CHEAT SHEET MIDTERM #2 – nucleic acids

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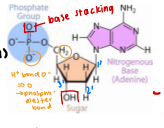
- interactions stabilizing 2° struct: hydrophobic base stacking (mostly 1D-1D) above + below strand + H-bonds between bases
  - ↳ stacking allows for hydrophobic surfaces to be excluded from water, allowing water to have more motional freedom → ↑ stability
- linkage forming backbone of nucleic acid: covalent phosphodiester bond between sugar + phosphate
- Watson Crick purine - pyramidine base pairings = SAME geometry
  - pyr-pyr = too much space ⇒ kinking (strain) (1)
  - pur-pur = too little space ⇒ bulge (2 rings)



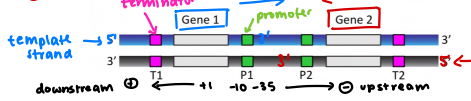
- genome: base pairs – hereditory info: amount of DNA gene: DNA seq. code for protein/mRNA
- new nucleotide added: 3' end w/ free OH group

transcription – DNA → RNA (mRNA)

Compare/contrast...	Eukaryotes	Bacteria
Chromosome structure	contains histones (nucleosomes)	X histones
Site of transcription	nucleus	cytoplasm
What is the promoter structure?	TATA box, 30 bp upstream	-10 box, -35 box
What are the proteins involved contacting the promoter?	general transcription factors	sigma factor
Is splicing (removal of introns) required? (5' cap, 3' poly A tail)	yes (RNA processing) introns X, exons remain	NO
Capping and tailing of mRNA?	yes, ↑ stability, X rapid degradation in cyto.	no
Site of translation	cytoplasm	cytoplasm
Can translation occur while transcription is still occurring?	NO, mRNA needs to be transported to cytoplasm	yes, translation + transcription happen at same place

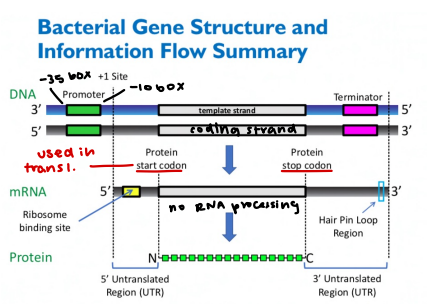
- specific factors → DNA seq. @ bases, major + minor grooves (promoter)
- RNA pol initiate transcription @ consensus seq. euk. (TATA box) bac. (-10, -35 box) upstream of (+1 site) (binding of SF.)
- bacterial gene: both RNA + DNA seq. = RBS, start codon // 5' cap (euk's RBS)
- DNA binding proteins bind (because ...): Specific non-cov. w/ exposed DNA seq., 3D structure → size, shape, charge, polarity → major + minor grooves
- consensus seq. = most common base in that base position
  - ↳ bind tightly → more expression ⇒ gene regulation + control (change base ↓ strength in bona → less trans.)
  - upstream/downstream according to direction of RNA polymerase is moving
    - ↳ downstream = direction RNA polymerase is moving (relativity) (towards terminator)
    - ↳ polymerase starts @ promoter, and moves downstream to terminater

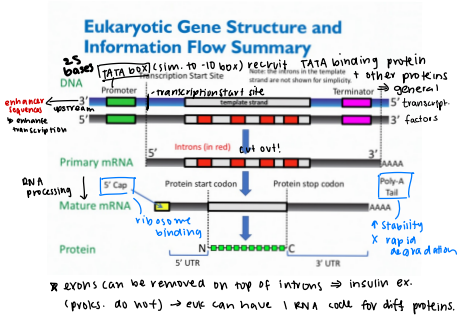
e.g. Q.



→ pos. of genes relative to each other: BOTH UPSTREAM from each other

← template strand





* exons can be removed on top of introns ⇒ insulin ex. (proks. do not) → euk can have 1 RNA code for diff proteins.

translation – mRNA → protein

need:
- ribosomes → all ribosomes ⇒ mRNA, tRNA, rRNA
- initiation factors
- charged tRNA
- template mRNA

open reading frame: AUG, 3 base pairs non-overlapping → codons

- triplet codon code = redundant degenerate → > 1 codon can code for same a.a. (read 5'-3', anti-codon = 3'-5') (universal too)

tRNA wobble effect

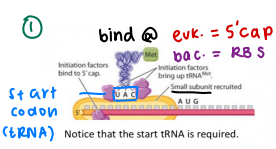
ANTIPARALLEL

- due to # of possible base pair combos.
  - → G-U can pair quite easily in third position
    - ↳ first 2 same base, end can be switched (G-U pairs)
    - ↳ that's why less tRNAs than expected 61 for 61 amino acids

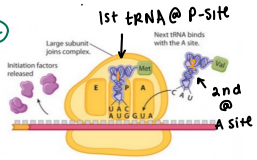
e.g. codons UUA UUG CUU CUC CUA CUG
anti-codons AAU AAC GAA GAG GAU GAC
- ↳ both UUA + UUG can bind to AAU
- ↳ both CUU + CUC can bind to GAG
- ↳ both CUA + CUG can bind to CAU

translation mechanism

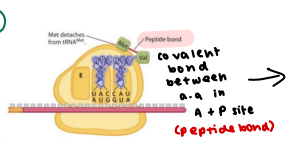
1. euk. binds on 5' cap, bacteria binds on RBS (ribosome → binding point of mRNA)
   - ↳ scans until finds codon (AUG) ↳ RBS attaches to specific position + distance from start codon
     - ↳ adding b.p = translation ↳ adding base pairs before start codon = no translation
2. large ribosome unit attaches with the first tRNA (anti-codon of AUG → UAC) in the P (peptidyl) site
   - ↳ RBS makes complementary interactions w/ nucleotides in rRNA part of ribosome
     - → euks. assemble at 5' cap (along w/ starting tRNA) and scans along mRNA → start codon
3. 2nd tRNA enters ribosome @ A (amino-acyl acceptor) site, and first peptide bond is made
   - ↳ when peptide bond forms, it is actually part of the rRNA (rather than protein portion of ribosome) that catalyzes Rx
4. first tRNA moves to the E (exit) site and is ejected as the ribosome moves, 2nd tRNA moves to P site, and then next tRNA enters at A site, REPEATS until end codon (release factor ⇒ release of polypeptide)



