

* Determine Where to Start. "Initiation" 年 月 日

replication origin X1

Ori

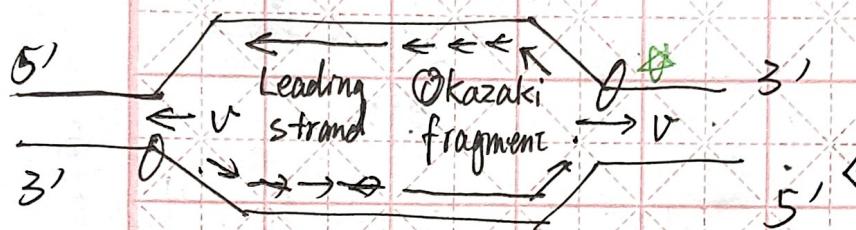
Xn

A T rich sequence

initiator protein

"Elongation"

* replication fork → bubble.

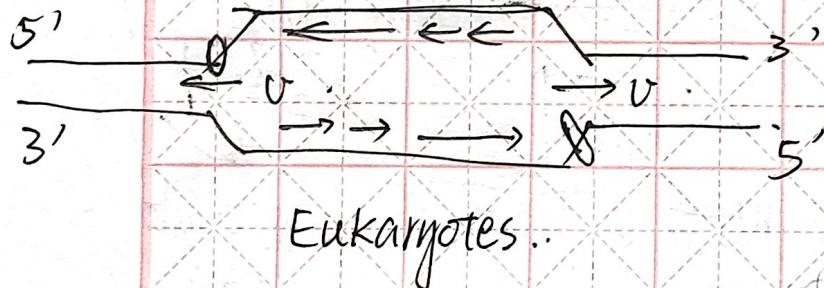


DNA helicase < 5'-3'
3'-5'

template DNA.

New DNA < Leading strand
Lagging strand

single strand DNA binding protein

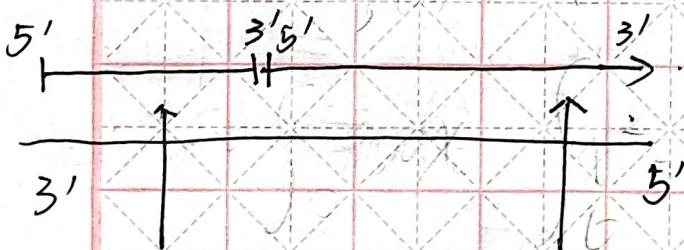


SSB., in E.coli

RPA, in Eukaryotes.

Asymmetrical

Asymmetrical



RNA primer

new DNA

(RNA polymerase)

DNA primase, in E.coli

DNA · pol. δ (DNA primase), in Eukaryotes.

pol II, in E.coli

pol ε : leading strand.

δ : lagging strand.

(Okazaki fragment)

