

# DNA, RNA, & Flow of Genetic Information

DNA & RNA are long linear polymers, called nucleic acids.

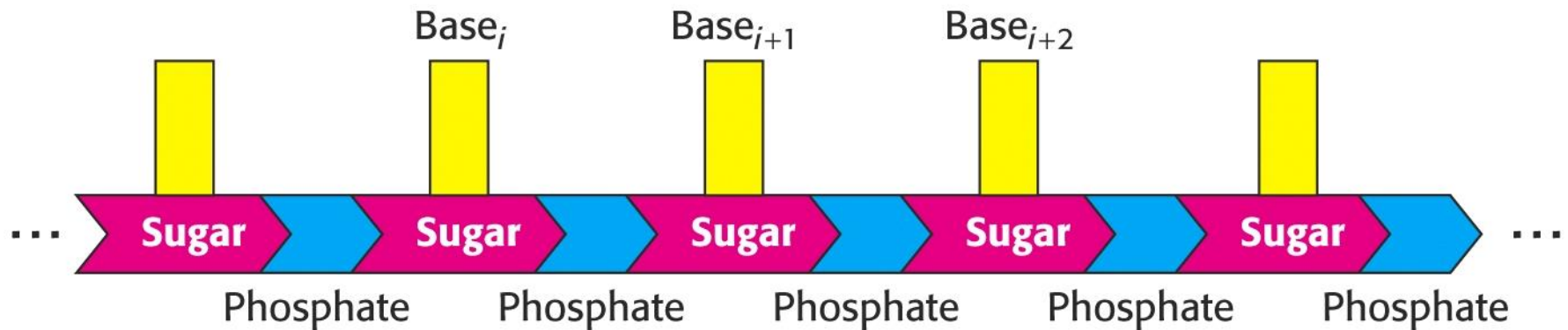
Genetic information is stored in a sequence of 4 kinds of bases along the chain, and is passed from one generation to the next

## Chapter 5: Outline

- 5.1 A nucleic acid consists of 4 kinds of bases linked to a sugar-phosphate backbone
- 5.2 A pair of nucleic acid chains with complimentary sequences can form a double-helical structure
- 5.3 DNA is replicated by polymerases that take instructions from templates
- 5.4 Gene expression is the transformation of DNA information into functional molecules
- 5.5 Amino acids are encoded by groups of three bases starting from a fixed point
- 5.6 Most eucaryotic genes are mosaics of introns & exons

# Polymeric structure of nucleic acids

Linear polymers of covalent structures, built from similar units



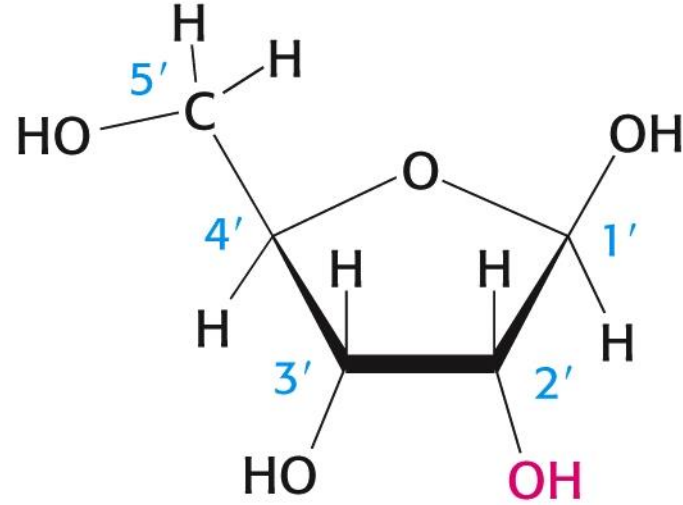
Sequence of bases uniquely characterizes nucleic acids  
Represents a form of linear information

Backbone is constant: repeating units of sugar-phosphate

# Different pentose sugars in RNA & DNA

TEST

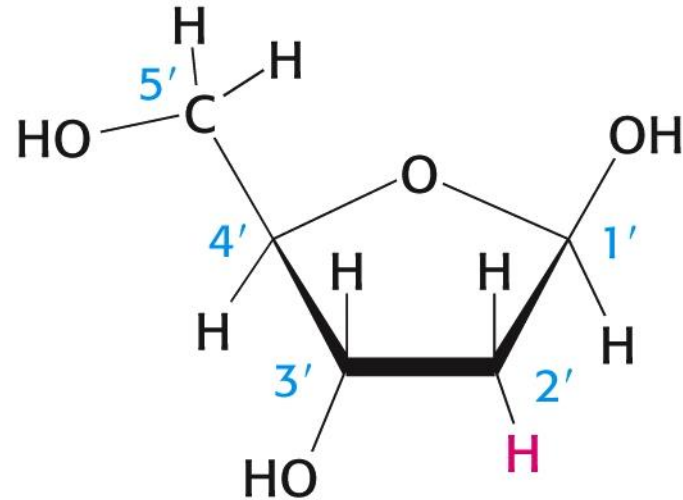
RNA



**Ribose**

Sugar carbons have prime numbers, to distinguish them from atoms in bases

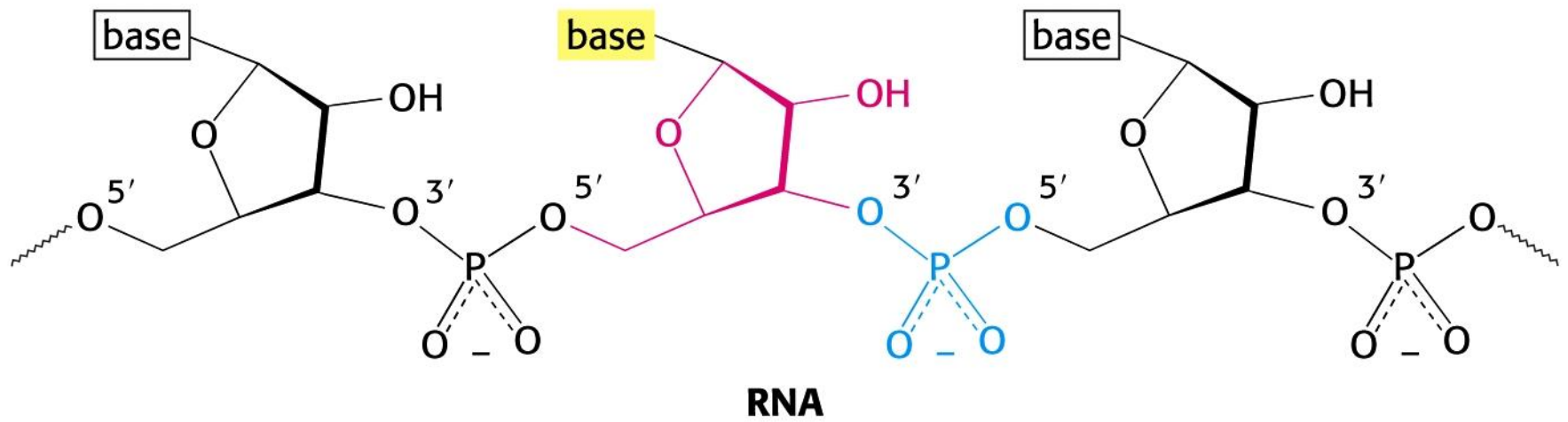
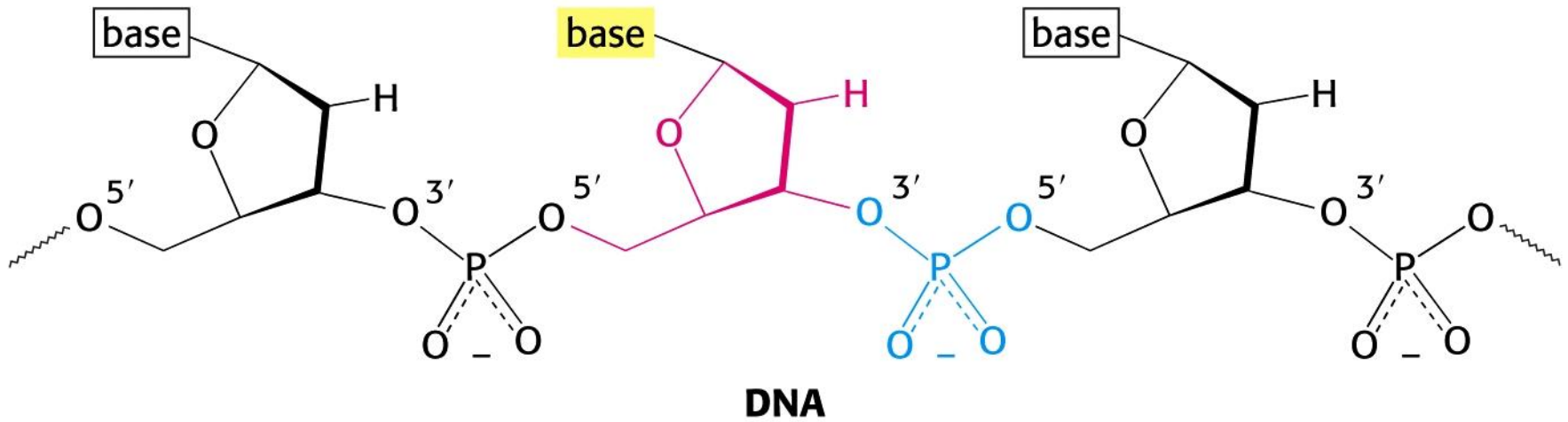
DNA



**Deoxyribose**

# Backbone of DNA & RNA

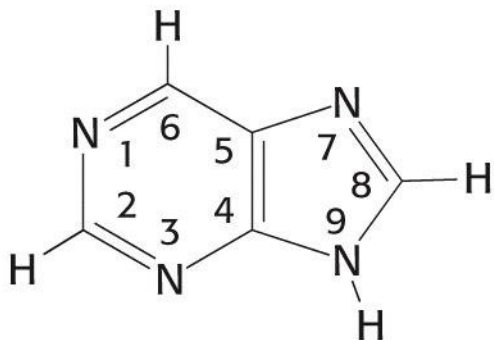
## 3'-to-5' phosphodiester linkages



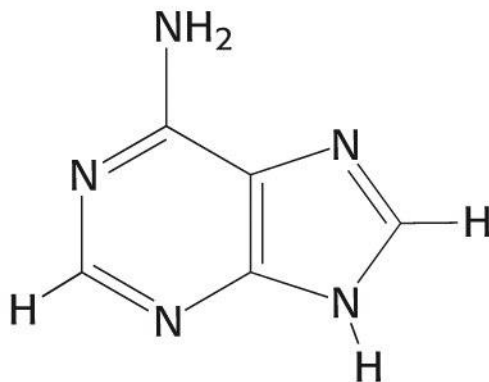
Sugar, red. Phosphate, blue

# Purines & Pyrimidines

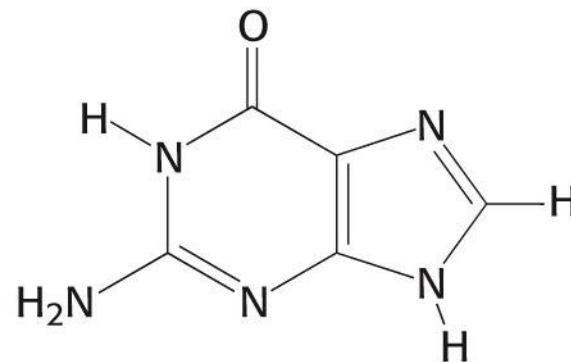
## PURINES



**Purine**

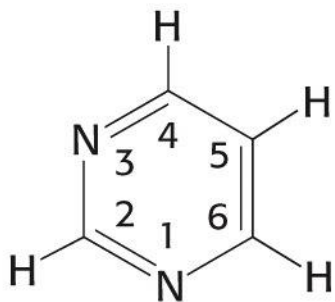


**Adenine**

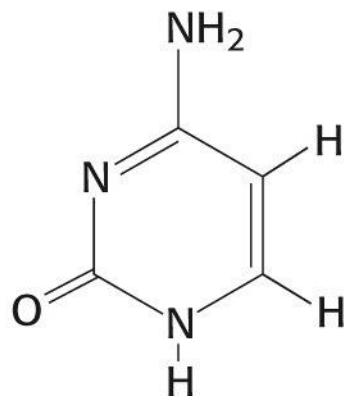


**Guanine**

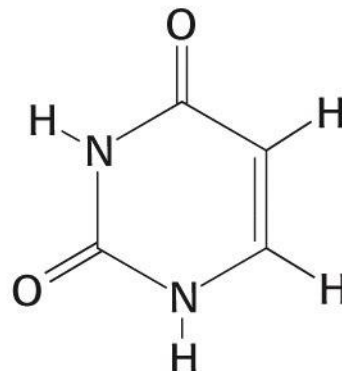
## PYRIMIDINES



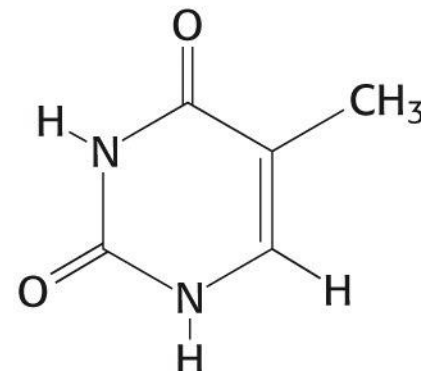
**Pyrimidine**



**Cytosine**



**Uracil**



**Thymine**

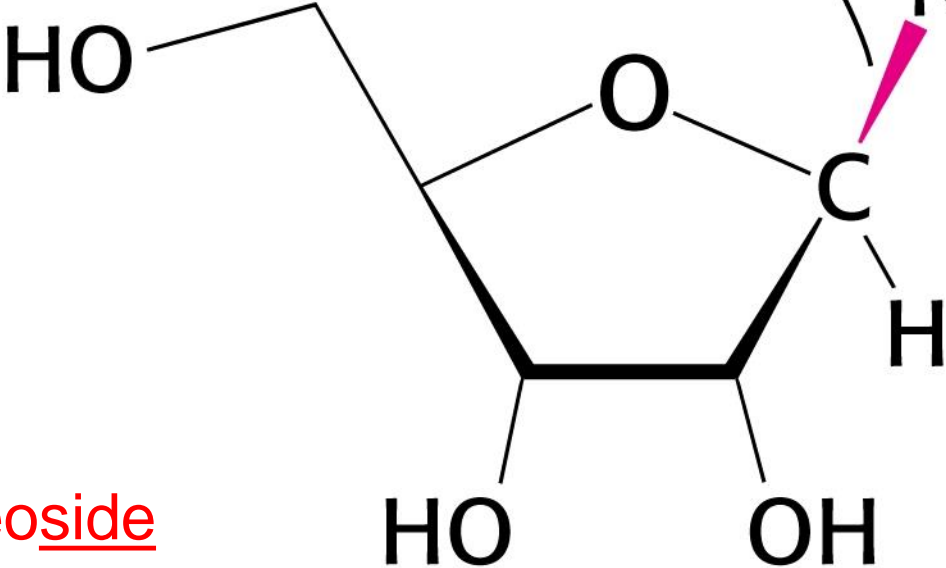
Note: ring atom #s

RNA

DNA

# Sugar - base linkage

$\beta$ -Glycosidic linkage



Base above plane of sugar, linkage is  $\beta$

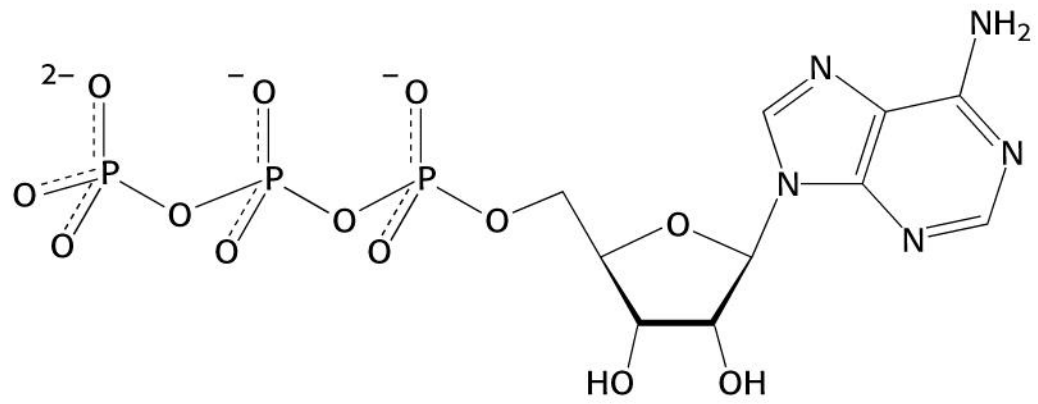
Nucleoside

RNA: adenosine, guanosine, cytidine, & uridine

DNA: deoxyadenosine, deoxyguanosine, deoxycytidine, & thymidine

# Nucleotides: monomeric units of nucleic acids

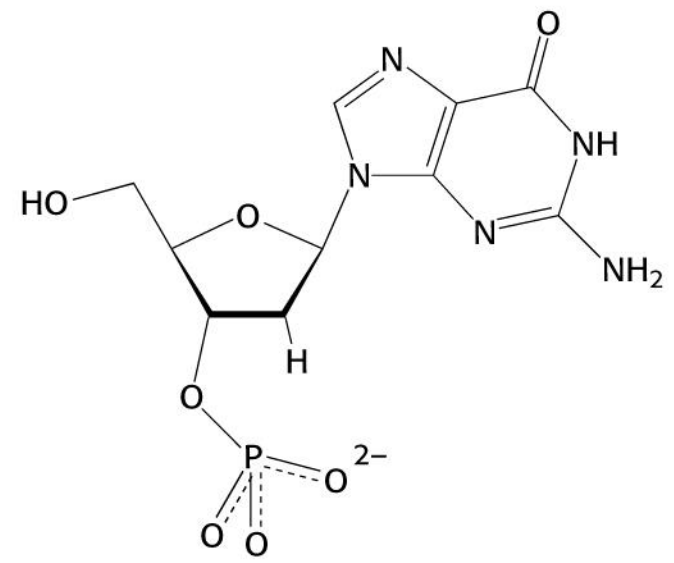
Adenosine 5'-triphosphate



5'-ATP

5' nucleotide - most common

Deoxyguanosine 3' monophosphate

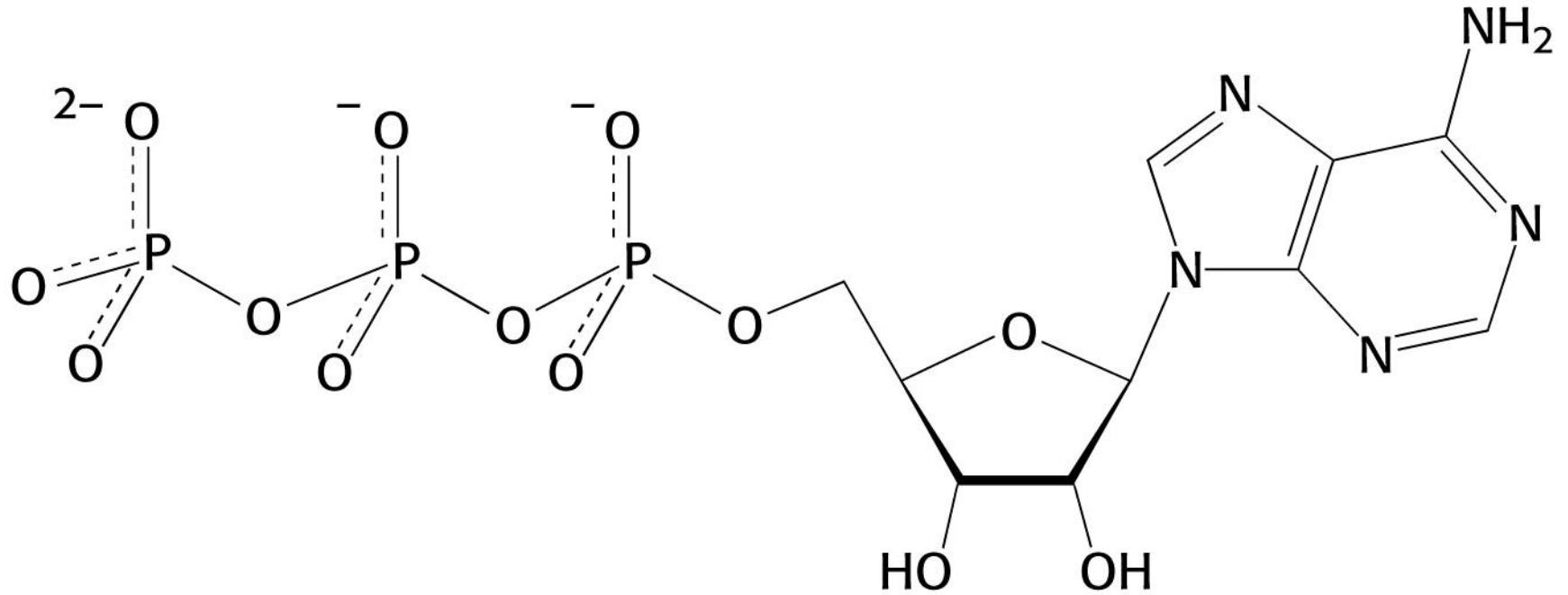


3'-dGMP

3' nucleotide

**Nucleotide**: nucleoside joined to one or more phosphate groups by an ester linkage

# Adenosine 5'-triphosphate



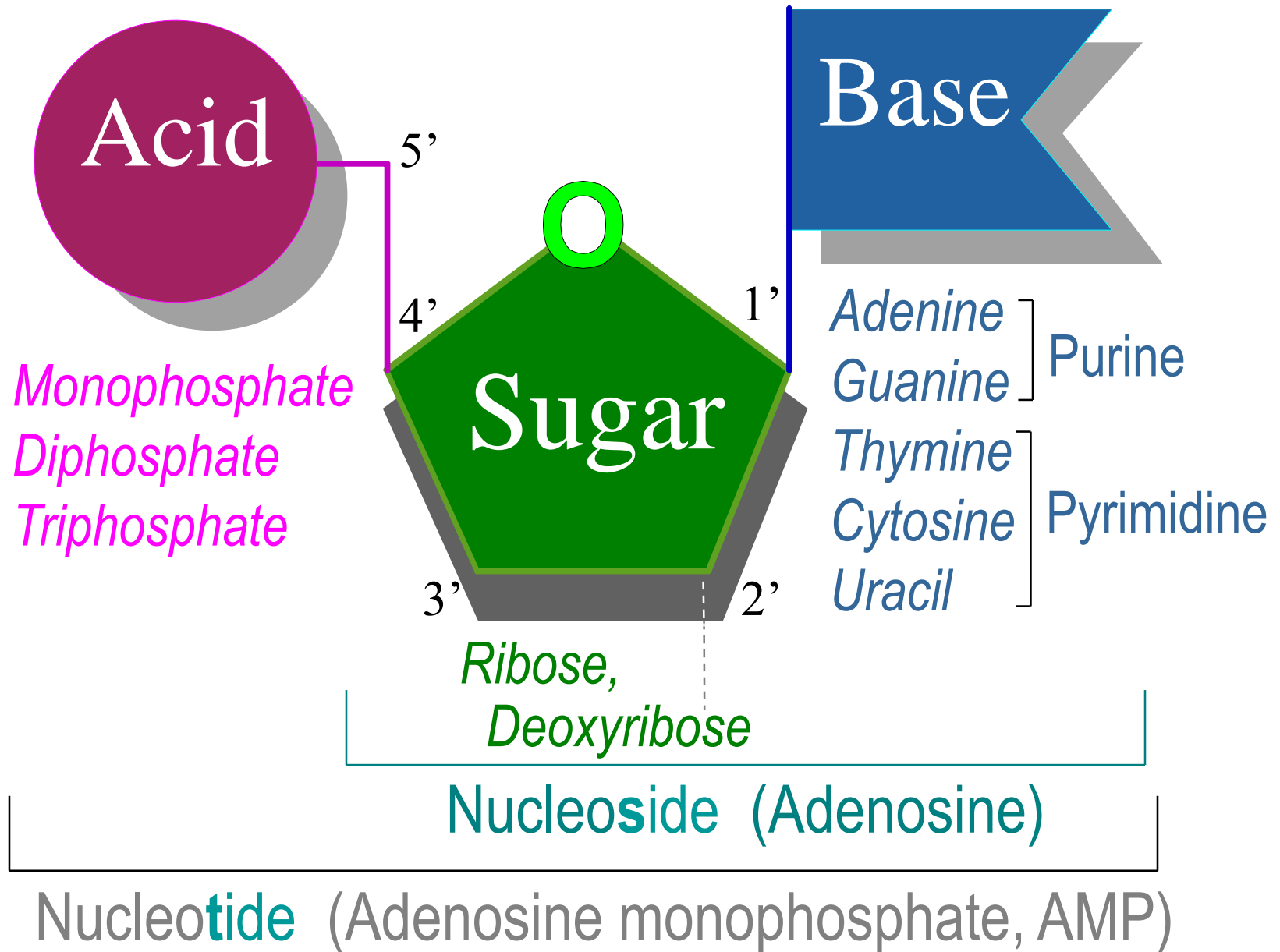
**5'-ATP**

Adenosine linked to sugar C1'

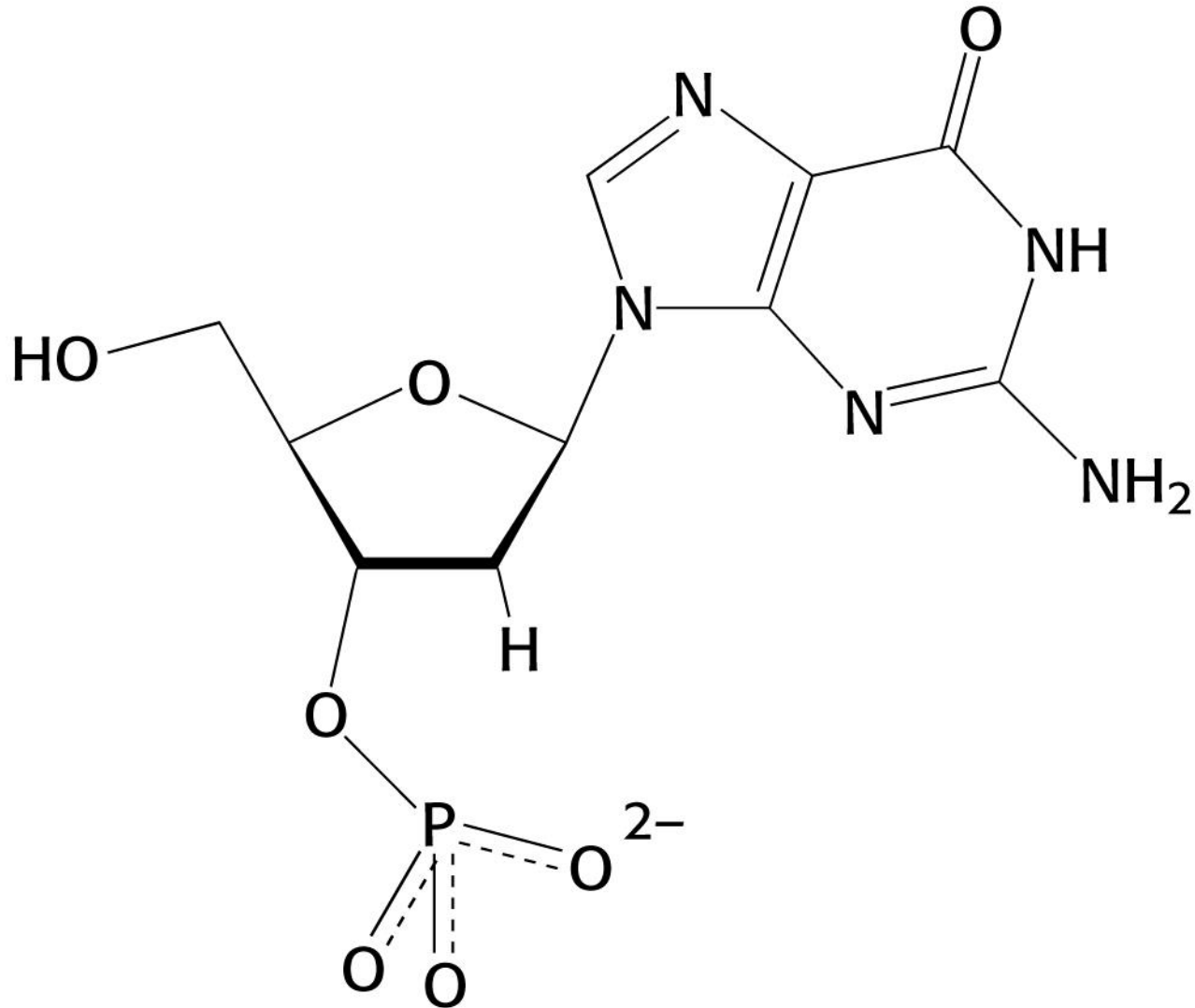
Triphosphate linked to sugar C5'



