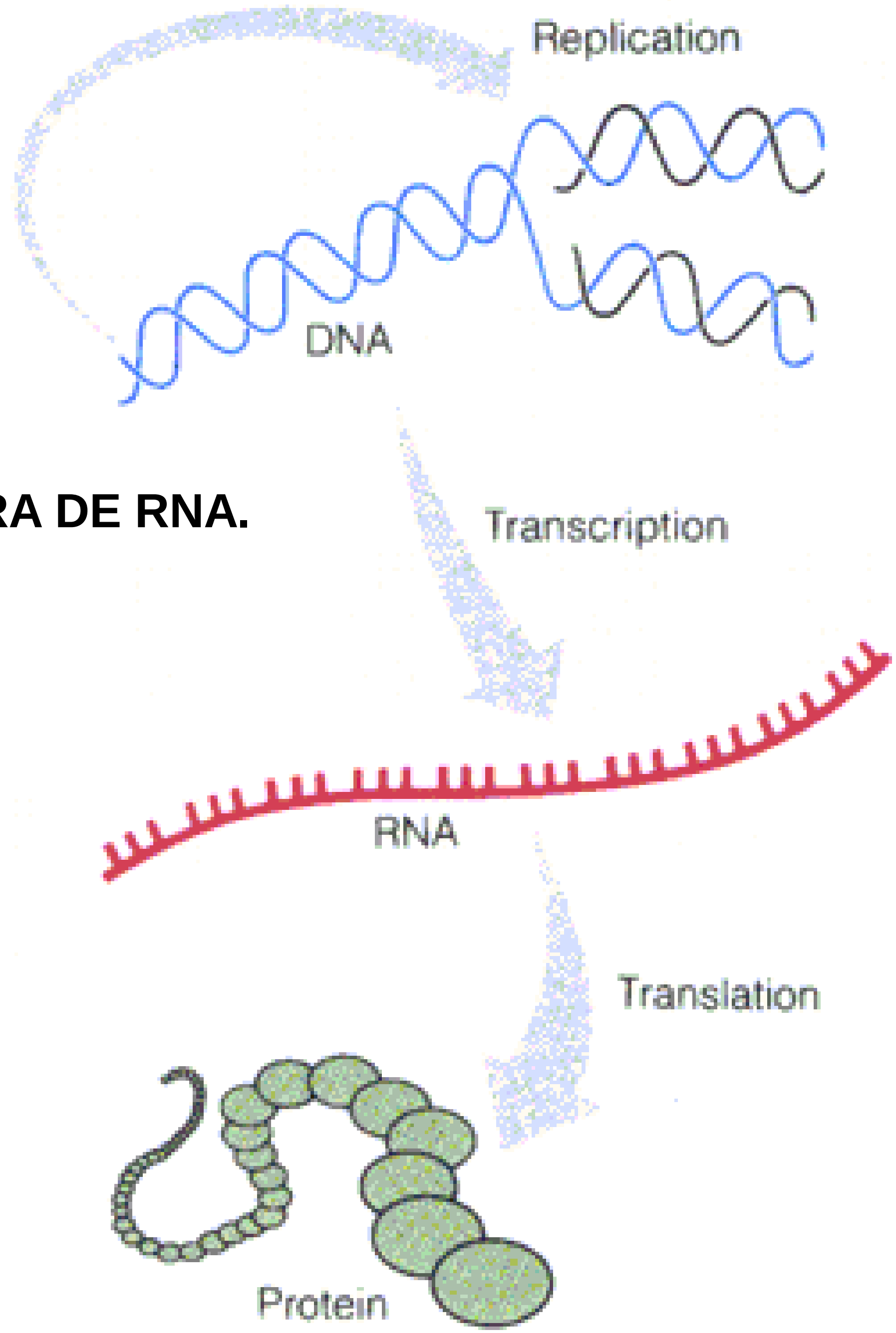
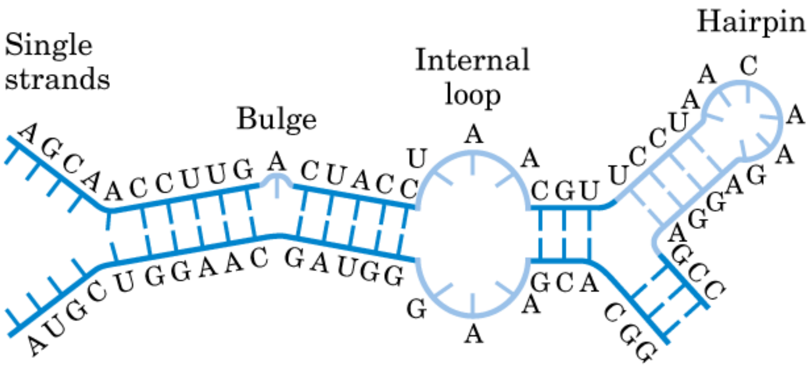
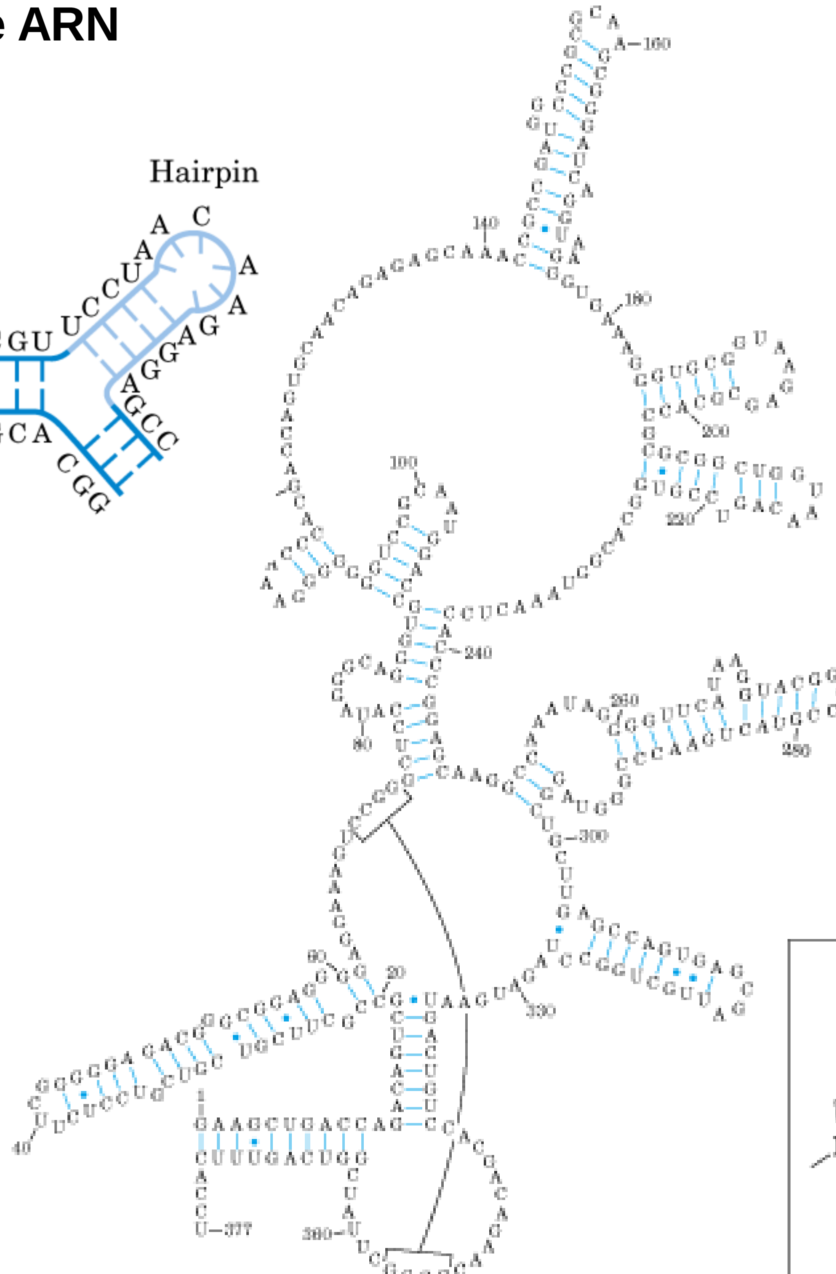
ACIDOS NUCLEICOS: ESTRUCTURA DE RNA.

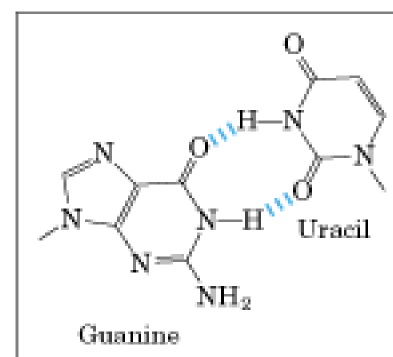


Estructura secundaria de ARN

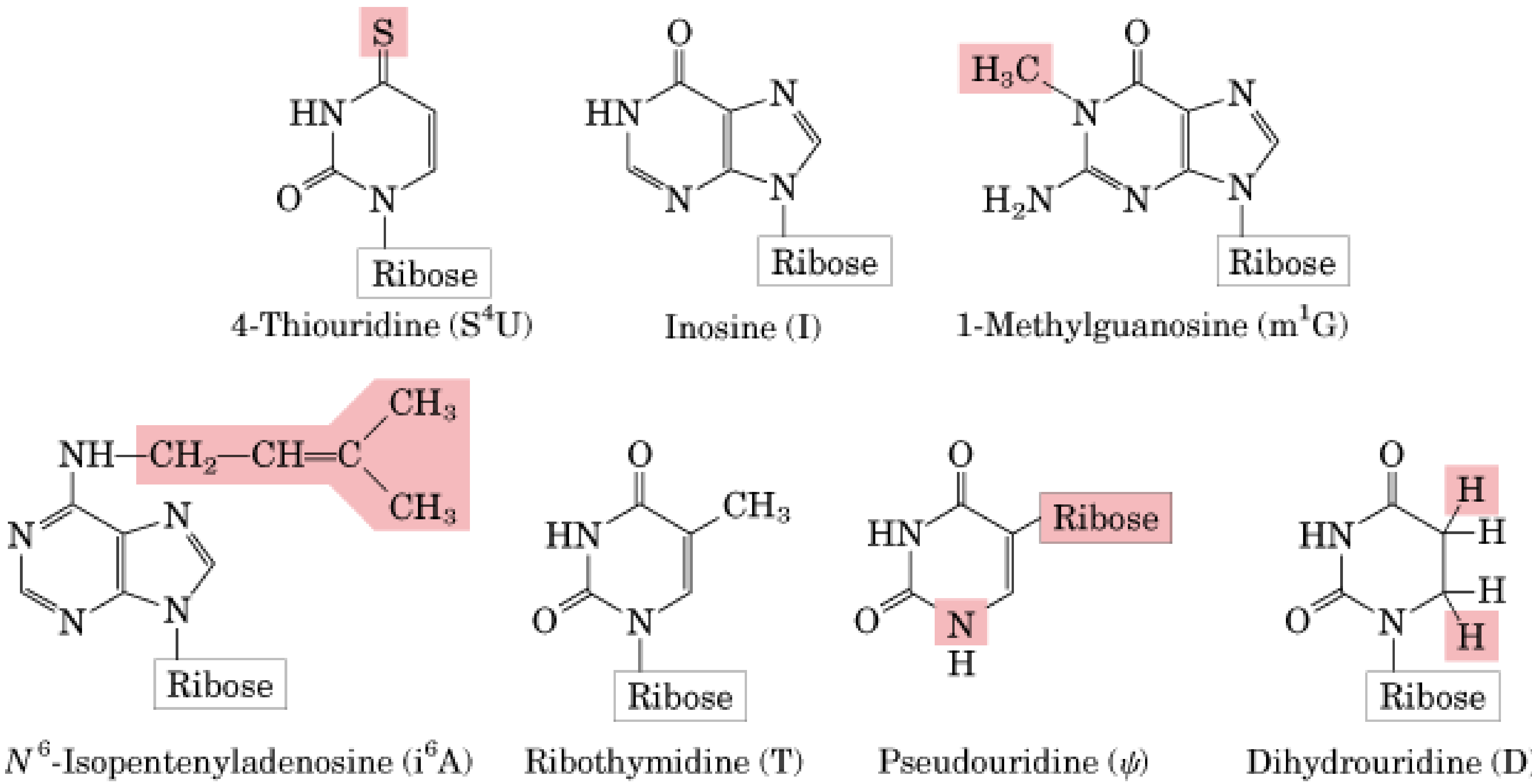


(a)