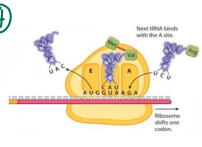
- small subunit
- binding @ 5' cap / RBS
- find start codon



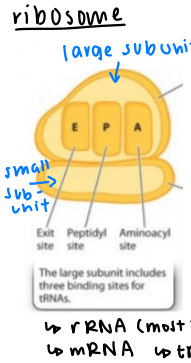
- large subunit → P site
  - ↳ next binds @ A site
- inhibition factors released



- peptide bond forms between 1st + 2nd a.a (P + A site)
- (AUG + ____)
- (Met)



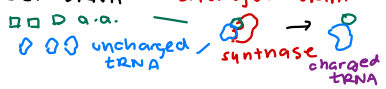
- 1st a.a. → E site (exit)
- 2nd → P site
- 3rd → A site
- ribosome shifts 1 codon



- ↳ rRNA (most #)
- ↳ mRNA ↳ tRNA

(tRNA + correct a.a.)

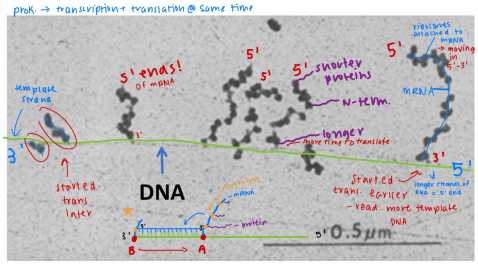
- aminoacyl-tRNA synthase: catalyze the covalent attachment of a.a to correct tRNA → charged tRNA
  → each a.a. has a specific aminoacyl-tRNA ★ real translaters

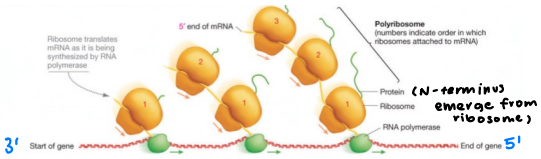


- DNA → proteins = 2 step process (why?)
  - more places to control protein synthesis
  - more proteins can be produced in a given time (making proteins from multiple mRNA templates vs. 1 DNA template)

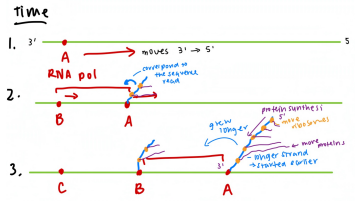
Electron Micrographs.

bacteria - can see transcription + translation @ SAME TIME

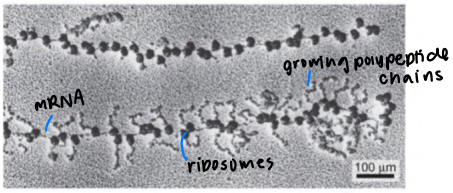


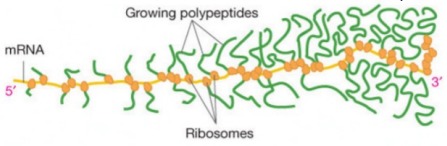


- christmas tree transcription



euk. - only can see translation





★ translate DNA → protein

temp. 3'-A CG-5' (complimentary, but w/ U's, anti-parallel)
coding: 5'-TGC-3' (complementary, anti-parallel)
mRNA: 5'-UGC-3' (same, T→U)

★ translate protein → DNA

mRNA: 5'-UCG-3'
coding: 5'-TCG-3' (same, U→T)
temp: 3'-AGC-5' (comp. anti-p complementary anti-parallel w/ T's)

Mutations

- wild type: the natural state of an organism isolated from nature
- genotype: the hereditary (genetic) info within an organism's genome
- phenotype: the resulting expression of the genotype within an organism resulting in observable traits
- mutant: an organism with a changed genotype, usually in a specific location in the DNA
- mutation: a change in the genotype

point mutation ★

- mutation that changes a single base in the DNA, eventually resulting in a change in base pair if not repaired
  ↳ incorrect DNA copying during rep. ↳ chemical mutagens ↳ environmental damage (UV light)
- silent mutation: changes codon, but not the resulting a.a
- missense mutation: changes codon, new a.a.
- nonsense mutation: point mutation that creates a new stop codon
- Deletion mutation
  - sections of DNA can be removed ("deleted") and remaining DNA joined together
    ↳ can remove sections of genes, promoters, terminators

e.g. a missence point mutation changes a base in the template strand, will this change phenotype?
- in current cell + 1 of the daughter cells

not all mutations in a protein coding region causes change in phenotype. Why?
- Silent mutation + the codon code = degenerate → some amino acids have >1 codon and a mutation in a codon can result in the same a.a. ⇒ no change in shape / f(x)
- similar amino acid substitution: might not lead to change in protein folding / f(x) (e.g. hydrophic + similar size switch = ok)

e.g. Label