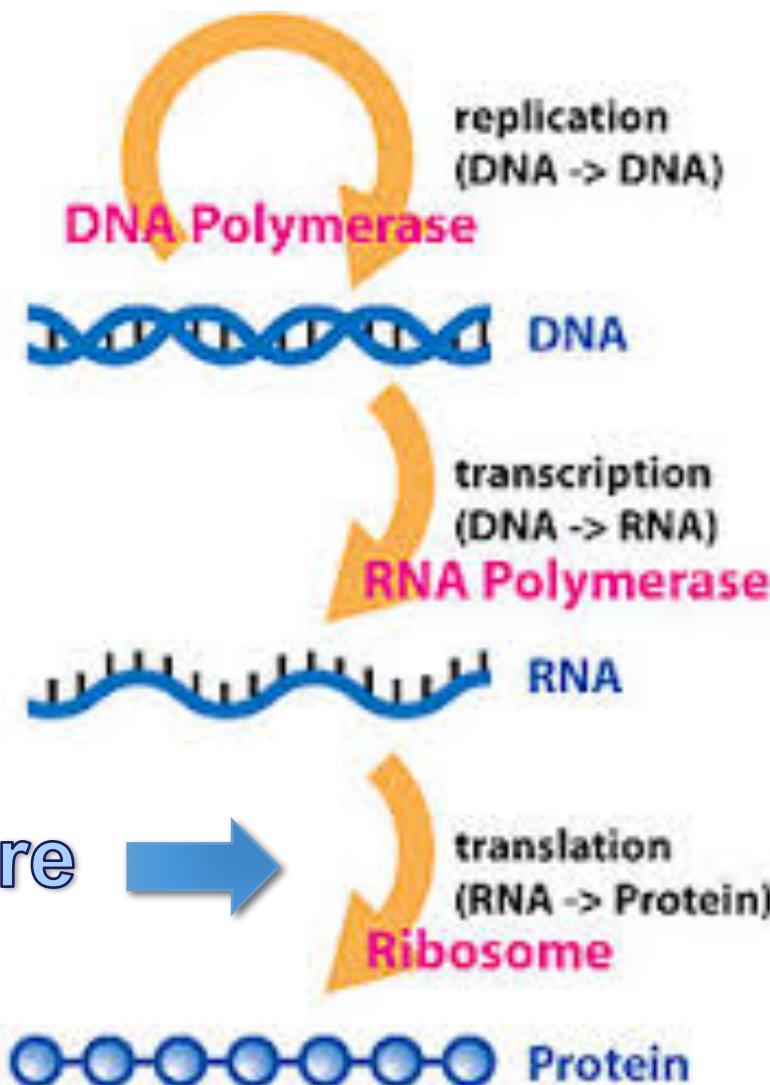
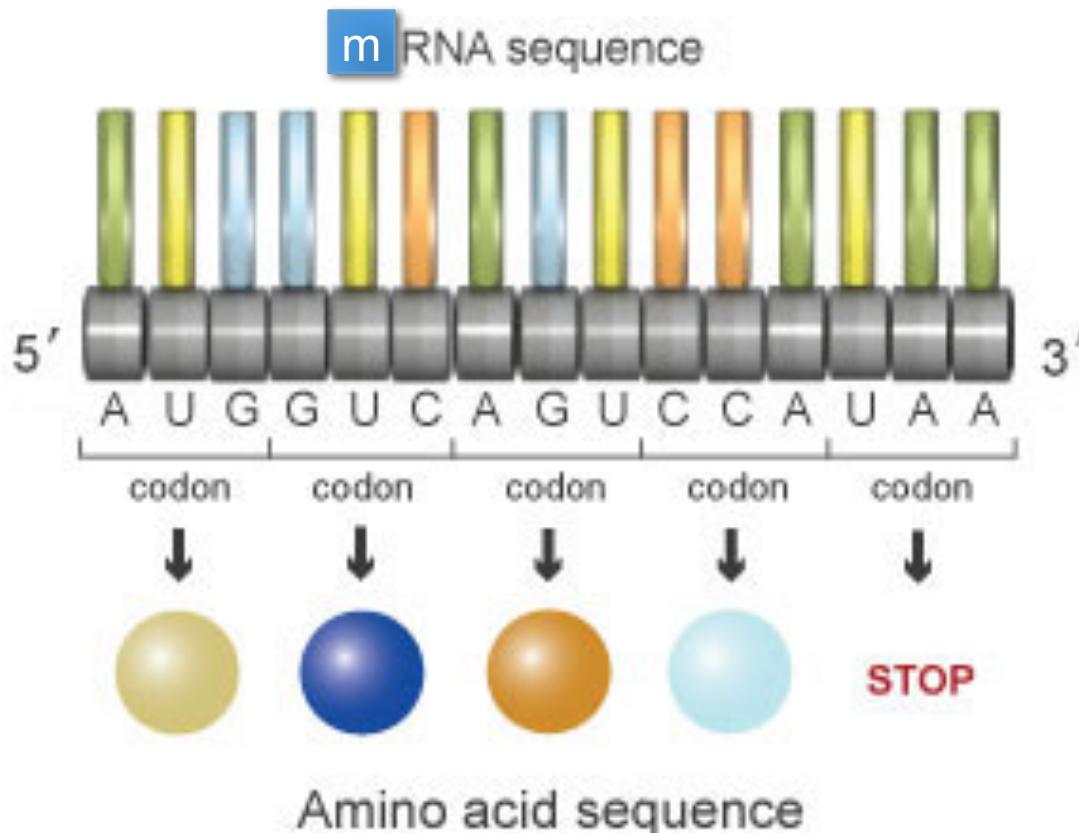