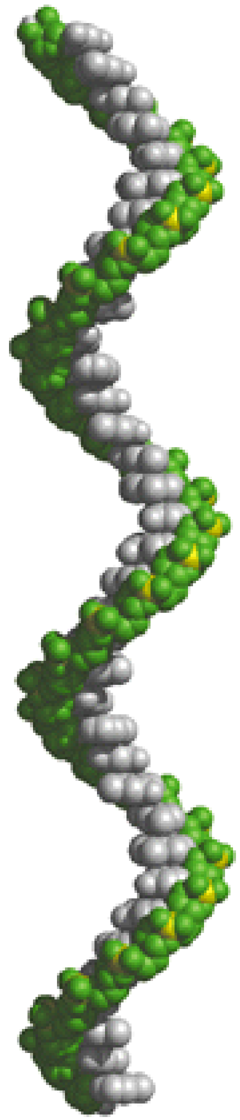
Otras bases nitrogenadas presentes en ARN

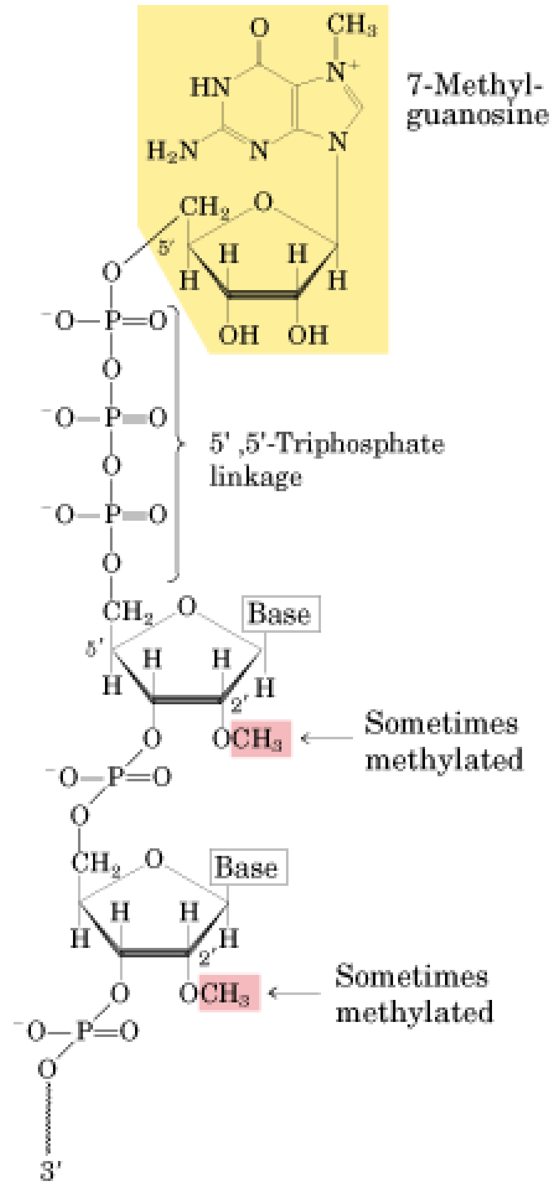


Las bases son modificadas en reacciones postranscripcionales

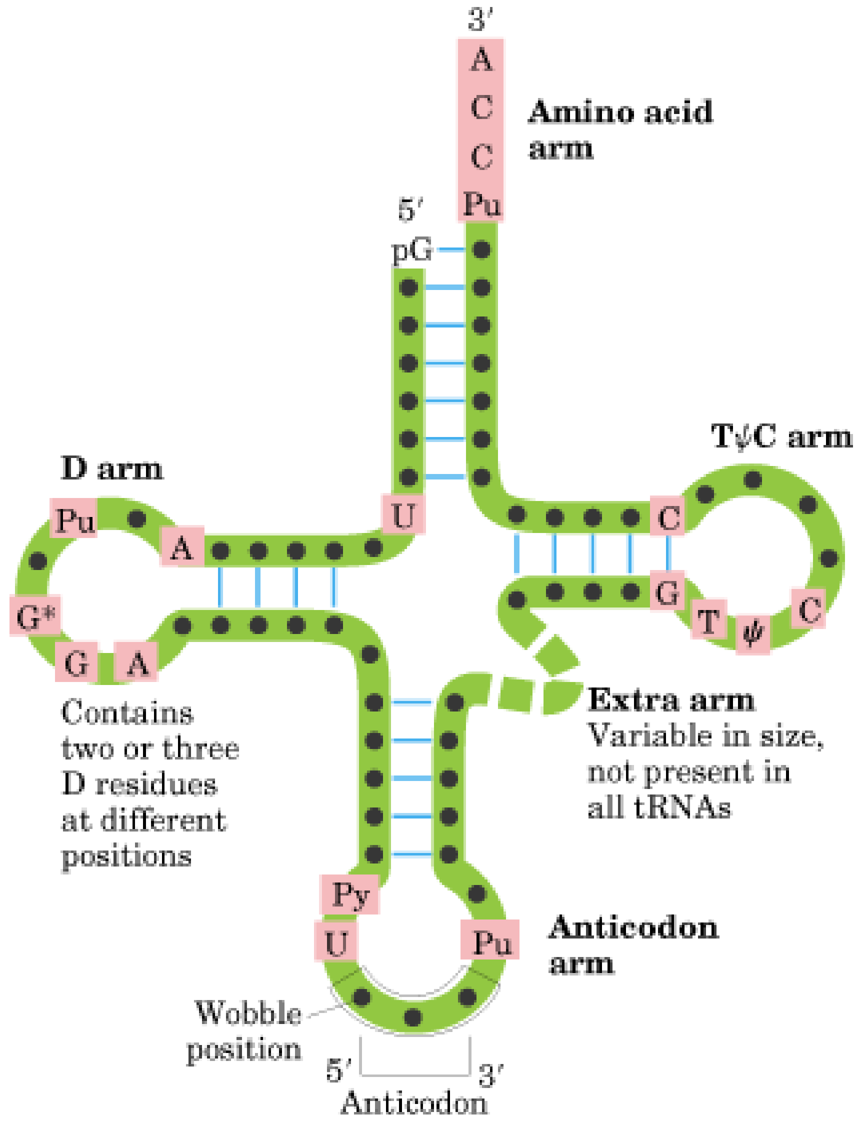
ARNm

5'cap del ARN_m



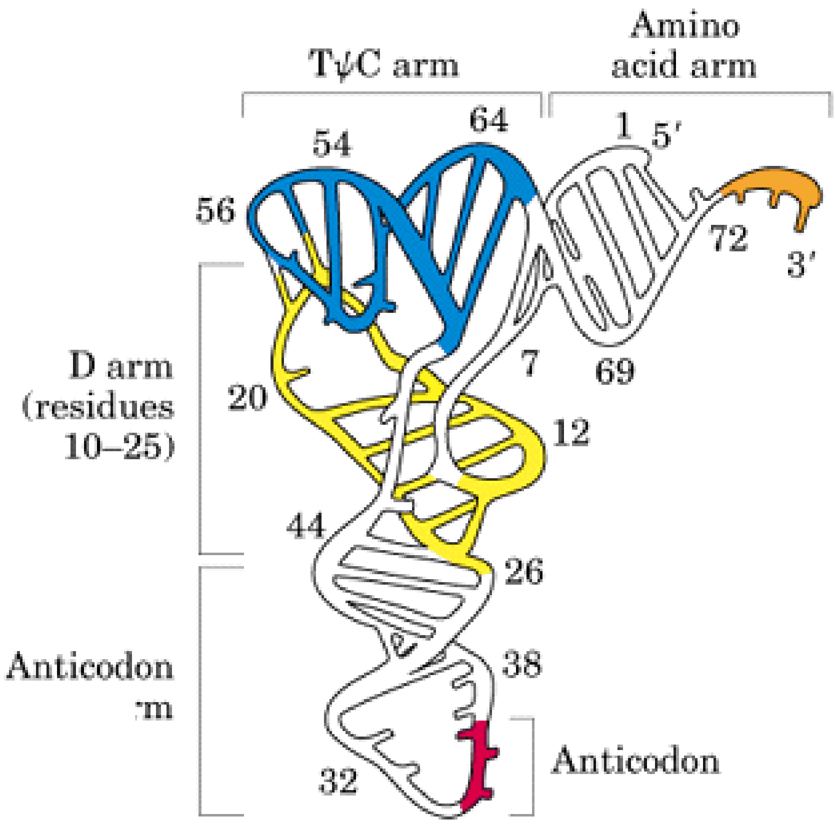


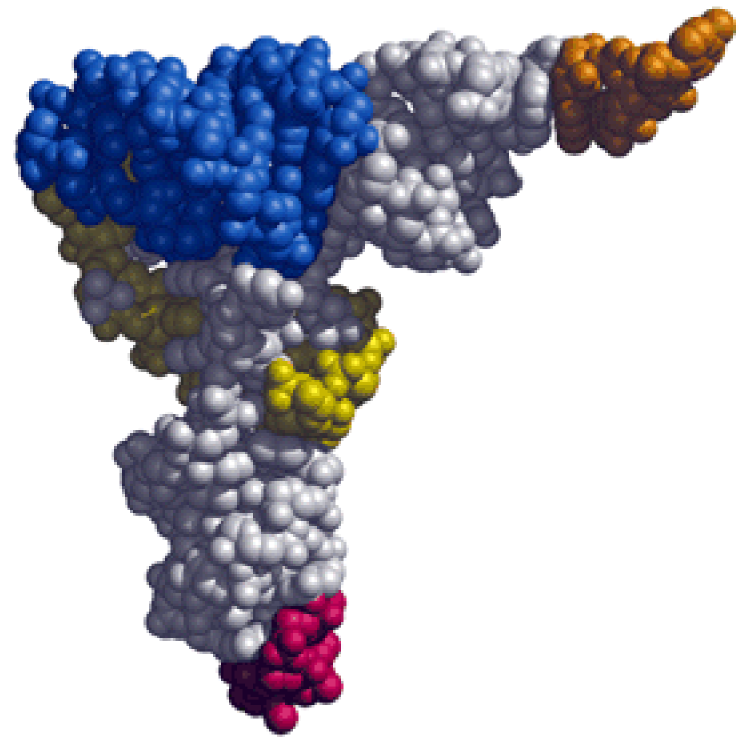
ARN$_t$



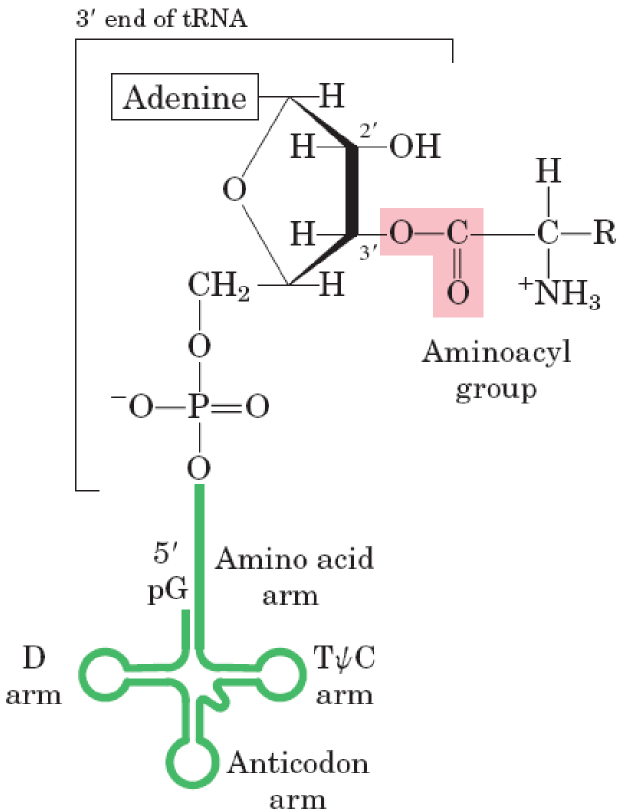
General cloverleaf secondary structure of tRNAs. The large dots on the backbone represent nucleotide residues; the blue lines represent base pairs. Characteristic and/or invariant residues common to all tRNAs are shaded in pink. Transfer RNAs vary in length from 73 to 93 nucleotides. Extra nucleotides occur in the extra arm or in the D arm. At the end of the anticodon arm is the anticodon loop, which always contains seven