# Basic Structure of Nucleic Acids

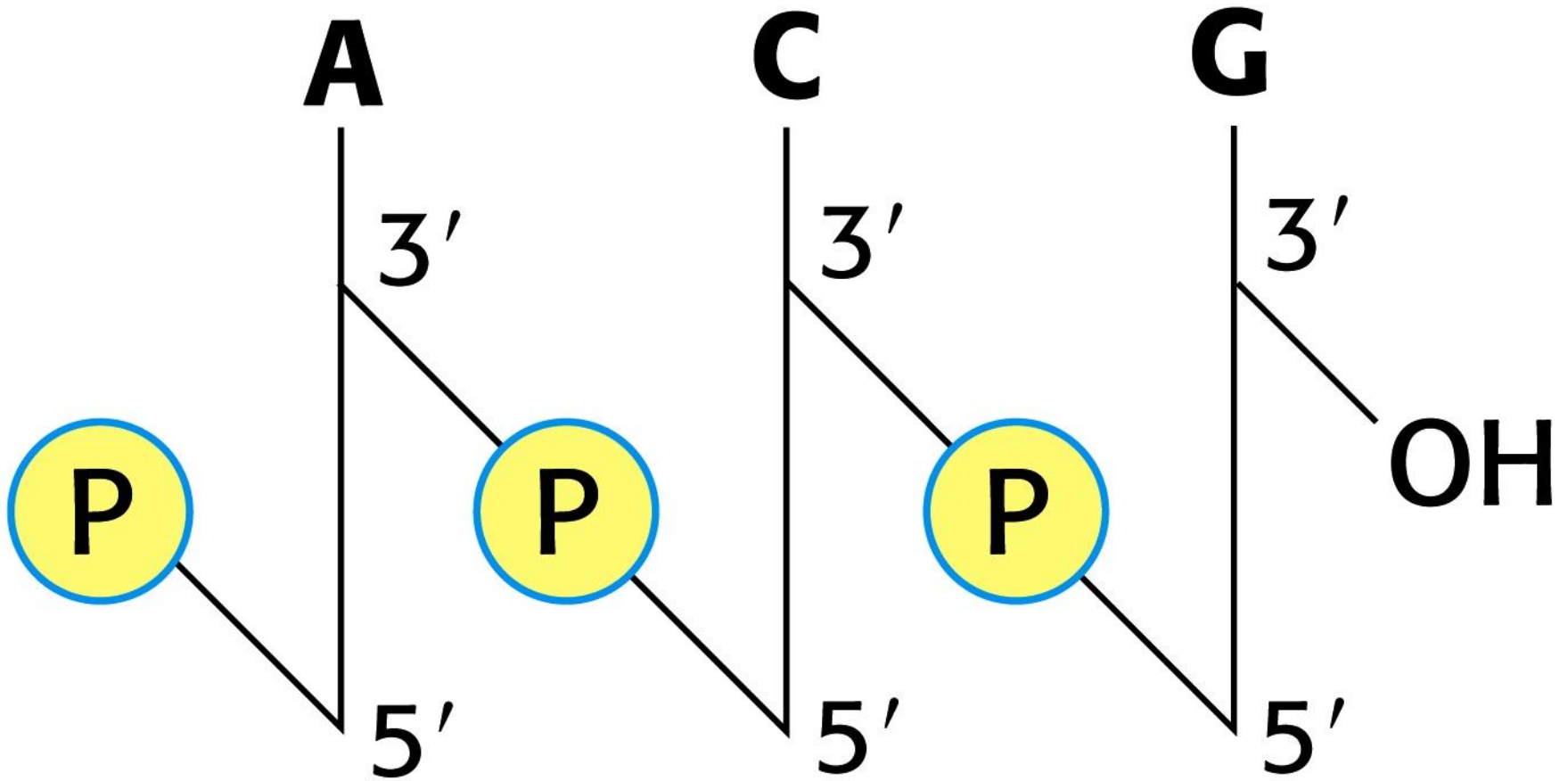


# Deoxyguanosine 3'-monophosphate



**3'-dGMP**

# Structure of DNA chain



5' end, phosphate attached

3' end, free hydroxyl group

# The Two Chains of DNA Are Antiparallel

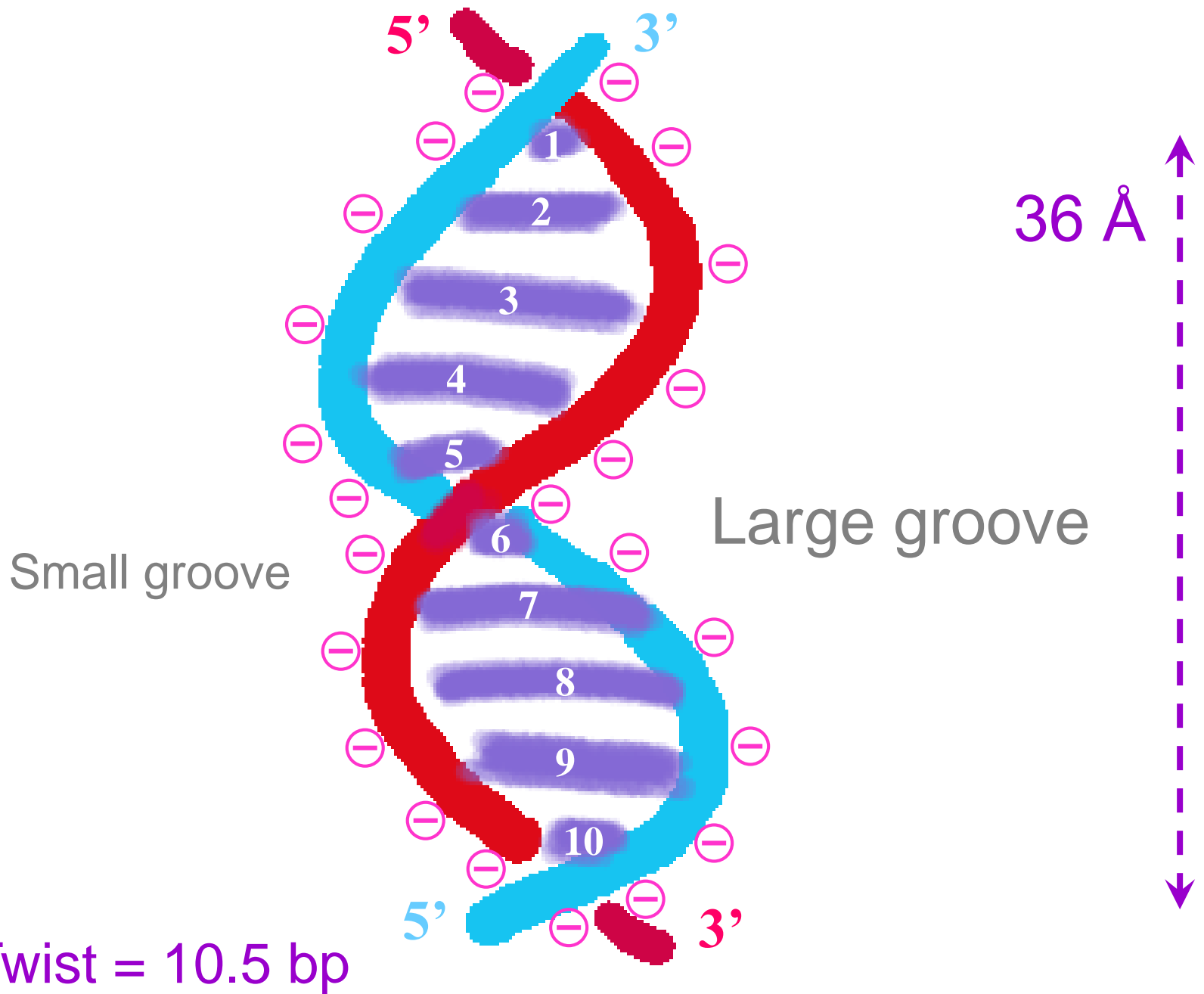
5' → 3'

5' pApTpCpGpApTpCpG-OH 3'

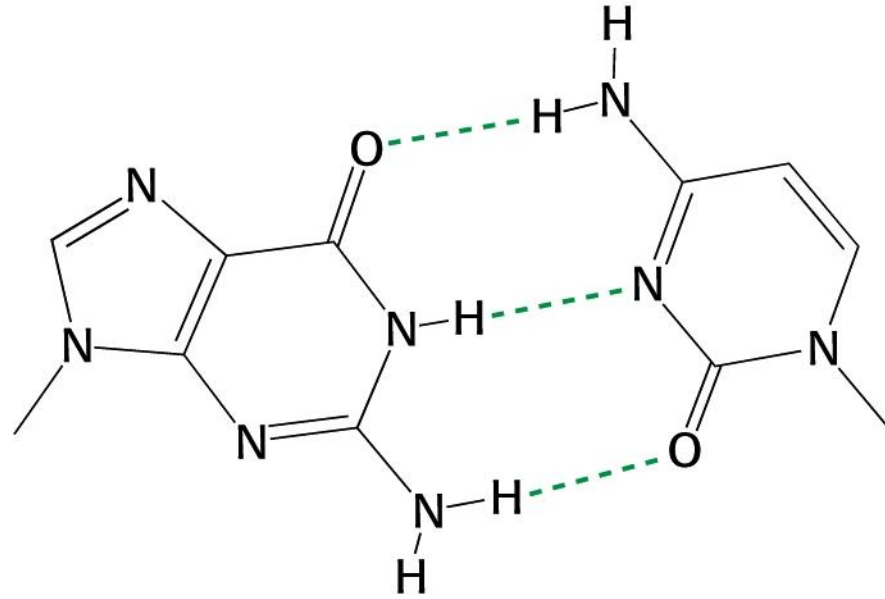
3' HO-TpApGpCpTApGpCpT 5'

3' ← 5'

# Characteristics of Double Helix

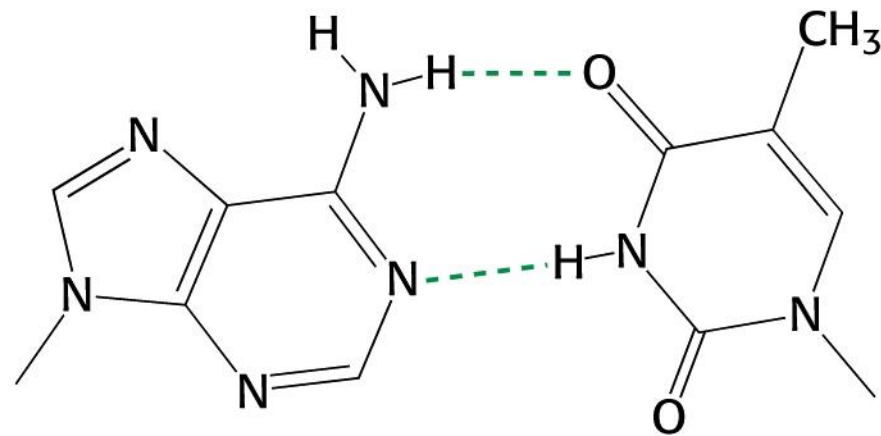


# Watson and Crick base pairs



**Guanine**

**Cytosine**



**Adenine**

**Thymine**

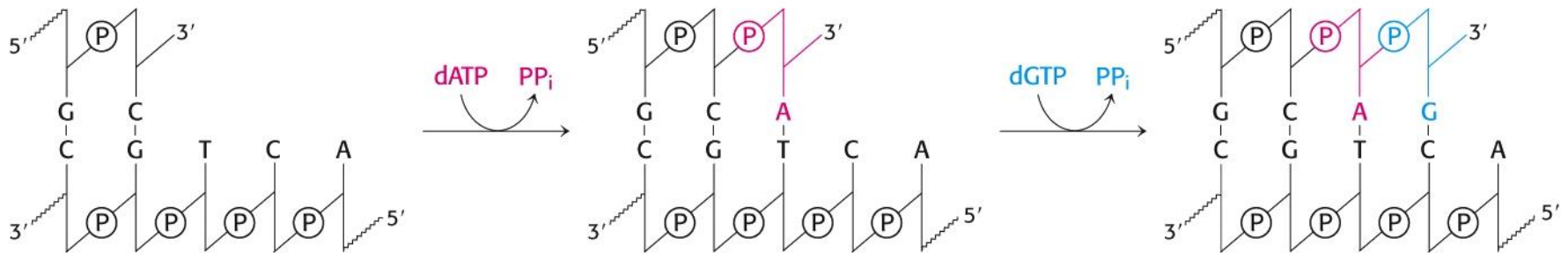
Essentially the same shape

# DNA polymerization reaction

By DNA polymerase

Step by step addition of deoxyribonucleotide units to a DNA chain

New DNA chain assembled directly on a preexisting DNA template



Primer & template required

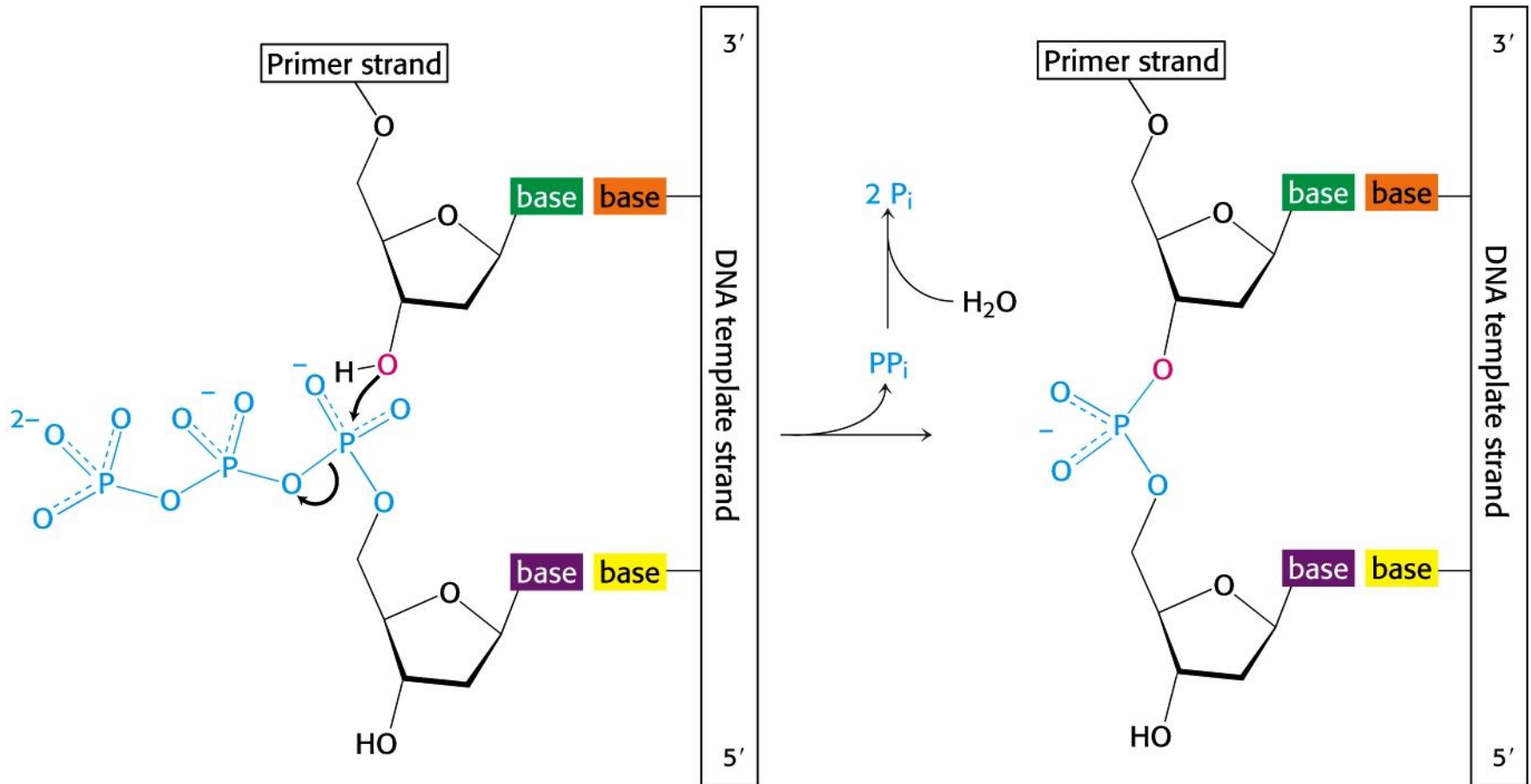
Activated precursors required: dATP, dGTP, TTP, dCTP

Also required:  $\text{Mg}^{2+}$  ion

# DNA replication, phosphodiester bridge

Nucleophilic attack by 3'-hydroxyl group of primer on innermost phosphorus atom of deoxynucleotide triphosphate (dNTP)

Elongation proceeds, 5' -to- 3'

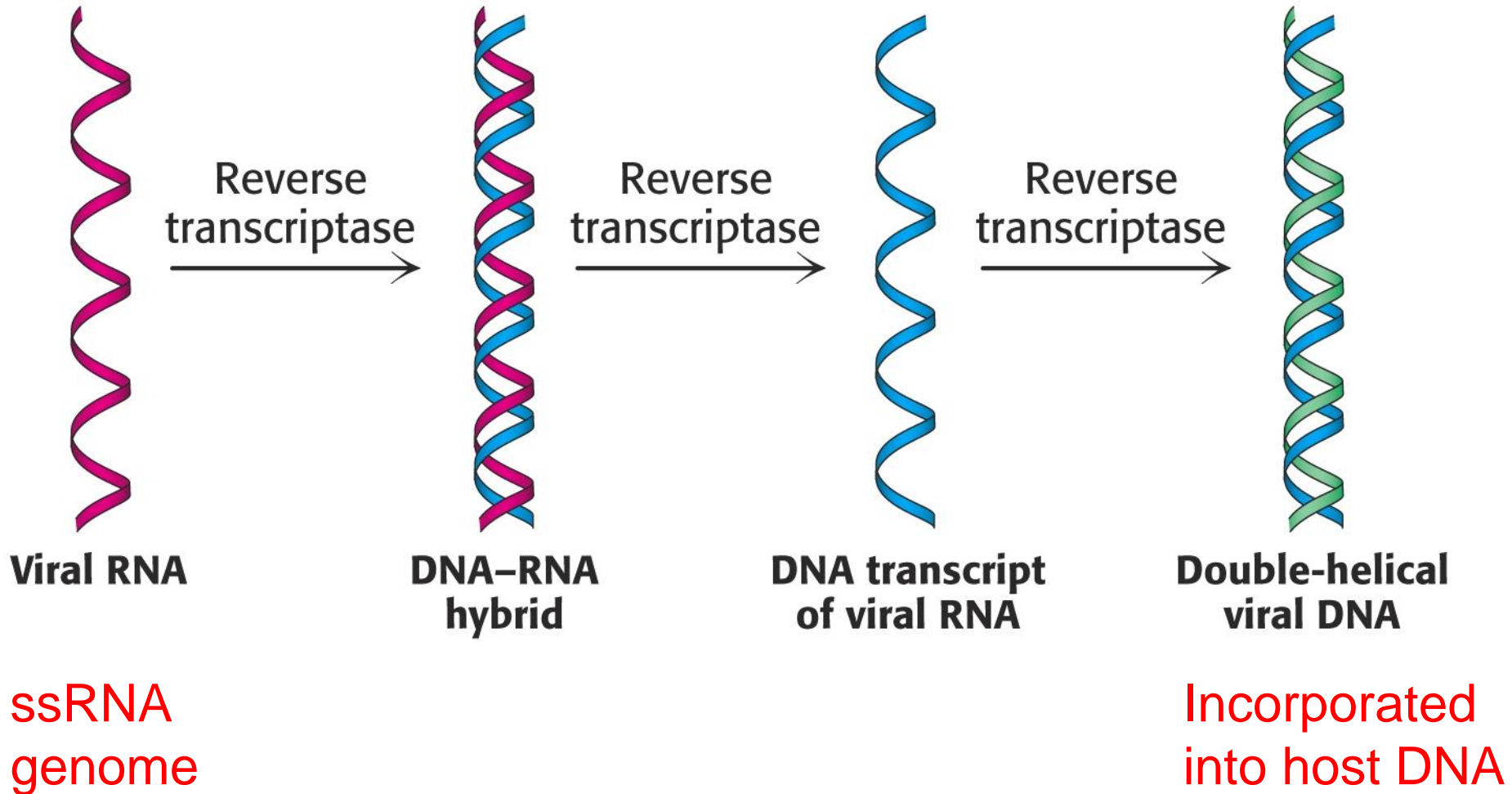


Hydrolysis of pyrophosphate (PP<sub>i</sub>) helps drive polymerization



# Retroviruses reverse flow of information

Reverse transcriptase brought into cell by the virus (eg. HIV-1)



# Roles of RNA in gene expression

**TABLE 5.2** RNA molecules in *E. coli*

Type	Relative amount (%)	Sedimentation coefficient (S)	Mass (kd)	Number of nucleotides
Ribosomal RNA (rRNA)	80	23	$1.2 \times 10^3$	3700
		16	$0.55 \times 10^3$	1700
		5	$3.6 \times 10^1$	120
Transfer RNA (tRNA)	15	4	$2.5 \times 10^1$	75
Messenger RNA (mRNA)	5		Heterogeneous	

Messenger RNA: template for translation (protein synthesis)

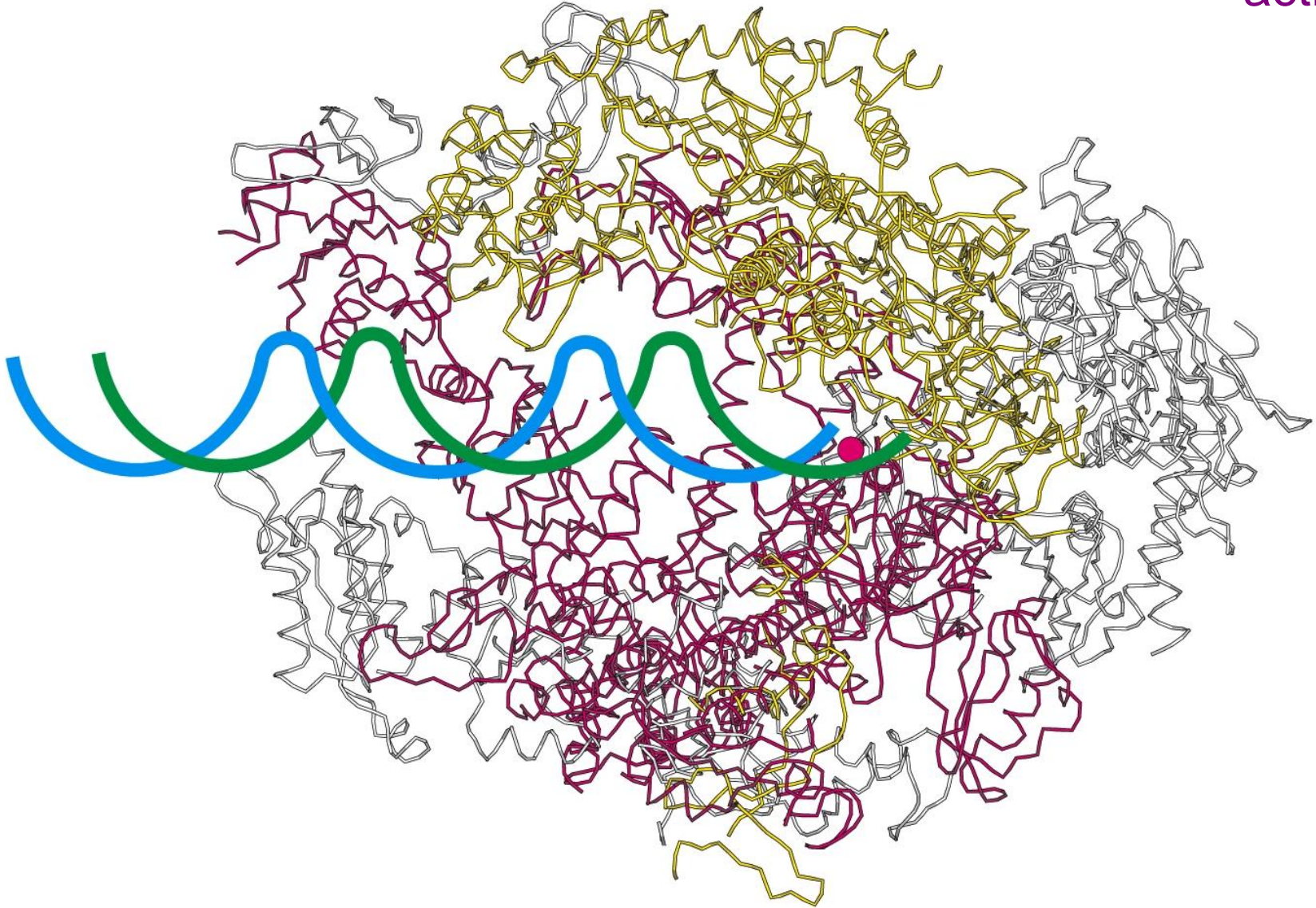
Transfer RNA: carriers of activated AAs to ribosomes (at least one kind for each of 20 AAs)

Ribosomal RNA: major component of ribosomes (play structural and catalytic roles)