TRANSLATION & HW3 DETAILS

The Central Dogma



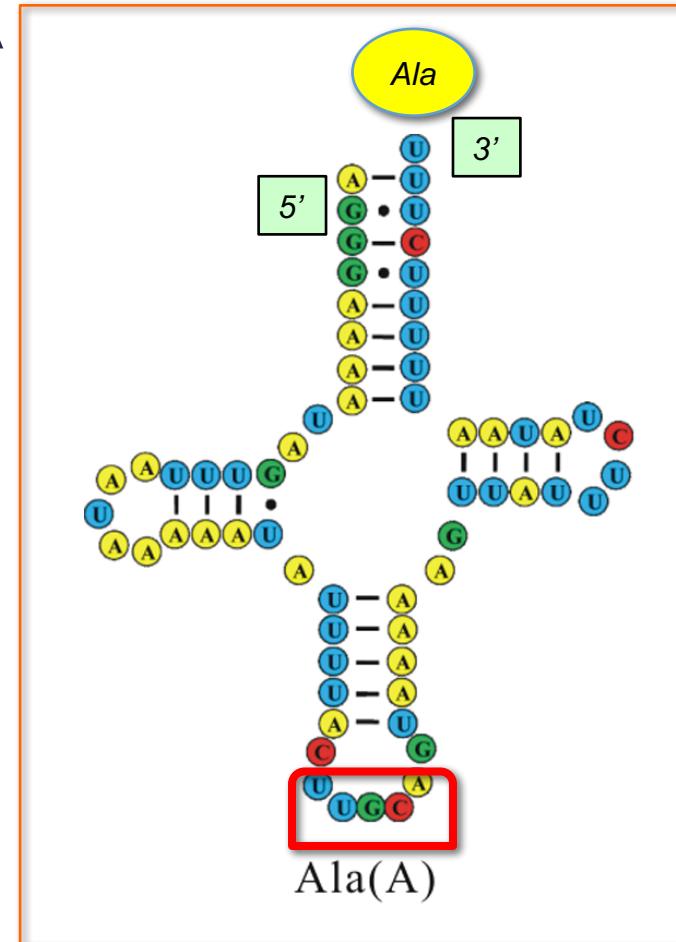
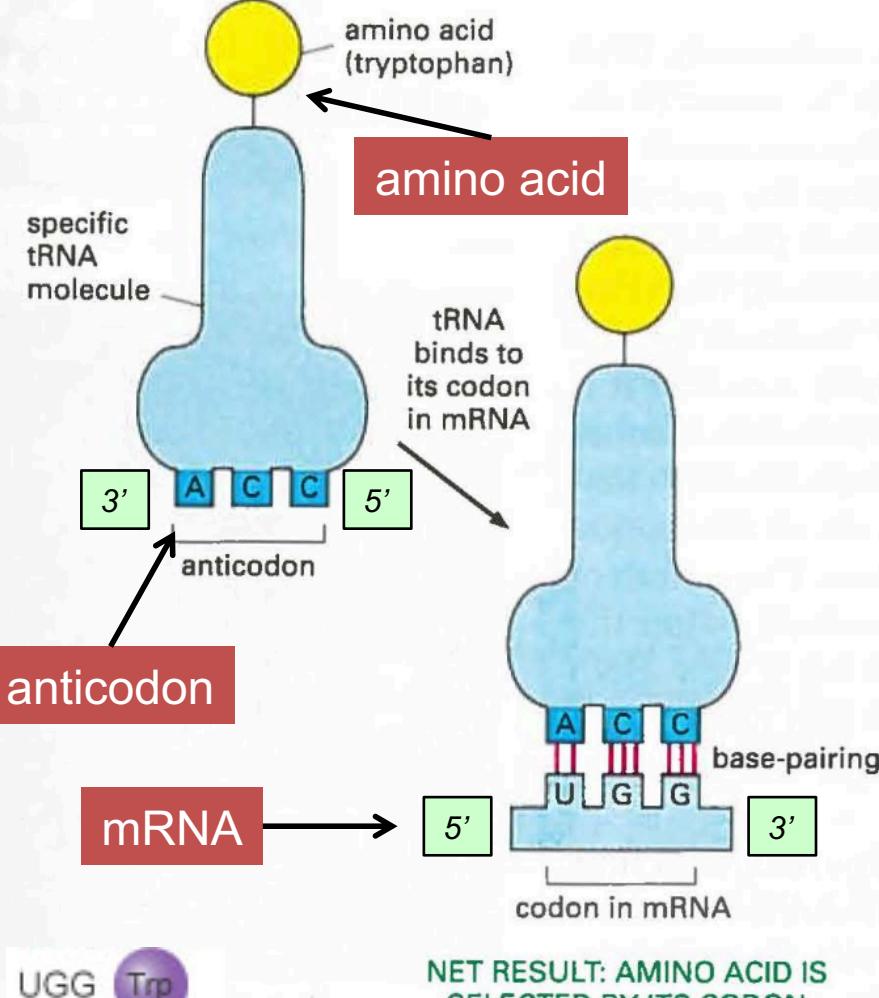
Goal: Convert Instructions in mRNA to a Peptide



