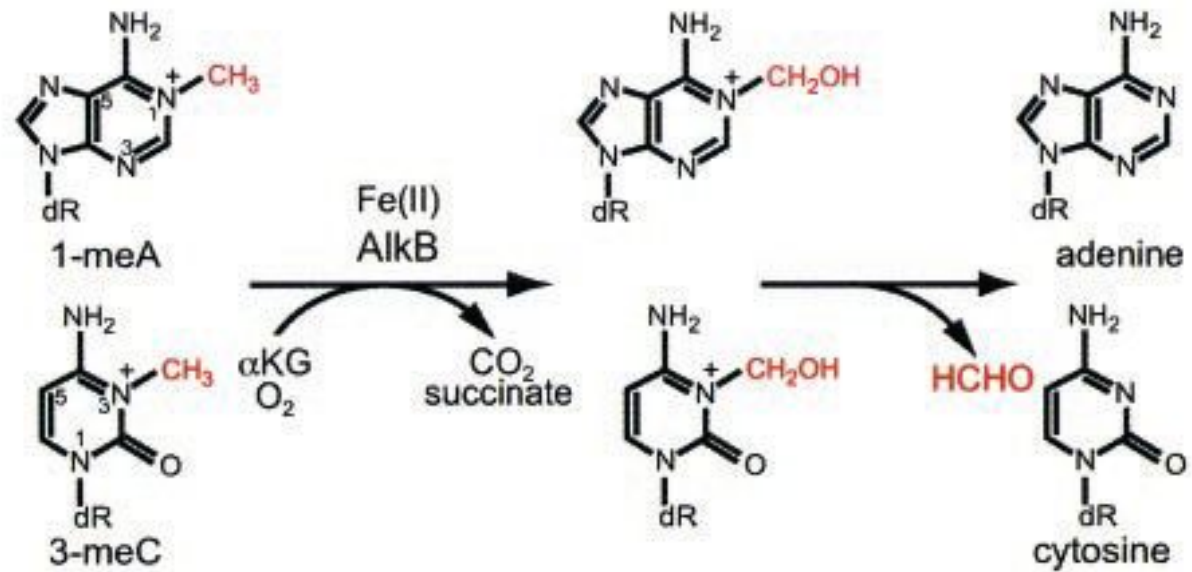


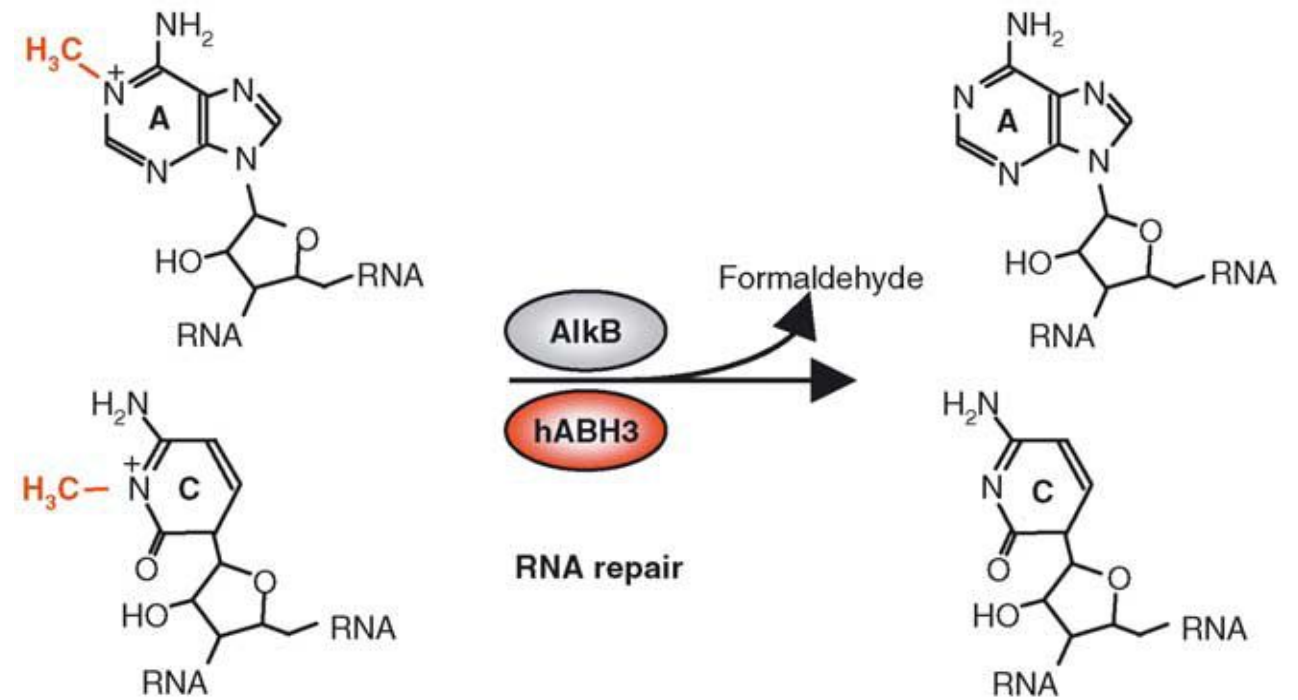