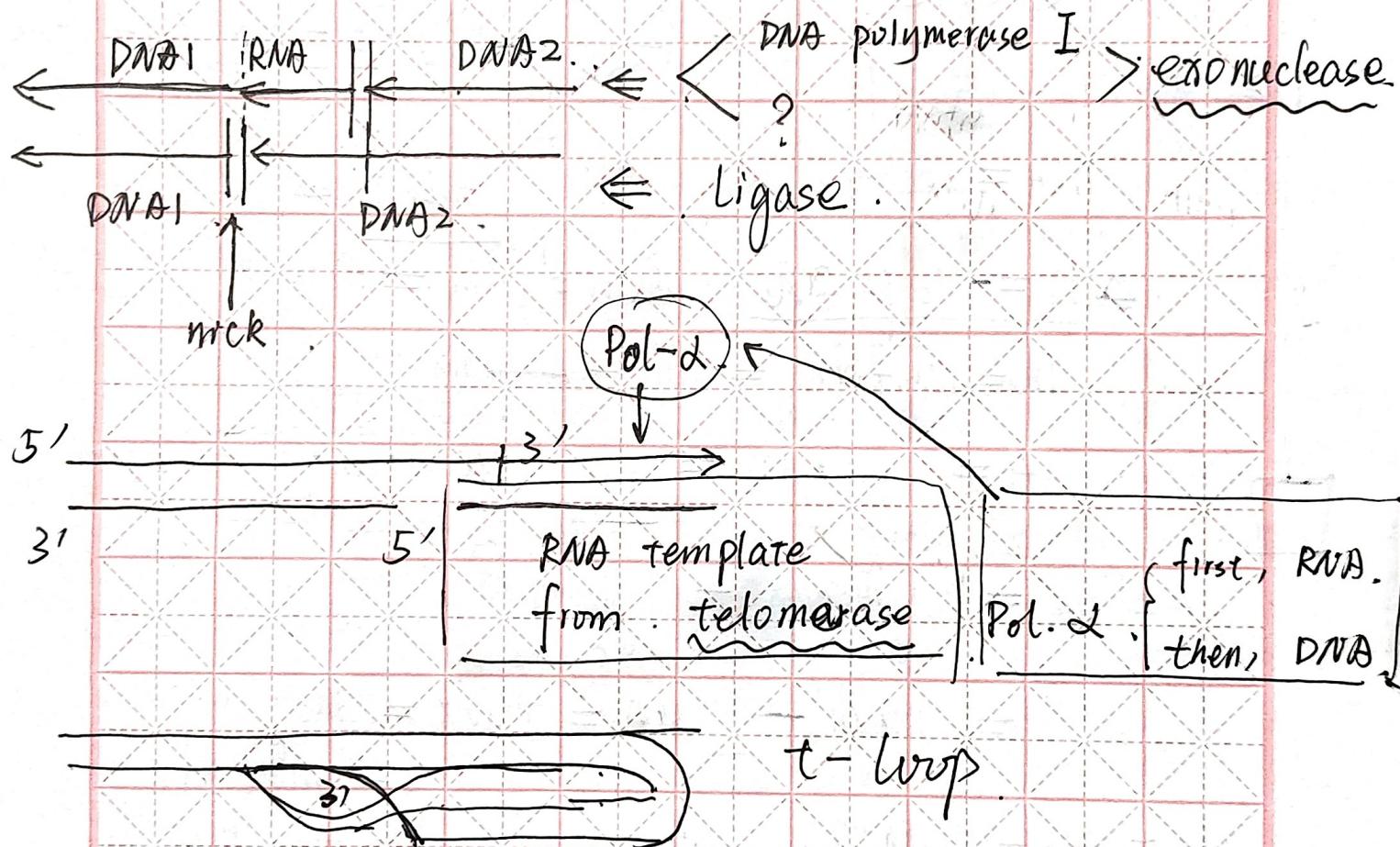
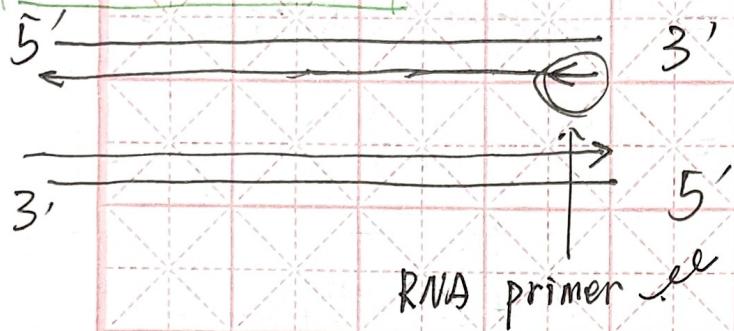
$$10 \times 15 = 150$$

in. Eukaryotes.

* 班级

Termination 姓名 _____

年 ____ 月 ____ 日

Telomere

topo-isomerase → release torsional stress

Polymerization

proof reading

~~ DNA pol. ; Exonucleolytic .

MutS
MutL

methylation : >; strand-directed mismatch .

clamp

* DNA Primase → RNA primer.

Pol. d.

DNA Polymerase → pol III, pol ε / δ ⇒ processive

pol I ~ exonuclease.

ligase.

DNA pol. d.

As a primase. → RNA primer.

Synthesizing DNA in telomere.

Topoisomerase. → reversible nuclease.

to release torsional stress.

Transcription. (DNA → RNA).

Outline :

In E.coli.

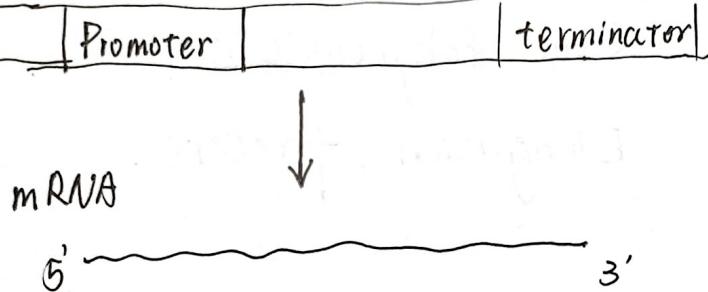
Promoter Recognition.