unpaired nucleotides. The D arm contains two or three D (5,6-dihydrouridine) residues, depending on the tRNA. In some tRNAs, the D arm has only three hydrogen-bonded base pairs.

Estructura tridimensional de un ARN$_t$





Estructura general y forma de unión un aminoácido al extremo 3' terminal de un ARN_t



Aminoacil ARN_t sintetasas

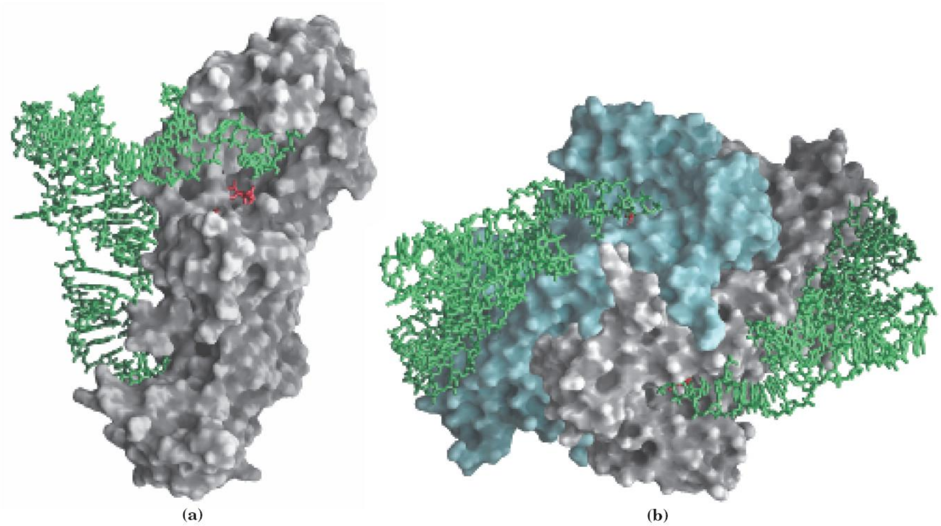
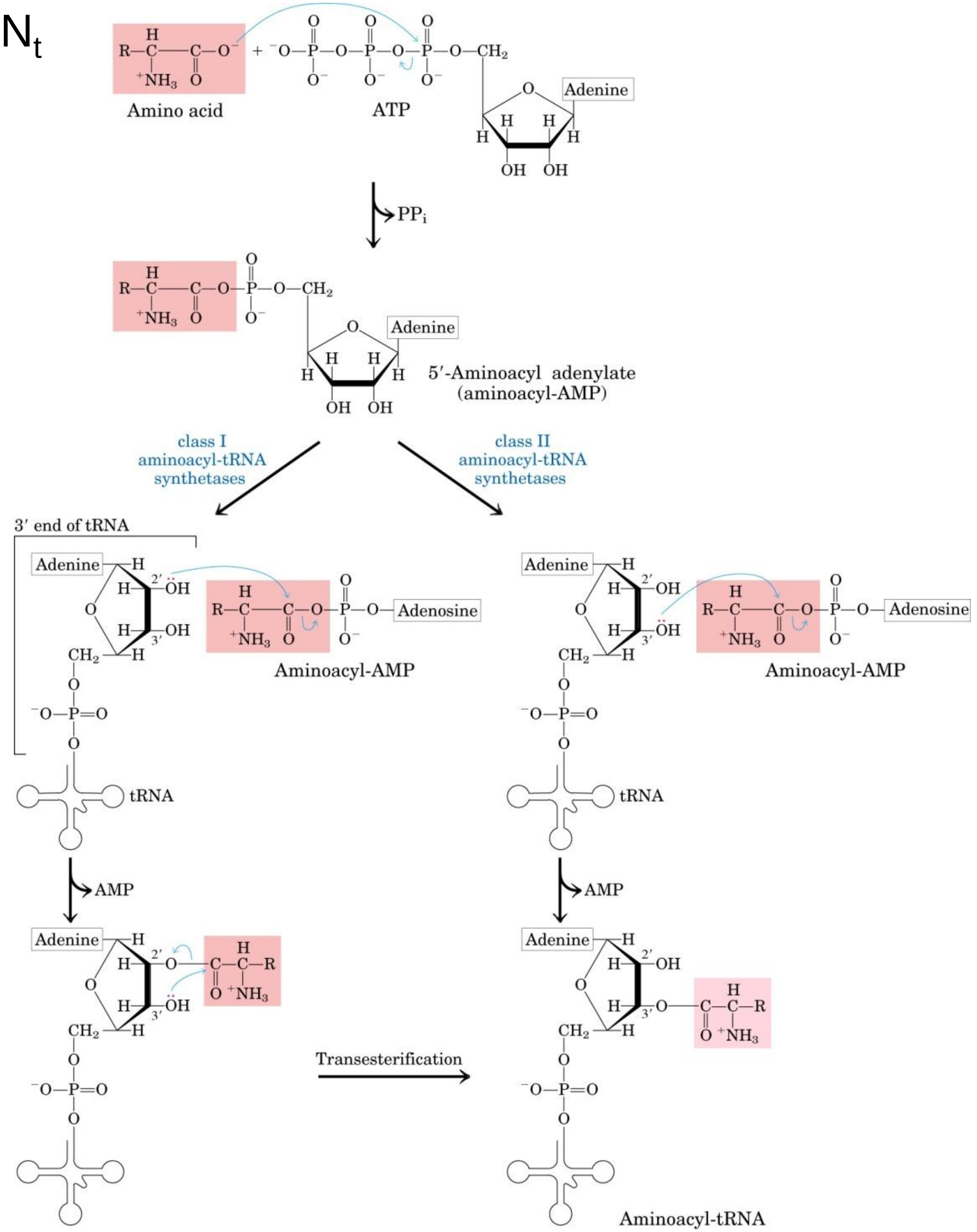


FIGURE 27–17 Aminoacyl-tRNA synthetases. Both synthetases are complexed with their cognate tRNAs (green stick structures). Bound ATP (red) pinpoints the active site near the end of the aminoacyl arm. **(a)** Gln-tRNA synthetase from *E. coli,* a typical monomeric type I synthetase (PDB ID 1QRT). **(b)** Asp-tRNA synthetase from yeast, a typical dimeric type II synthetase (PDB ID 1ASZ).