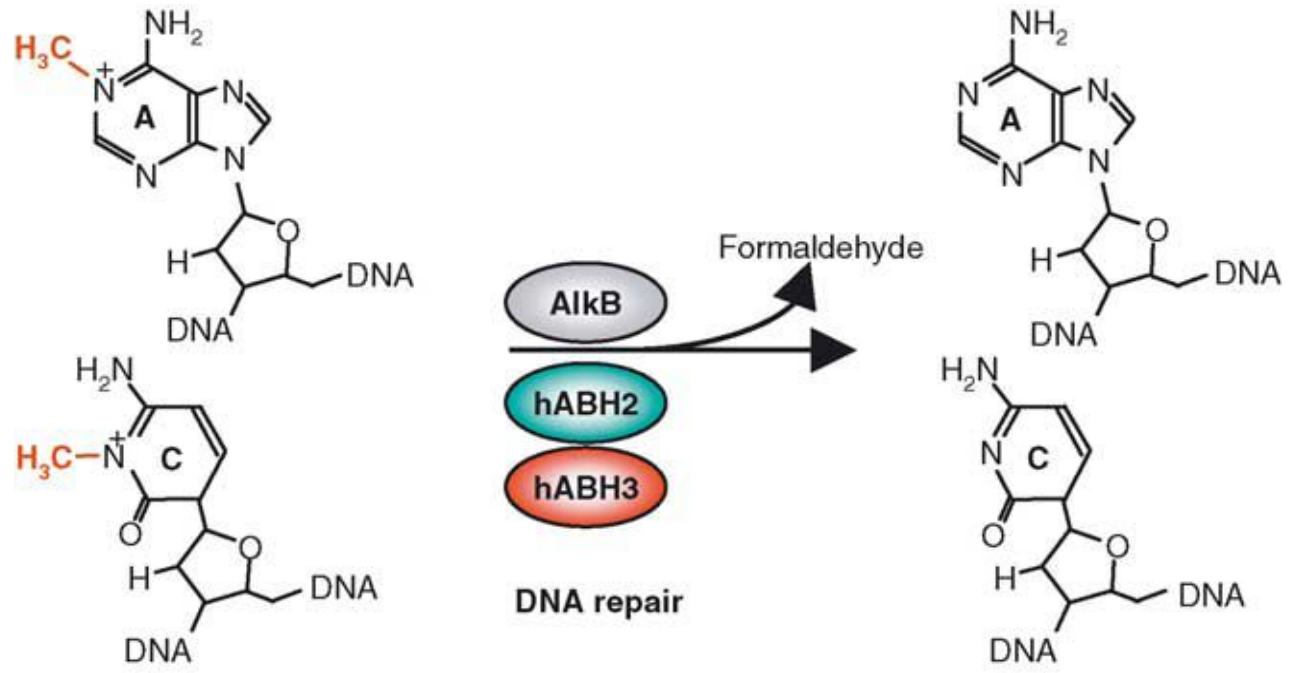
MMR