		Second nucleotide					
		U	C	A	G		
First nucleotide	U	UUU Phe UUC UUA Leu UUG	UCU UCC UCA UCG	UAU UAC UAA STOP UAG STOP	UGU UGC UGA STOP UGG Trp		
	C	CUU CUC Leu CUA CCA CCG	CCU CCC Pro	CAU His CAC	CGU CGC Arg		
A	A	AUU AUC Ile AUA AUG Met	ACU ACC ACA ACG	AAU AAC Asn AAA AAG Lys	AGU AGC Ser AGA AGG Arg		
	G	GUU GUC Val GUA GUG	GCU GCC GCA GCG	GAU GAC Asp GAA GAG Glu	GGU GGC Gly GGA GGG		

- Methionine
- Valine
- Serine
- Proline

Transfer Mechanism: tRNA



Anticodon: 5' UGC 3'

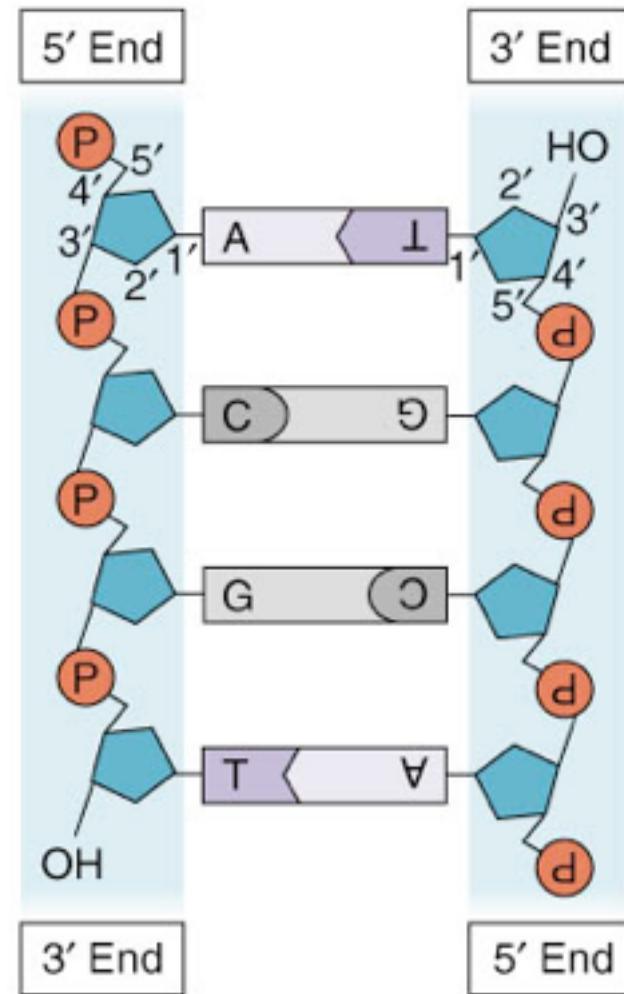
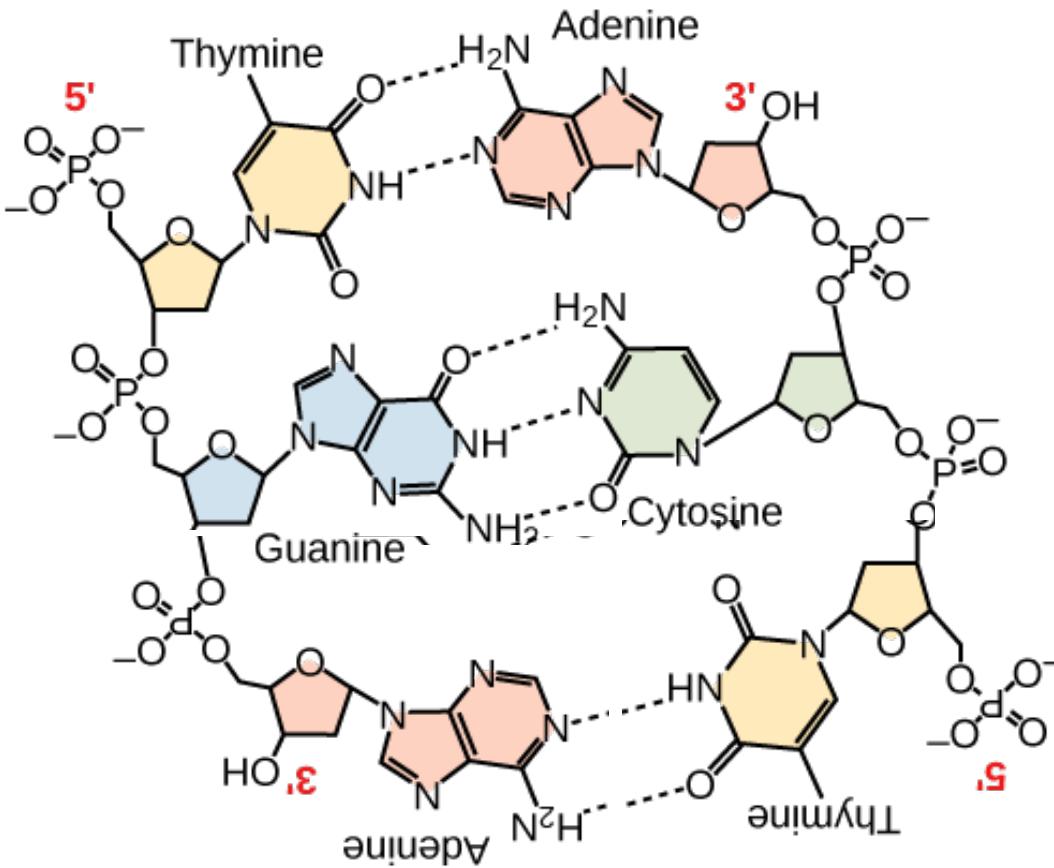
Codon: 3' ACG 5'
= 5' GCA 3'

GCU
GCC
GCA
GCG

Ala

Figure 1-9, Alberts et. al.,
Molecular Biology of the Cell (eReserves)

Question from Last Lecture: Why Antiparallel Pairing?