Mecanismo de aminoacilación de ARN$_t$ Catalizado por ARN$_t$sintetasas

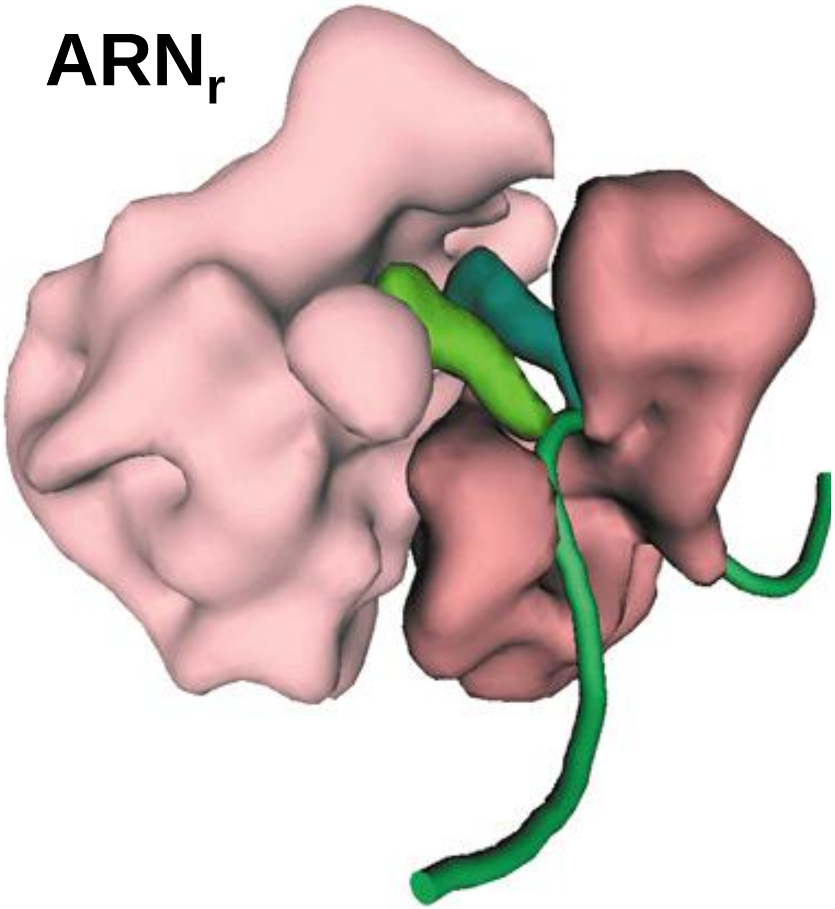


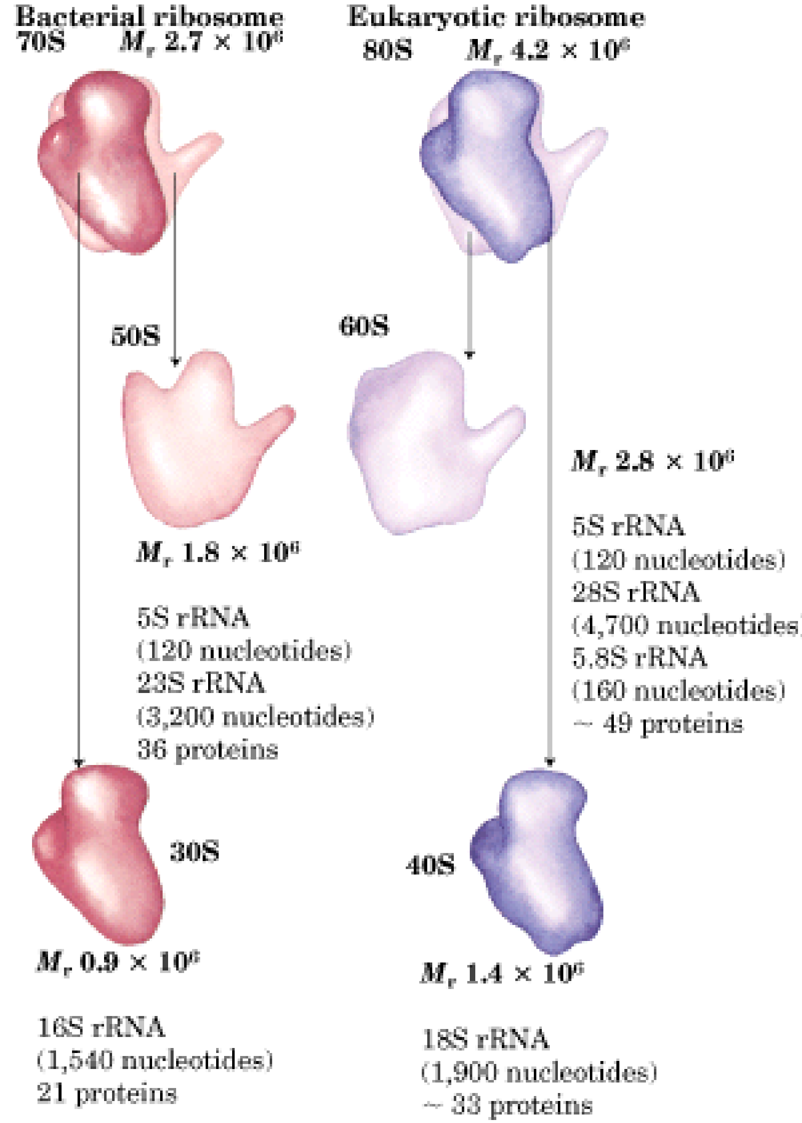
Two Classes of Aminoacyl-tRNA Synthetases*

Class I	Class II
Arg	Ala
Cys	Asn
Gln	Asp
Glu	Gly
Ile	His
Leu	Lys
Met	Phe
Trp	Pro
Tyr	Ser
Val	Thr

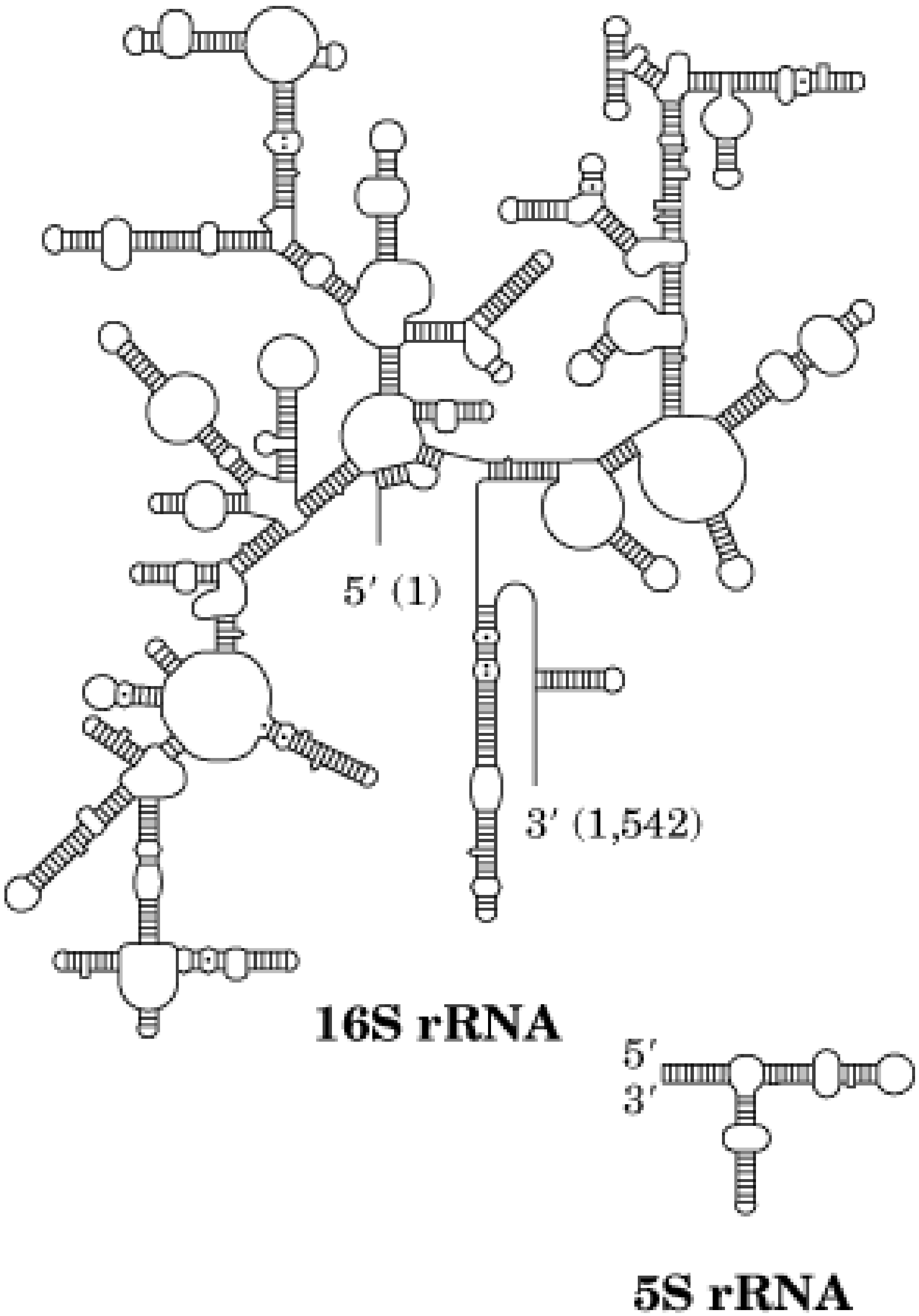
*Here, Arg represents arginyl-tRNA synthetase, and so forth. The classification applies to all organisms for which tRNA synthetases have been analyzed and is based on protein structural distinctions and on the mechanistic distinction outlined in Figure 27–16.

ARN$_r$

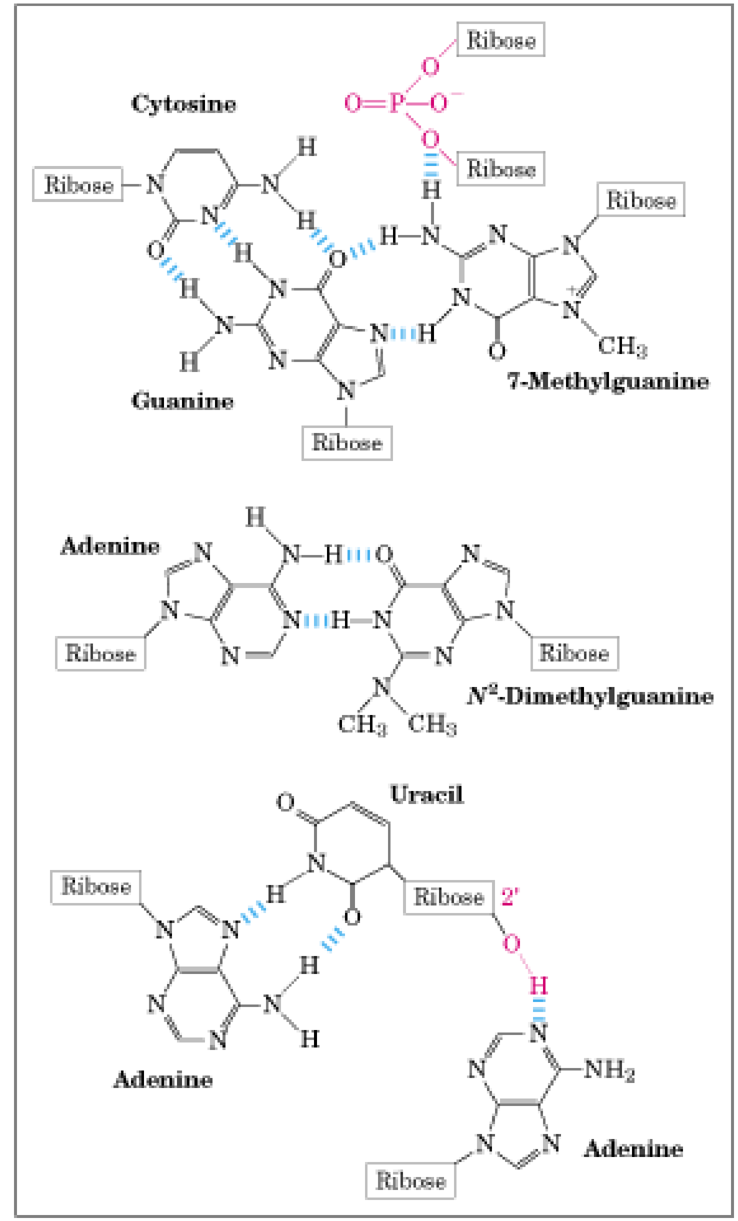



Bacterial ribosome
70S M_r 2.7 × 10^6
50S
M_r 1.8 × 10^6
5S rRNA
(120 nucleotides)
23S rRNA
(3,200 nucleotides)
36 proteins
30S
M_r 0.9 × 10^6
16S rRNA
(1,540 nucleotides)
21 proteins
Eukaryotic ribosome
80S M_r 4.2 × 10^6
60S
M_r 2.8 × 10^6
5S rRNA
(120 nucleotides)
28S rRNA
(4,700 nucleotides)
5.8S rRNA
(160 nucleotides)
~ 49 proteins
40S
M_r 1.4 × 10^6
18S rRNA
(1,900 nucleotides)
~ 33 proteins