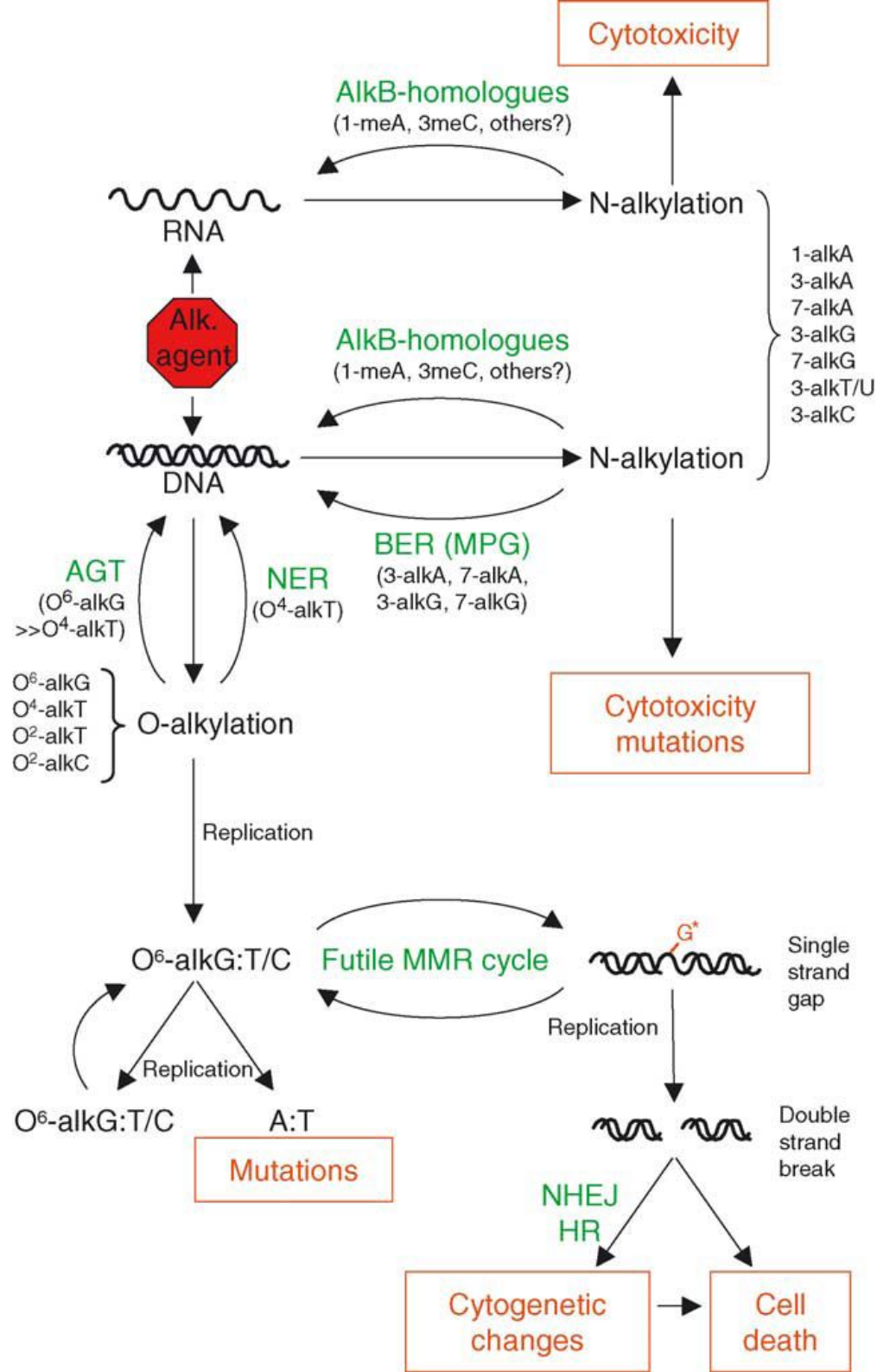






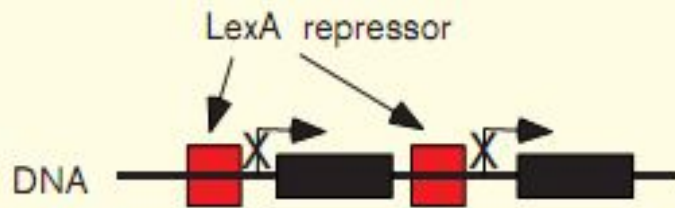
A.**B.**