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Peptides are Translated by the Ribosome

Bacterial Ribosome
(blue & green), over 50
proteins and rRNA molecules

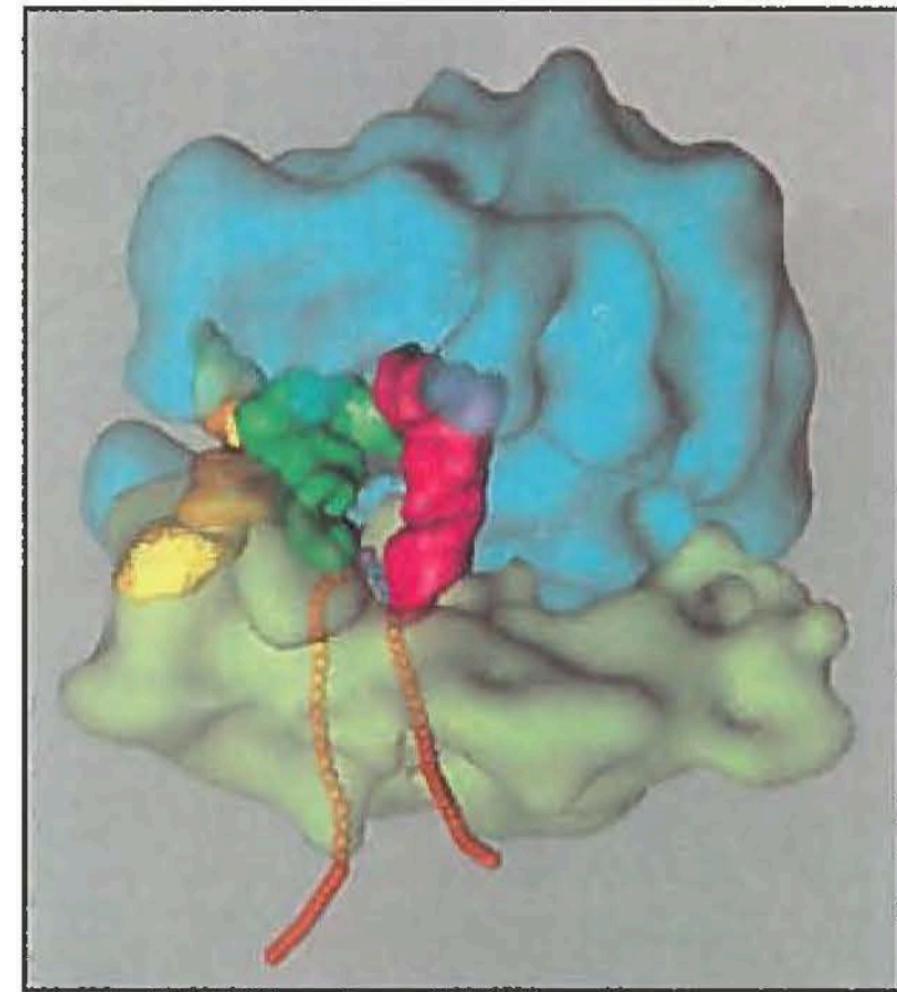
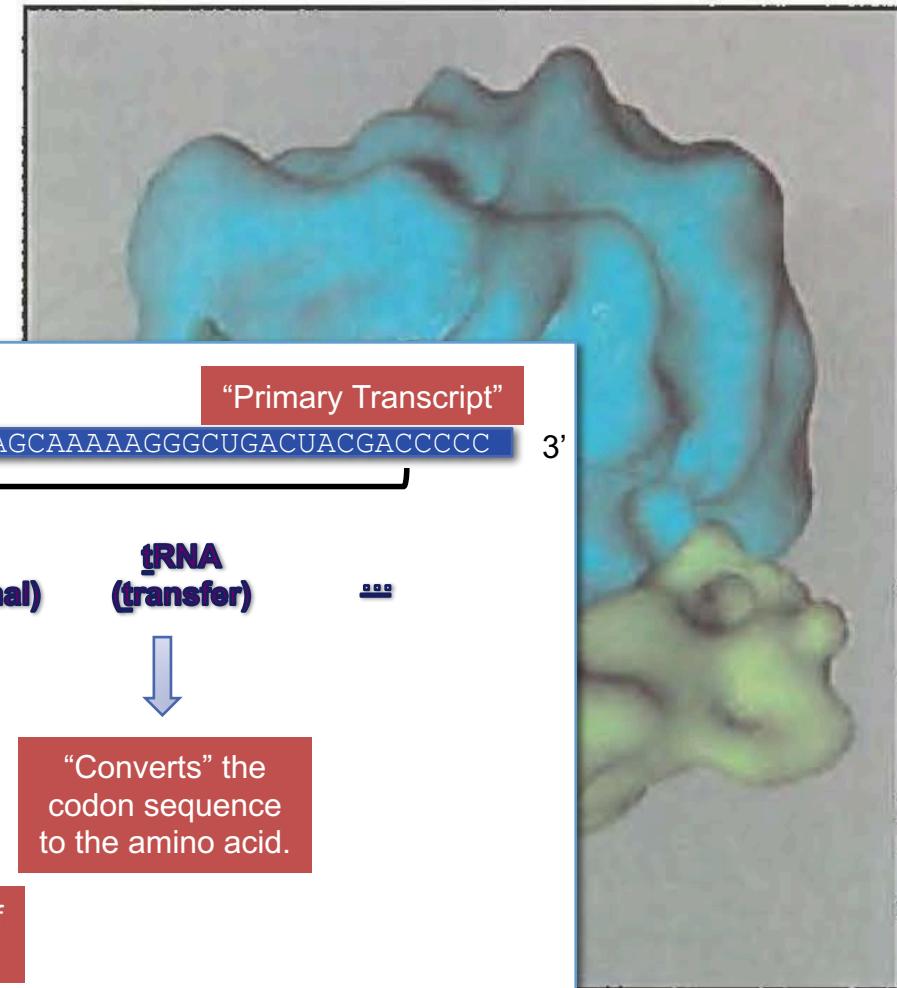