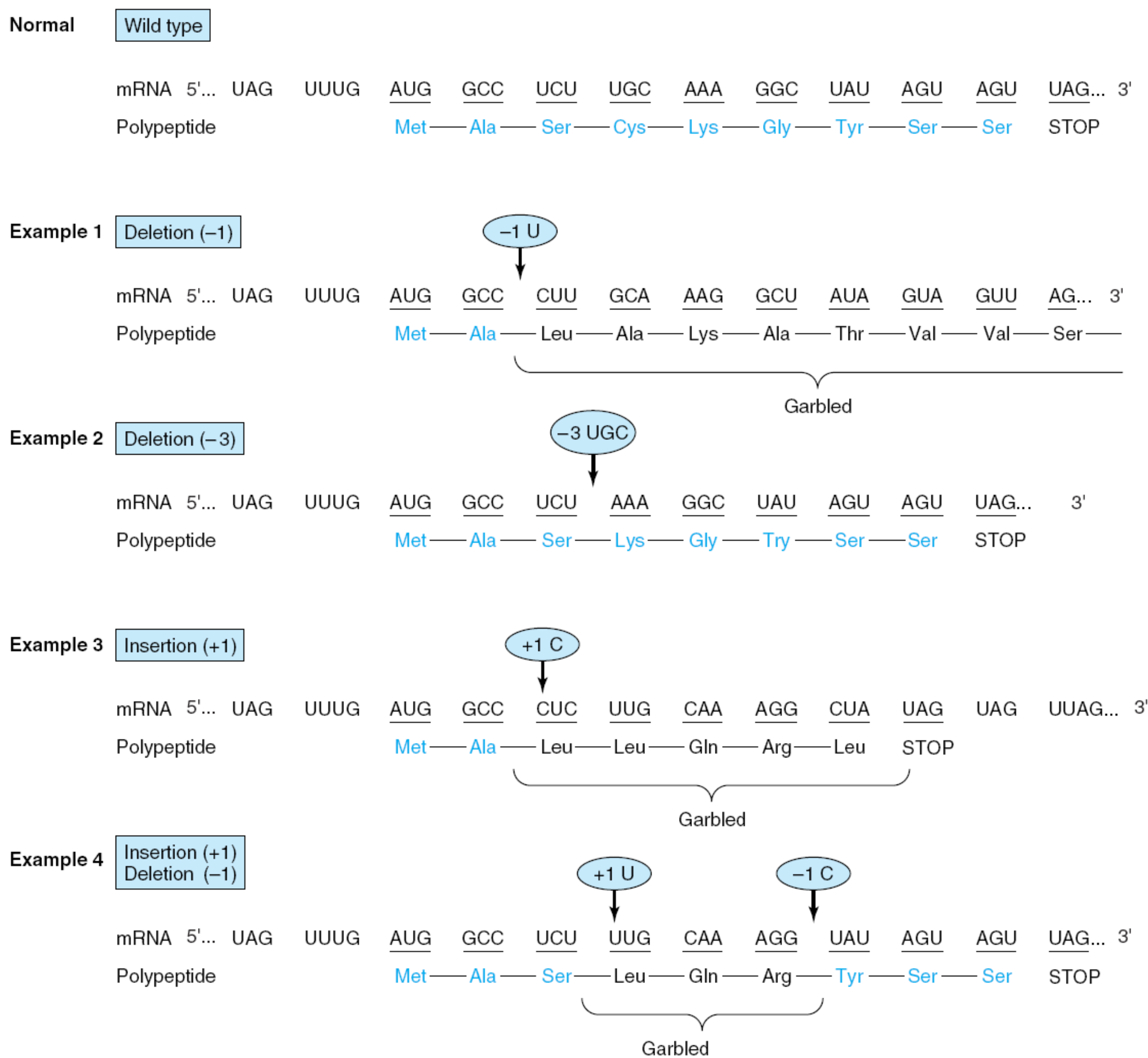
Estructura secundaria de ARN$_r$ bacterianos



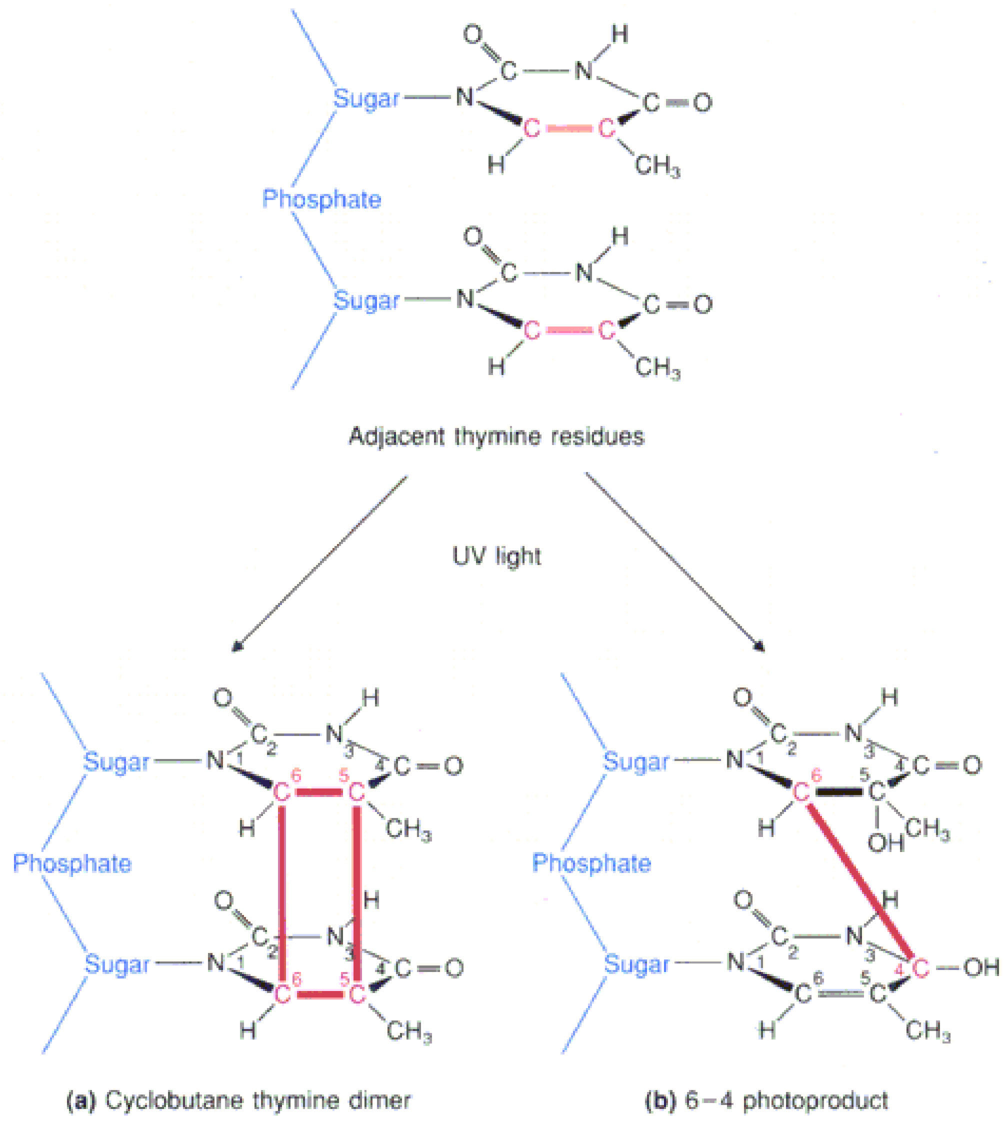
Algunos apareamientos encontrados en ARN$_r$