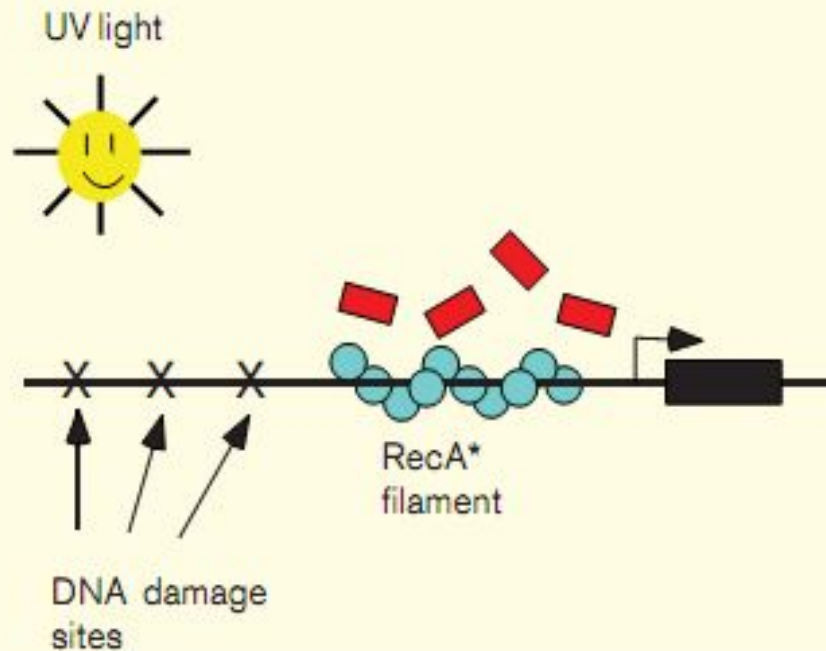
SOS

(a) SOS System off

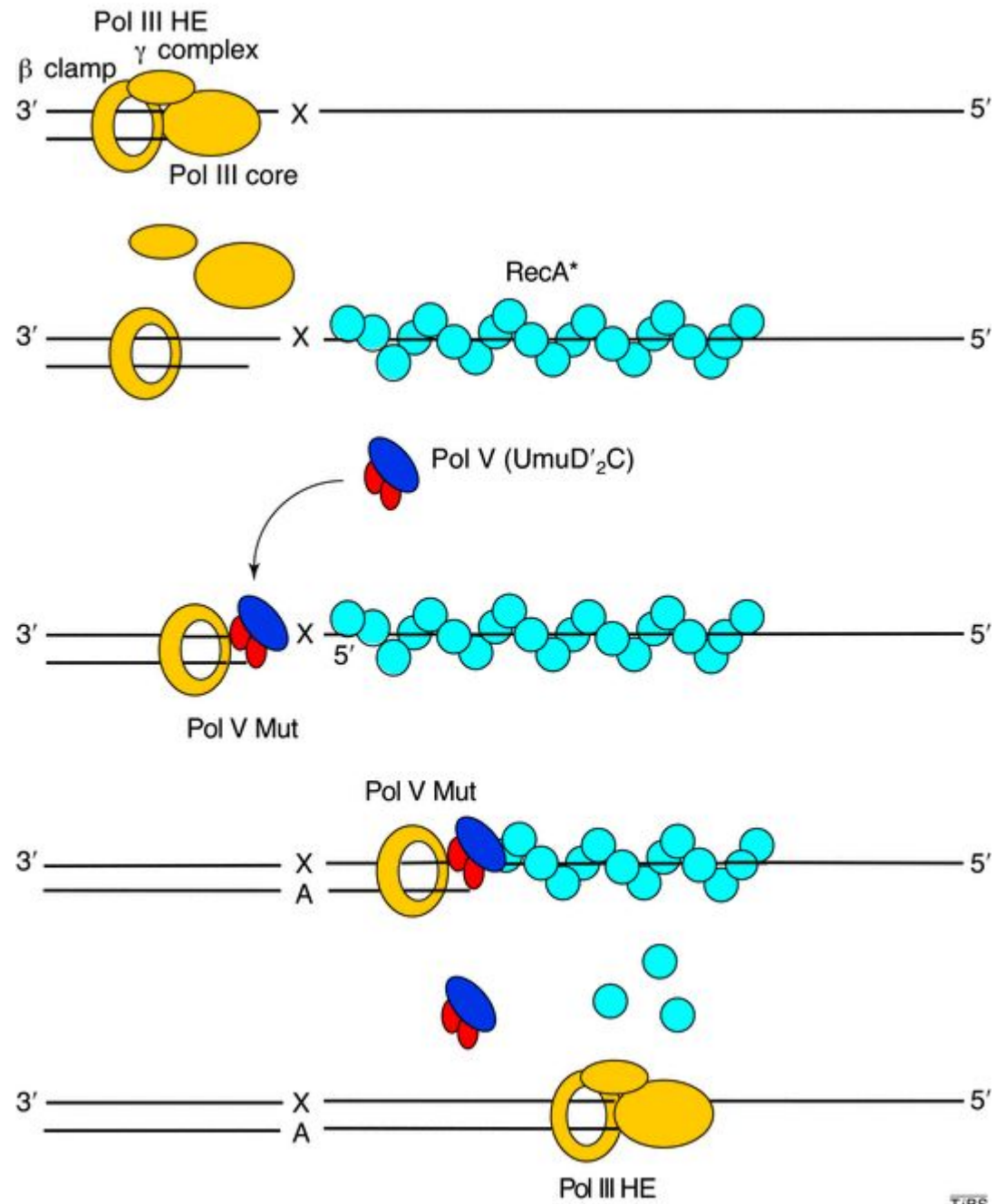


SOS genes repressed