Figure 1-10, Alberts et. al.,
Molecular Biology of the Cell (eReserves)

Peptides are Translated by the Ribosome

Bacterial Ribosome
(blue & green), over 50
proteins and rRNA molecules



Three tRNAs
(yellow, green)

Peptides are Translated by the Ribosome

Bacterial Ribosome
(blue & green), over 50
proteins and rRNA molecules

mRNA molecule
(orange beads)

Three tRNA molecules
(yellow, green, and pink)

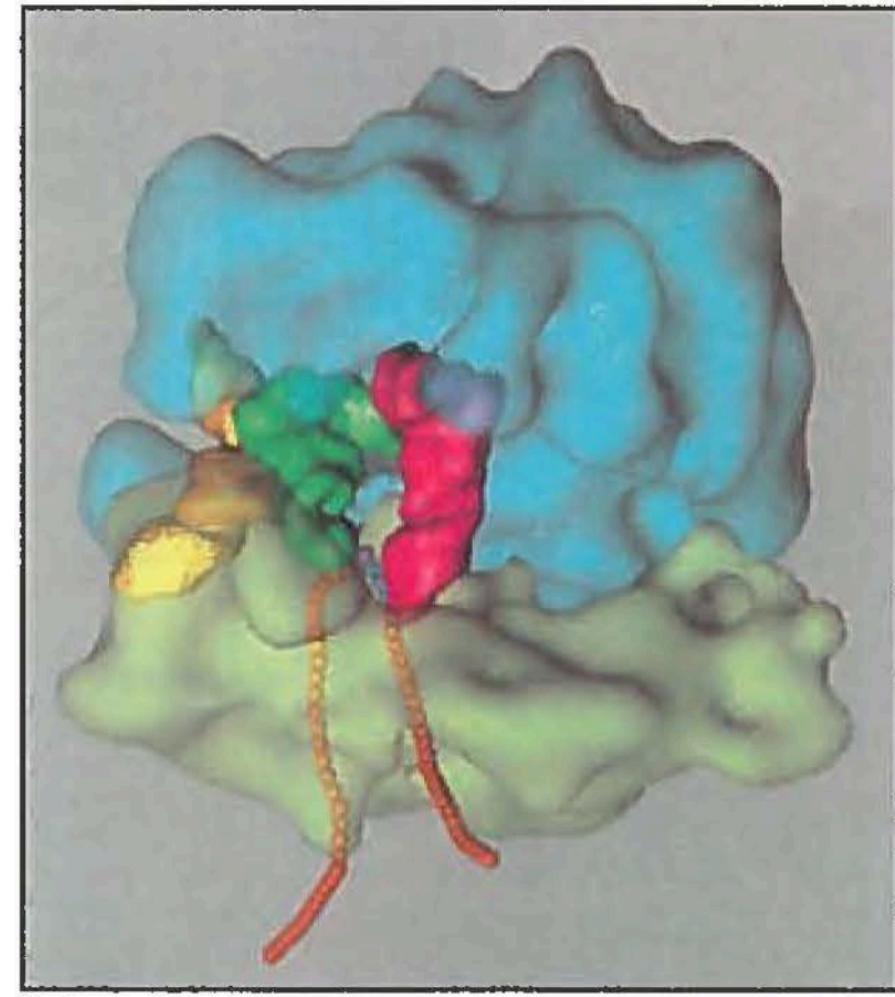
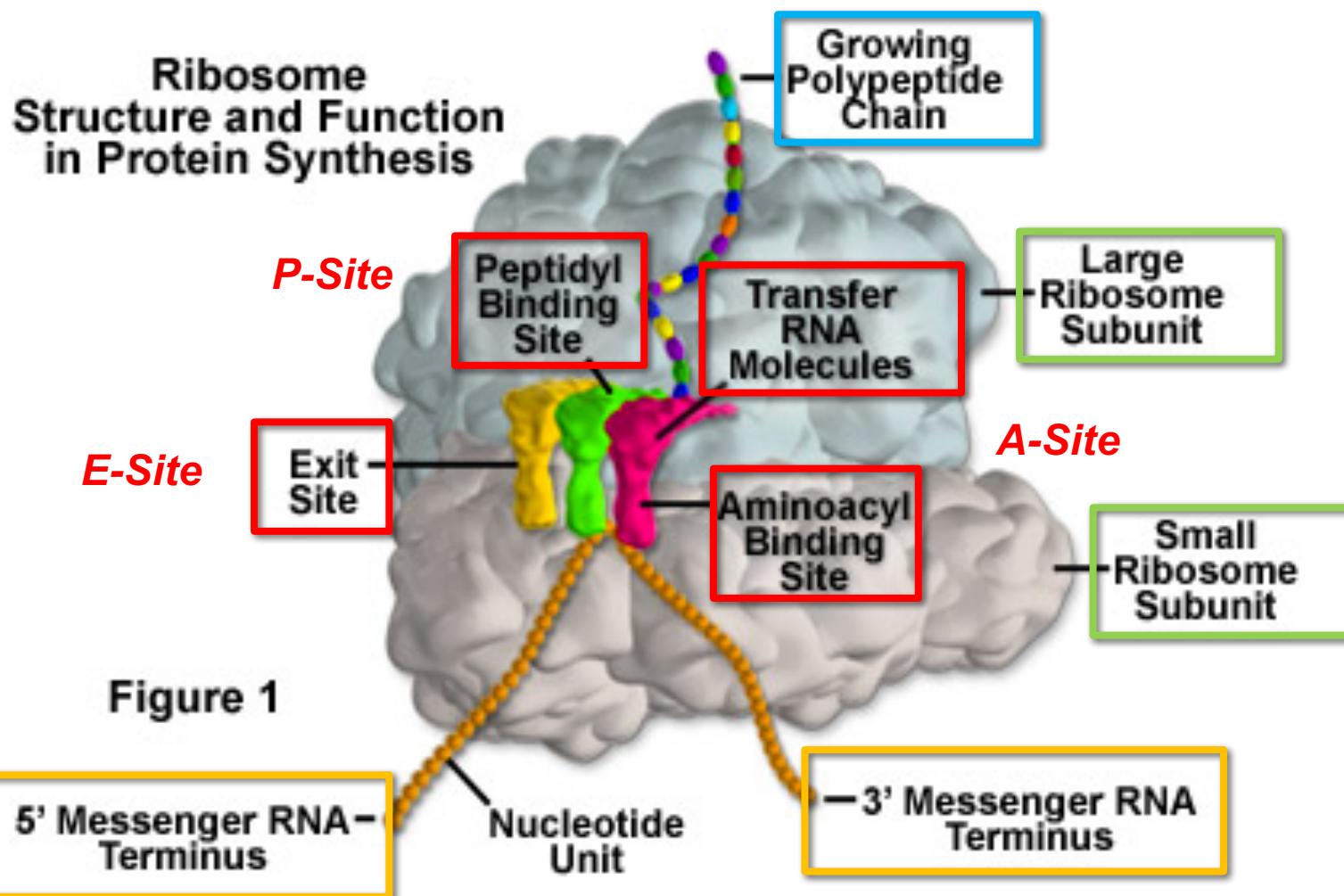
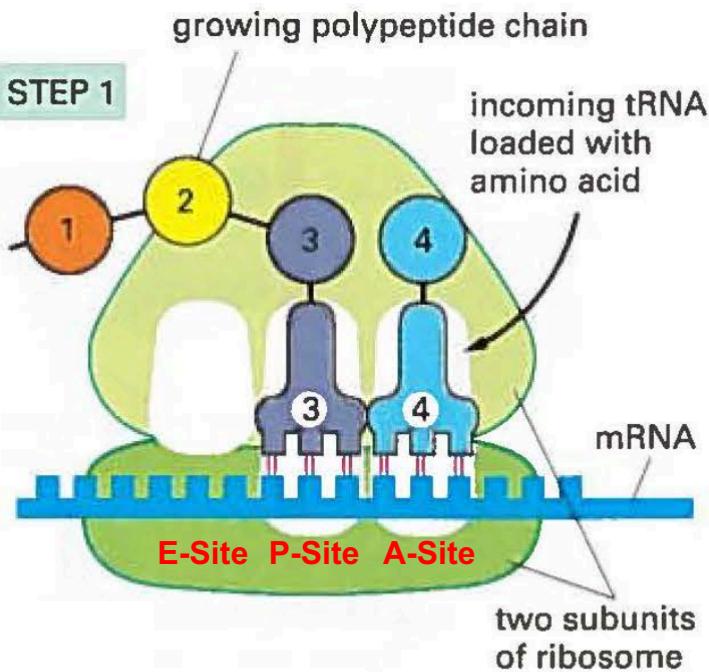