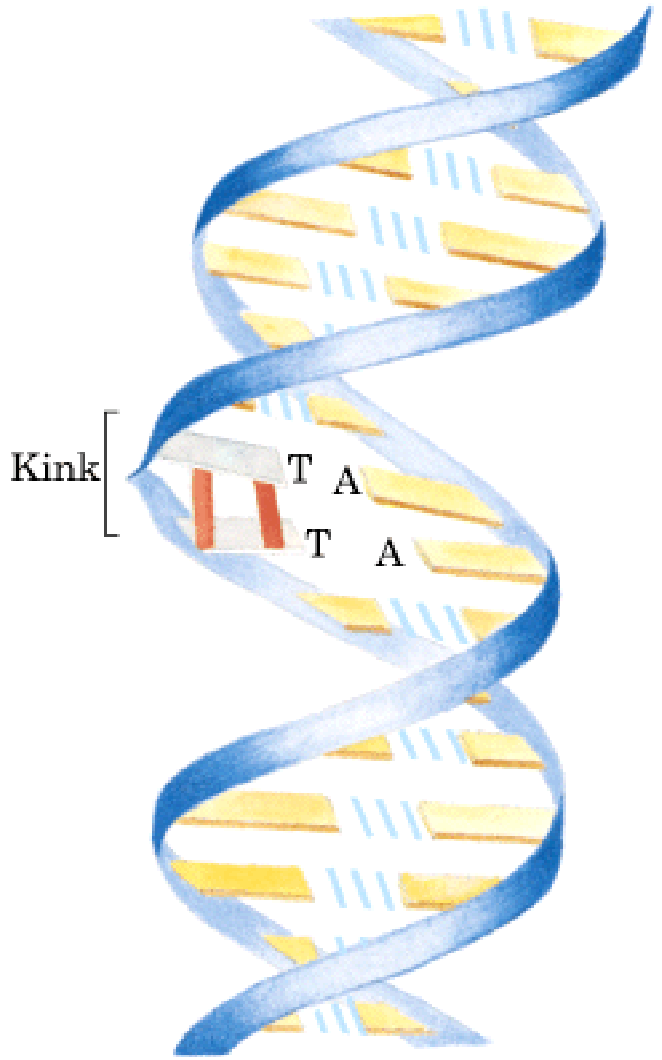


Mutaciones: su naturaleza molecular
Deleciones e inserciones

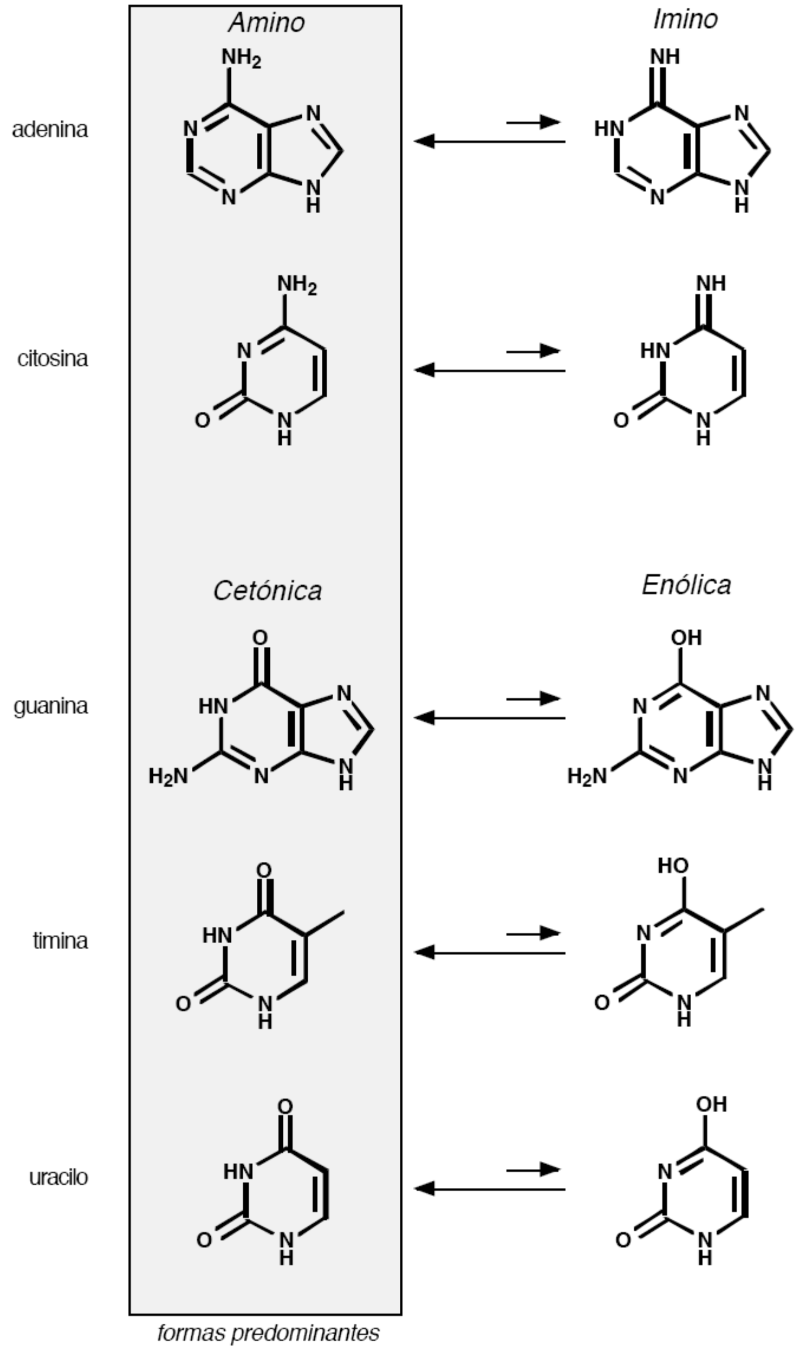


Agentes mutagénicos : Radiaciones
Formación de dímeros de timina

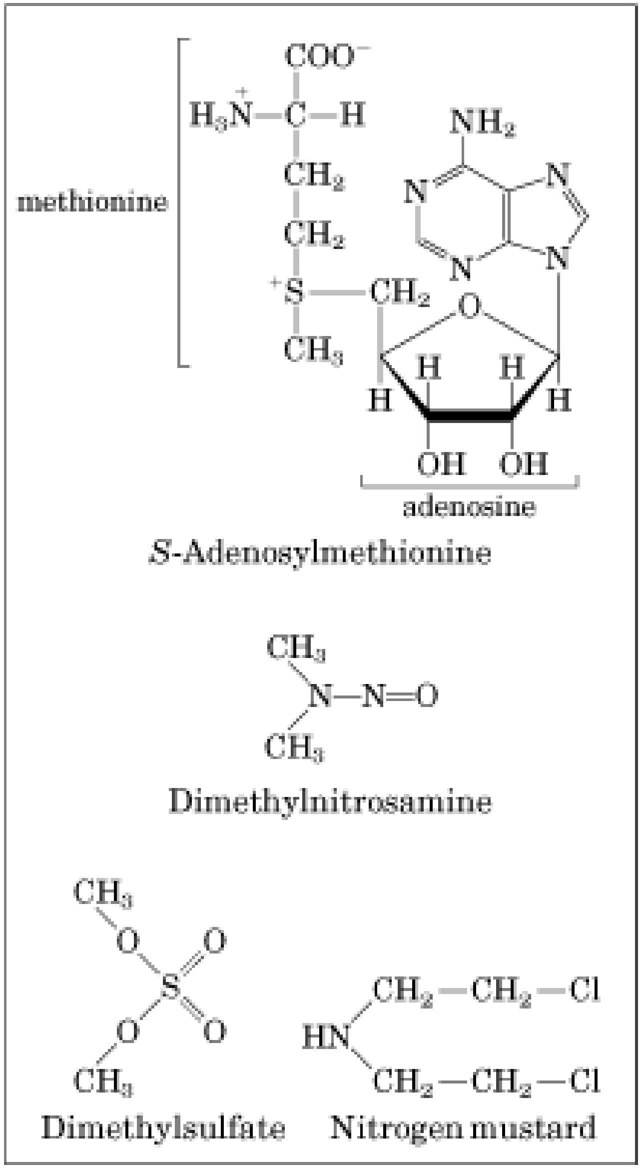


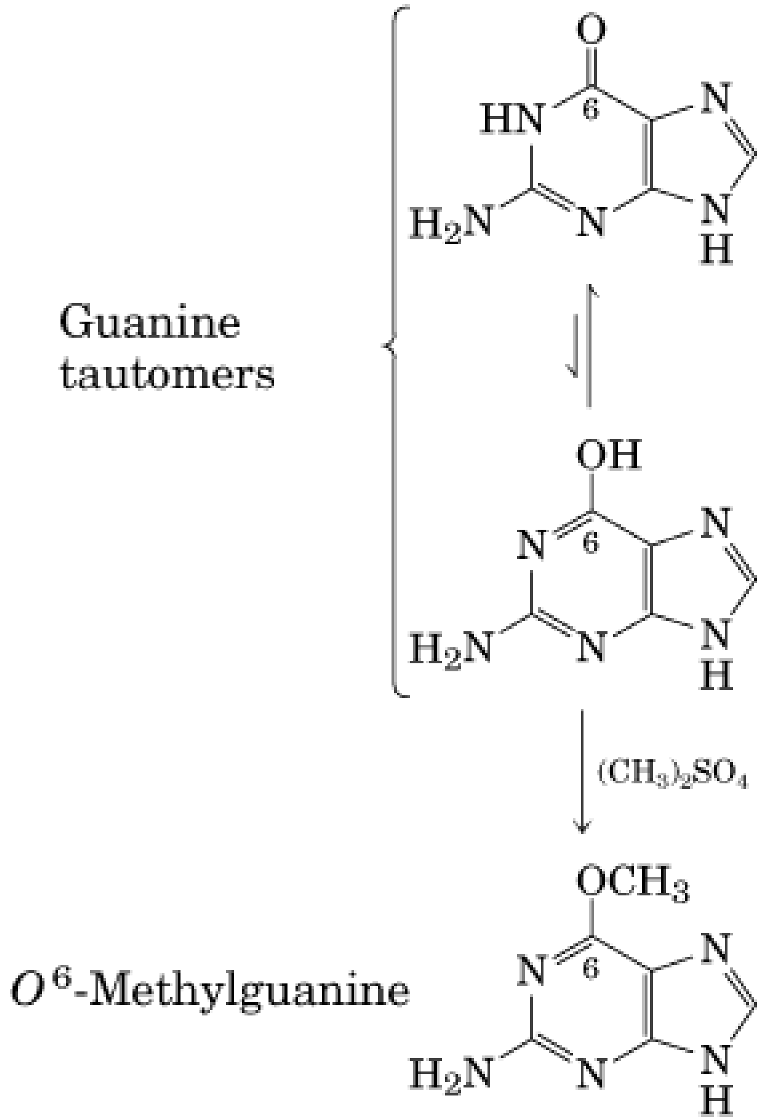


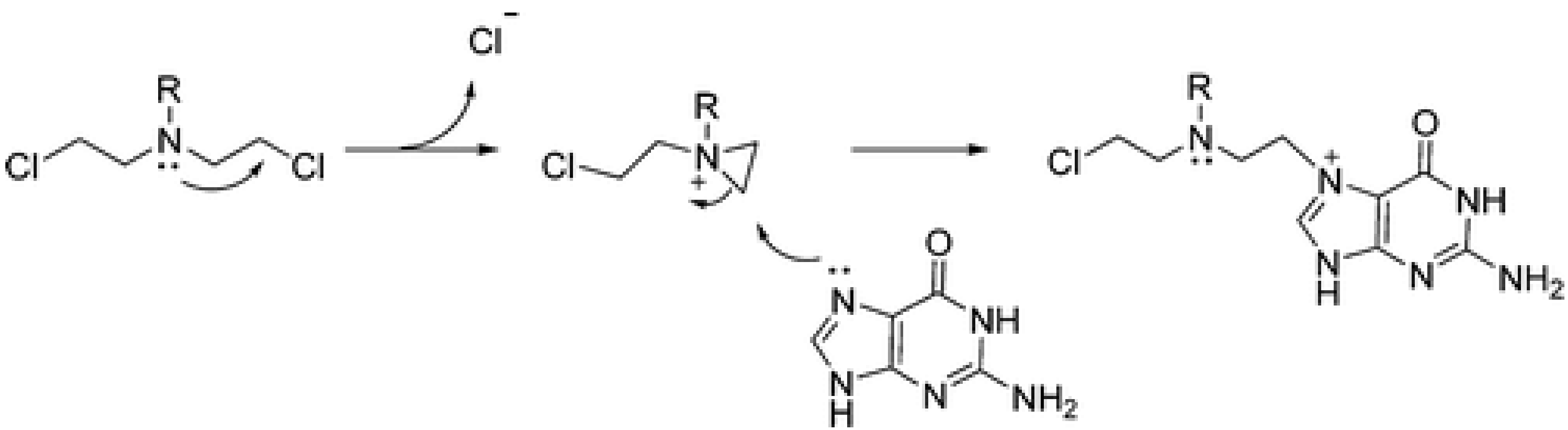
Formas tautómeras de las bases nitrogenadas

