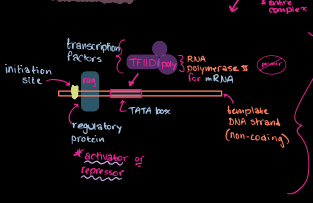
the central dogma

DNA

transcription : nucleus

① INITIATION



promoter — special DNA sequence that says where to start transcription
- transcription initiation site
- where RNA polymerase binds w/o primers!
- includes:
  - a) sigma factors / transcription factors } to help RNA polymerase bind (e.g. TFID) ↳ positive or negative
  - b) TATA box — DNA sequence for starting site
  - c) regulatory protein
  - d) transcription initiator site

② ELONGATION : synthesize

*depending on type of RNA being made

- RNA polymerase II unwinds DNA + reads from 3' → 5'
  - ↳ will build in 5' → 3' using ribonucleoside triphosphates
  - ↳ will proofread a little

} exergonic rxn! ENERGY! ↳ to catalyze phosphodiester bonds between nucleotides

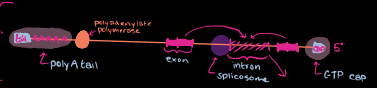
③ TERMINATION

- DNA sequence that codes to stop transcription *code will not be used in polypeptide

PROKARYOTES: signals to end pre-mRNA ← name when still in nucleus

EUKARYOTES: many proteins involved + no specific DNA termination sequence

↳ pre-mRNA is modified



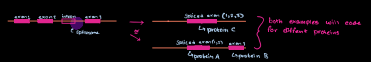
modification of pre-mRNA

a) Addition of poly A tail at RNA's 3' end to stabilize molecule
↳ POLYADENYLATION
* uses polyadenylate polymerase

b) addition of GTP cap at RNA's 5' end to:
① help mRNA bind to ribosome
② prevent digestion in cytoplasm by ribonuclease
③ promote translation

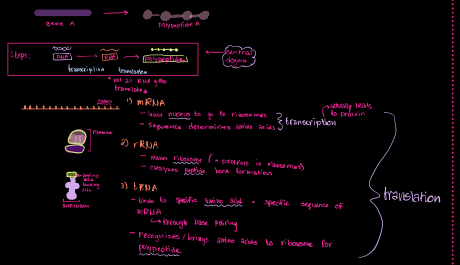
c) RNA splicing by spliceosomes → made of proteins + small RNA
- removes introns and connects exons
  - ↳ non-coding regions
  - ↳ expressed / transcribed regions

alternative splicing - exons can be spliced into various combinations to yield different proteins



gene expression

relationship: 1 gene codes for 1 polypeptide



transcription : DNA → RNA
- requires template DNA strand (3')
- requires 4 nucleotide triphosphates (ATP, GTP, CTP, UCT)
- an RNA polymerase
  * specific to type of RNA
  - tRNA → RNA polymerase I
  - mRNA → RNA polymerase II } catalyzes synthesis of RNA from DNA template
  - tRNA → RNA polymerase III

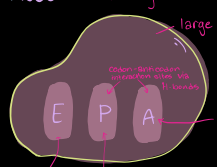
translation : Synthesis of polypeptide

RNA

- occurs in ribosomes * made of proteins + rRNA
  * in cytoplasm or RER

① tRNA reads mRNA codons

② tRNA delivers corresponding amino acid



* tRNA is specific for each amino acid (20)
* codons can code for same amino acid

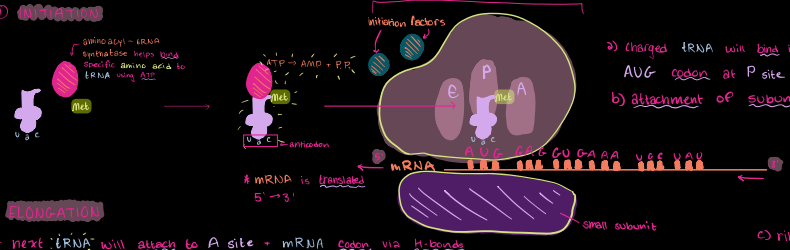
CODONS: mRNA — more codons (64) than amino acids (20)
↳ essential vs non-essential

* AUG — start codon
  - ↳ all proteins start with
  - ↳ codes for Methionine
  - * ↑ issue if mutation is for start codon

* UAA, UAG, UGA — stop codons
  - ↳ all proteins end with one * never written in polypeptide code

INITIATION COMPLEX : both subunits, mRNA, tRNA (methionine) * put together via initiation factors

① INITIATION

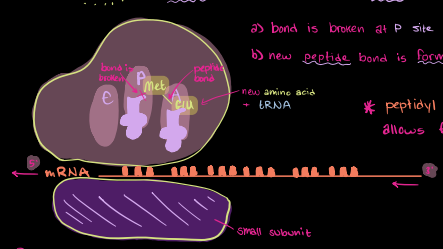


a) charged tRNA will bind its anticodon to mRNA's AUG codon at P site
b) attachment of subunits

* mRNA is translated 5' → 3'

② ELONGATION

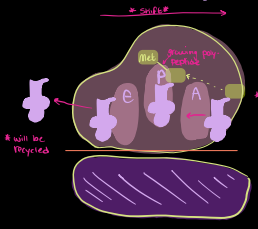
- next tRNA will attach to A site + mRNA codon via H-bonds



a) bond is broken at P site between old tRNA + amino acid (methionine)
b) new peptide bond is formed with amino acids at A and P sites ↳ tRNA

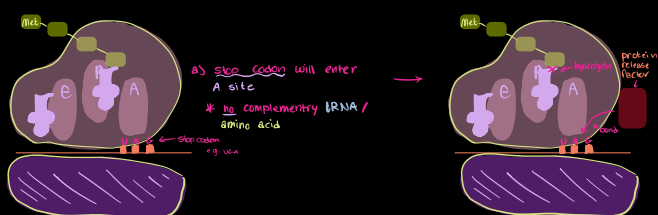
* peptidyl transferase activity called ribozyme allows for this activity by large subunit

c) ribosome will move so non-bonded tRNA can exit



* new tRNA enters at A site to form peptide bond with previous amino acid

③ TERMINATION

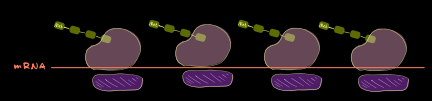


a) stop codon will enter A site
* no complementary tRNA / amino acid

b) stop codon will bind to a protein release factor

c) bond between tRNA + amino acid at P site will be hydrolysized

d) seperation of polypeptide chain + ribosome(s)
* if multiple ribosomes are working on mRNA + many polypeptides growing it is a polysome



* polypeptide will now be modified after signal sequence sends protein to RER / golgi

POLYPEPTIDE