# RNA polymerase

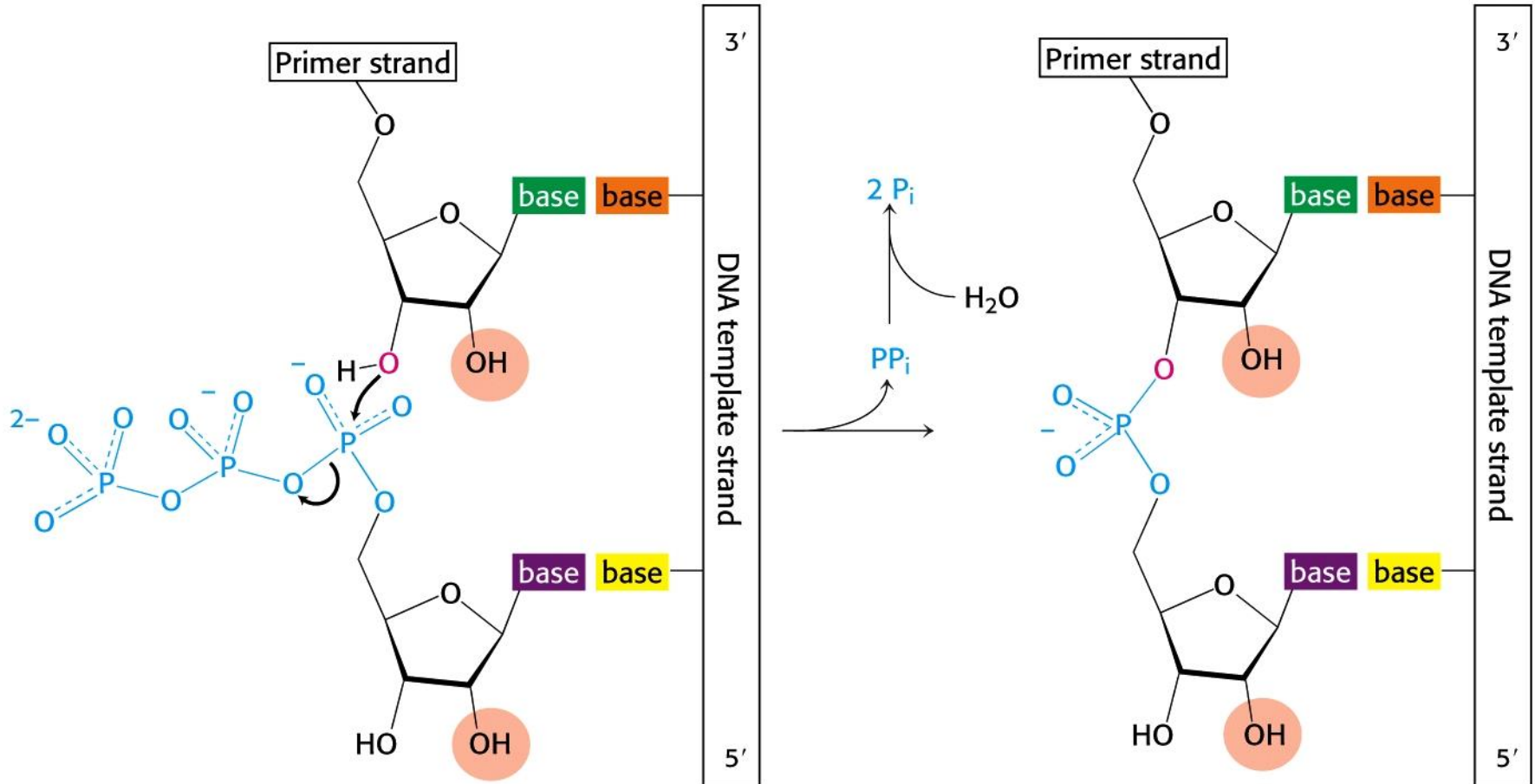
“claw” shape to hold DNA to be transcribed

Mg<sup>2+</sup> ion at active site



# Transcription reaction - RNA polymerase

## Nucleophilic attack by 3' hydroxyl group



**Requirements:** a template, activated precursors (NTPs), & Divalent metal ion, Mg<sup>2+</sup> or Mn<sup>2+</sup>

# RNA polymerase: instructions from DNA templates

**TABLE 5.3** Base composition (percentage) of RNA synthesized from a viral DNA template

DNA template (plus strand of $\phi$ X174)		RNA product	
A	25	25	U
T	33	32	A
G	24	23	C
C	18	20	G



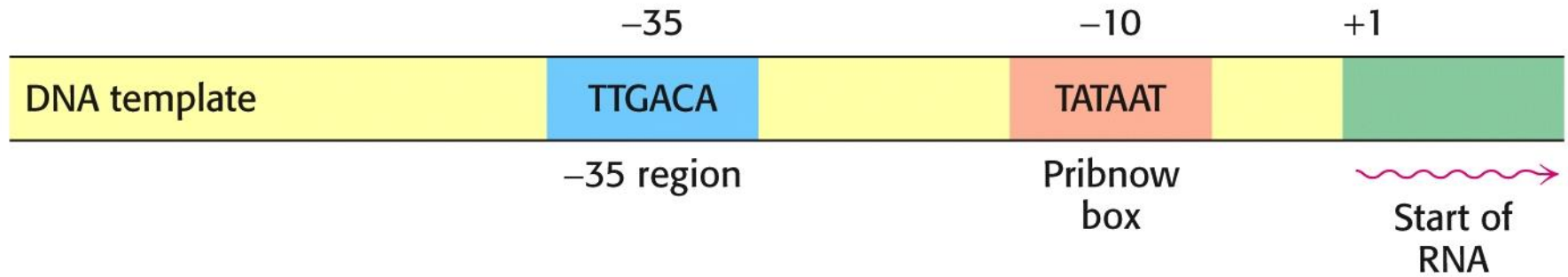
# mRNA & DNA complementarity

5'—GCGGCGACGCGCAGUUAUCCACAGCCGCCAGUUCGCGUGGCGGCAUUUU—3'	<b>mRNA</b>
3'—CGCCGCTGCGCGTCAATTAGGGTGTCTGGCGGTCAAGGCGACCGCCGTAAAA—5'	<b>Template strand of DNA</b>
5'—GCGGCGACGCGCAGTTAATCCCACAGCCGCCAGTTCGCTGGCGGCATTT—3'	<b>Coding strand of DNA</b>

mRNA sequence is the complement of that of the DNA template & is the same as that of the coding DNA strand, except for T in place of U

# Prokaryotic promoter

Consensus sequences centered at -10, & -35



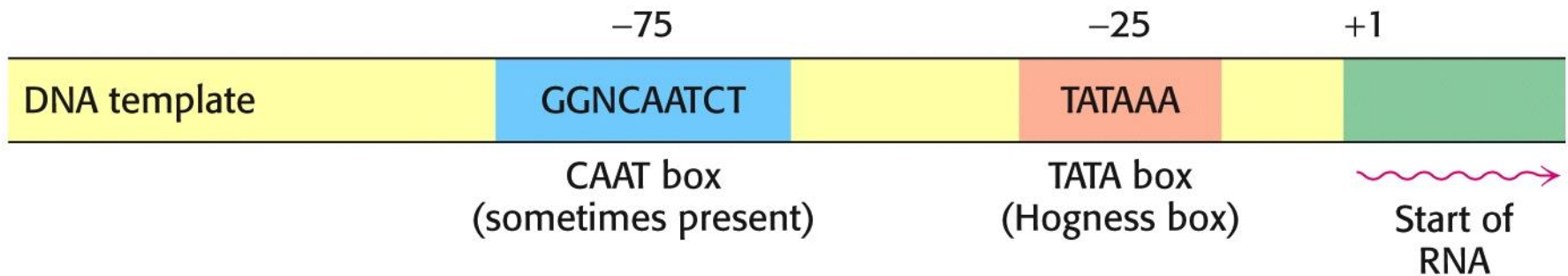
(A)

**Prokaryotic promoter site**

Promoter sites specifically binds RNA polymerase,  
& determine where transcription begins

# Eukaryotic promoter

Consensus sequences centered at -25 & -75



(B)

**Eukaryotic promoter site**

Eukaryotic promoters are further stimulated by enhancer sequences (can be at a distance of several kb from start site on either its 5' or 3' side)

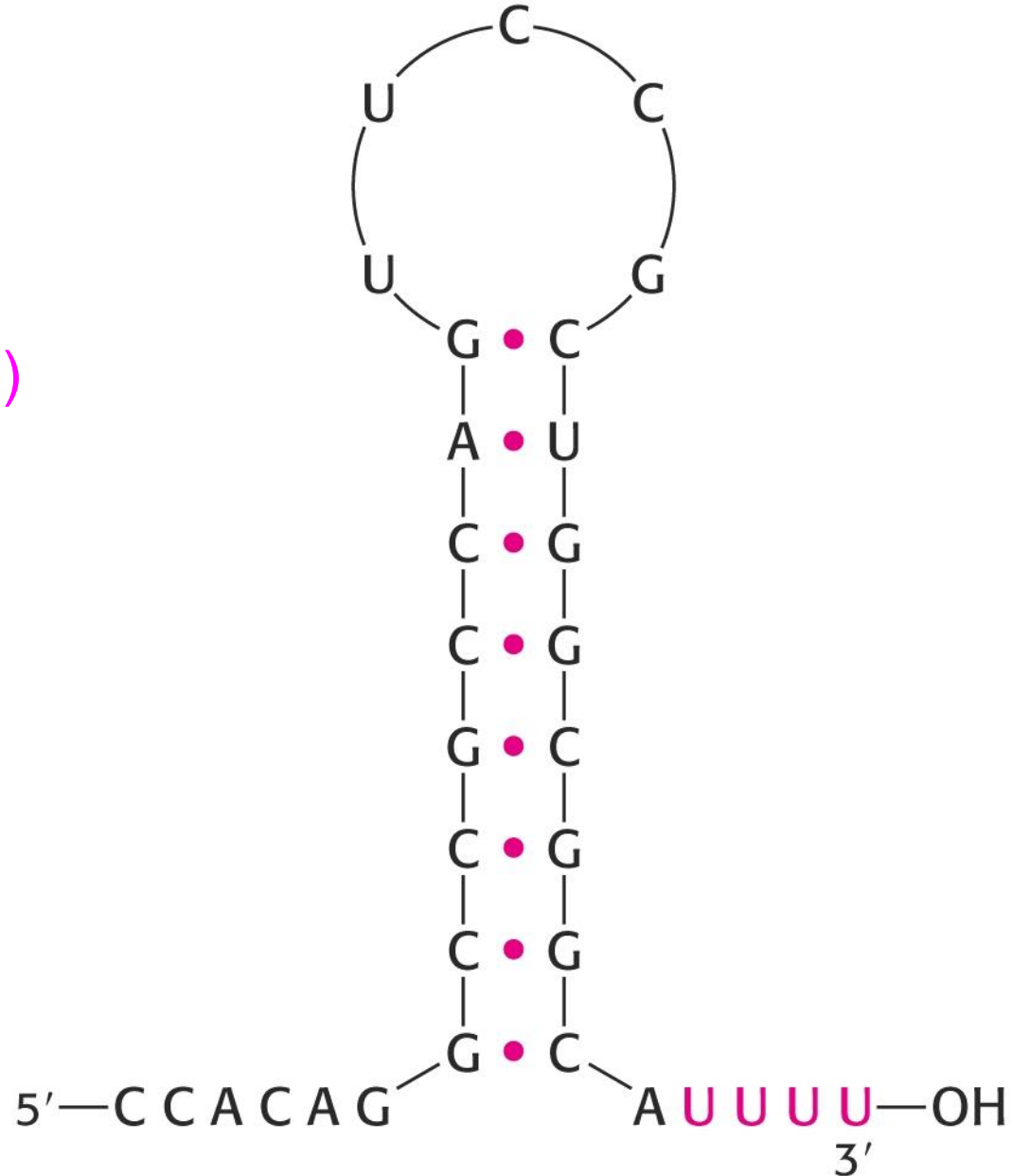


# Termination signal in *E. coli*

Sequence at 3' end  
of mRNA:

Hairpin loop  
followed by a  
string of uridines (U)

Alternatively,  
transcription ended  
by action of  
Rho protein



# mRNA modification in eukaryotes

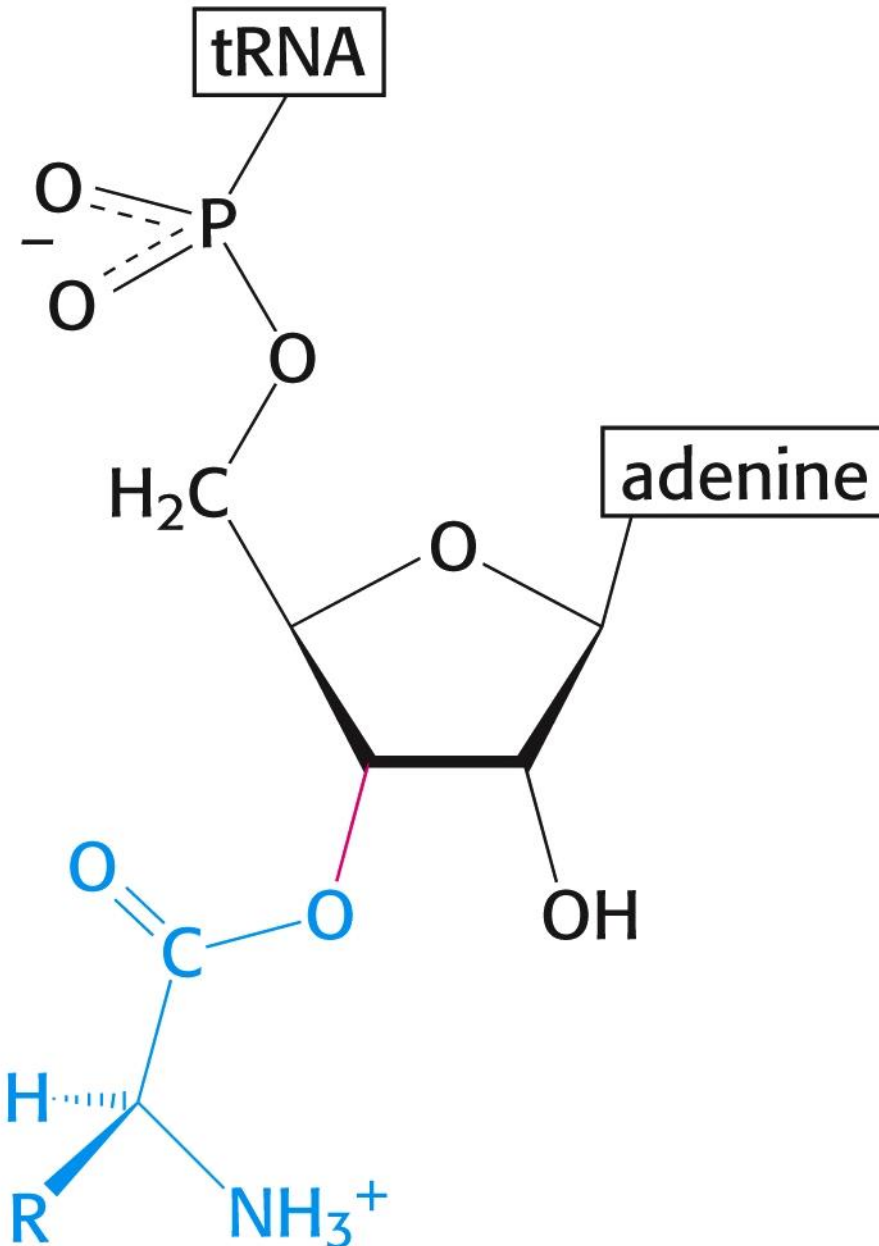
(Less known about transcription termination in eukaryotes)

mRNA is modified after transcription



A “cap” structure is attached to 5’ end & a sequence of adenylates, the poly(A) tail, is added to the 3’ end

# Amino acid attached to tRNA



Amino acid esterified to 3'-hydroxyl group of terminal adenosine of tRNA

Amino acid is in an activated form

Whole molecule is, *aminoacyl* - tRNA

# Aminoacyl - tRNA, symbolic diagram

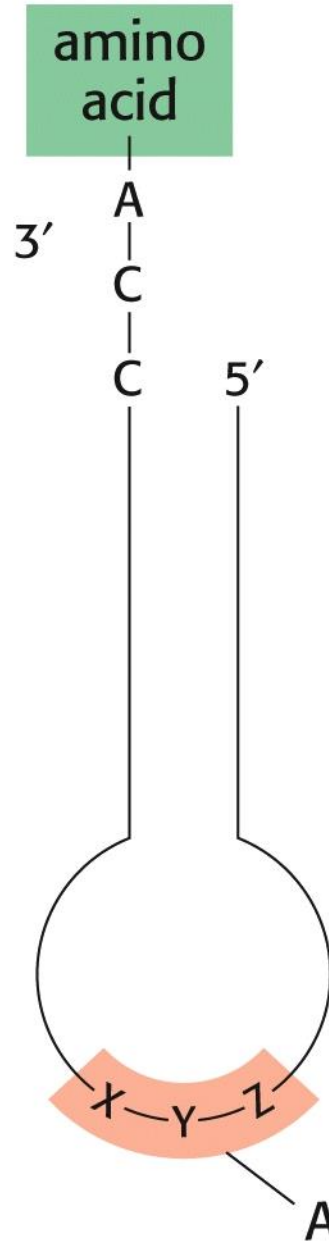
1961, Crick & Brenner,  
the genetic code:

3 nucleotides encode  
an amino acid,

Code is nonoverlapping,

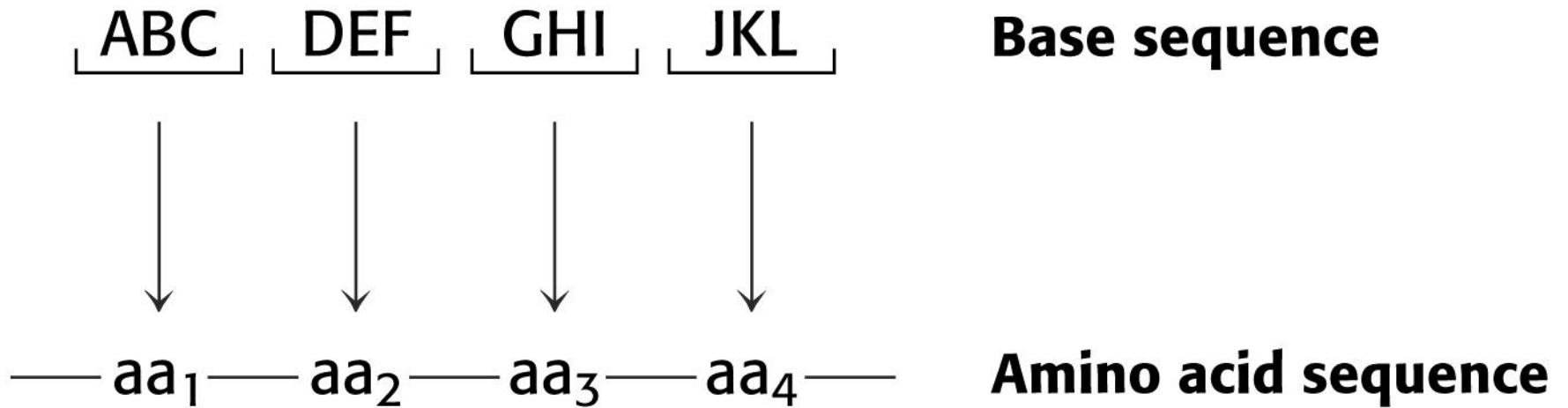
Code has no punctuation,

Code is degenerate,  
(some AAs encoded by  
more than one codon)



The anticodon is the  
template-recognition  
site

# Genetic code, **nonoverlapping**



# Genetic code, **no punctuation**

Sequence of bases is read in blocks of 3 bases from a fixed starting point

Start



ABC | DEF | GHI | JKL | MNO

aa<sub>1</sub> — aa<sub>2</sub> — aa<sub>3</sub> — aa<sub>4</sub> — aa<sub>5</sub>

# Genetic code, degenerate (64 codons, 20 aa<sub>s</sub>)

**TABLE 5.4** The genetic code

First position (5' end)	Second position				Third position (3' end)
	U	C	A	G	
U	Phe	Ser	Tyr	Cys	U
	Phe	Ser	Tyr	Cys	C
	Leu	Ser	Stop	Stop	A
	Leu	Ser	Stop	Trp	G
C	Leu	Pro	His	Arg	U
	Leu	Pro	His	Arg	C
	Leu	Pro	Gln	Arg	A
	Leu	Pro	Gln	Arg	G
A	Ile	Thr	Asn	Ser	U
	Ile	Thr	Asn	Ser	C
	Ile	Thr	Lys	Arg	A
	Met	Thr	Lys	Arg	G
G	Val	Ala	Asp	Gly	U
	Val	Ala	Asp	Gly	C
	Val	Ala	Glu	Gly	A
	Val	Ala	Glu	Gly	G

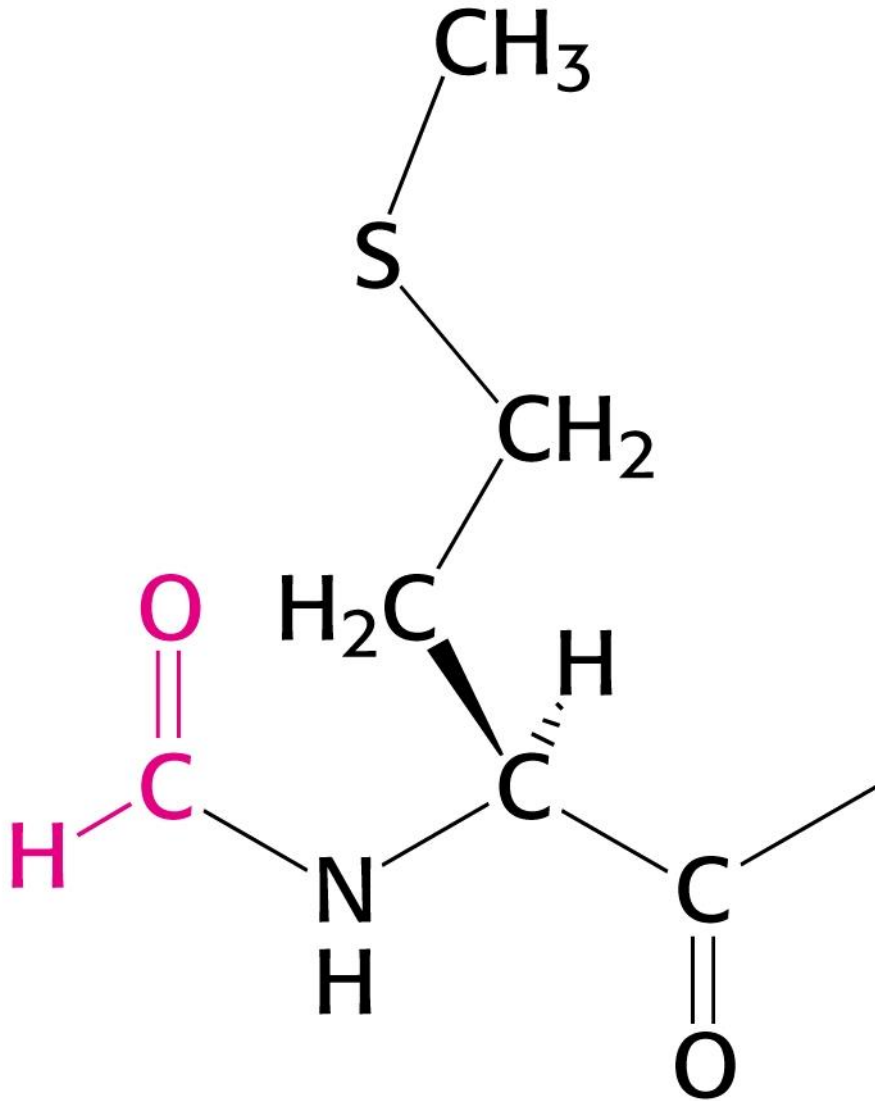
Trp & Met, one codon each,  
 other 18 aa<sub>s</sub>, two or more codons,  
 Leu, Arg, & Ser, six codons each,  
 Synonyms, codons for same aa,  
 Synonyms differ in last base,  
 3 stop codons, designate translation termination

*Note:* This table identifies the amino acid encoded by each triplet. For example, the codon 5' AUG 3' on mRNA specifies methionine, whereas CAU specifies histidine. UAA, UAG, and UGA are termination signals. AUG is part of the initiation signal, in addition to coding for internal methionine residues.

## Translation initiation: start codon

Messenger RNA is translated into proteins on ribosomes, large molecular complexes of proteins & ribosomal RNA

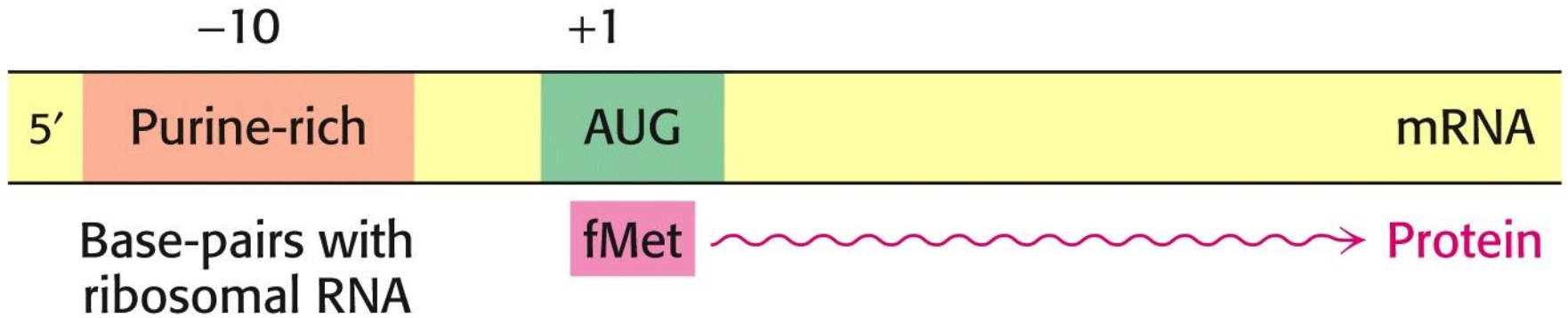
Initiator tRNA carries fMet (formylmethionine) to AUG (& sometimes GUG) in prokaryotes, but initiation is more complex



**fMet**

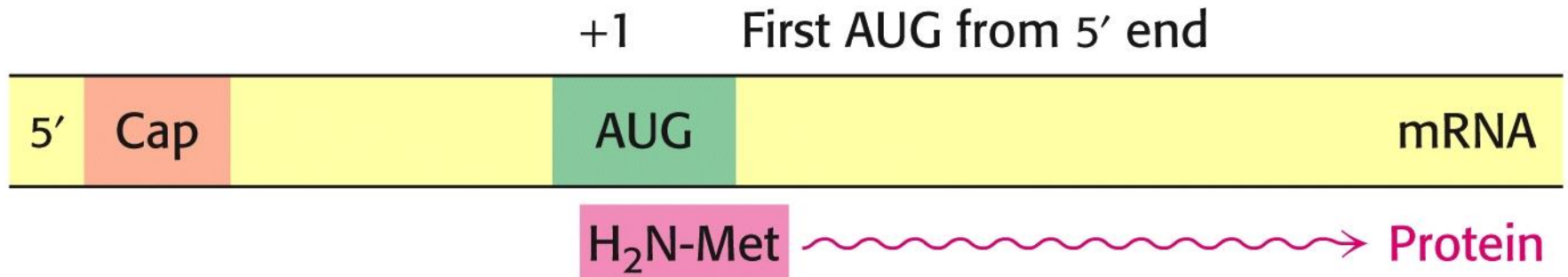


# Prokaryotic translation start



(A) **Prokaryotic start signal**

# Eukaryotic translation start



(B) Eukaryotic start signal

# Genetic code, **universal**, except...

Nearly but not absolutely universal

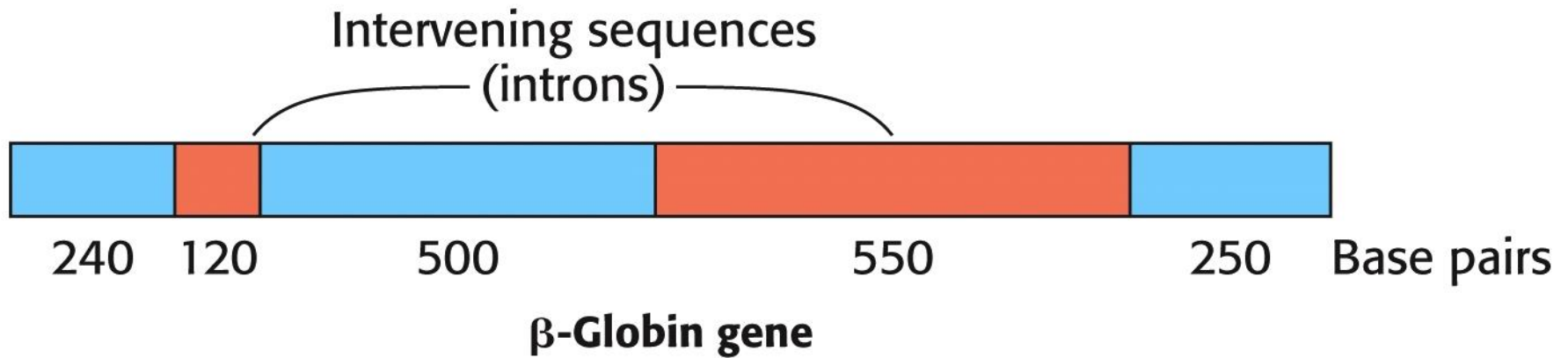
**TABLE 5.5** Distinctive codons of human mitochondria