Initiation.

Elongation.

Termination.

DNA



In Eukaryotes.

① ✓

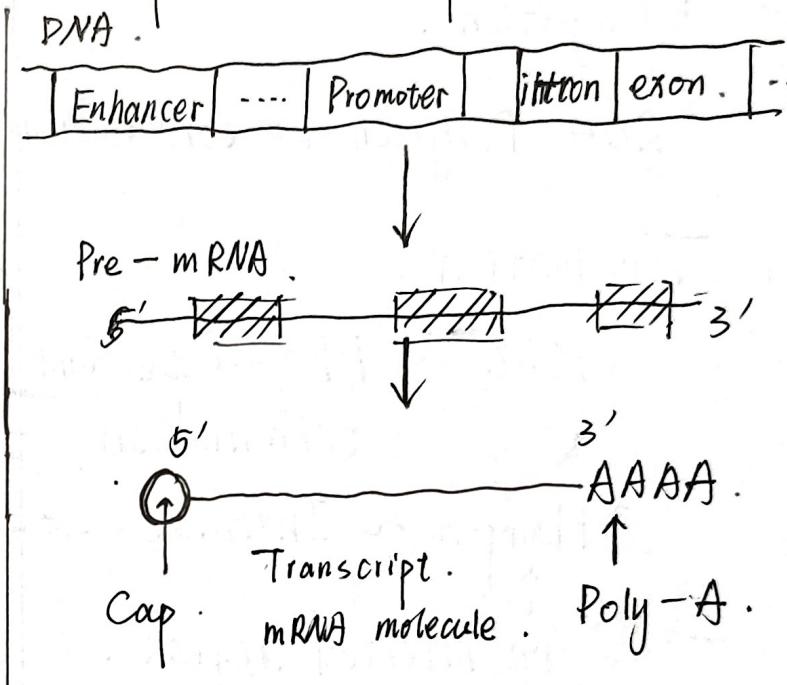
② ✓

+ accompanied by "RNA processing"

③ ✓

④ ✓

+ follow-up work: Exportation.



Tools.

1. Promoter Recognition.

RNA polymerase holoenzyme

the core enzyme.

σ sigma (σ) factor.

general transcription factors (TF)

TF II D.

TBP (TATA-binding protein)

TF II H

a protein kinase.

Activator

Mediator; Chromatin-modifying Proteins.

2. Initiation.

RNA Polymerase core enzyme
 Holoenzyme
 σ factor.

RNA Polymerase II.
 transcriptional activator
 Mediator

General transcription factors (TF)

→ Chromatin-modifying Proteins.

{ Chromatin remodeling complexes
 Histone-modifying enzymes.

3. Elongation.

RNA Polymerase core enzyme.

RNA Polymerase II.

Elongation factors.

4. Termination.

Rho. ~ Rho-dependent termination.

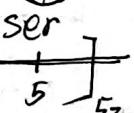
* Hairpin ~ Intrinsic
 an inverted repeat sequence.

④ RNA processing

Outline. (In Eukaryotes)

5'-Cap.

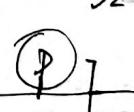
Capping Proteins.



RNA Splicing

Spliceosome (snRNA).

Splicing Proteins.



Poly A. tail.

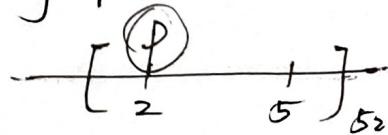
3'-end processing proteins.

④ Selectively Exported from Nucleus.

mRNA.