by LexA protein

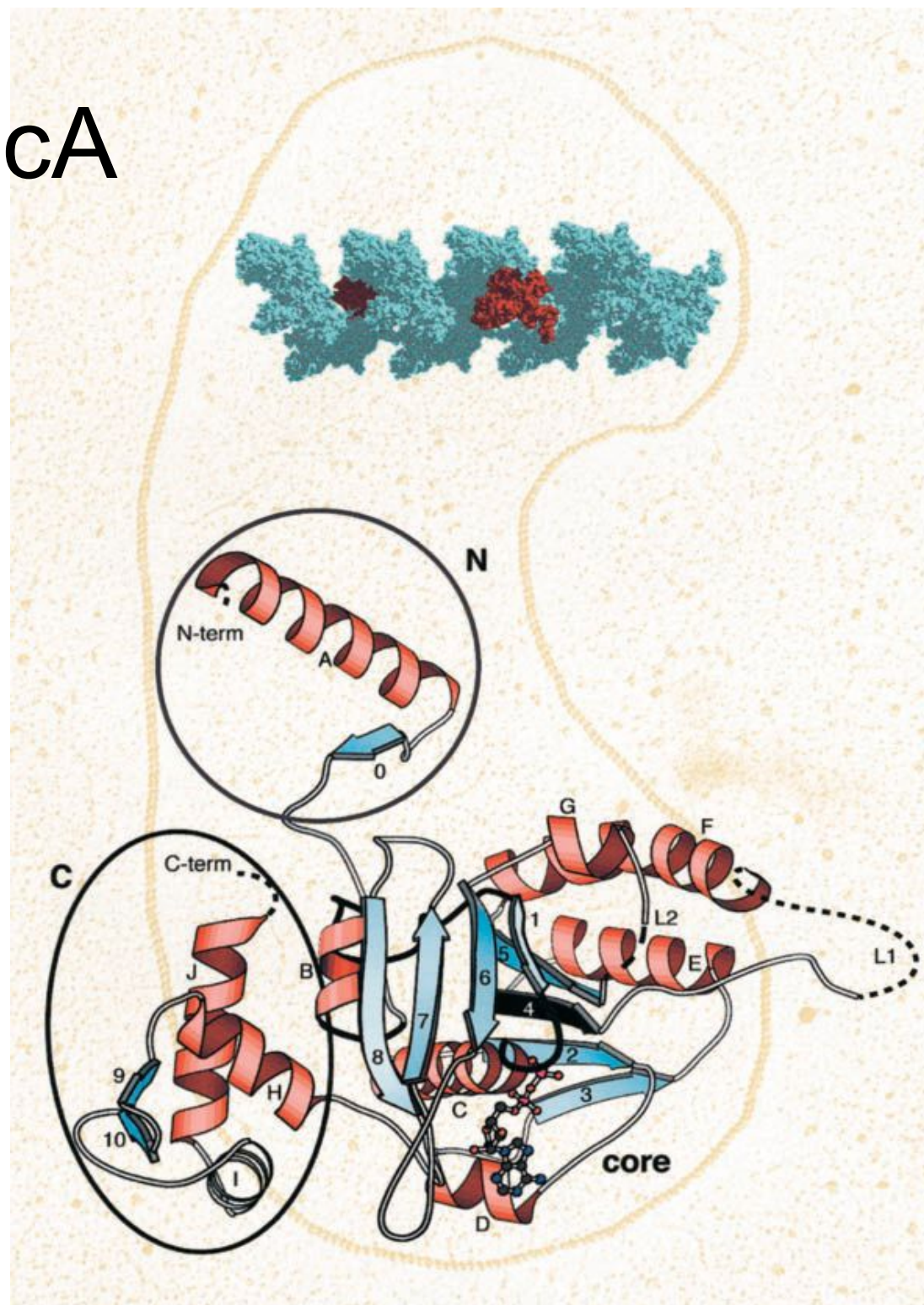
(b) SOS System On



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