Codon	Standard code	Mitochondrial code
UGA	Stop	Trp
UGG	Trp	Trp
AUA	Ile	Met
AUG	Met	Met
AGA	Arg	Stop
AGG	Arg	Stop

Ciliated protozoa read UAA & UAG as codons for aa<sub>s</sub> instead of stop signals. UGA is their only stop

# Eukaryotic genes: mosaic of introns & exons

Introns (intervening sequences), brown

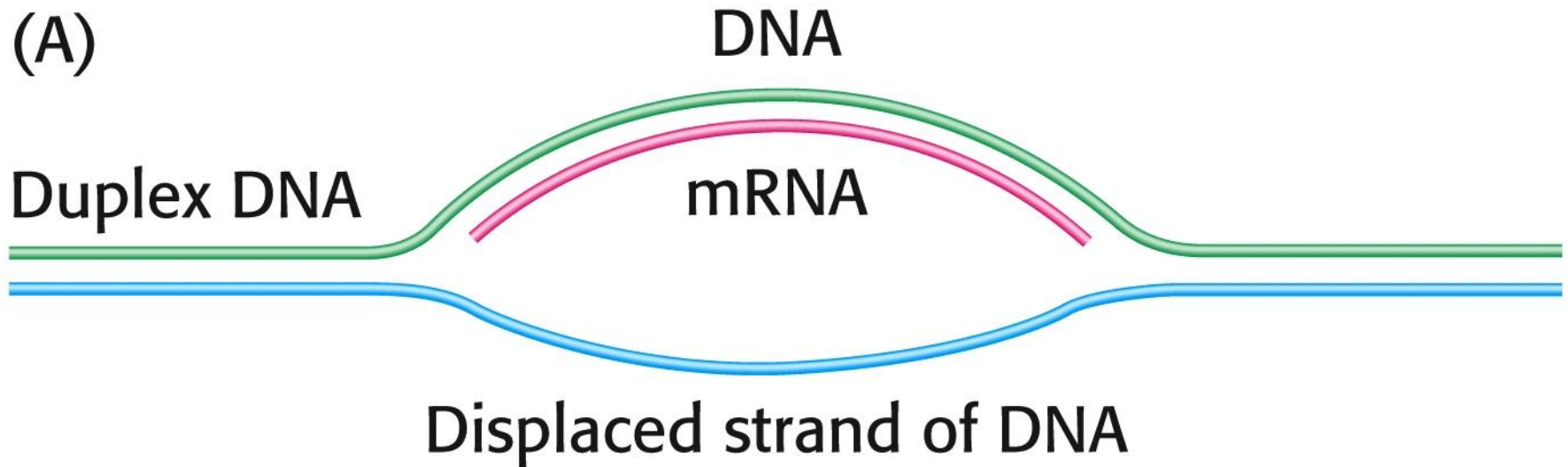


Exons (expressed sequences), blue

# Detecting introns by EM

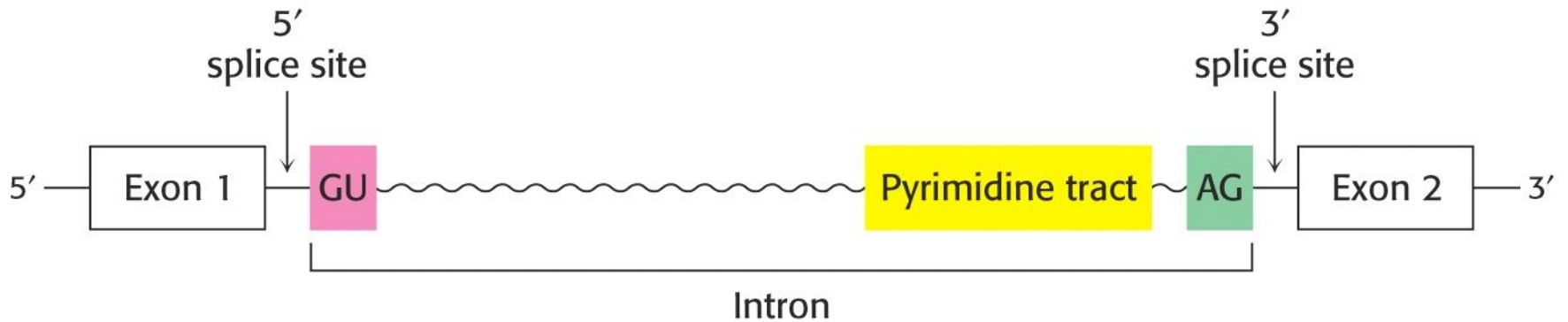
mRNA hybridized to corresponding genomic DNA

Single loop indicates gene is continuous



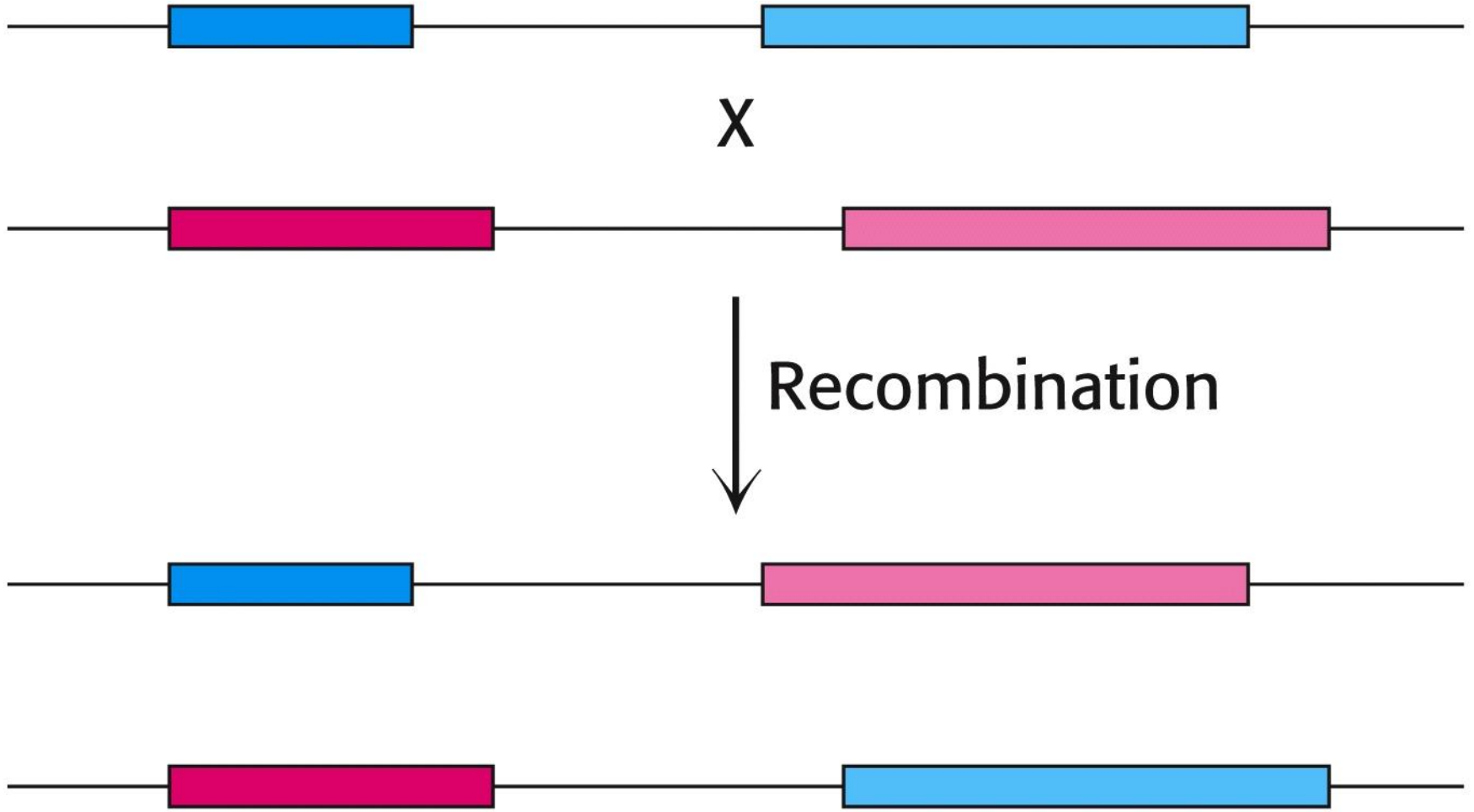
# Splicing at consensus sequences

Introns excised by *spliceosomes* (assemblies of proteins & small RNAs)



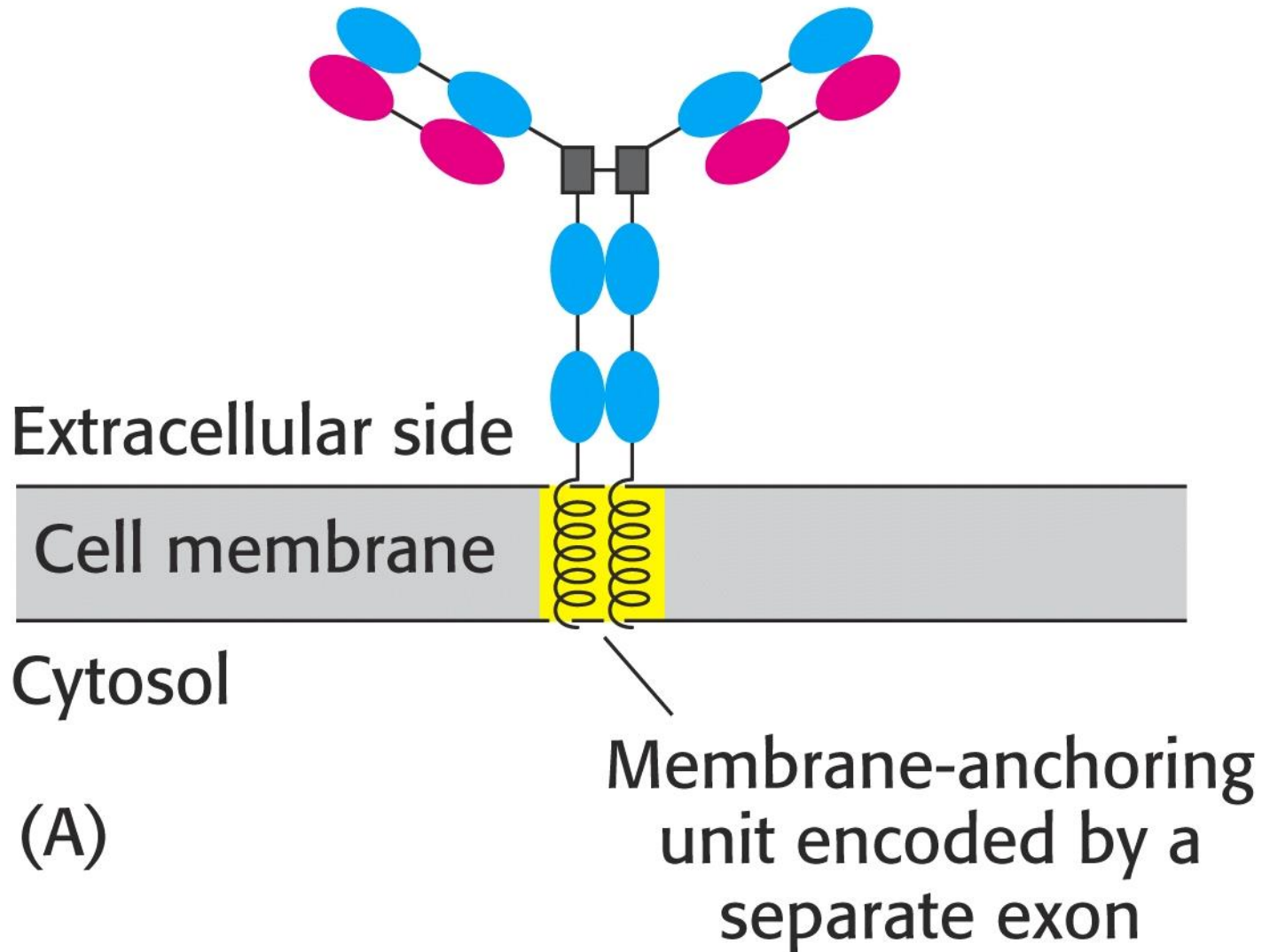
# Exon shuffling

Shuffling expands genetic repertoire



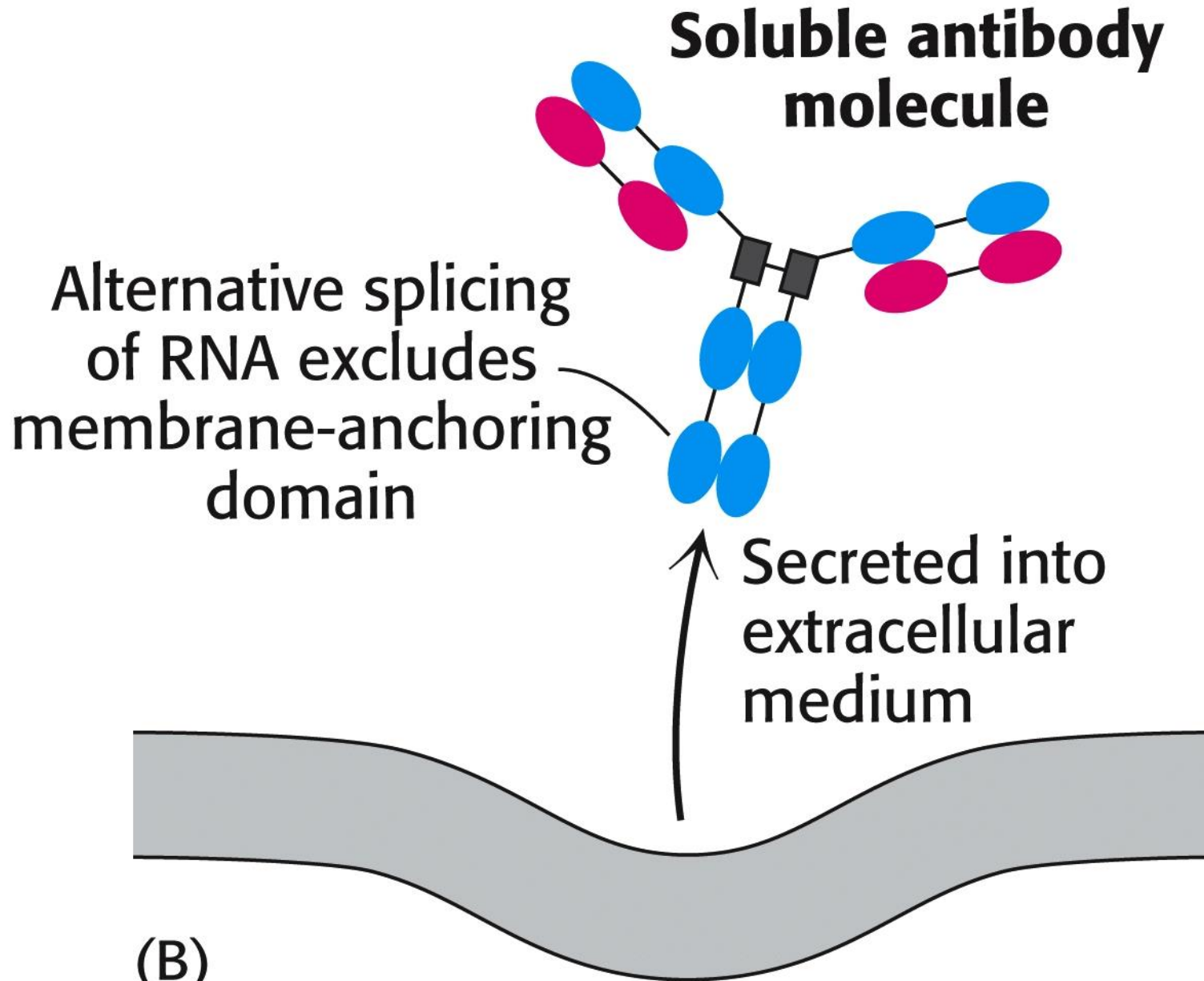
# Alternative splicing, 1st variation

## Membrane-bound antibody molecule





# Alternative splicing, 2nd variation





## Biosynthesis of purine and pyrimidine nucleotides

- all cells needs ribonucleosides, deoxyribonucleosides and their phosphates
- purine and pyrimidine basis from food are not used
- **Synthesis of purine and pyrimidine nucleotides are coordinated**

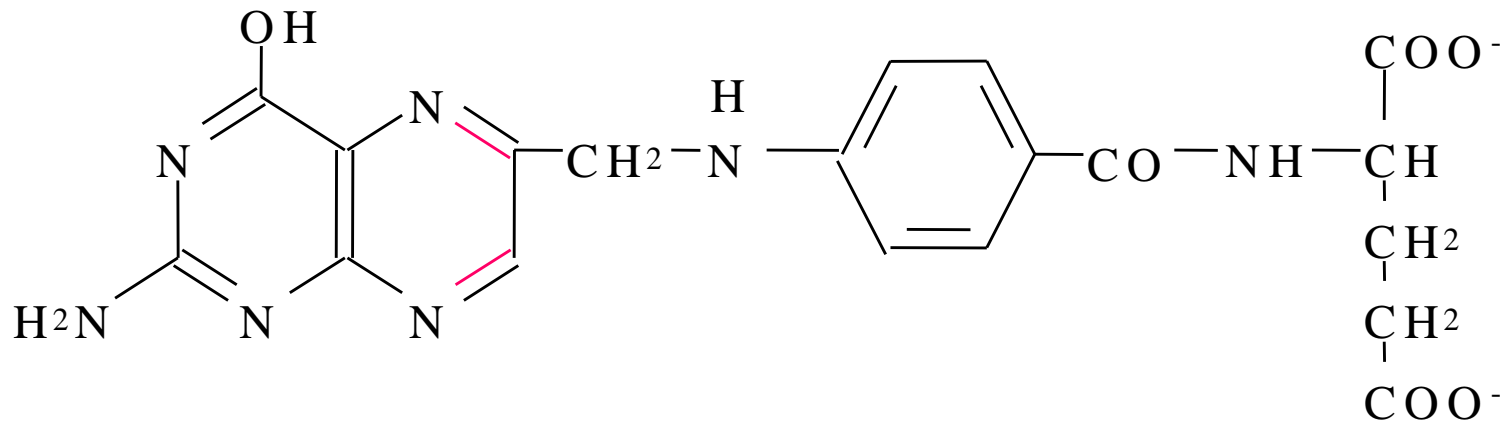
# Precursore molecules

- 3 main compounds:
- **tetrahydrofolate**
- **glutamine**
- **PRPP – 5-phosphoribosyl-1-pyrophosphate**

# Importance of folic acid for biosynthesis of NA bases

Green leafy vegetables,  
liver, whole grains, yeast, k

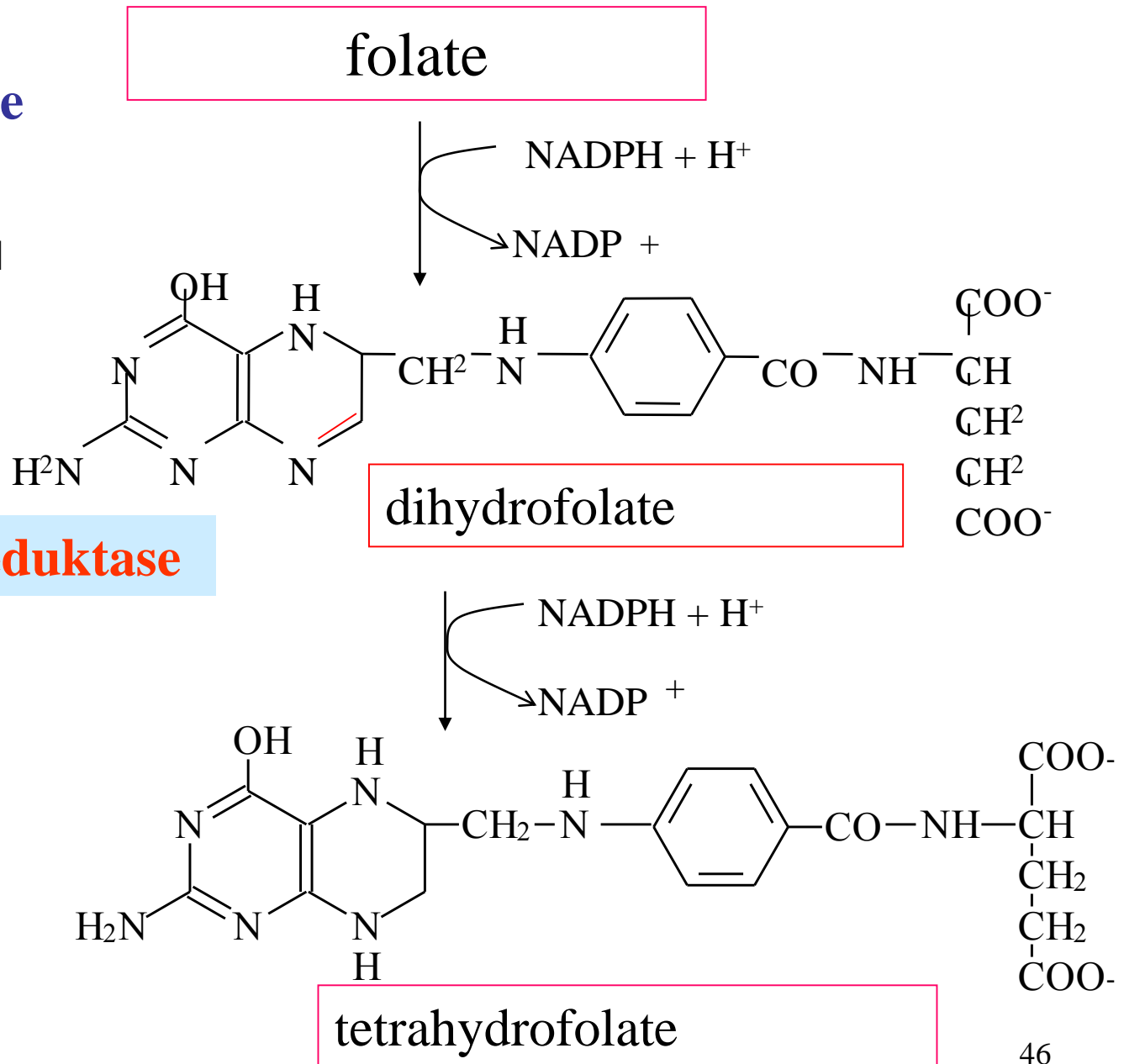
Folate



Used form in human is tetrahydrofolate

# Formation of tetrahydrofolate

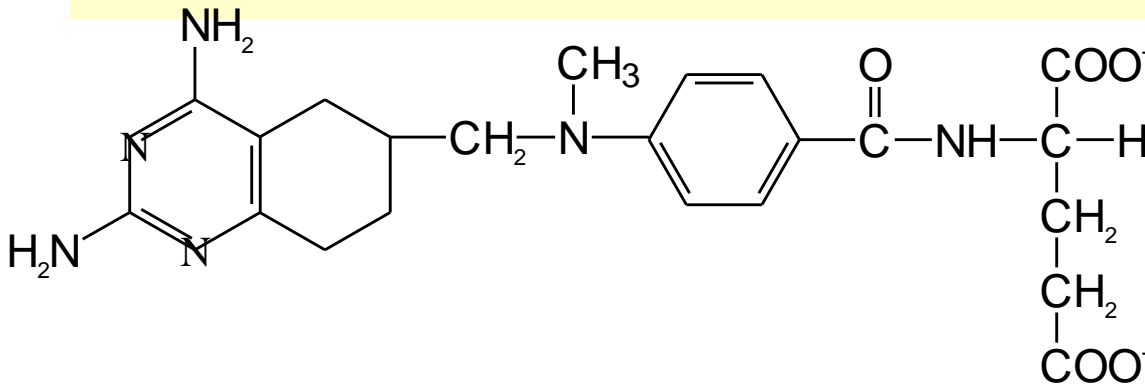
## DEHYDOGENATION



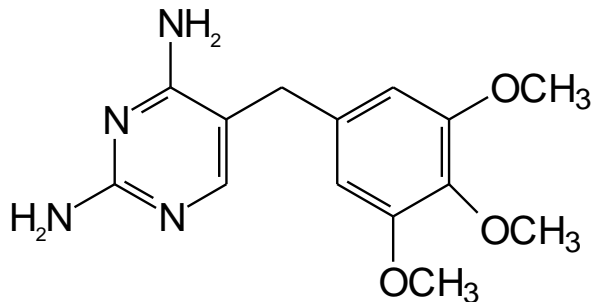
**(dihydro)folatereduktase**

# Inhibitors (dihydro)folatereductase:

Methotrexate (anticancer agent)

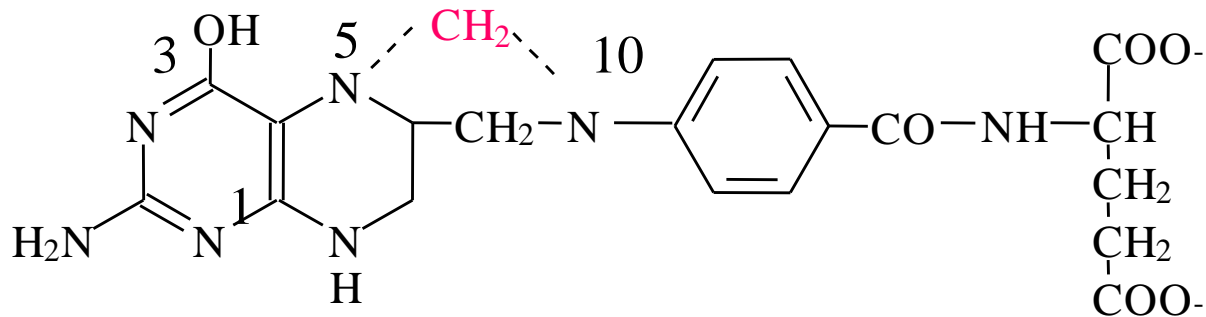


Trimethoprim (bacteriostaticum)

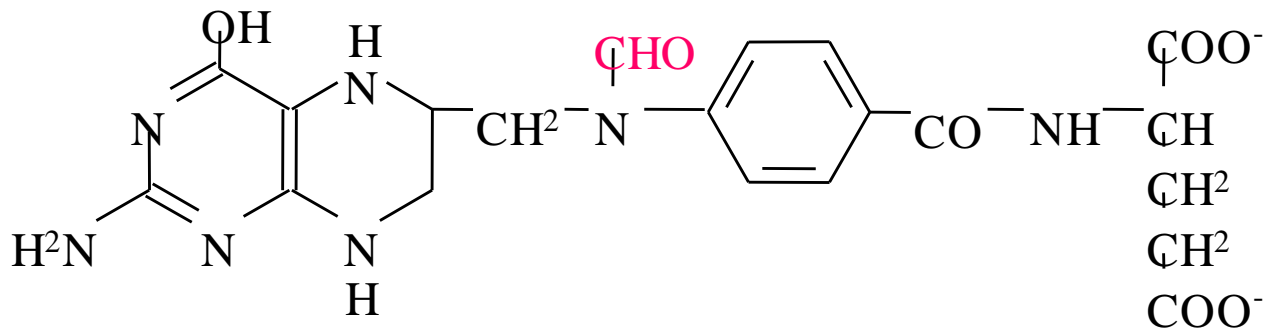


# Using of tetrahydrofolate

## N-5,N-10- methylen H<sub>4</sub>F – synthesis of thymine



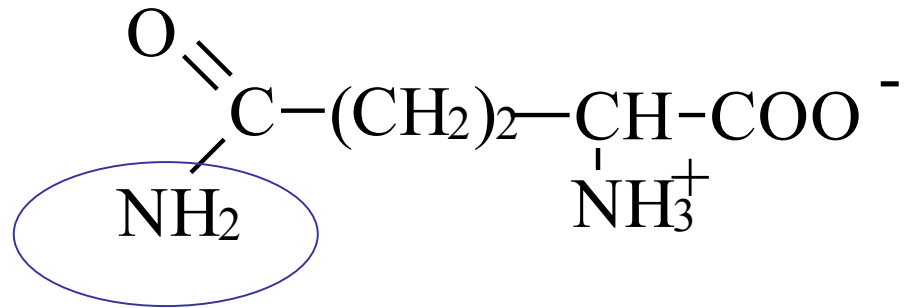
## N-10-formyl H<sub>4</sub>F – synthesis of purins