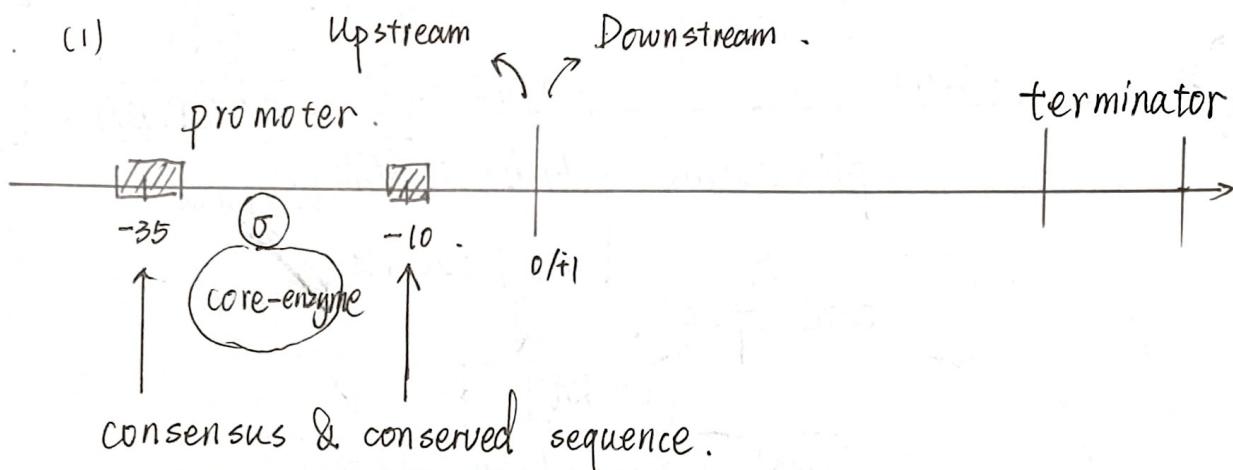
nuclear transport receptor

NPC = nuclear pore complexes



Functions and Interactions among Them

1. (1)



(2) activator

mediator

RNA polymerase II.

enhancer

TATA box

INR.

TBP -30

0/+1

DNA distortion

as a landmark

TFIID.

TFIIF

Kinase

CTD (52×7)

* histone modifying enzyme

* chromatin remodeler complex

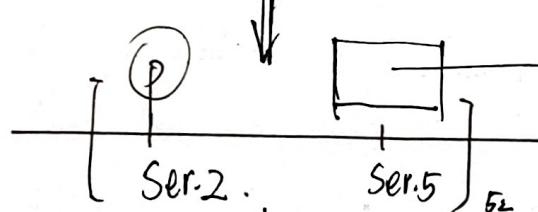
Capping Proteins

disengage from the cluster.
and start elongation.

elongation Pol.

Splicing Proteins.

Start A New Round.