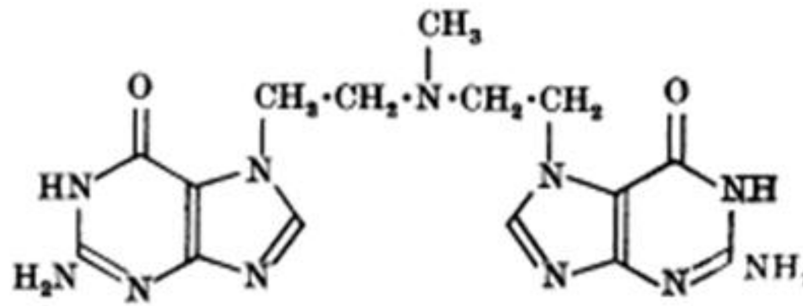


Agentes alquilantes

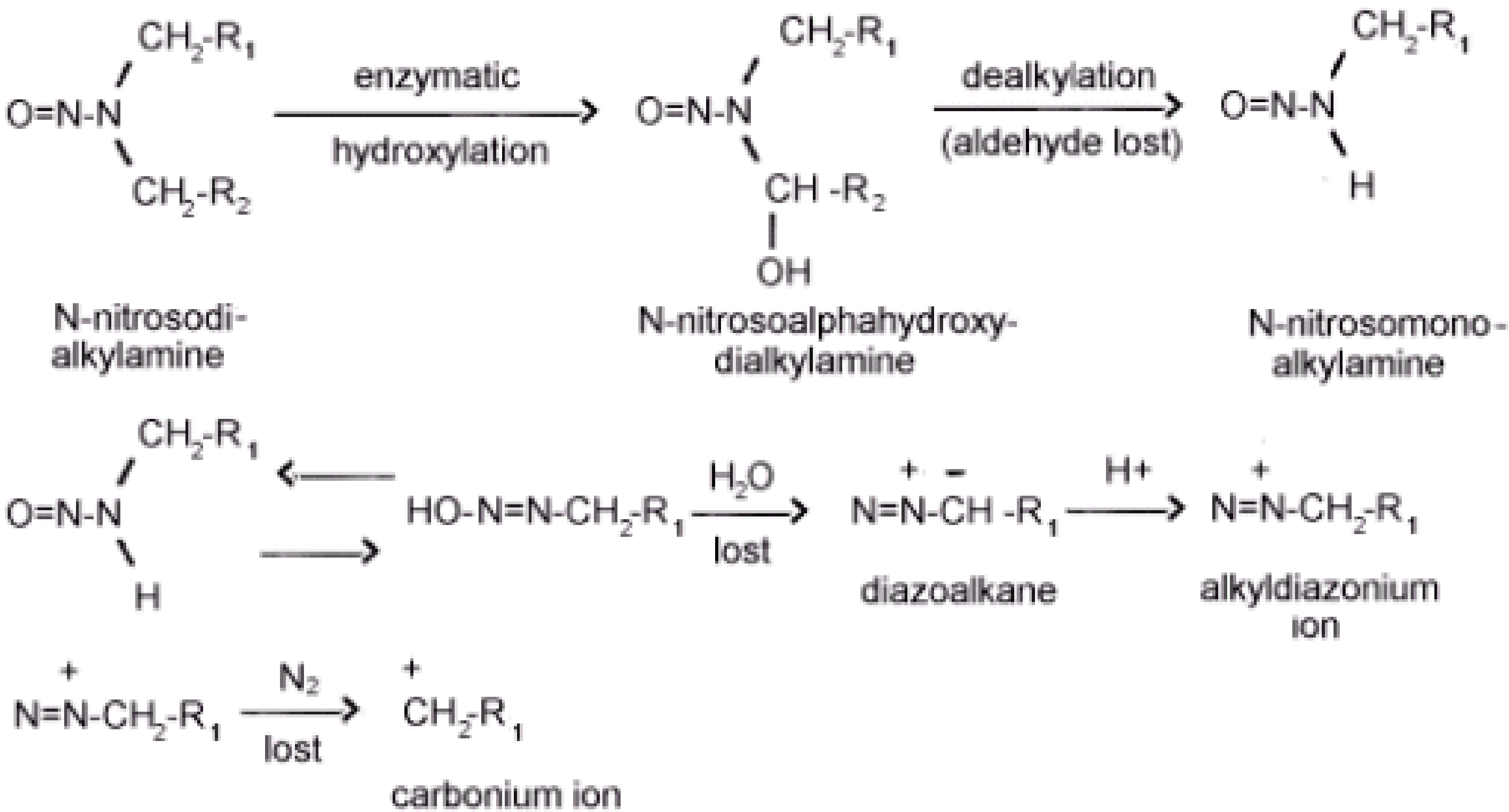


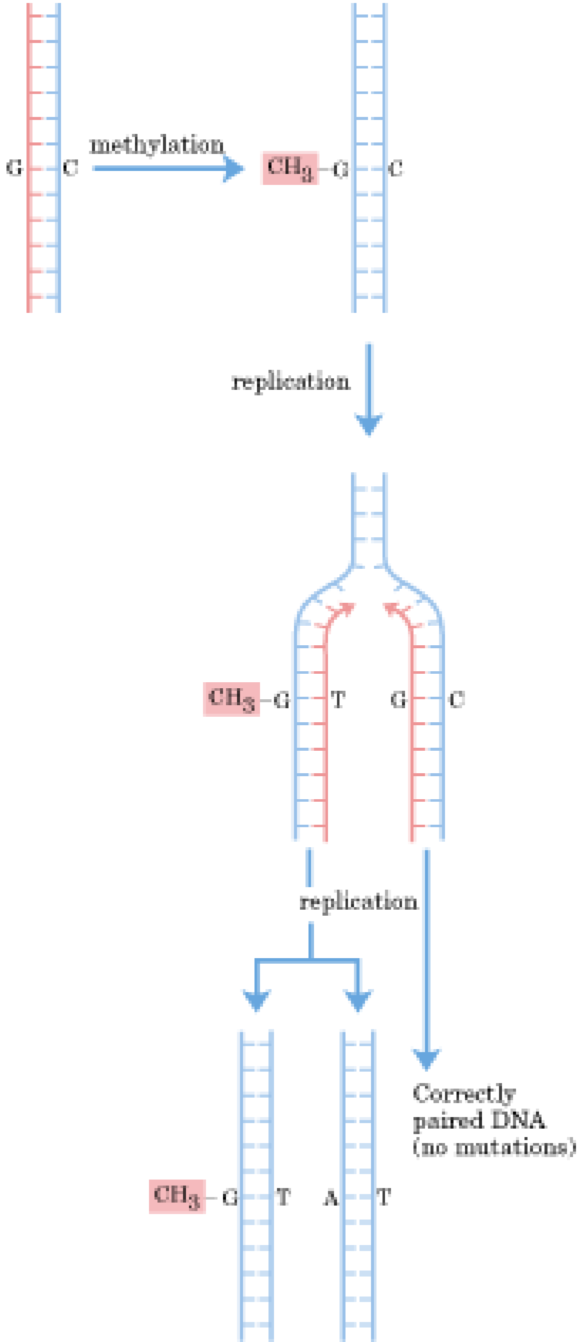


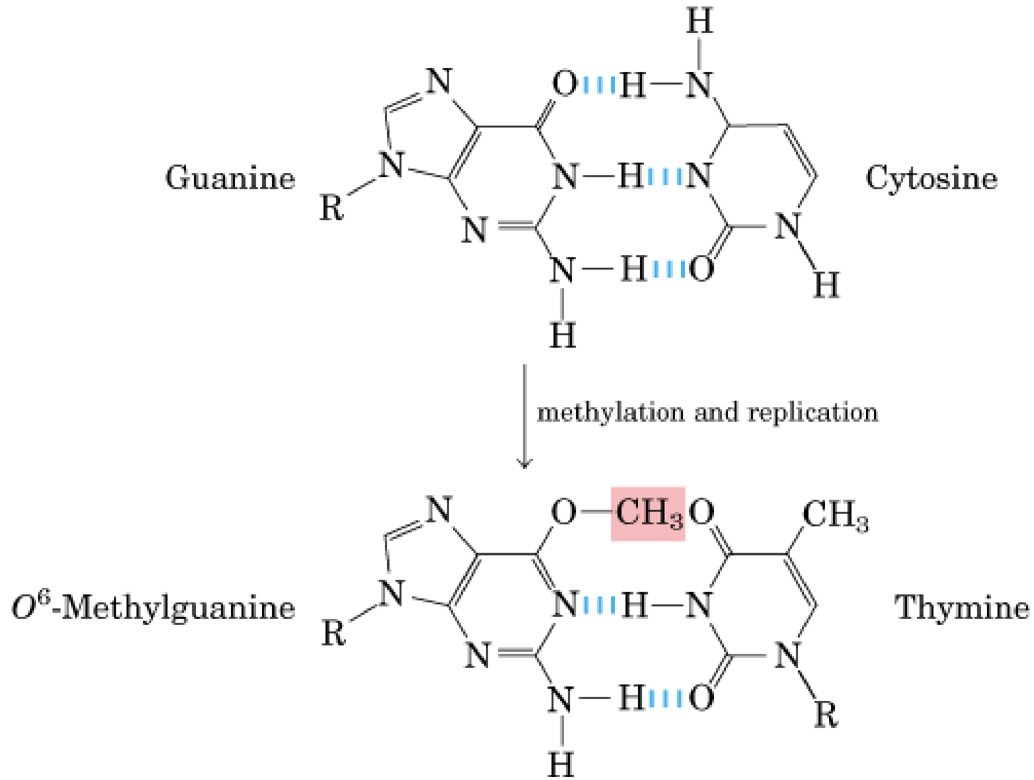




(II)


enzymatic
hydroxylation
dealkylation
(aldehyde lost)
N-nitrosodi-alkylamine
N-nitrosoalphahydroxy-dialkylamine
N-nitrosomono-alkylamine
H2O
lost
H+
diazoalkane
alkyldiazonium ion
N2
lost
carbonium ion


G
C
methylation
CH3–G
C
replication
CH3–G
T
G
C
replication
Correctly
paired DNA
(no mutations)
CH3–G
T
A
T

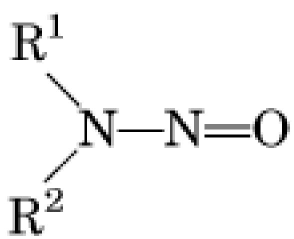

Guanine
Cytosine
methylation and replication
O6-Methylguanine
Thymine

(a)