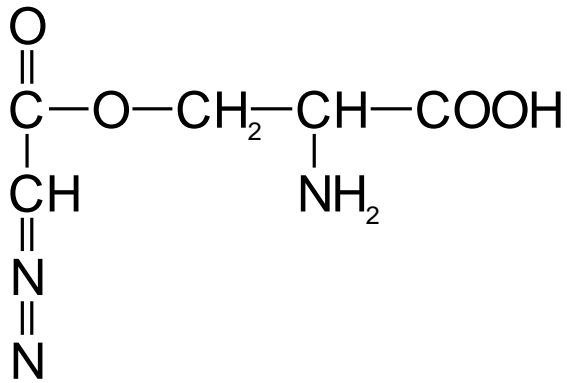


# Importance of glutamin for purine and pyrimidine biosynthesis

- Donor of aminogroup



# Glutamine antagonists inhibits synthesis of purines and pyrimidines



azaserin

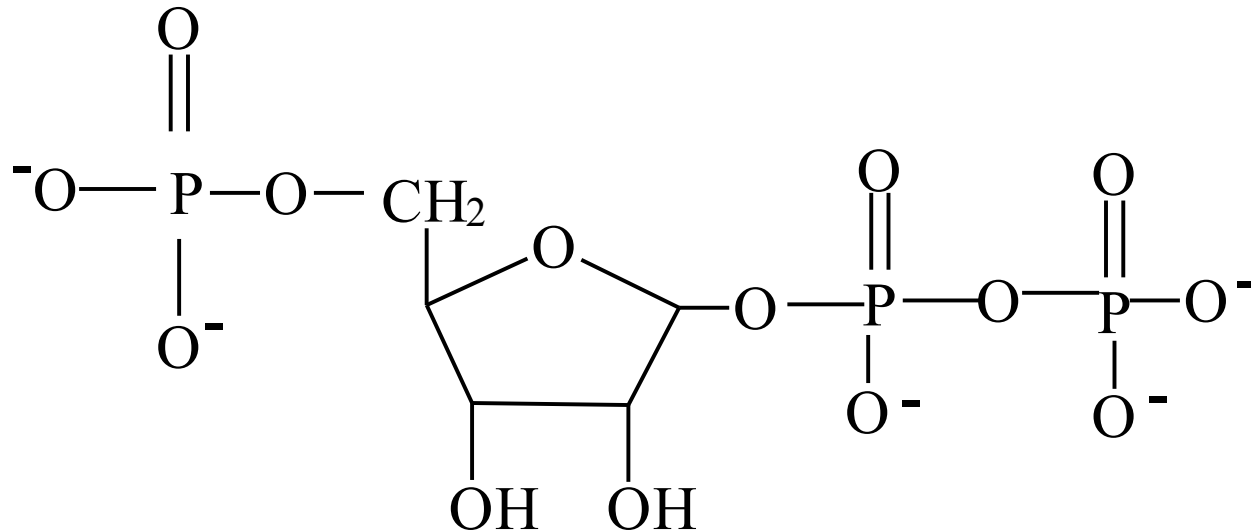
# PRPP - phosphorybosylphosphoribosylphosphate

## Necessary for synthesis:

Purine nucleotides

Pyrimidine nucleotides

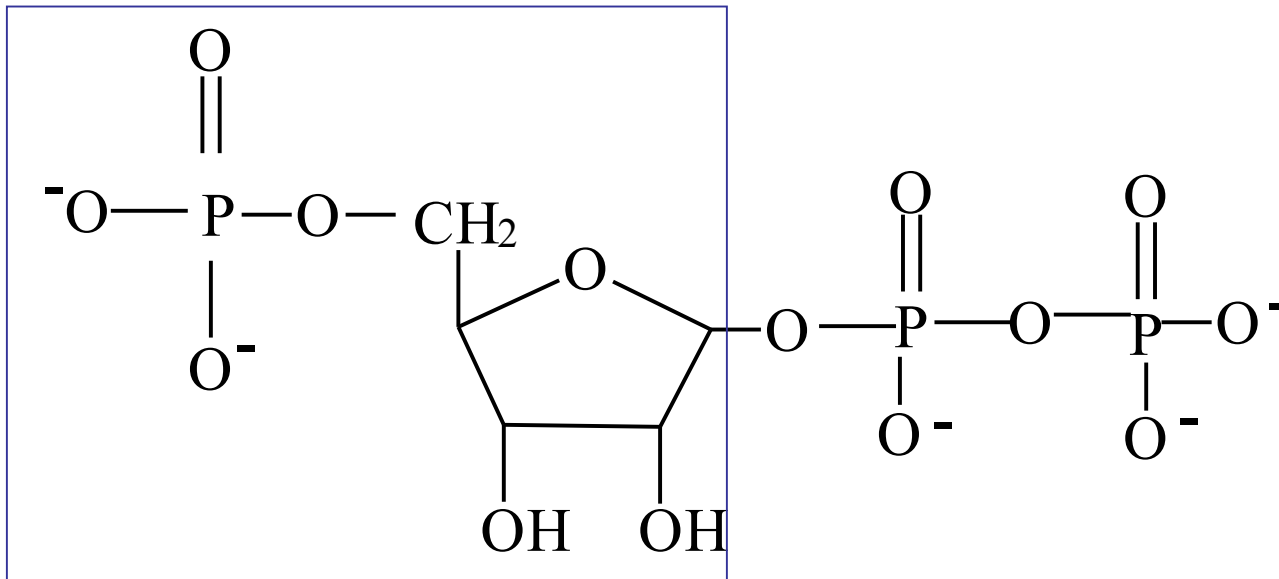
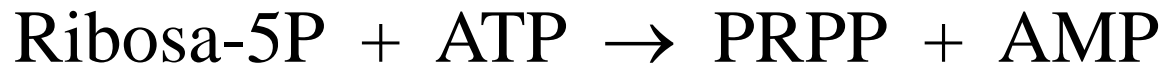
NAD<sup>+</sup>, NADP<sup>+</sup>



# Synthesis of PRPP

PRPP-synthetase

ribose-5-phosphate  
(pentose cycle),  
activated penthose



# Differences in purine and pyrimidine synthesis

Synthesis - *puzzle* – one part to others.

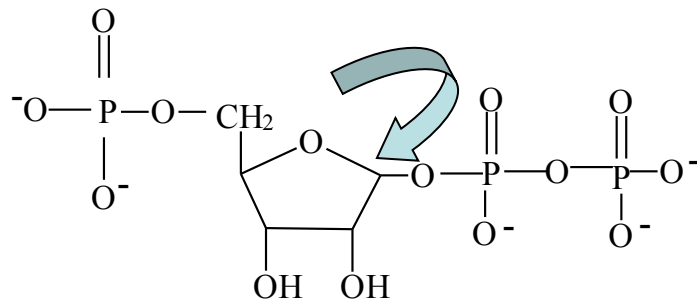
TEST

## Difference in the beginning :

- purines : first PRPP and than is form base
- Pyrimidines : first base and than ribosa-5-P from PRPP.

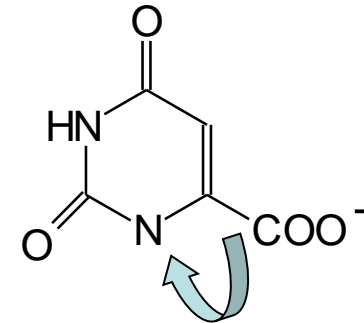
## Purins

First PRPP...



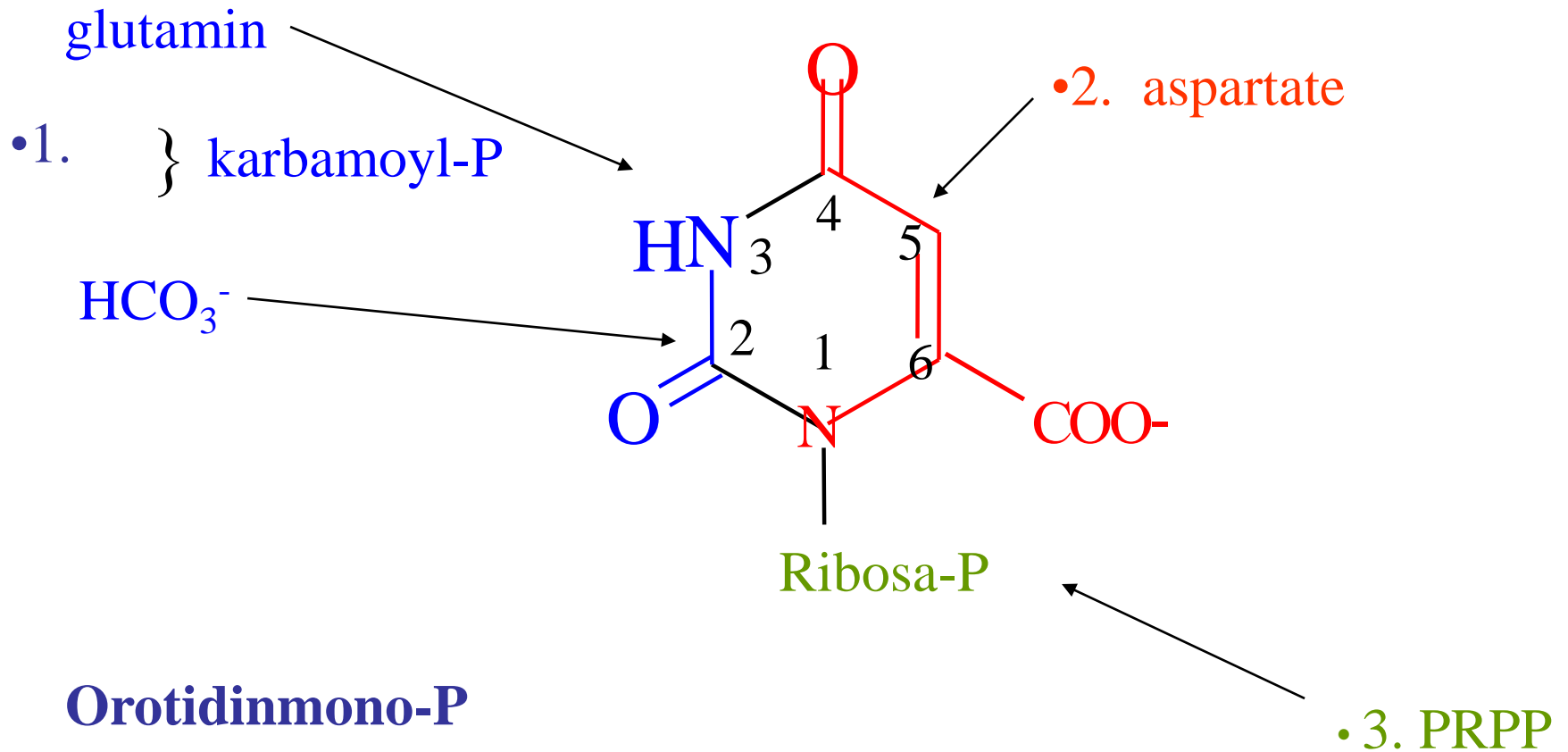
## Pyrimidins

First heterocycle ribose-P from PRPP



# BIOSYNTESIS of PYRIMIDINES

## Origin of atoms in pyrimidines



**Orotidinmono-P**

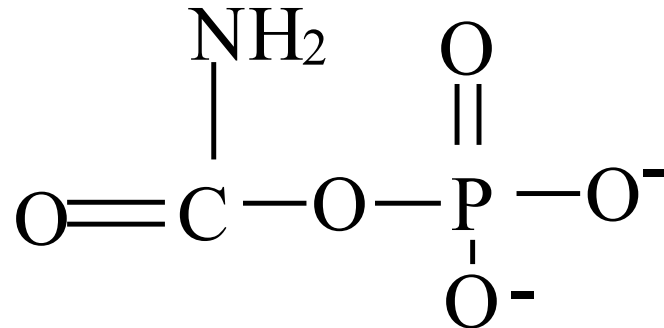
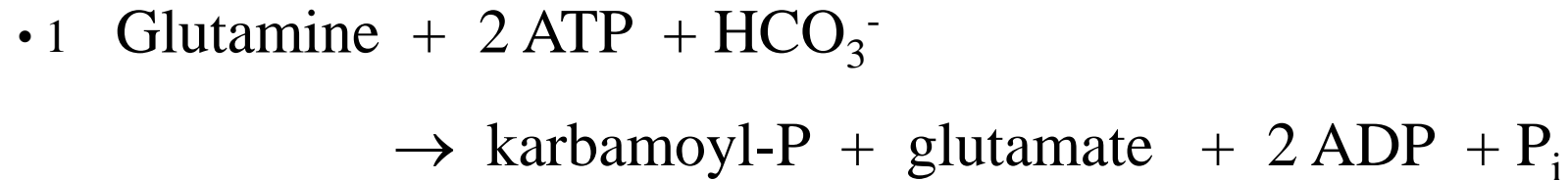
**Decarboxylation – uridin mono-P**

# • synthesis of karbamoyl -P

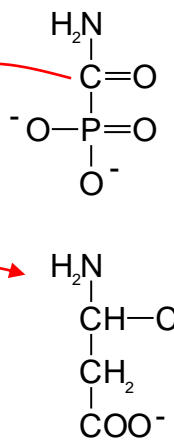
## CYTOPLASM

### Karbamoyl-P-synthetase

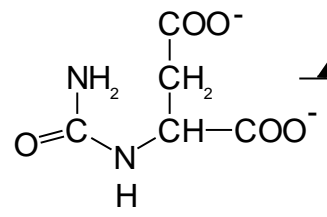
-energy, enzym **karbamoylphosphatesynthetase II**  
**Inhibition by UTP** („inhibition by product“) and  
**aktivation by ATP**.



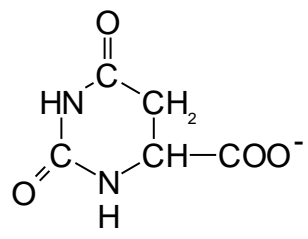
karbamoylP



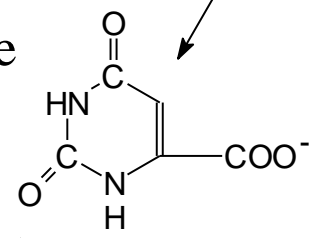
P<sub>i</sub>



karbamoylaspartate

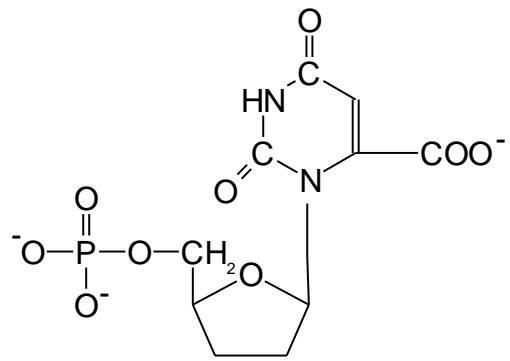


dihydroorotate

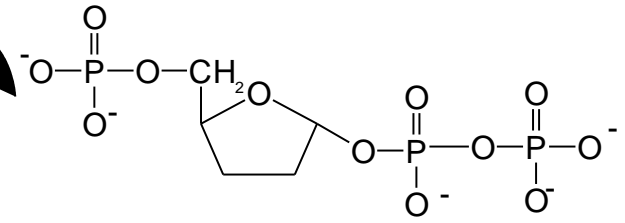


orotate

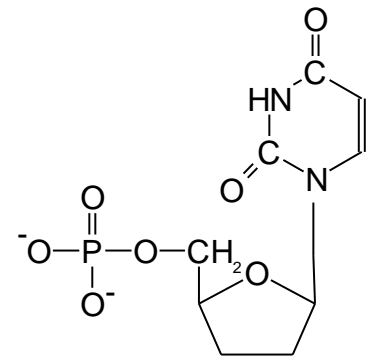
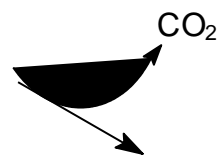
aspartate



Orotidinmono-P



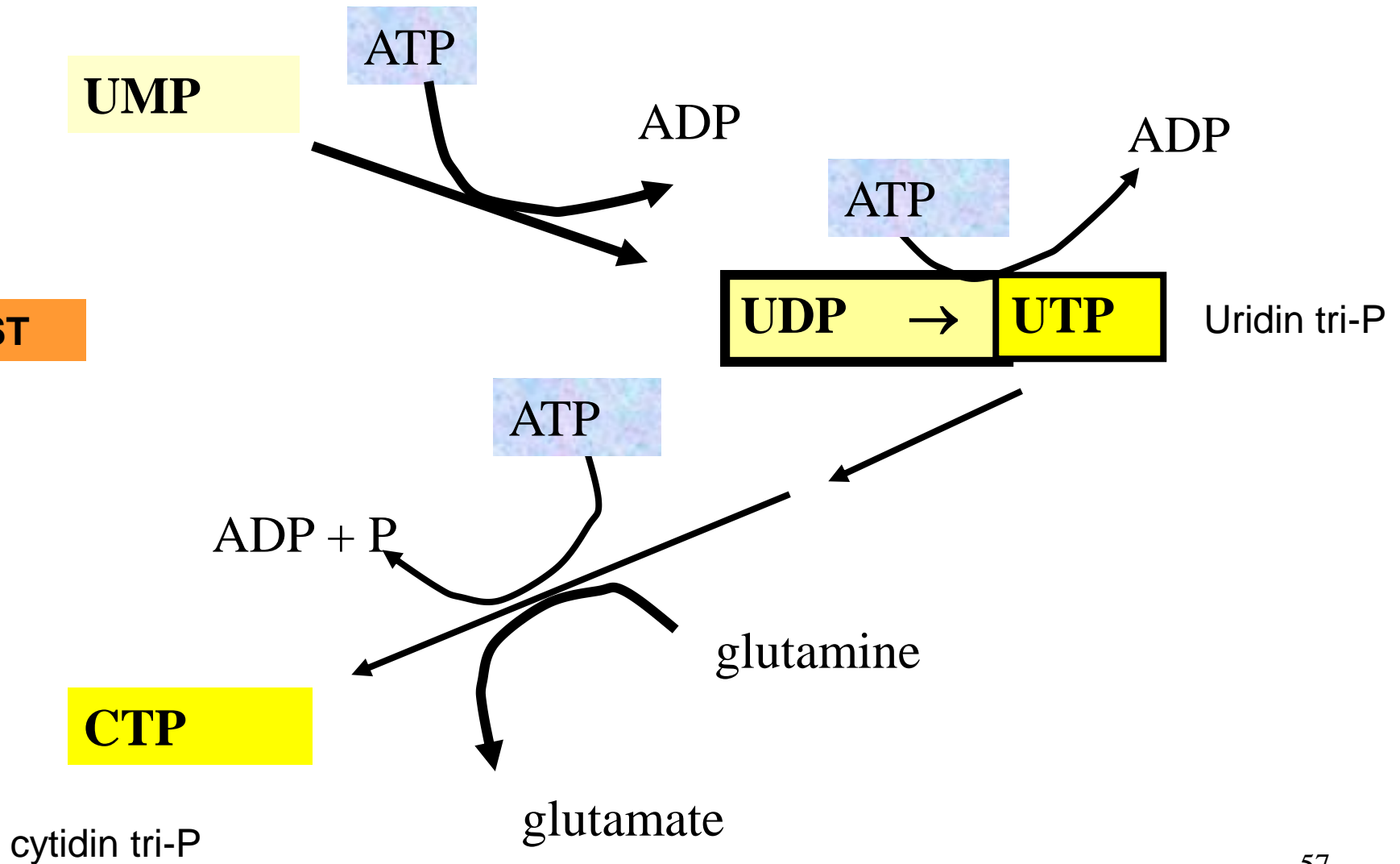
PRPP



Uridinmono-P (UMP)

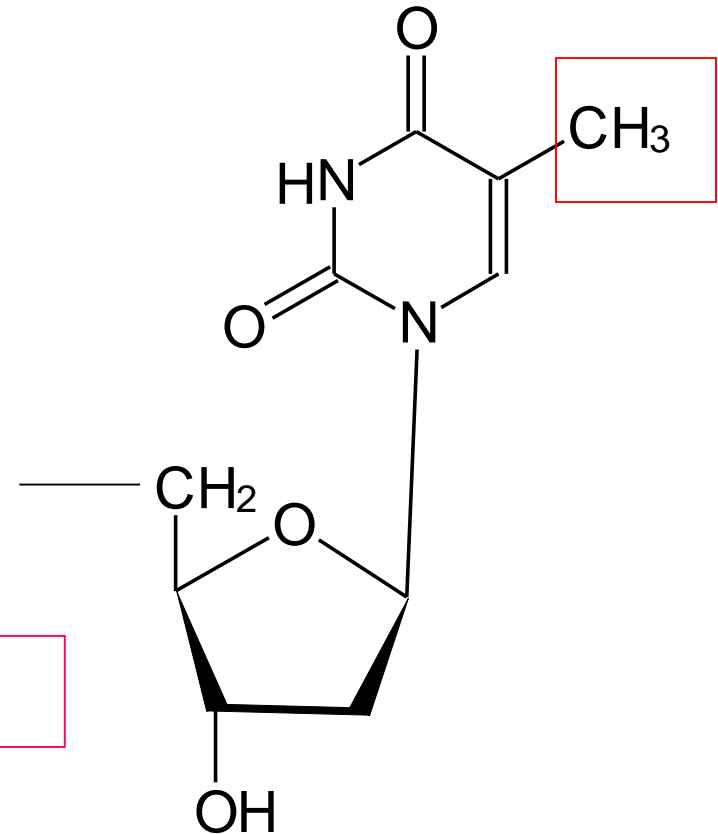


# Biosynthesis of UTP and CTP



# dTMP (methylation)

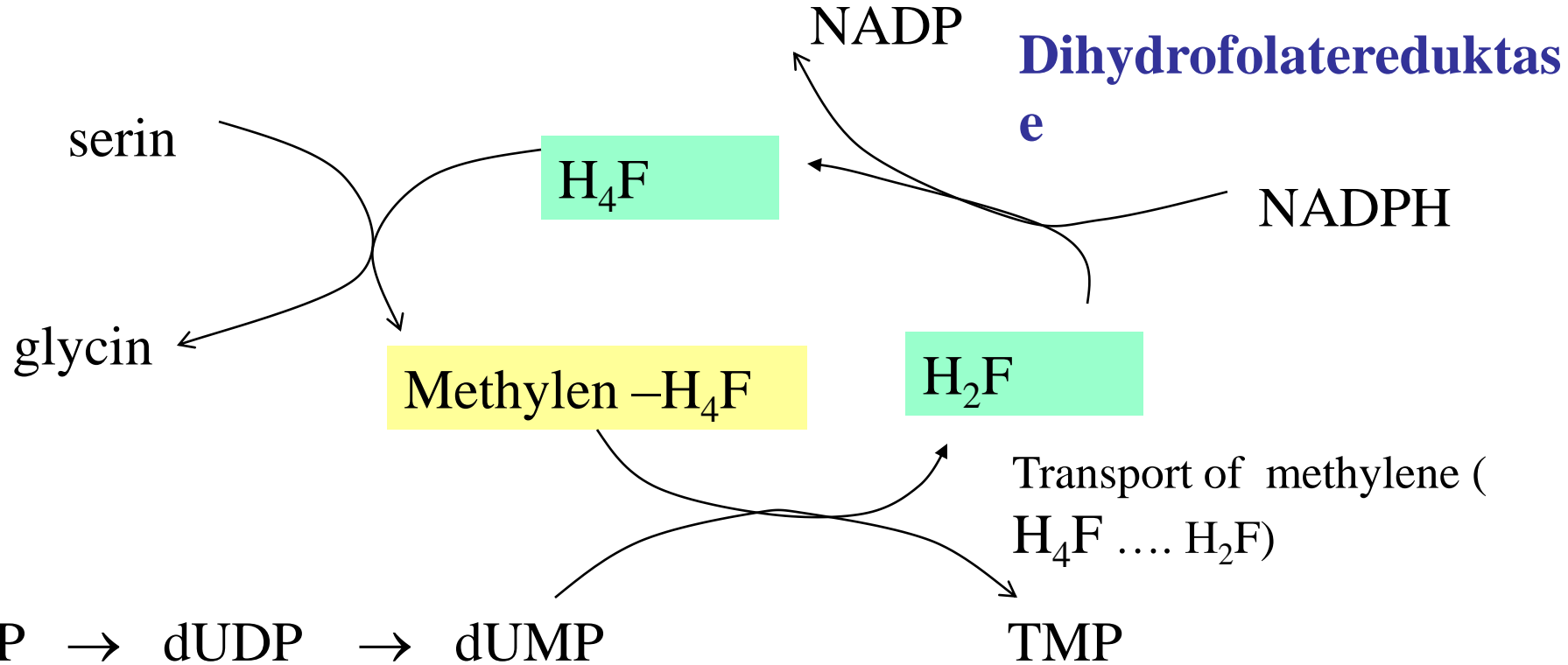
Deoxythymidintri-P



**Methylation- H<sub>4</sub>F**

Methylen group in H<sub>4</sub>F is reduced to methyl dUMP

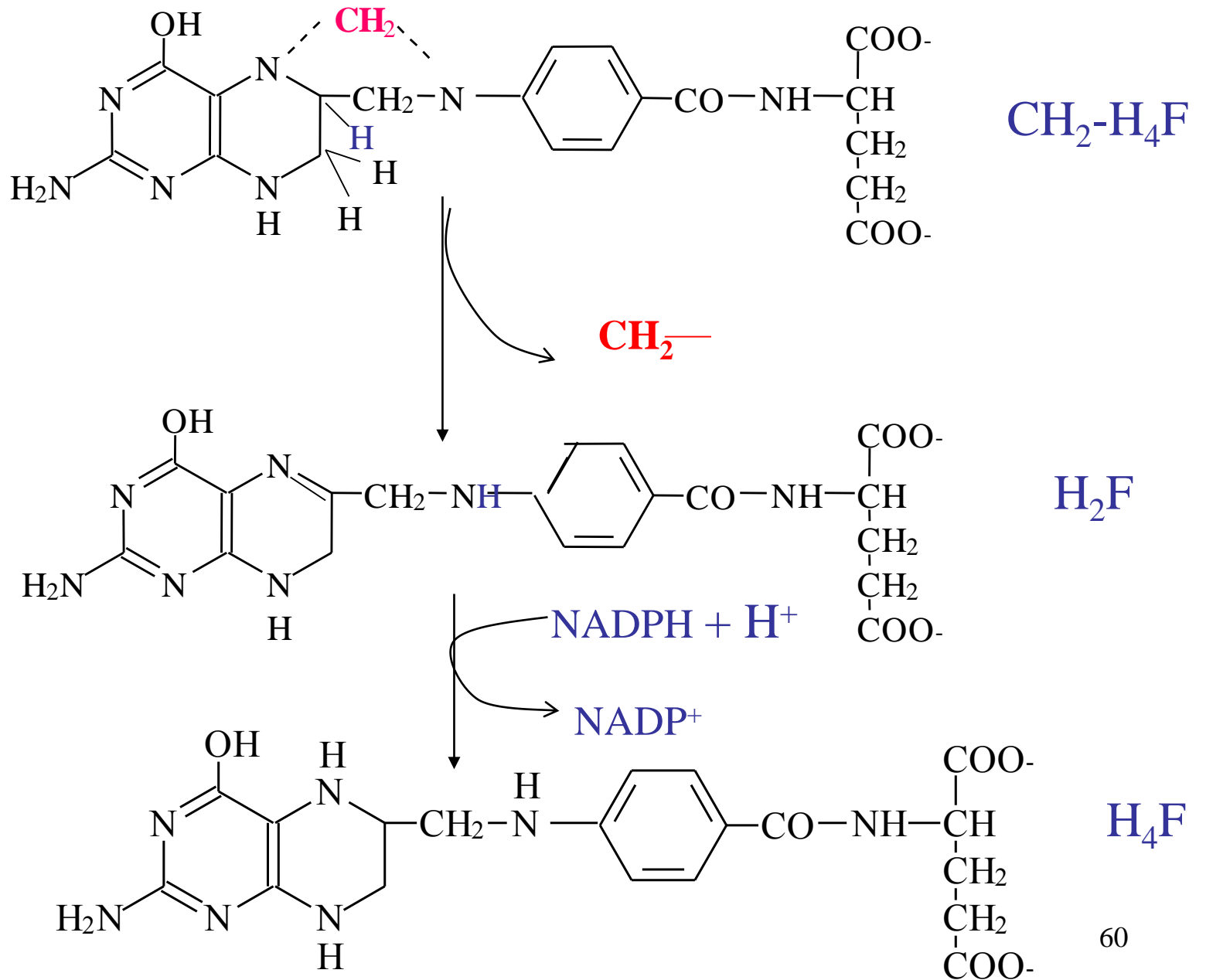
# Synthesis of TMP



TEST

**Thymidylatesynthase**  
(enzym dependent on folate)

Anticancer drugs



# **Dihydrofolate reductase - an objective antitumor therapy.**

Dihydrofolate reductase was the first enzyme for which focused antitumor therapy.