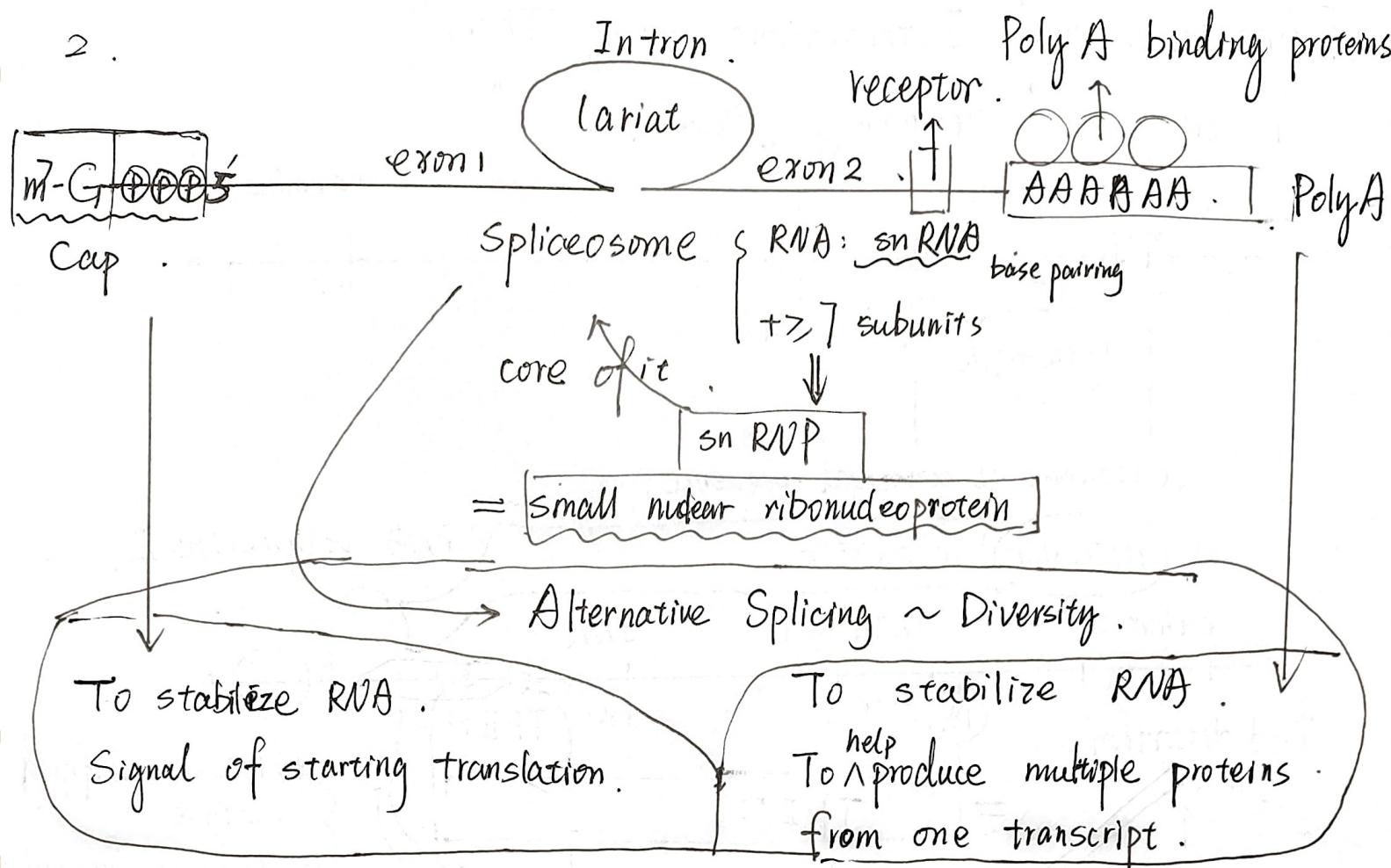


3'-end processing Proteins.

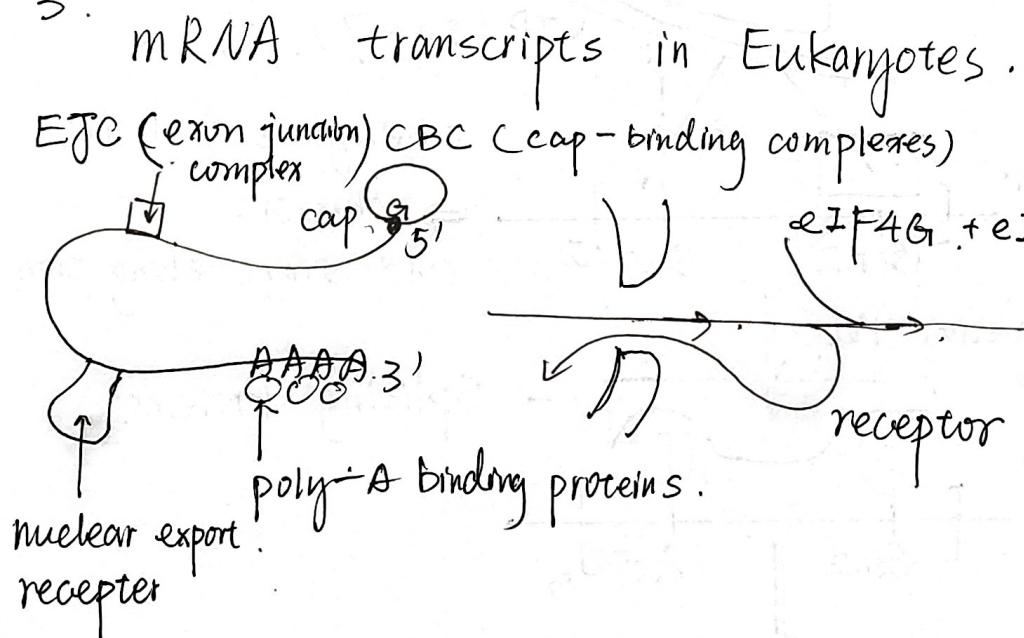
Dephasphorylated RNA polymerase II.

+ TF.

2.