Desaminación de bases: ácido nitroso

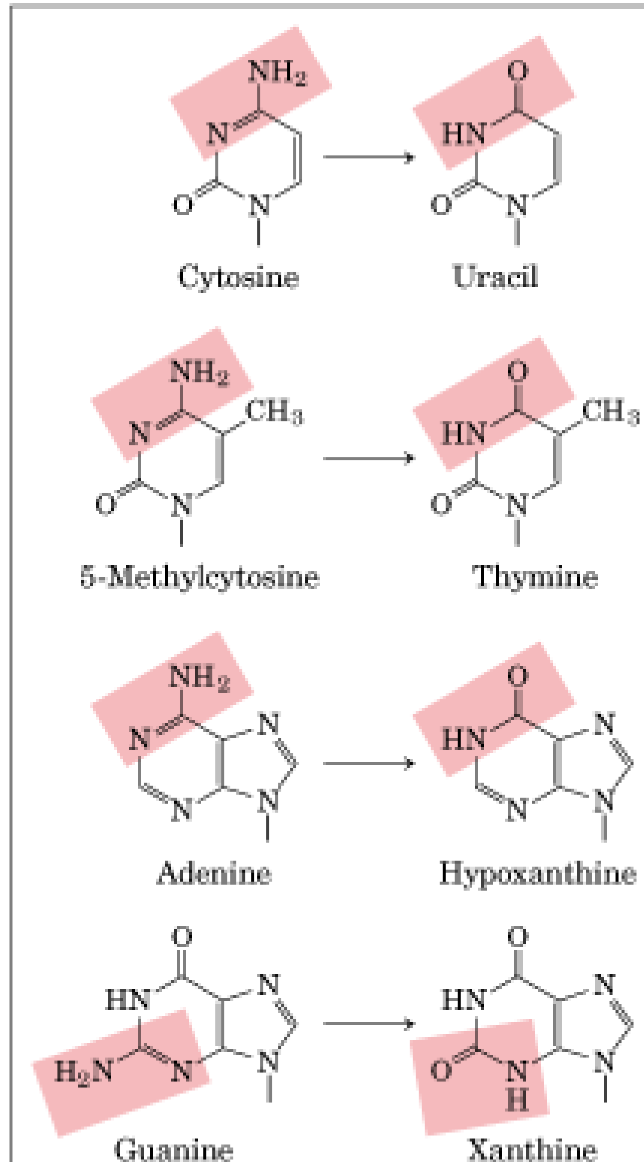
$NaNO_2$
Sodium nitrite

$NaNO_3$
Sodium nitrate

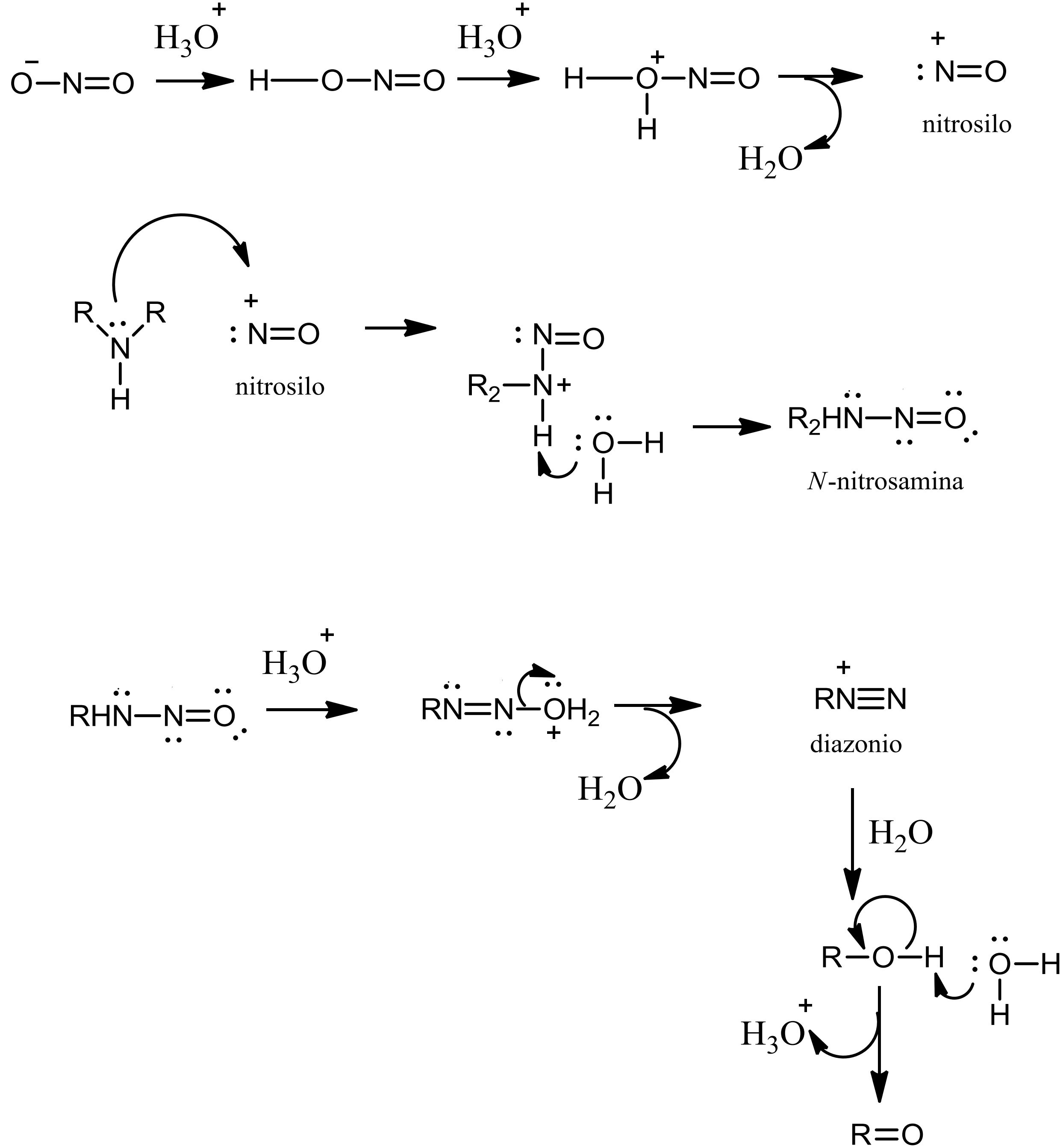


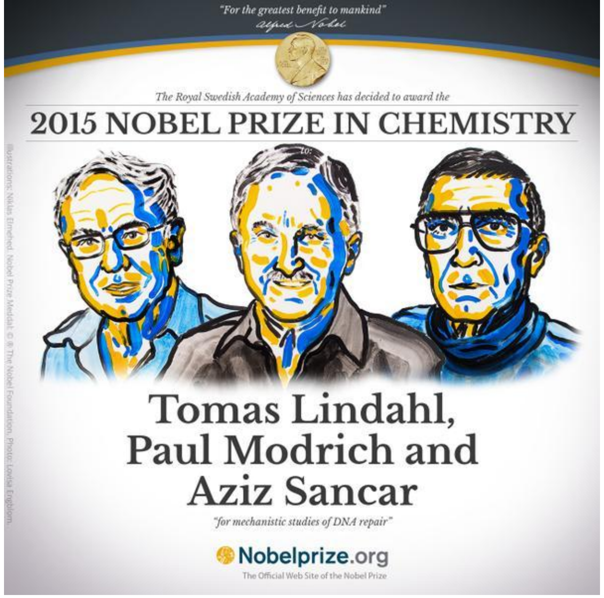
Nitrosamine

Nitrous acid precursors



Deamination


nitrosilo
nitrosilo
N-nitrosamina
diazonio



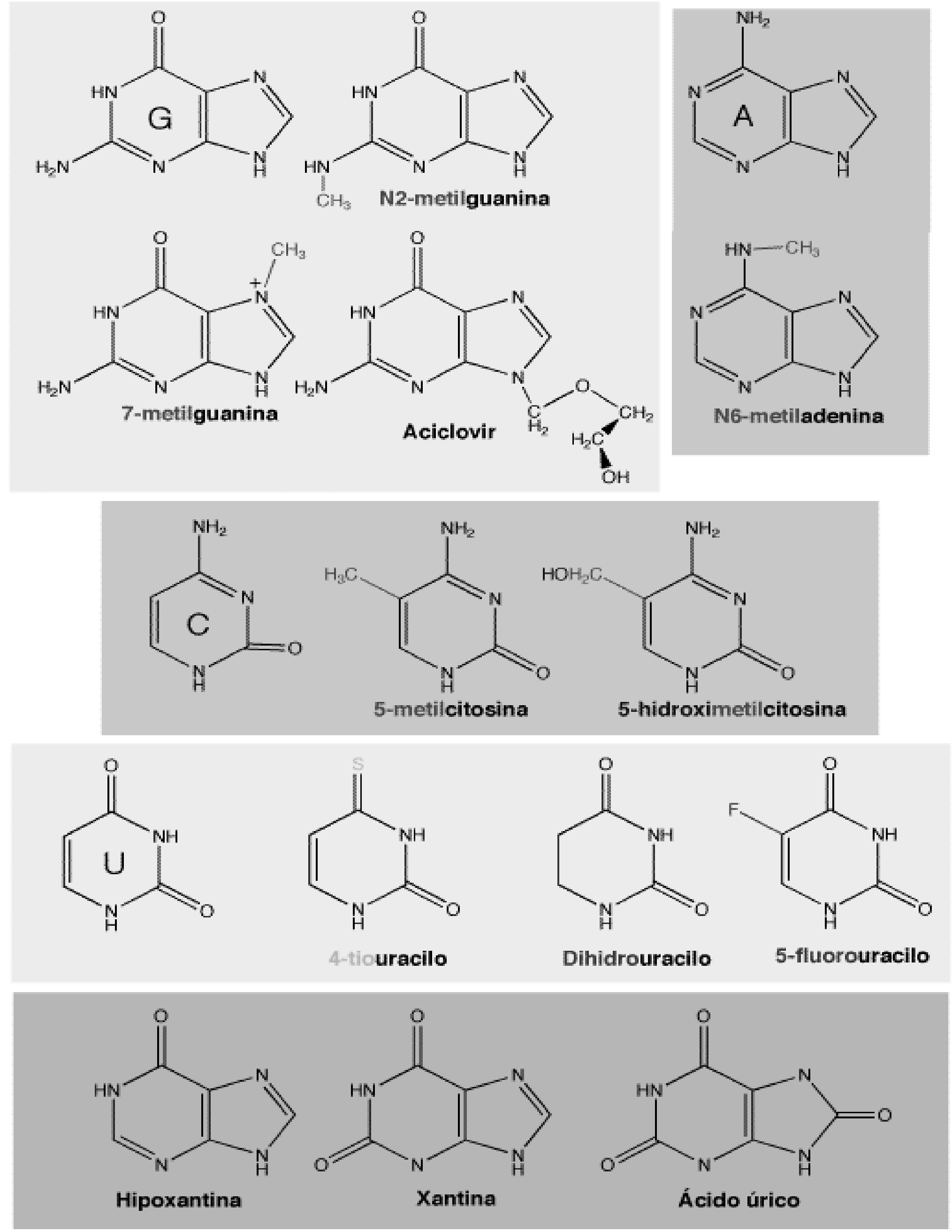
El sueco Tomas Lindahl, el estadounidense Paul Modrich y el turco Aziz Sancar- **Premio Nobel Química 2015**

Tomas Lindahl demostró que el ADN se descompone a un ritmo que debería haber hecho imposible el desarrollo de la vida en la Tierra. Esta visión le llevó a descubrir una maquinaria molecular, la reparación por escisión de base, que contrarresta constantemente el colapso de nuestro ADN.

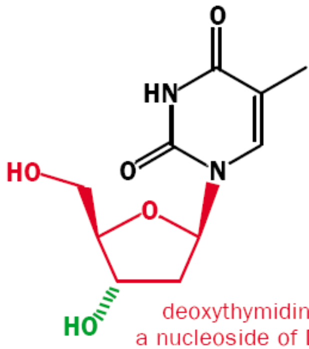
Aziz Sancar ha estudiado la reparación por escisión de nucleótidos, el mecanismo que utilizan las células para reparar el daño de los rayos UV al ADN. La célula también utiliza la reparación por escisión de nucleótidos para corregir defectos causados por sustancias mutagénicas, entre otras.

Paul Modrich ha demostrado cómo la célula corrige los errores que se producen cuando el ADN se replica durante la división celular. Este mecanismo, reparación de genes, reduce la frecuencia de errores durante la replicación del ADN en alrededor de mil veces.

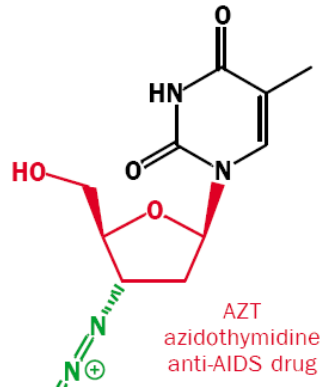
Derivados de bases con actividad farmacológica



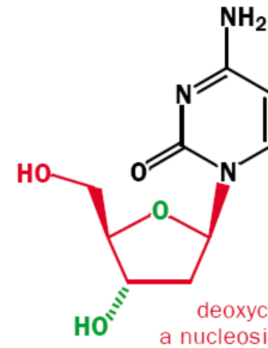
Derivados de nucleósidos con actividad farmacológica



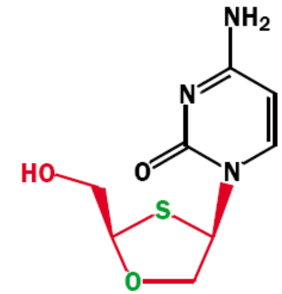
deoxythymidine
a nucleoside of DNA



AZT
azidothymidine
anti-AIDS drug

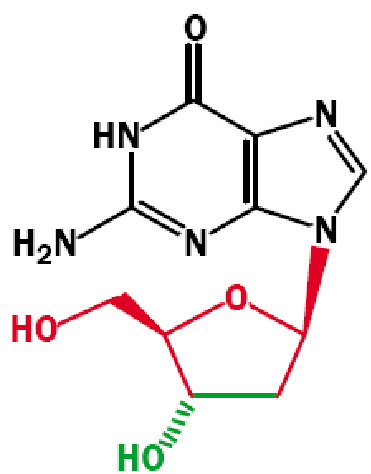


deoxycytidine
a nucleoside of DNA

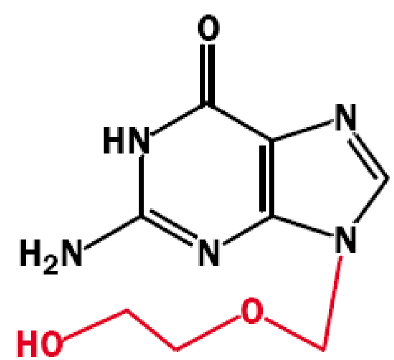


3-TC
lamivudine
anti-AIDS drug

deoxguanosine
a nucleoside of DNA



acyclovir
(Zovirax)
anti-herpes drug



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