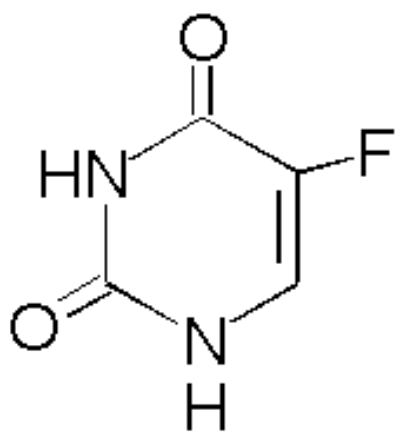
The first-used inhibitor was aminopterin.

It binds to the enzyme 1000 times tighter than folate, acts as a competitive inhibitor.

Currently used methotrexate and similar derivatives.

All drugs which affect the synthesis of purines and pyrimidines, deplete rapidly dividing cells - but not only cancer cells but also cells in the bone marrow and GI tract cells such as hair follicles.

thymidylate synthase



5-fluorouracil

The administration of fluorouracil



organism conversion to  
5-fluorodeoxyuridine monophosphate



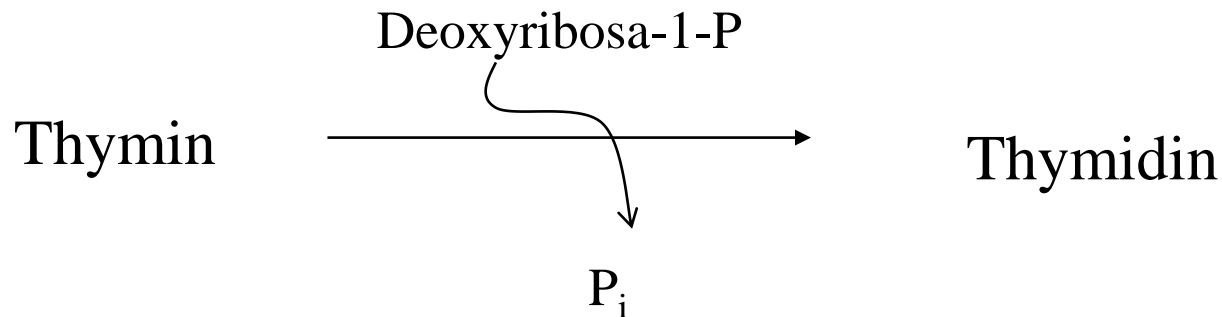
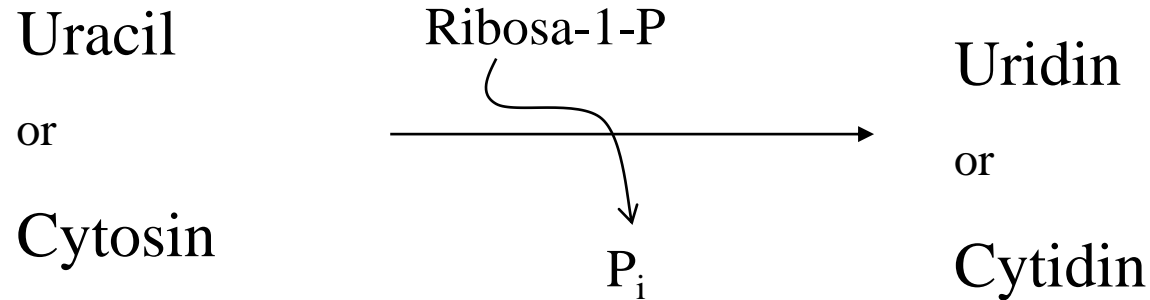
Competitive inhibition  
thymidylatesynthasy

Thymidylate synthase because it is blocked by a competitive inhibitor, which in effect prevents dTMP, resulting in a slowdown (disabling) of cell division.

**The cytostatic effect of a drug**

## 2. Synthesis of pyrimidins by *salvage pathway*

### 1. nukleosides



## 2. Kinase - phosphorylation

- $\text{thymidin} + \text{ATP} \rightarrow \text{TMP} + \text{ADP}$
- $\text{cytidin} + \text{ATP} \rightarrow \text{CMP} + \text{ADP}$
- $\text{deoxycytidin} + \text{ATP} \rightarrow \text{dCMP} + \text{ADP}$
- $\text{uridin} + \text{ATP} \rightarrow \text{UMP} + \text{ADP}$

**Salvage pathway – extrahepatal tissues**



# Regulation of biosynthesis of pyrimidins

## ☐ **Allosteric:**

- KarbamoylPsynthetase:  
inhibition by UTP, purins nucleotides,  
aktivation by PRPP

☐ dependence on cell cycle

KarbamoylP-synthetase in S phase is more sensitive to activation by PRPP

# Degradation of pyrimidins nucleotides

Pyrimidins – to the simple compounds – urine

pyrimidine base, we are able in our body break down into simpler components

STEPS:

a) Release of P

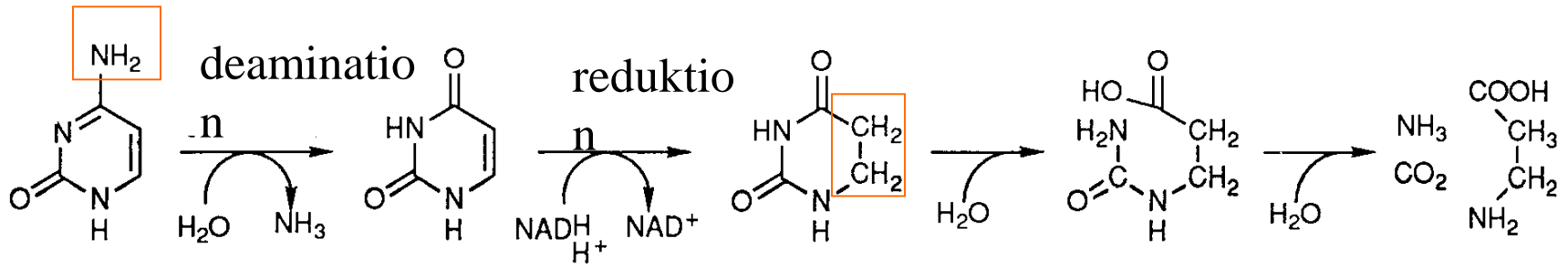
b) Release of sugar

c) Degradation of pyrimidin base

End products of cleavage of pyrimidines:

$\text{NH}_3$ ,  $\text{CO}_2$ ,  $\beta$ -alanin, ( $\beta$ -aminoisobutyrate)

Soluble metabolist – excretion by urine



$\beta$ -alanin

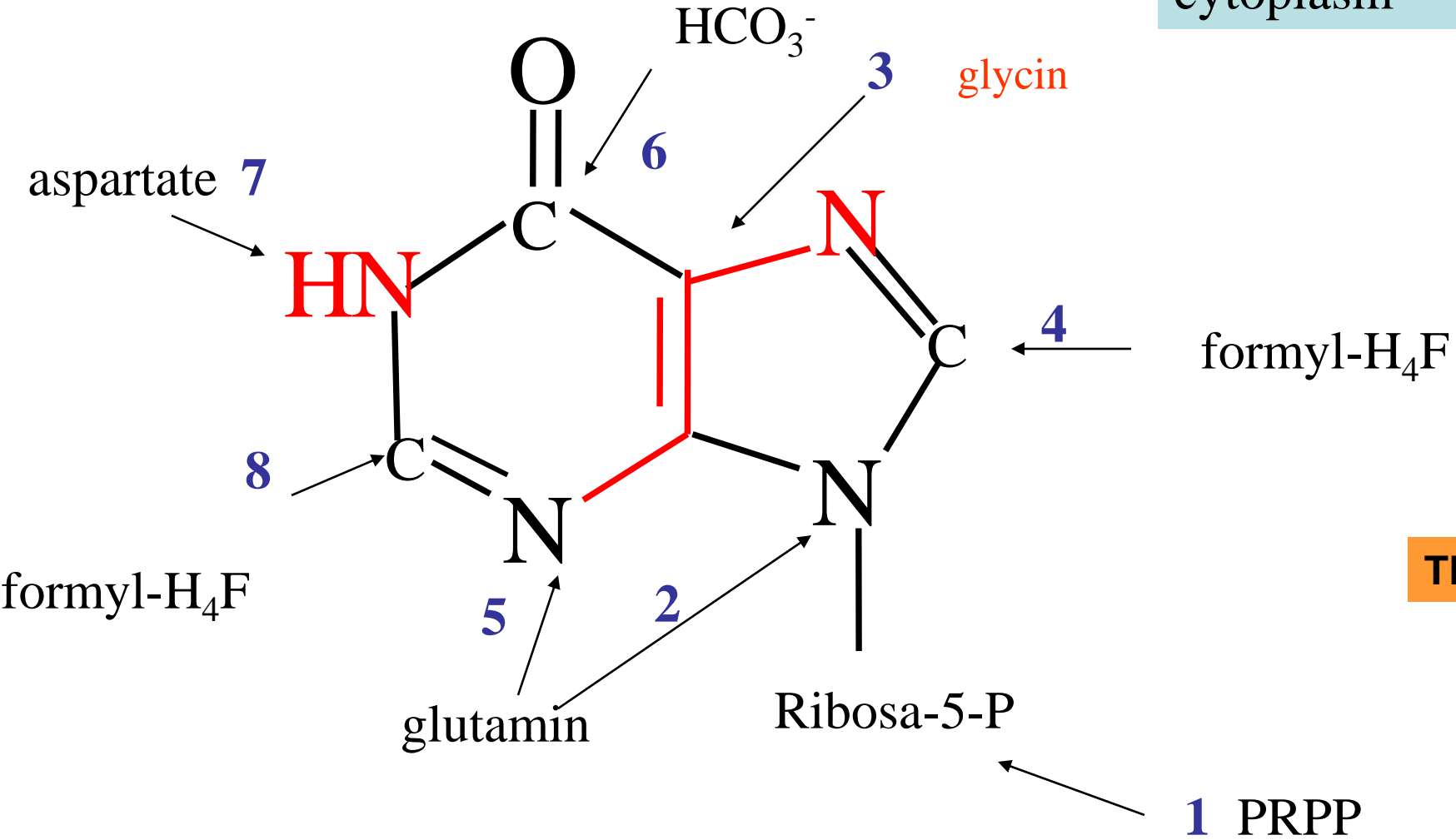
$\beta$ -aminoisobutyrate<sup>66</sup>

# Biosynthesis of purins

(multienzym complex)

liver

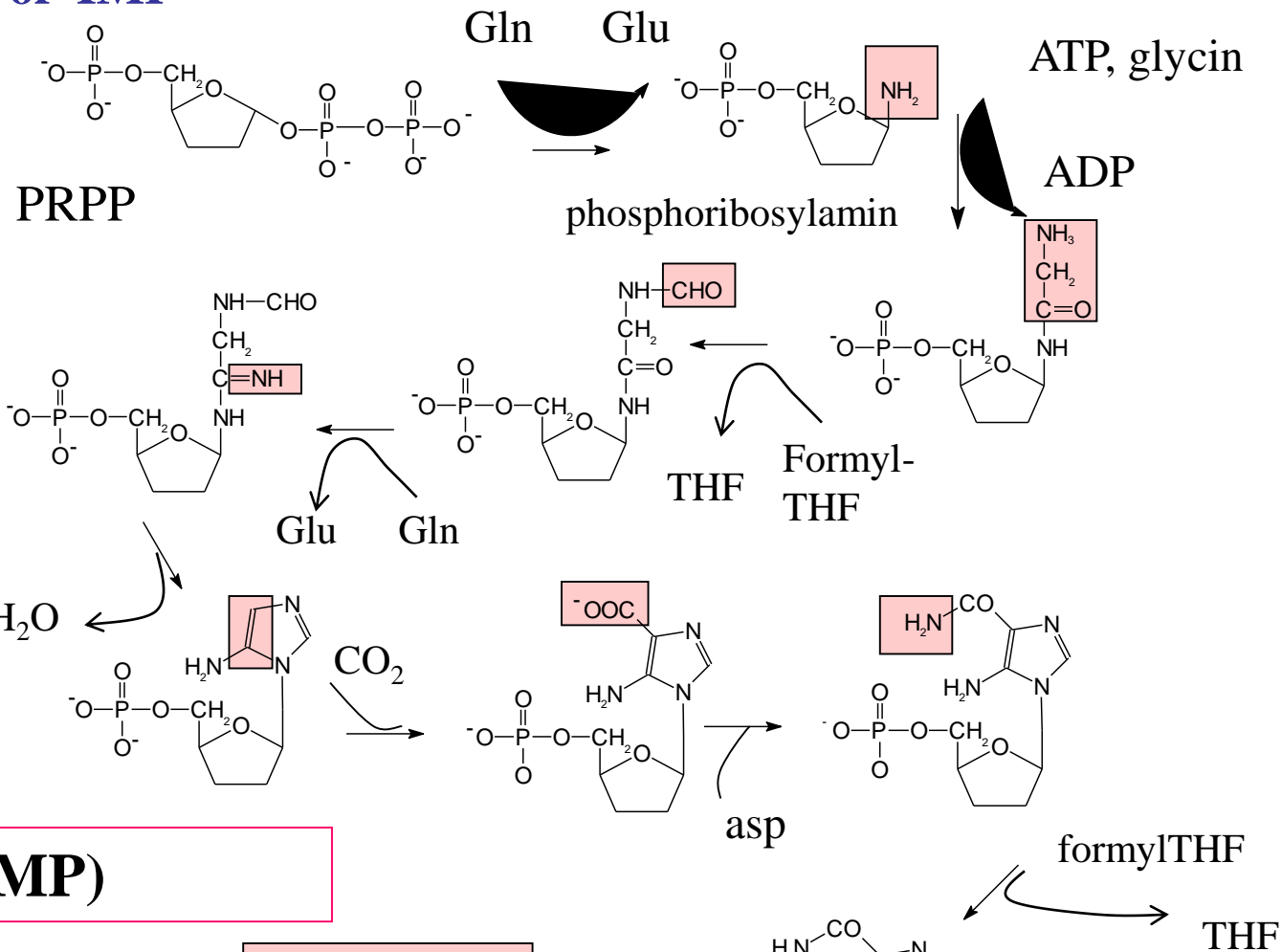
cytoplasm



TEST

**Inosin-5-P (IMP)**

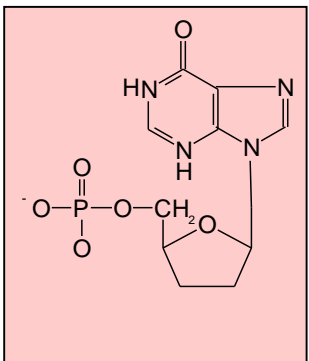
# Biosynthesis of IMP



TEST

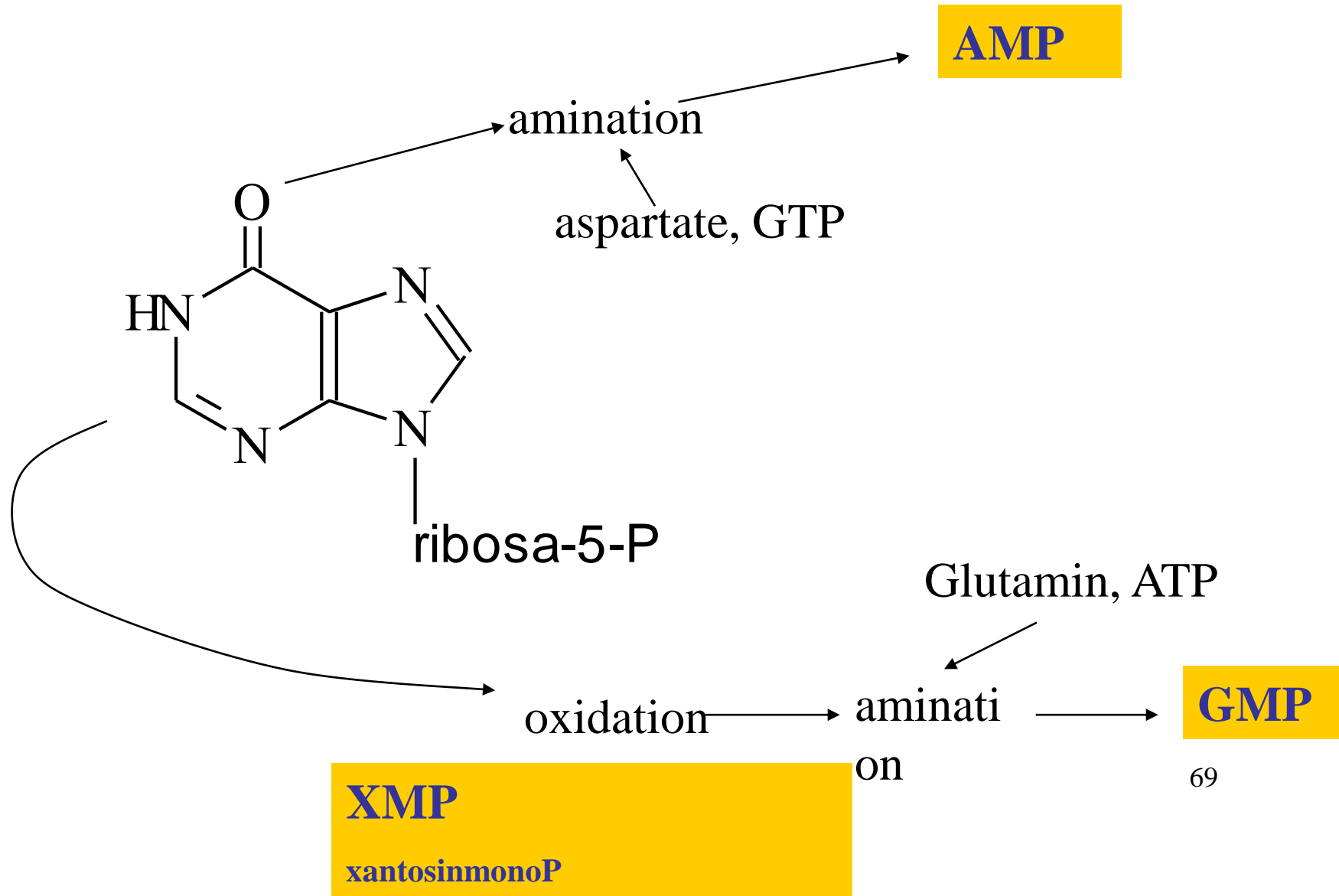
Inosin-5-P (IMP)

inosinmonophosphate



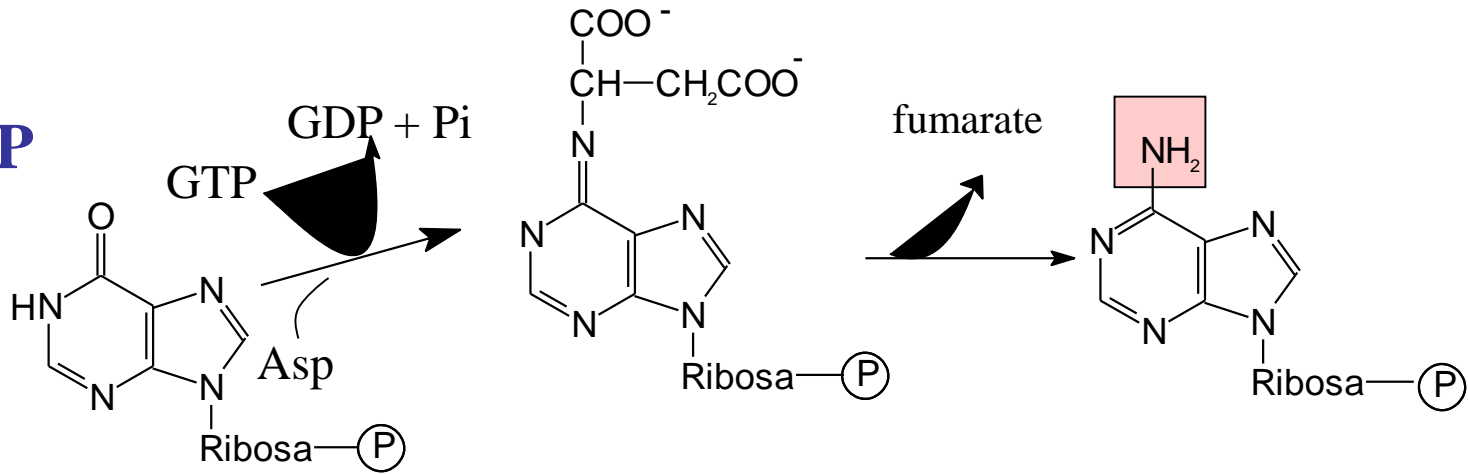
# Inosin-5-P (IMP)

Initial substance for synthesis of other basis

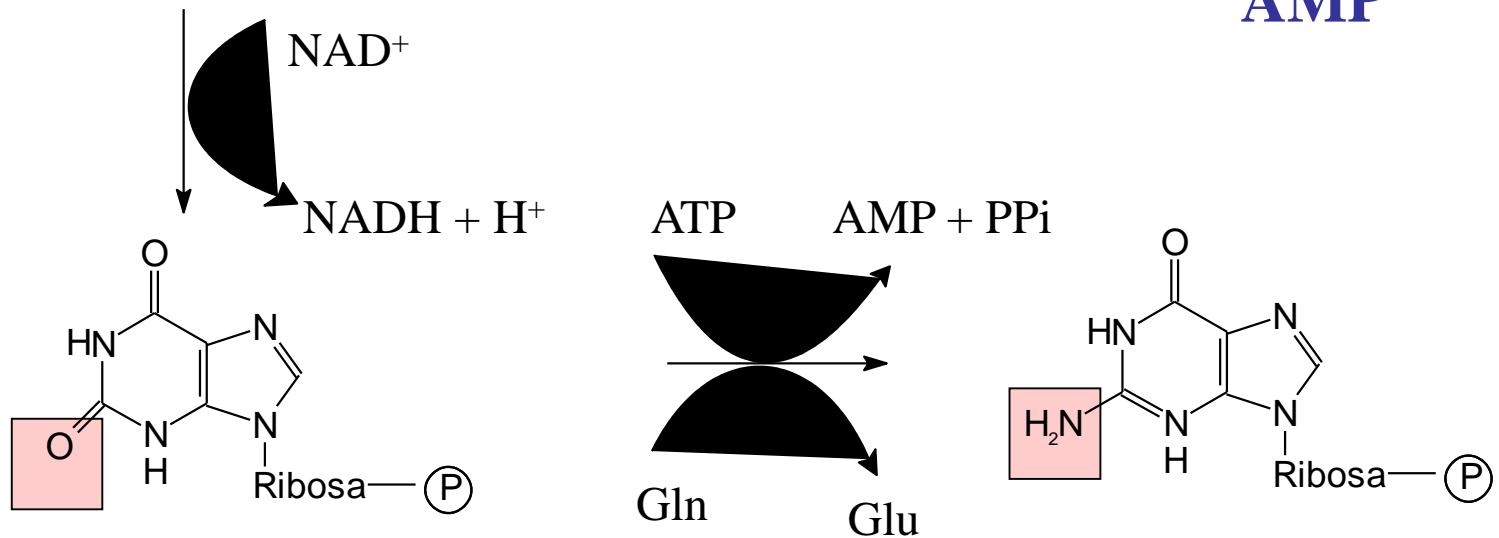


# Synthesis of AMP and GM

**IMP**



**AMP**

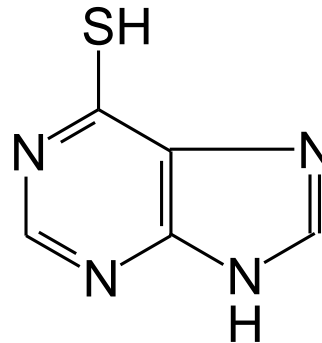


**XMP**

**GMP**

## Inhibitors of syntesis of purins (cytostatics)

- inhibitors dihydrofolate reductase
- analogy glutamin (azaserin)
- 6-merkaptopurin- inhibition of change IMP to AMP and GMP