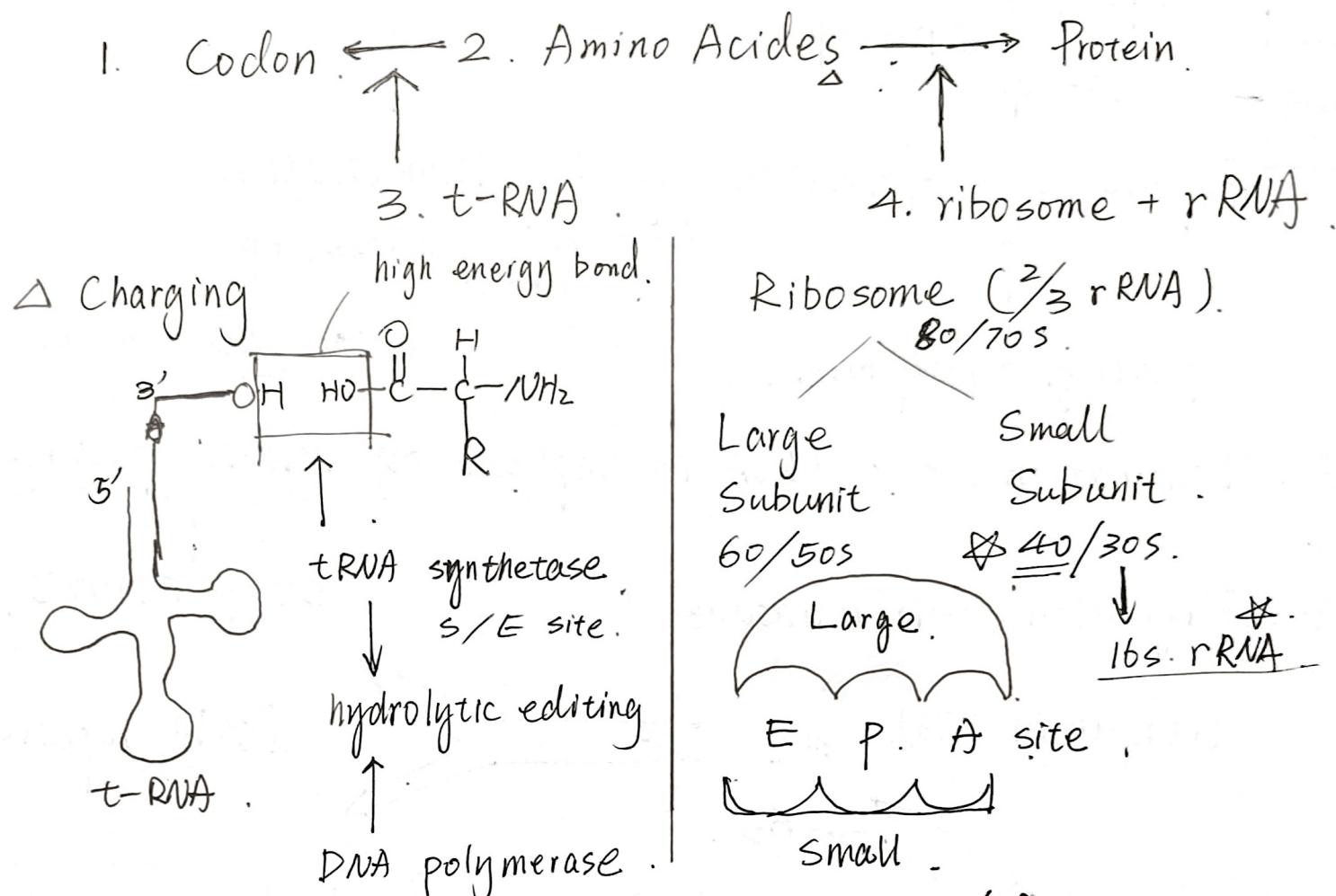


3.



Translation . (RNA → Protein)

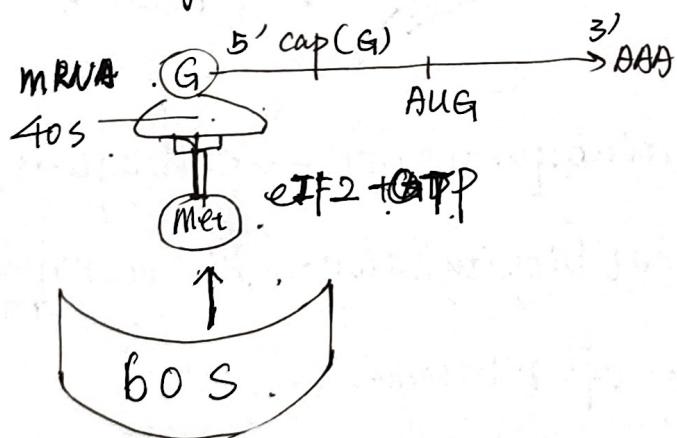
* Ingredients.