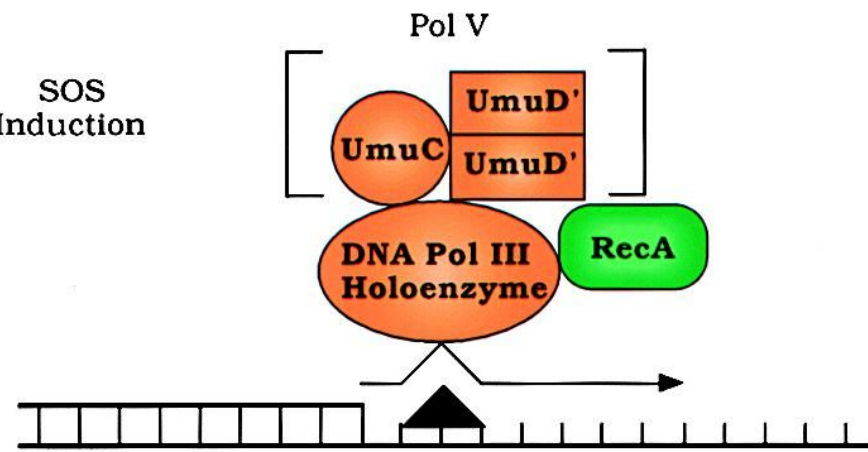


RecA

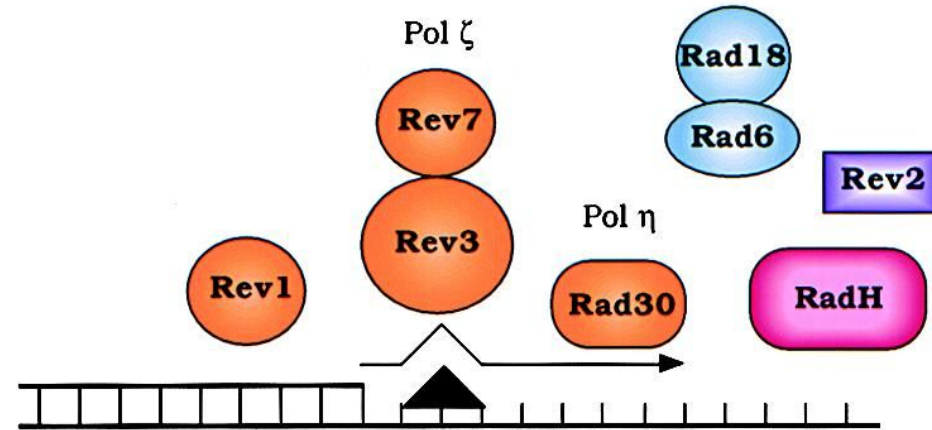


A.