merkaptopurin

# Syntesis of purins by salvage pathway

## Extrahepatal tissue

phosphoribosyltransferas

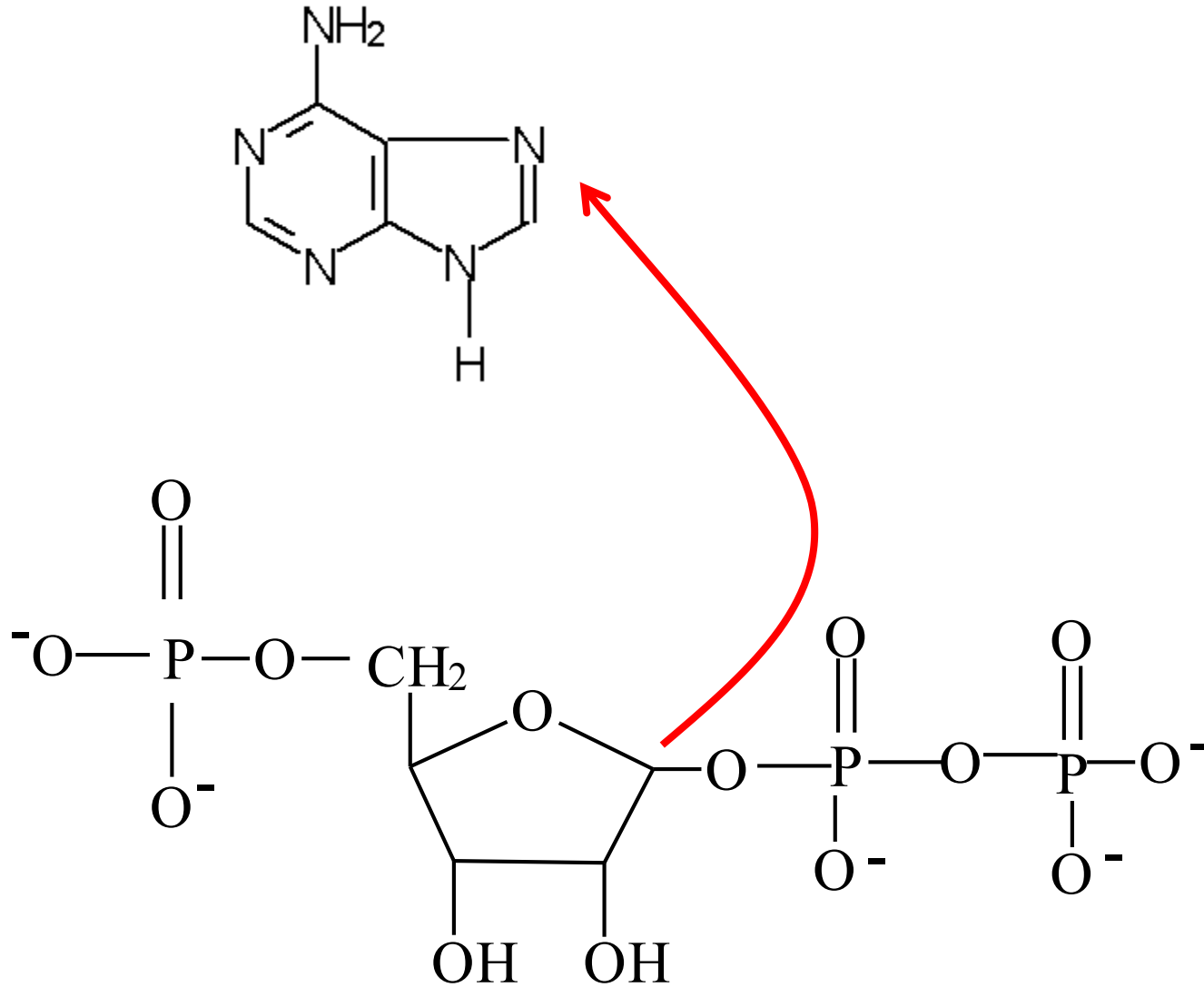
e



Recyclation of purins **phosphoribosyltransferase**



# phosphoribosyltransferase



AMP adeninphosphoribosyltransferase

# **Phosphoribosyltransferase deficiency causes Lesch-Nyhan syndrome**

**hereditary disease**

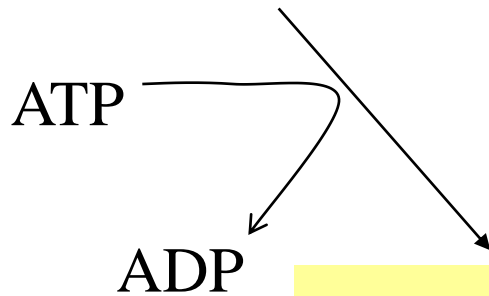
**overproduction purine bases**

**accumulation of uric acid - DNA**

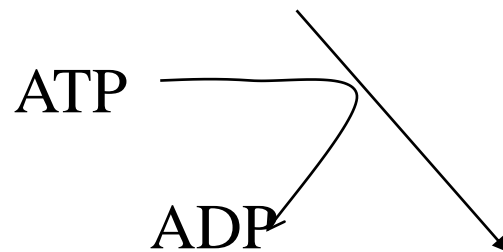
**mental retardation, self-mutilation**

# Syntesis of nukleotiddiP and triP

nukleosidmonoP

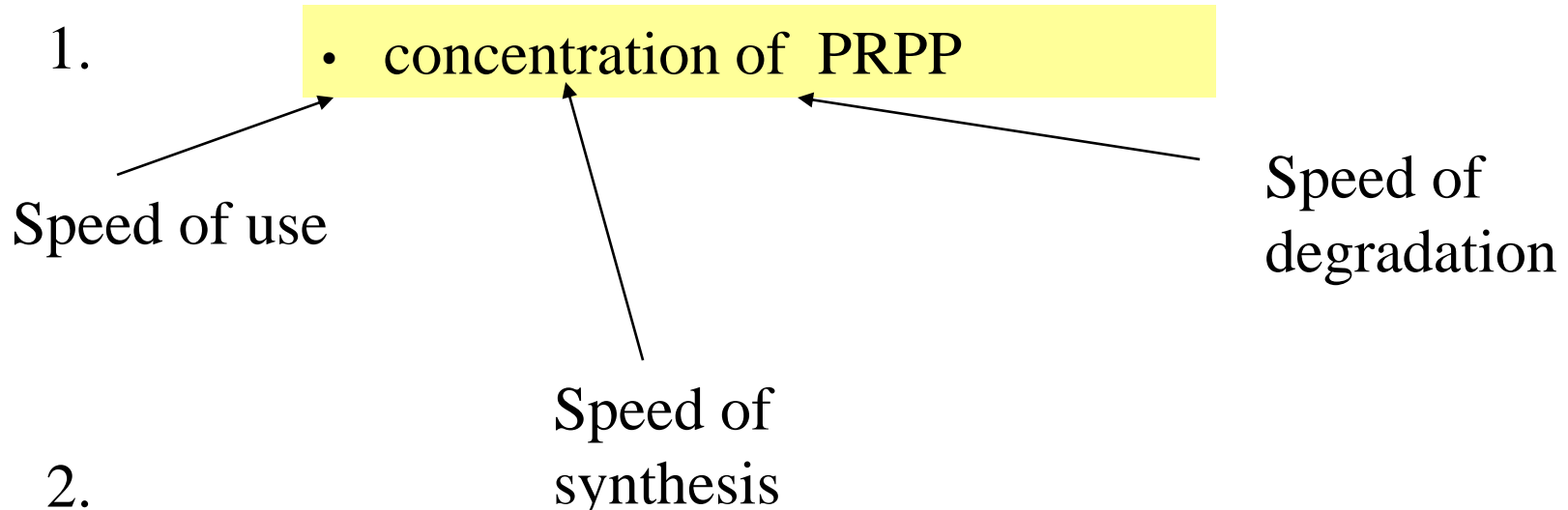


nukleotiddiP

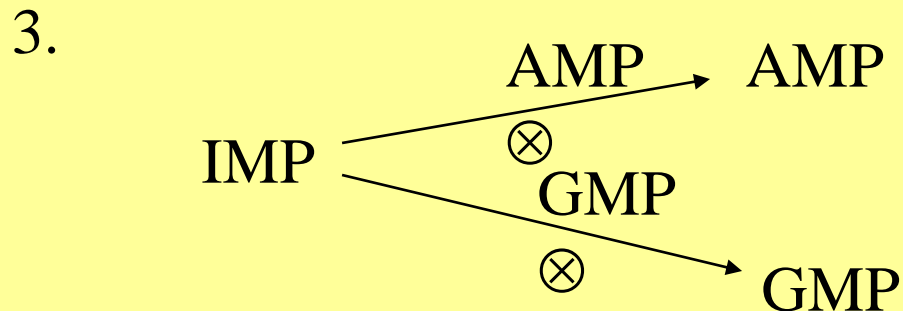


nukleotidtriP

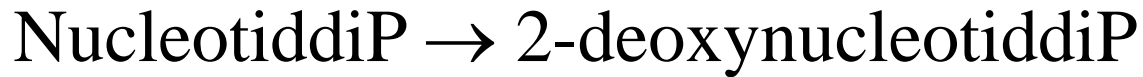
# Regulation of biosynthesis of purins



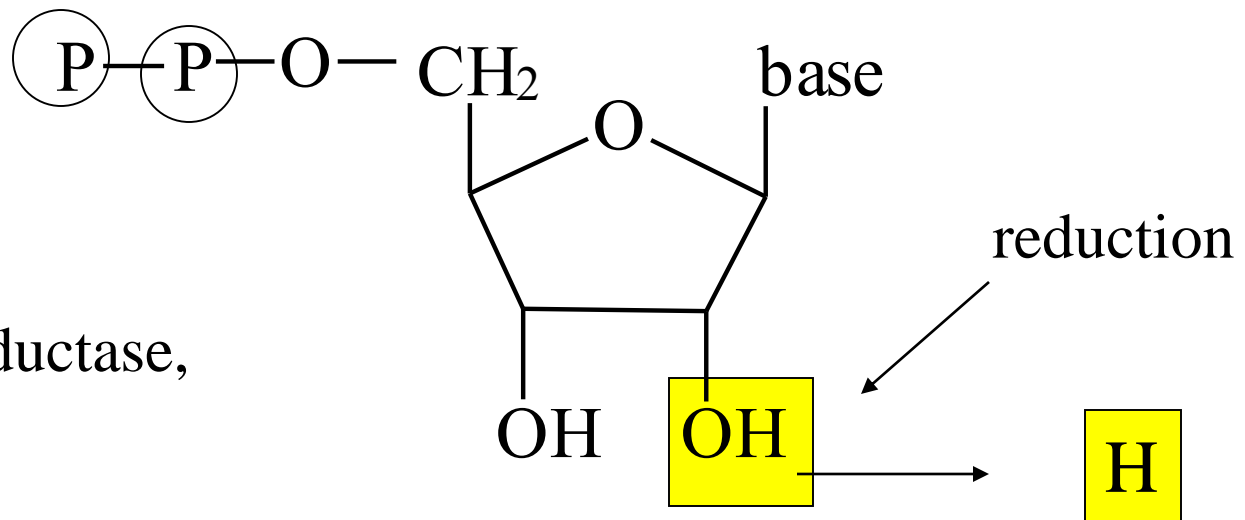
2. • inhibice PRPP-glutamylamidotransferase by AMP and GMP (end products)



# 2-deoxyribonucleotides



thioredoxin,  
thioredoxinreductase,  
NADPH

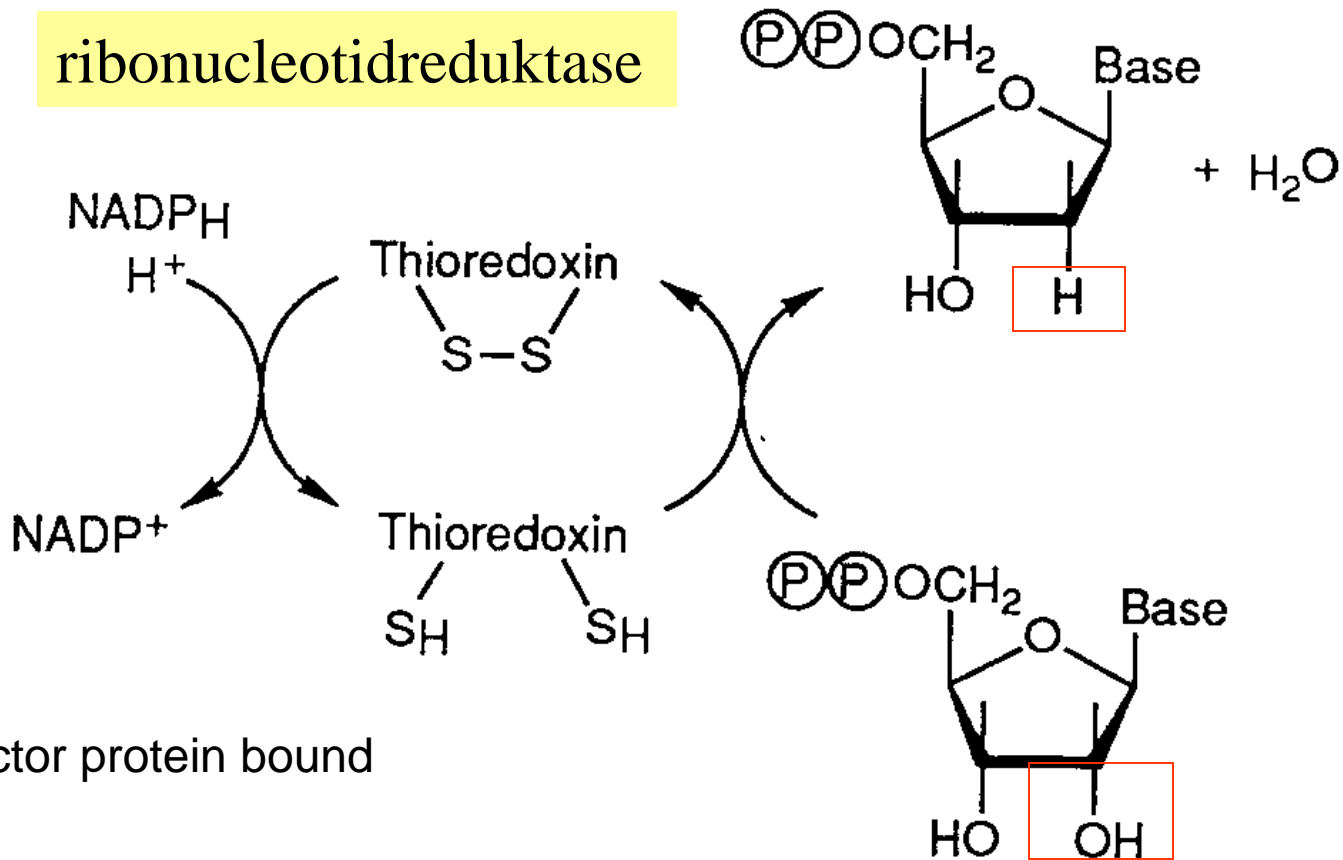


**Thioredoxinreductase - Se**

deoxygenati  
on

# Nukleotiddiphosphate → deoxynucleotiddiphosphate

ribonucleotidreduktase



cofactor protein bound

# Degradation of purines

liver

Cleavage of P

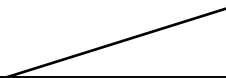
AMP, GMP,  
IMP, XMP

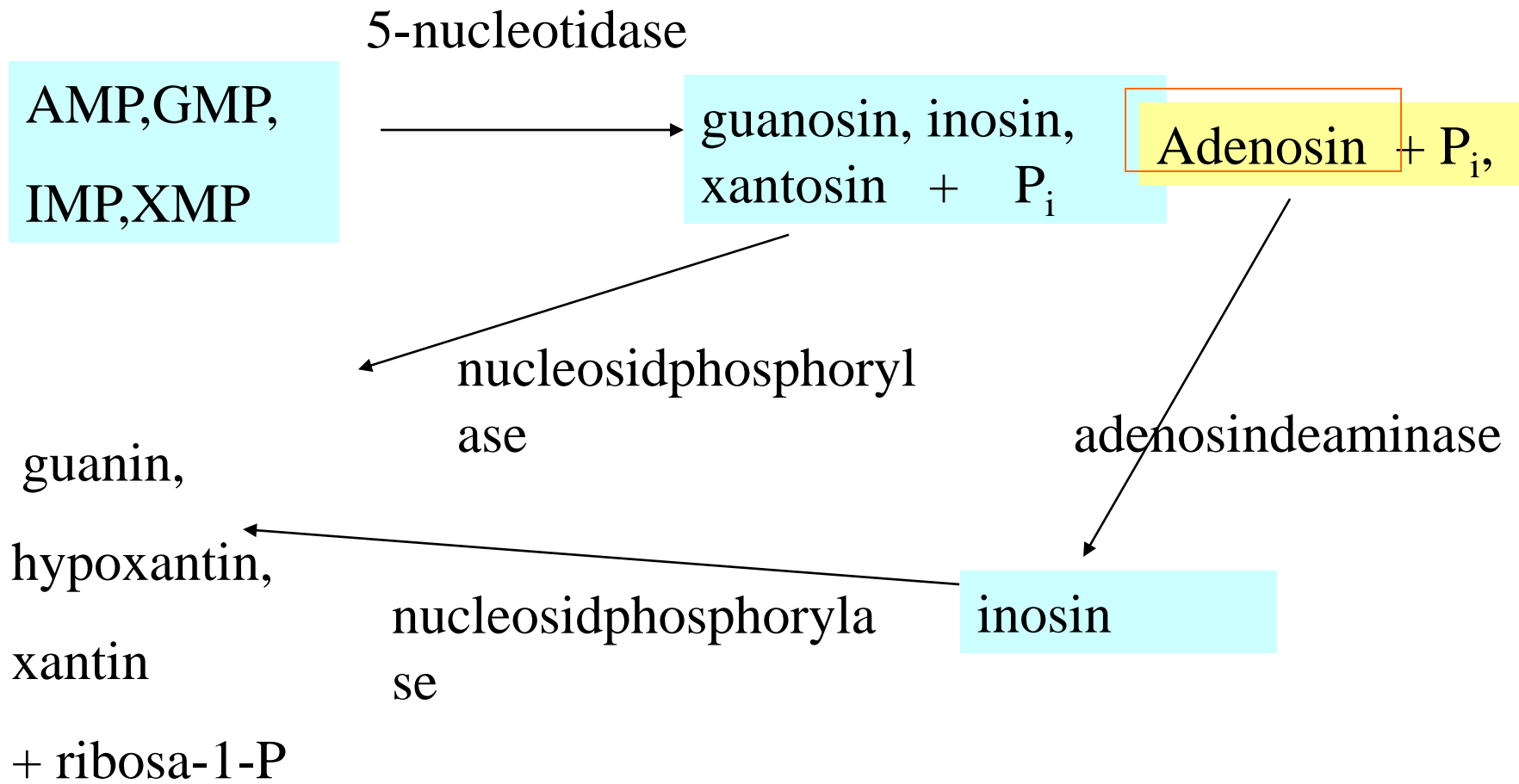
5-nukleotidase



guanosin, inosin,  
xantosin + P<sub>i</sub>

Adenosin + P<sub>i</sub>







# adenosine deaminase deficiency

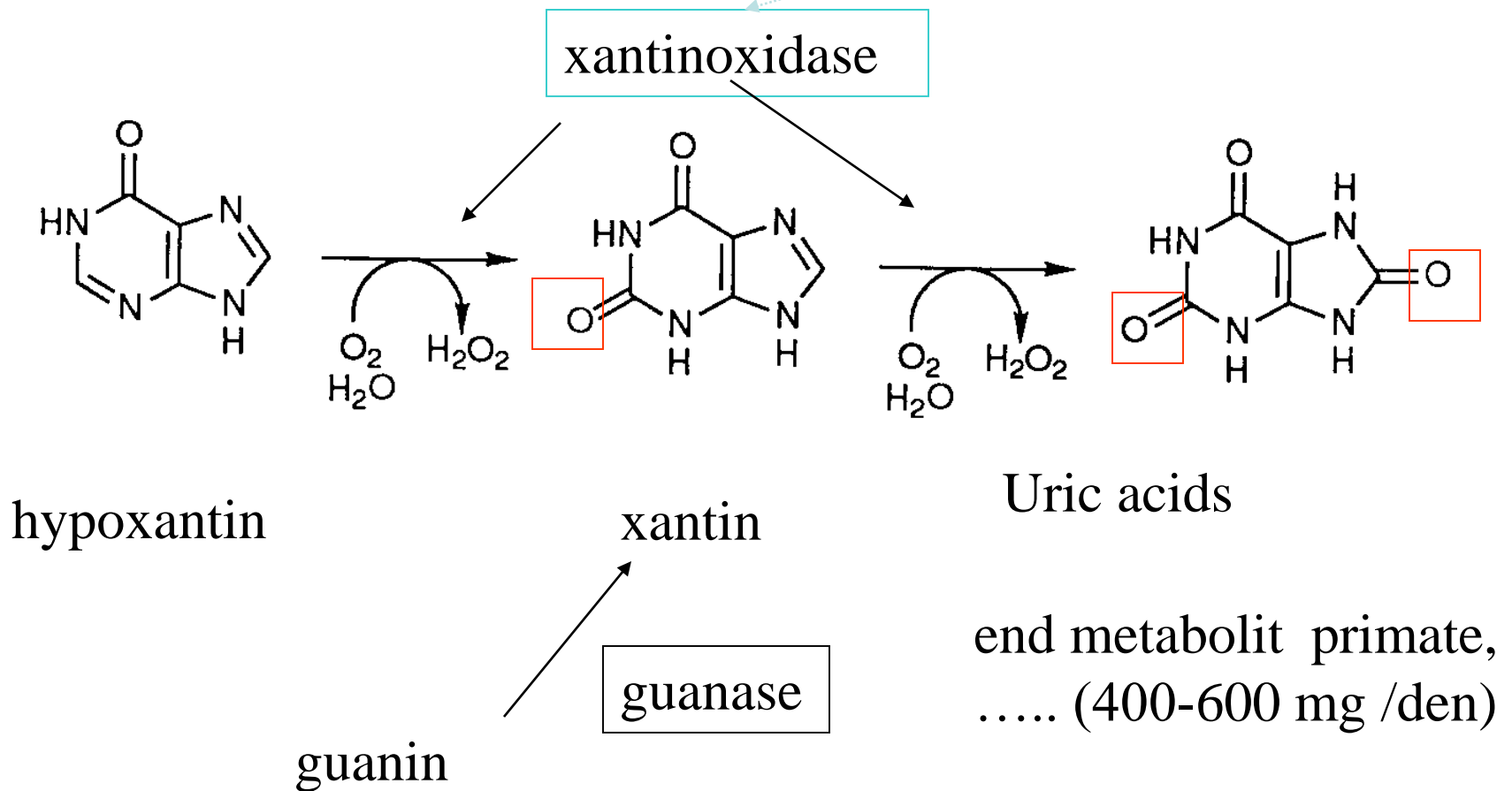
Enzyme deficiency leads to the accumulation of toxic deoxyadenosine, which affects immunocompetent cells

One of the causes of severe combined immunodeficiency (severe combined immunodeficiency disease-SCID).

# Degradation of purins

Inhibition by allopurinolem

TEST



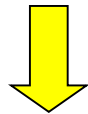
## Defects in metabolism of purins

### **gout**

- increasing of production and decreasing of excretion of uric acid
- defect in salwa pathway
  - (deficit hypoxantin-guaninphosphoribosyltransferase) (HGPRT)

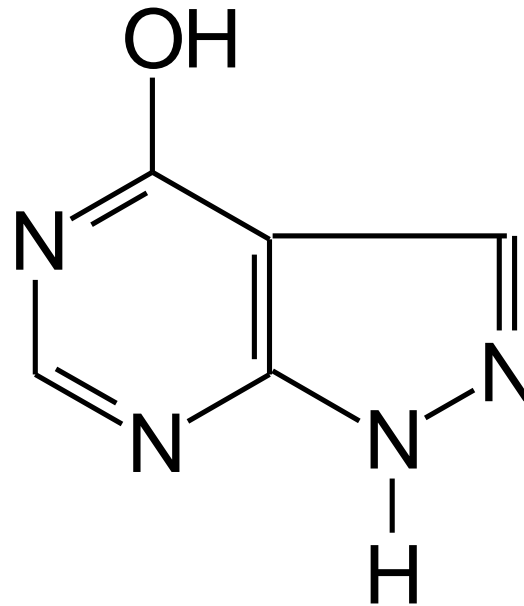


- decrease of clearance in kidney



**Keeping of crystals of UA in tissue**

## Allopurinol – competitive inhibitor xantinoxidasy



**Gout:** allopurinol inhibits the oxidation of hypoxanthine to xanthine

hypoxanthine is more soluble and more readily excreted

**hypouricemia**

**xanthin oxidase deficit (excretion of  
hypoxanthine and xanthine)**



# protein synthesis

# Synthesis of proteins - translations

Where: in cells containing nuclear DNA

Where cell: ribosomes (free or bound to the ER, mitochondria)

prokaryotes: transcription, editing, transcript and translation are spatially separated

eukaryotes: translation in progress to mature mRNA is transported to the cytoplasm



## Molecules which are necessary for protein synthesis?

Amino acids

A number of enzymes

protein factors

ATP and GTP

The inorganic ions ( $Mg^{2+}$ ,  $K^{+}$ )

## Effects of antibiotics on protein synthesis of prokaryotes

antibiotic effect

**Streptomycin** binds to the 30S ribosomal subunit, inhibits the formation of initiation complex errors in reading the mRNA.

**Tetracycline** binds to the 30S ribosomal subunit and inhibits the binding of aminoacyl-tRNA to A

**Chloramphenicol** binds to the 50S ribosomal subunit and inhibits peptidyltransferase

**Erythromycin** binds to the 50S ribosomal subunit and inhibits translocation

**Puromycin** Populated A-site of the ribosome, causing premature termination

## Protein folding (folding)

The nascent polypeptide chain is transported through the ribosome

Gradually getting out of a "protected" area of the ribosome and set its spatial folding

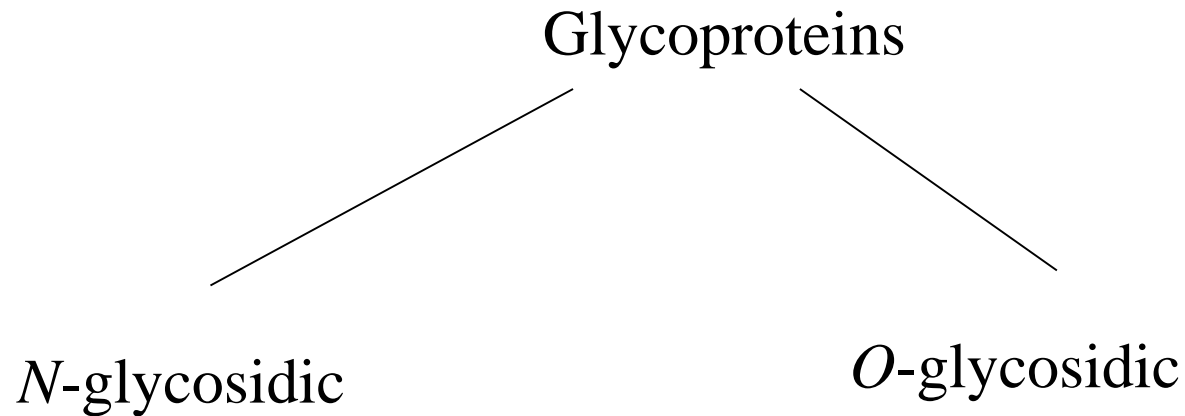
Folding (folding) is mediated by specific proteins - chaperones (heat shock proteins)

Faults in composing - Alzheimer's disease, BSE, cystic fibrosis ad.

# Post-translational modification of proteins

- Removing methionine residue
- Changing the length of the molecule (cleavage of the polypeptide chain)
- glycosylation
- acetylation
- carboxylation
- methylation
- prenylation
- hydroxylation
- Sulfation ad.