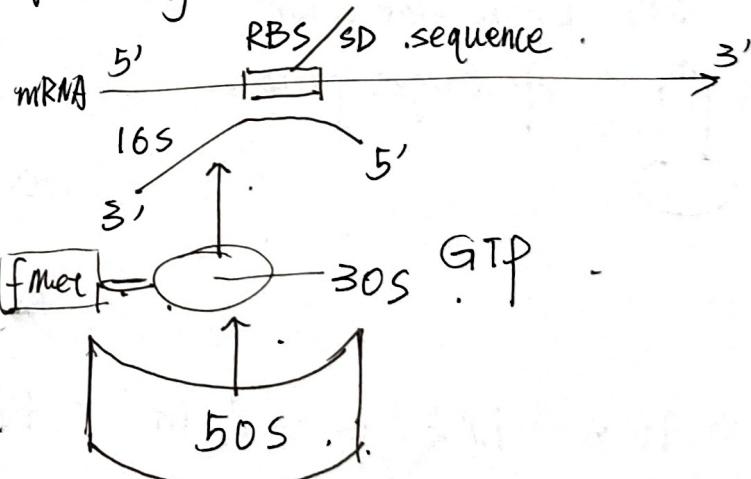
* The Process.

1. Initiation . ~ Find the 1st AUG (START CODON).

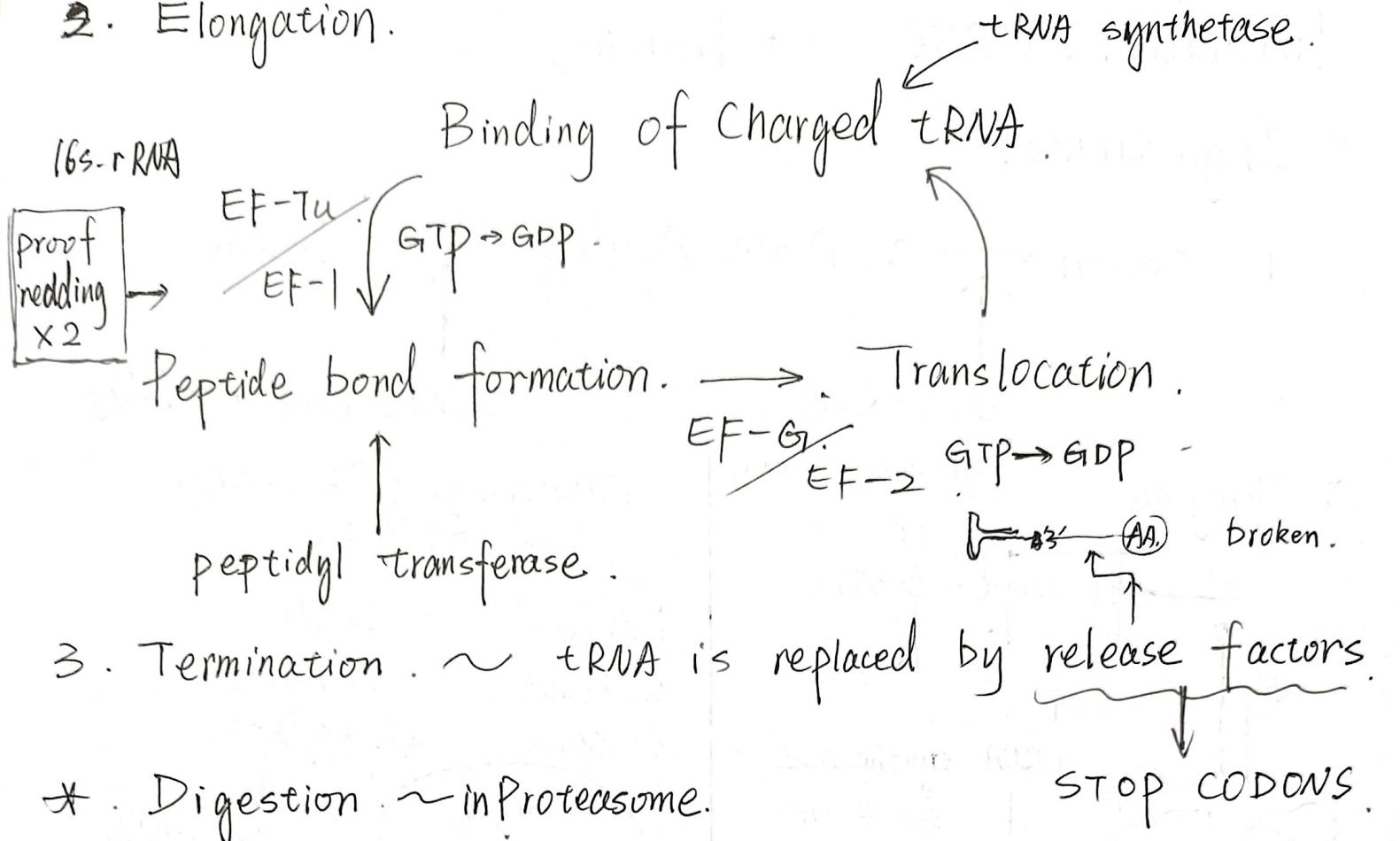
Eukaryotes



Prokaryotes

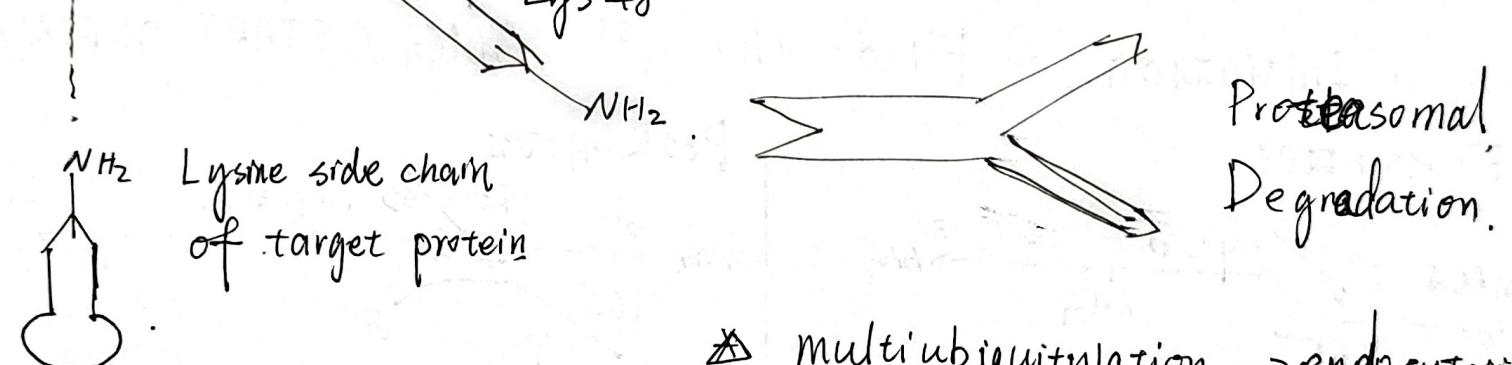
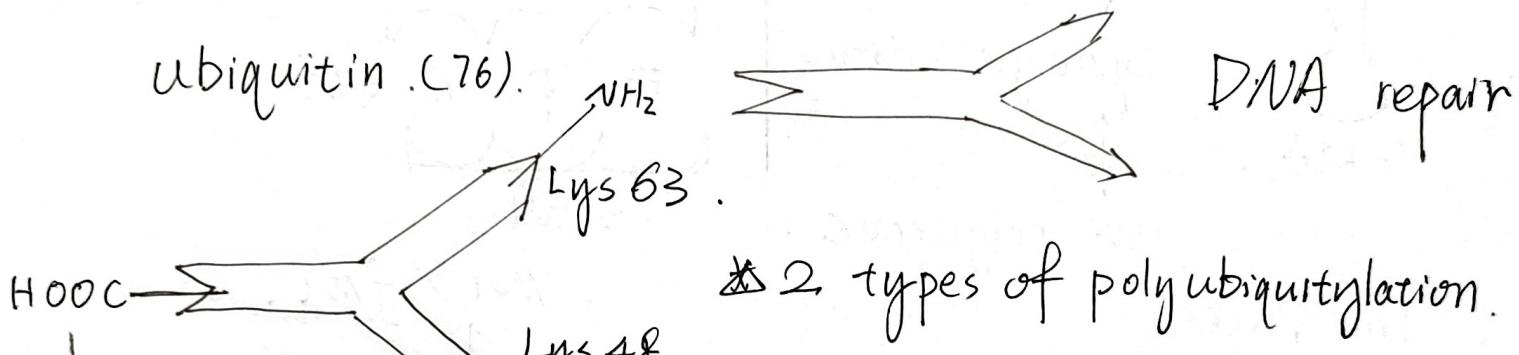


2. Elongation.



3. Termination. ~ tRNA is replaced by release factors.

* Digestion ~ in Proteasome.



- * multiubiquitylation → endocytosis.
- * monoubiquitylation → histone regulation

* 16S rRNA. is used in. { Binding of ribosome.

{ proof reading of binding of tRNA .