SOS
Induction

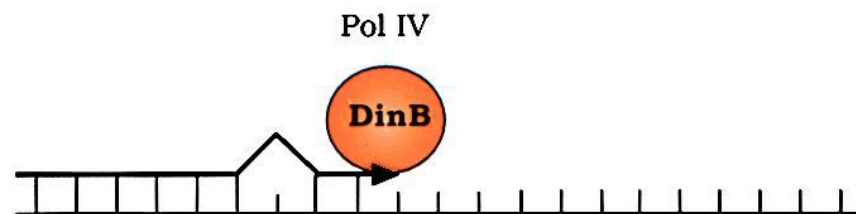


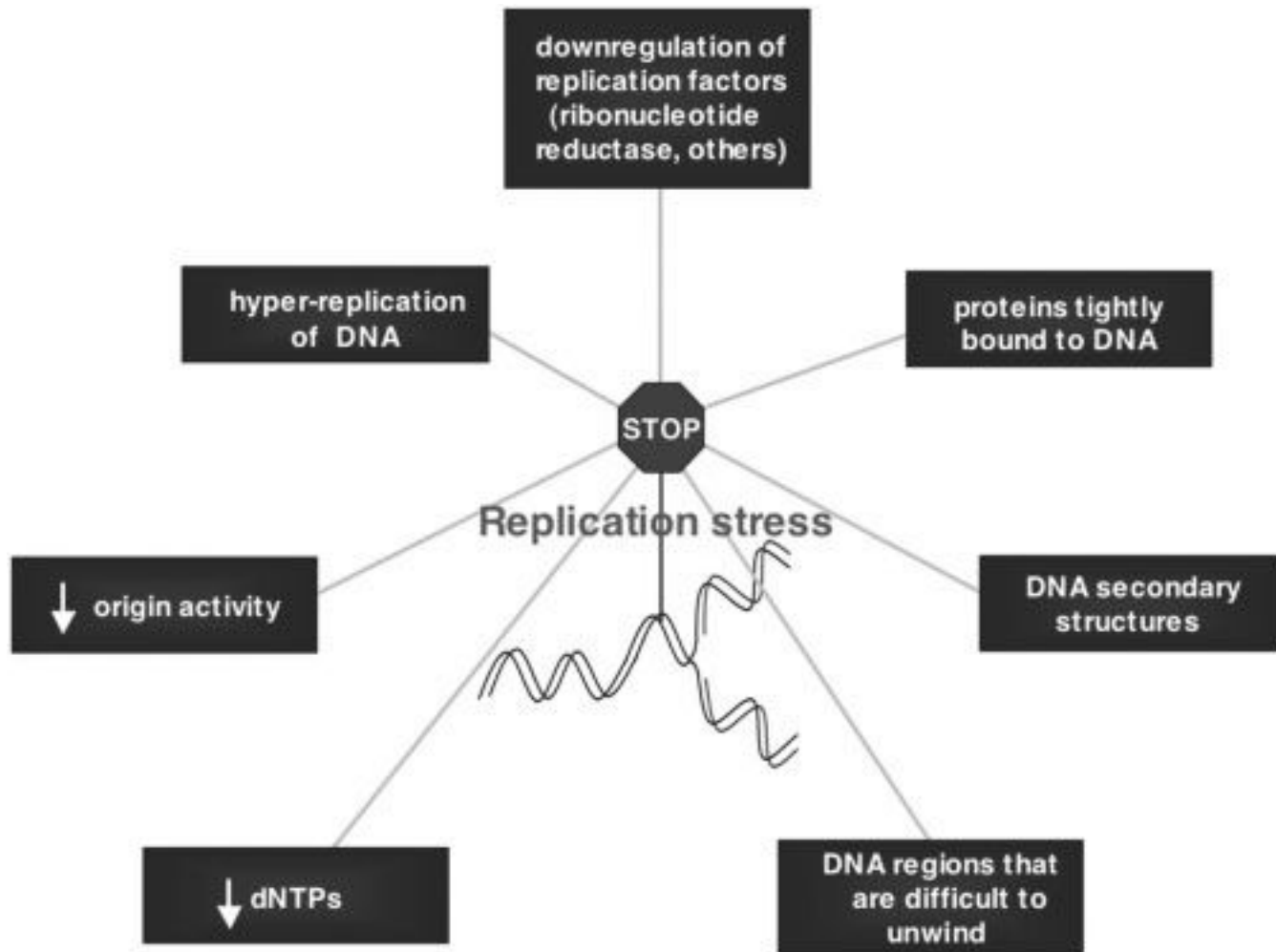