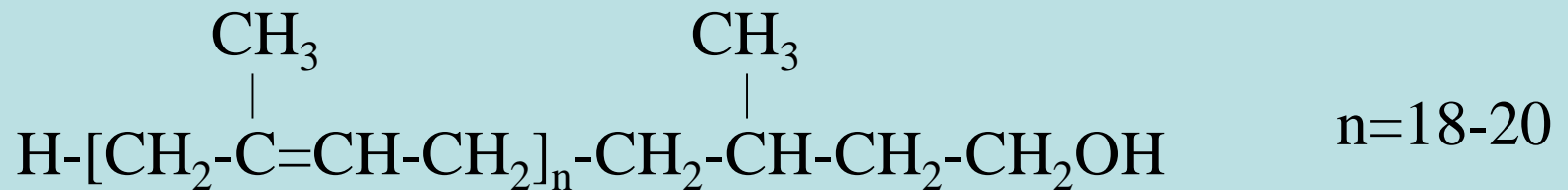
# Glykosylation of proteins



They differ in carbohydrate synthesis method

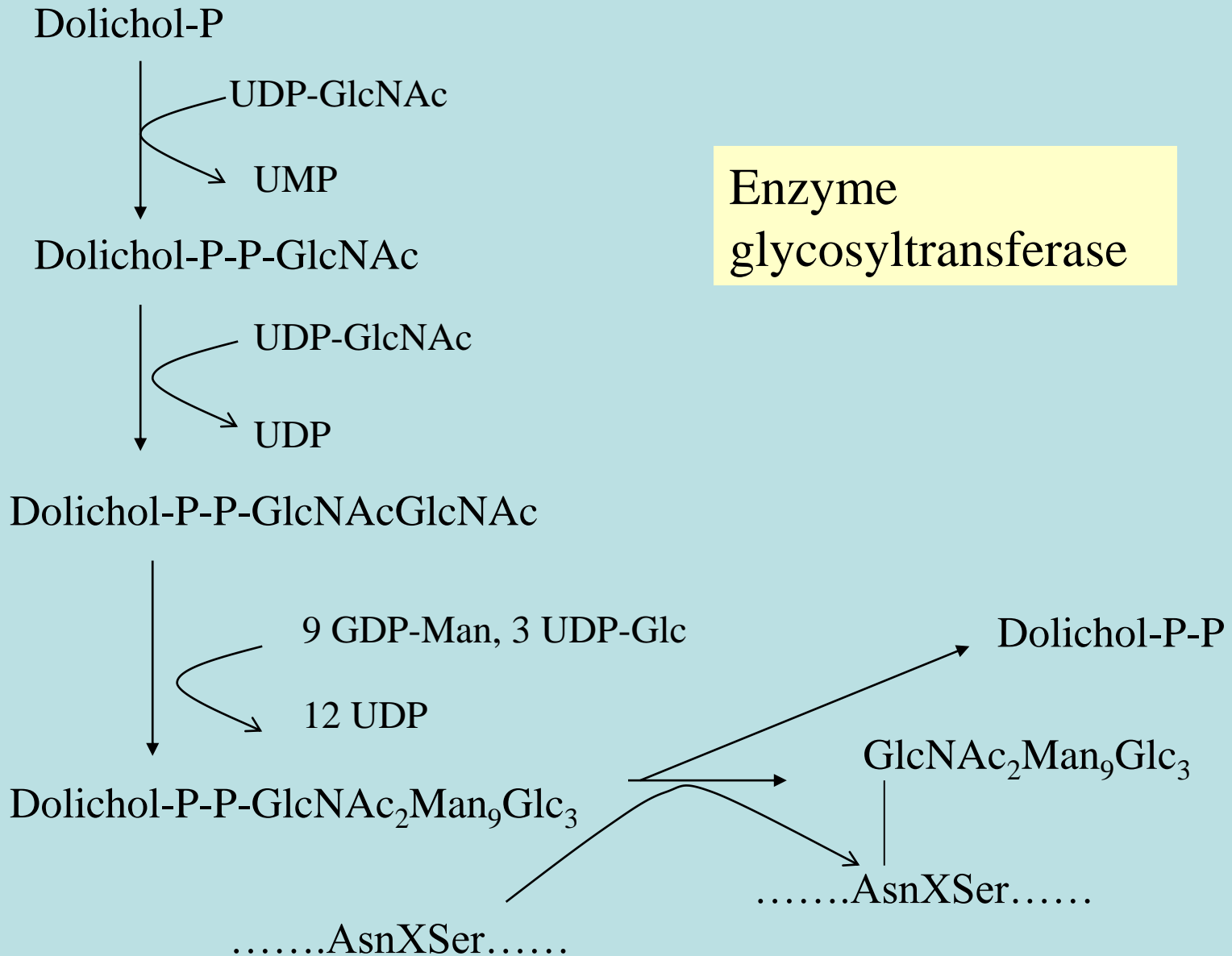
## Synthesis of N-glycoproteins

Synthesis of sugar components takes place outside the protein  
The base is polyisoprene dolichol (see synthesis of cholesterol)

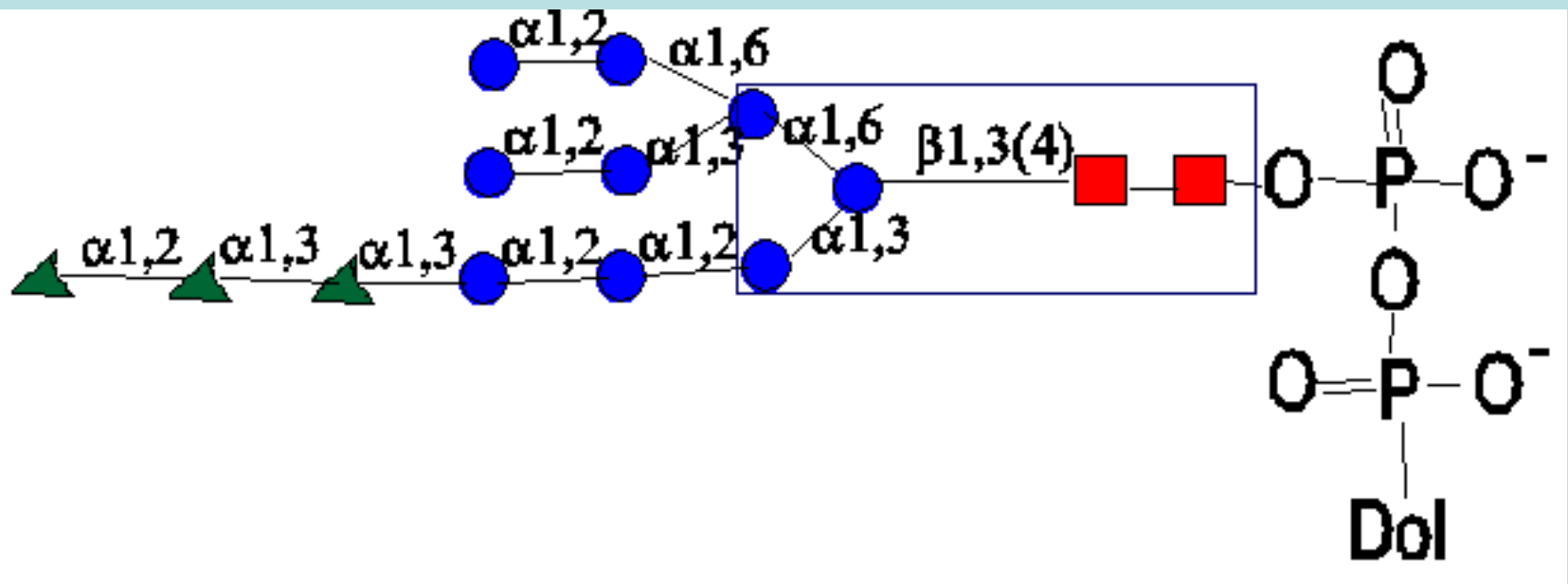


Dolichol diphosphate as it is bound in the ER membrane, the terminal phosphate is gradually adjoin the activated monosaccharides. Ready oligosaccharide is transferred to a protein is bound via asparagine N-glycosidic linkage. In plasma protein binding will take place finish oligosaccharide component.

# Glykosylation of dolichol



# The oligosaccharide precursor bound dolichol



glucose



mannose



N-acetylglucosamin

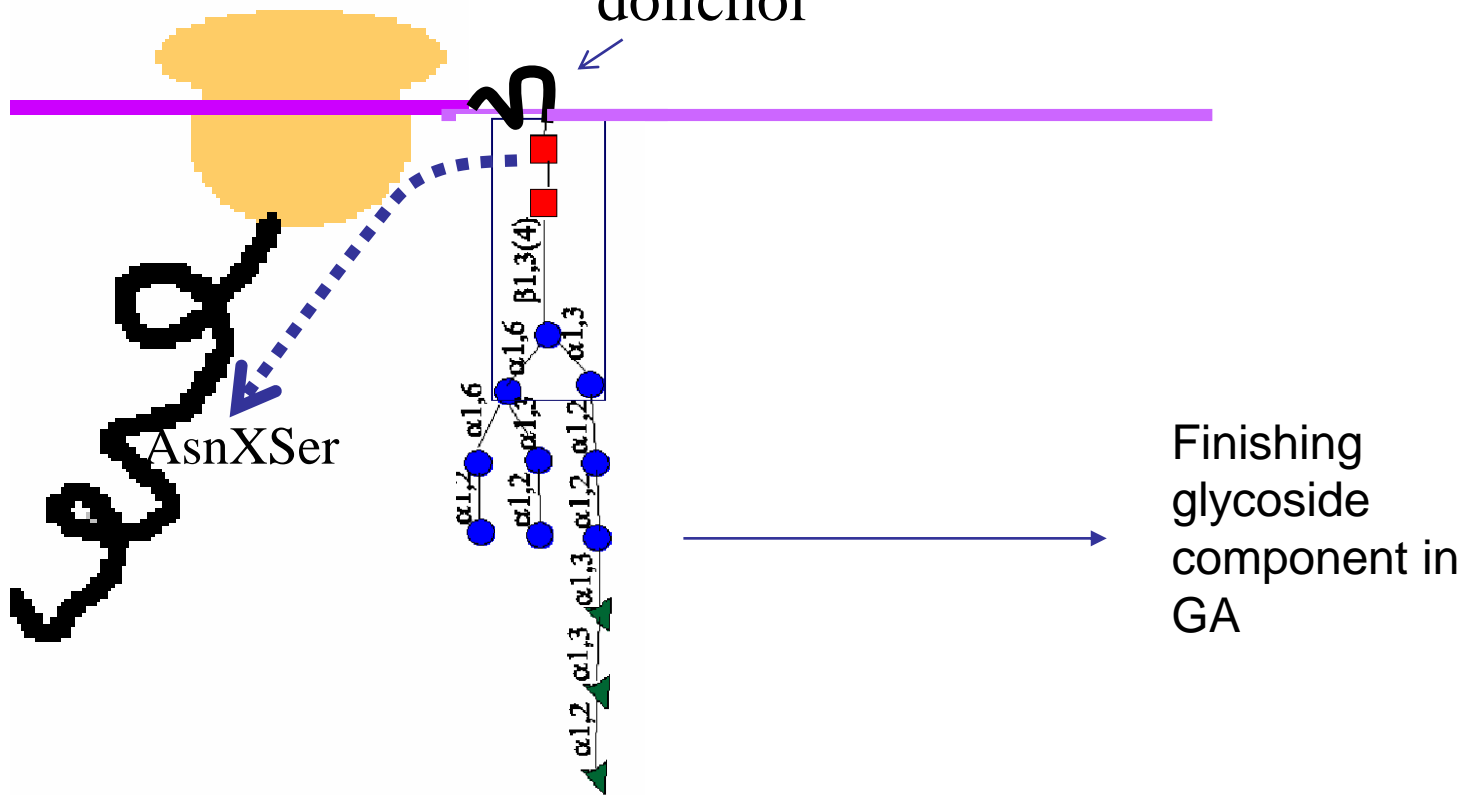


# Cotranslation glycosylation

cytoplasm

dolichol

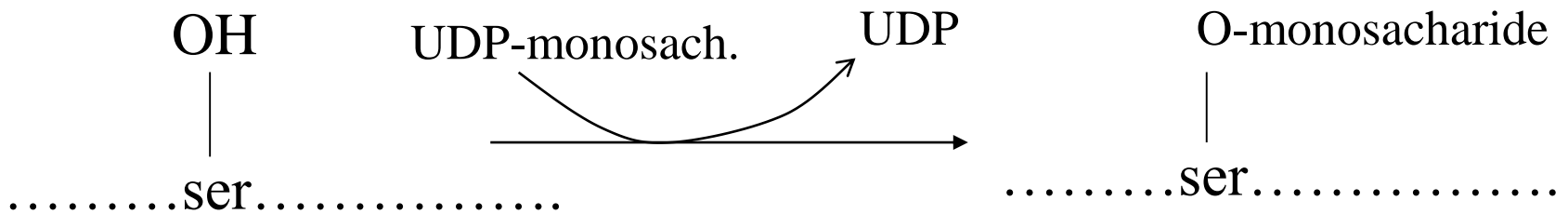
ER



Finishing  
glycoside  
component in  
GA

# Synthesis of O-glycoproteins

Takes place in the ER and the Golgi



Activated monosaccharides are sequentially attached  
O-glycosidic linkage

# Transport of proteins to subcellular and extracellular spaces (targeting)

Protein synthesis on free ribosomes



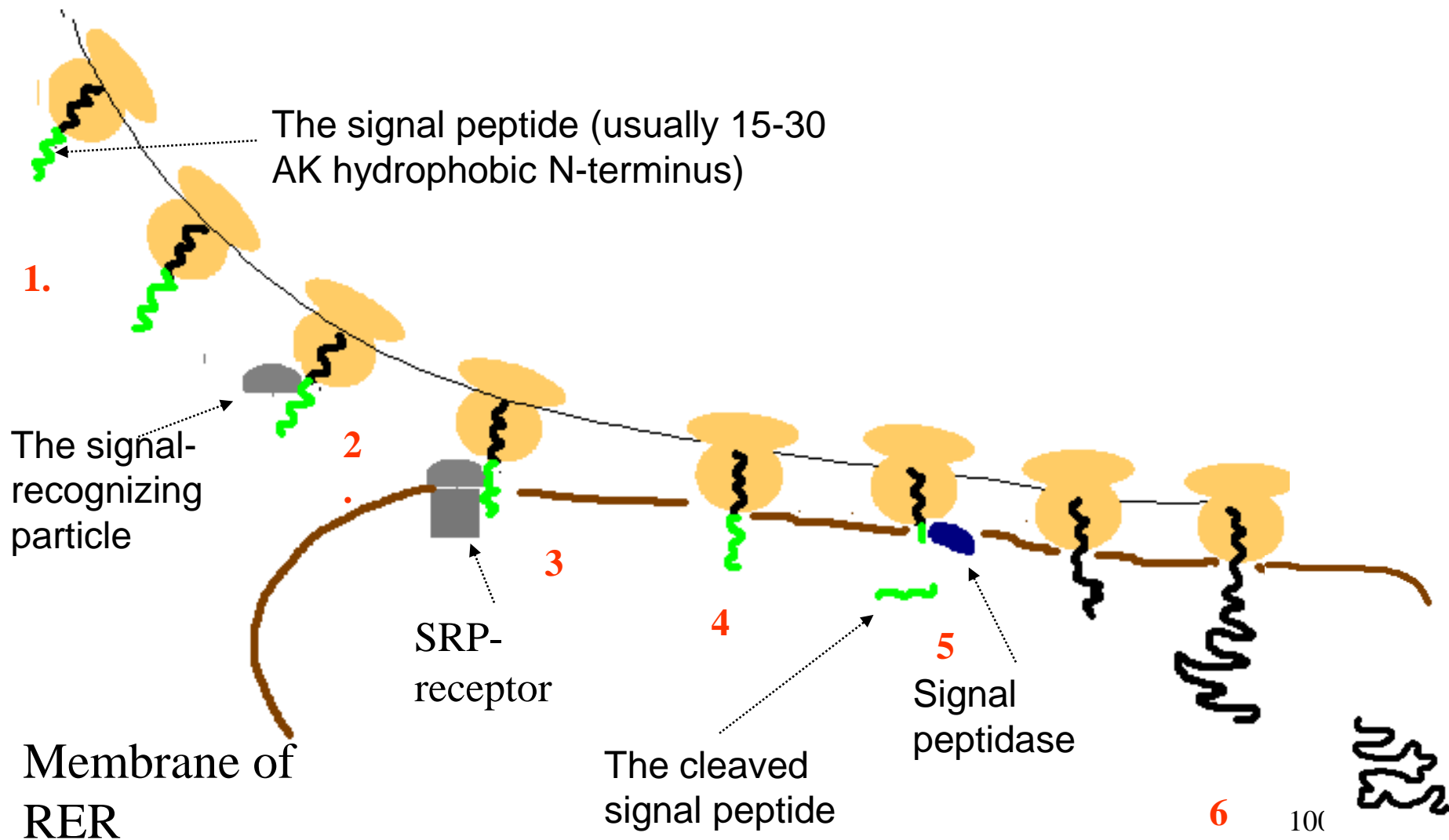
Proteins remain in the cytoplasm and are transported into the organelles (nucleus, mitochondria). AK contain a sequence which directs the transport

Protein synthesis on the RER



Transport into lysosomes, ER, Golgi apparatus or the membranes, secretion from a cell

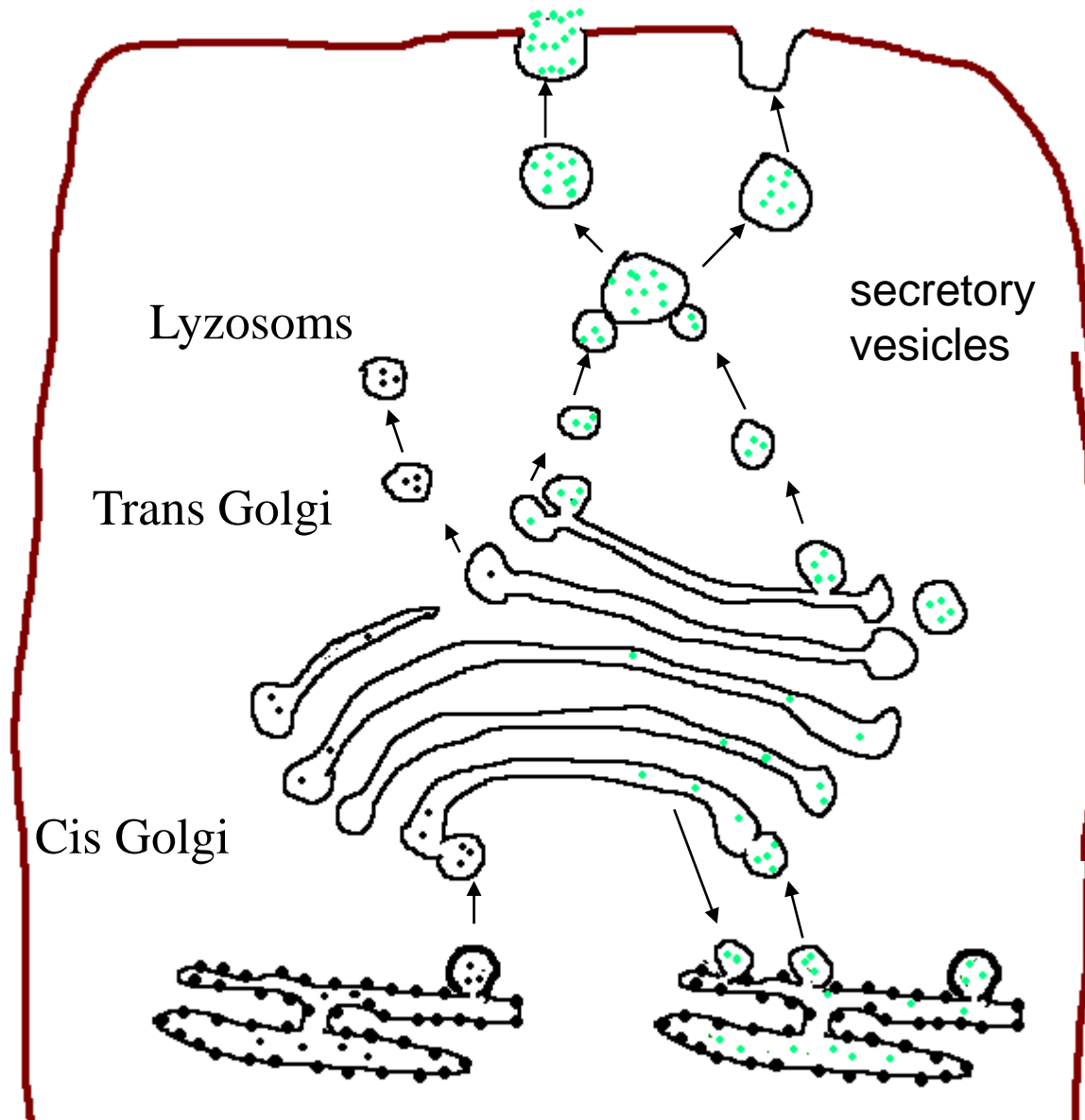
# Transport of proteins synthesized on the RER



# Transport of proteins synthesized on the RER

1. The translation begins in the cytosol
2. Once the signal peptide leaves the ribosome, it binds to the signal-recognizing particle (signal recognition particle-SRP). At the same time binds the ribosome and inhibits further synthesis
3. SRP particle binds to SRP receptor in the RER membrane and attaches to the ribosome RER
4. SRP is released and continues synthesis
5. Once the signal peptide penetrates the RER, signal peptidase deletes it
6. The synthesis of nascent protein and continues complete protein is released into the RER

# Transport of proteins synthesized on the RER



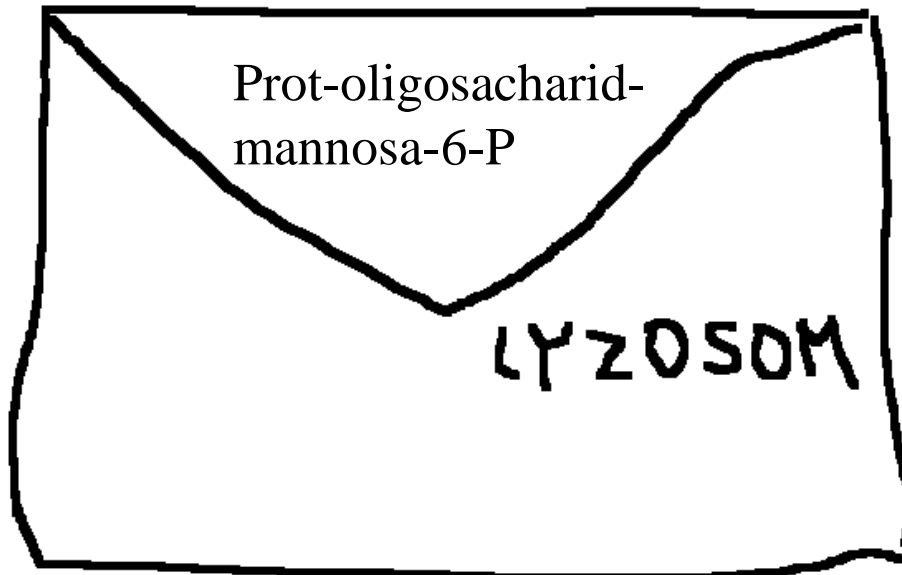
# Transport of proteins synthesized on the RER-cont.

1. Proteins synthesized on the RER are transported in the form of vesicles of the cis-Golgi
2. Here is a sorting center - structural features determine where the protein routing (sorting)
3. Some remain in the Golgi apparatus, while others are returned to the RER
4. Another wander in the form vesicles in the trans Golgi delivery
5. Here are separating lysosomes and secretory vesicles
6. The contents of secretory vesicles is released extracellularly
7. Hydrophobic proteins embedded in the membranes of vesicles become membrane proteins

## Principles of intracellular sorting (sorting)

Example 1:

Proteins destined for lysosomes are labeled N-linked oligosaccharide terminated with mannose-6-P



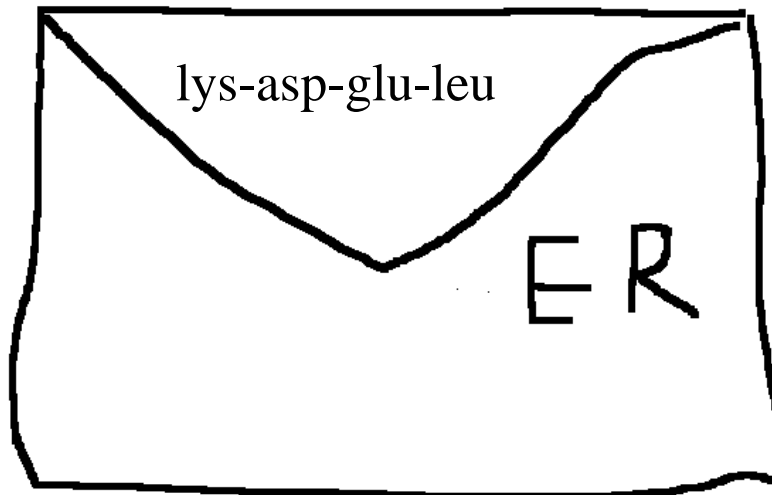
"Address" is recognized by specific membrane receptors in the Golgi, the protein is incorporated into a coated vesicle klathrinem



# Principles of intracellular sorting

Example 2:

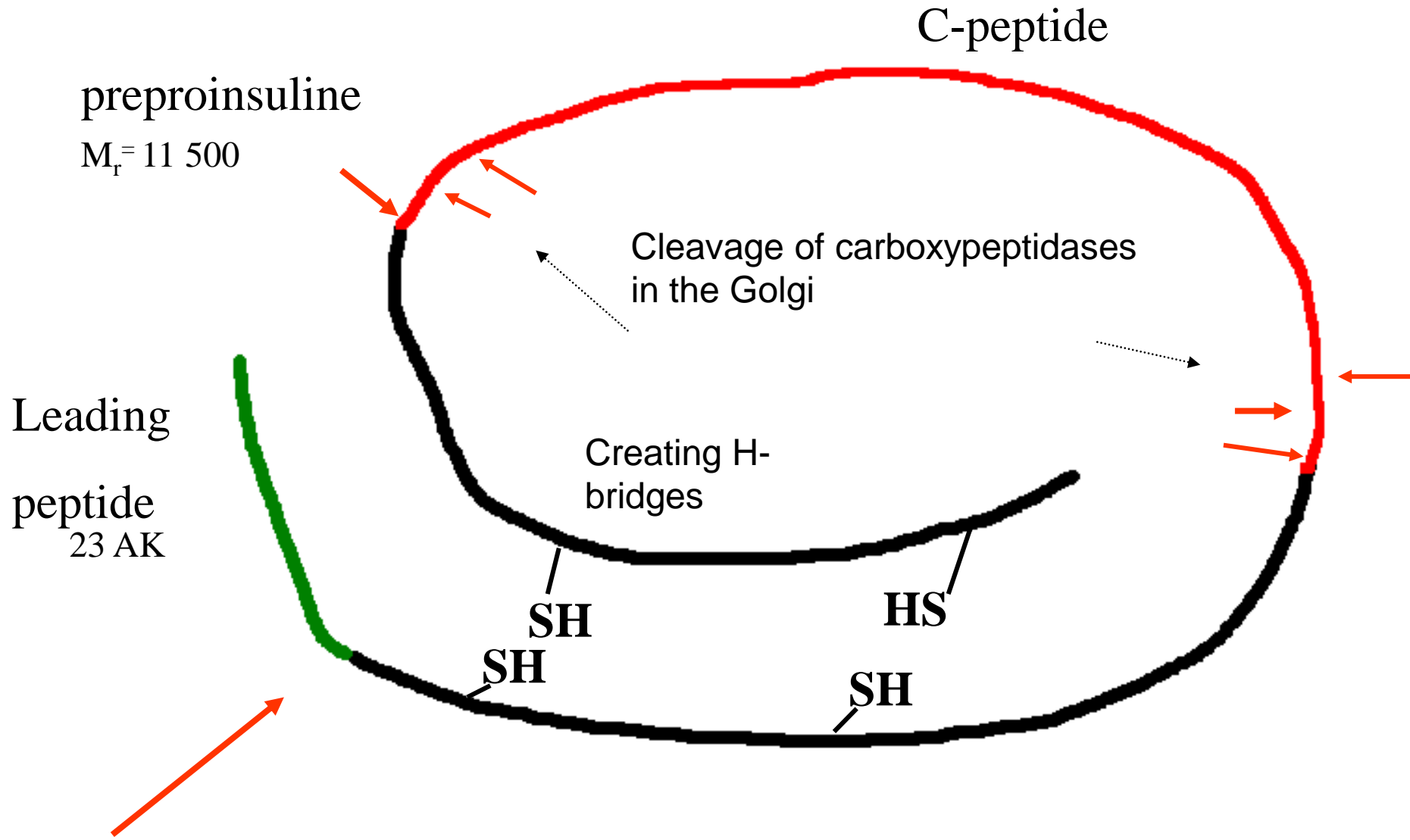
Proteins destined for the ER to the carboxyl terminus of the sequence Lys-Asp-Glu-Leu



The proteins are transported from the Golgi back to the ER

# Example posttranslational modifications: the synthesis of insulin

TEST



1 Cleavage of the peptide lead ER