B.



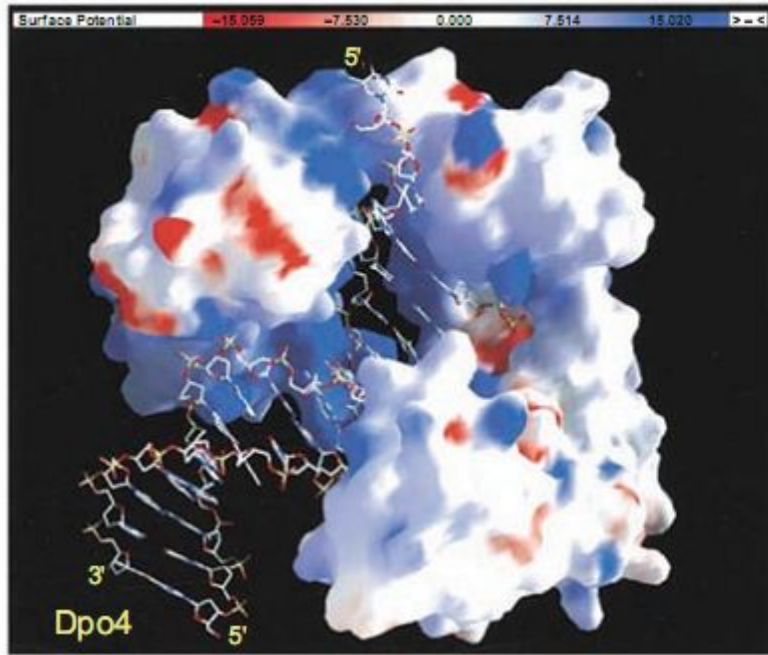
C.

SOS
Induction





A



B