Figure 1-10, Alberts et. al.,
Molecular Biology of the Cell (eReserves)

Peptides are Translated by the Ribosome



Translation by the Ribosome in 3 Steps

[YouTube Video](#)

Translation by the Ribosome in 3 Steps

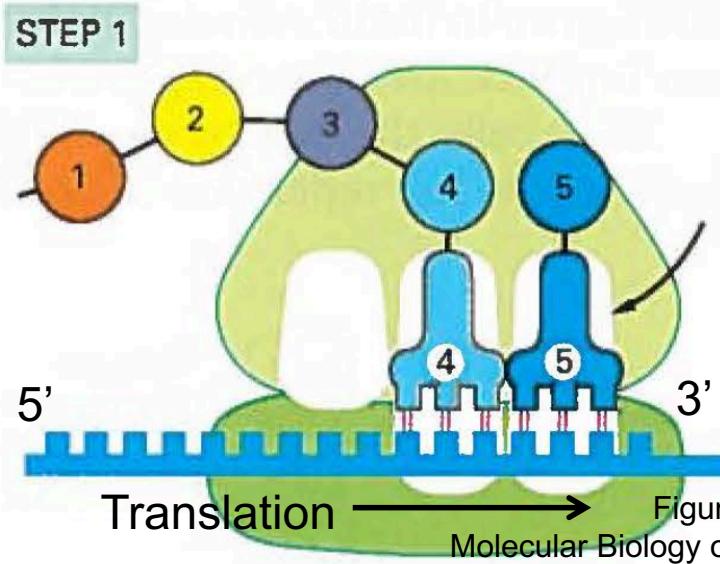
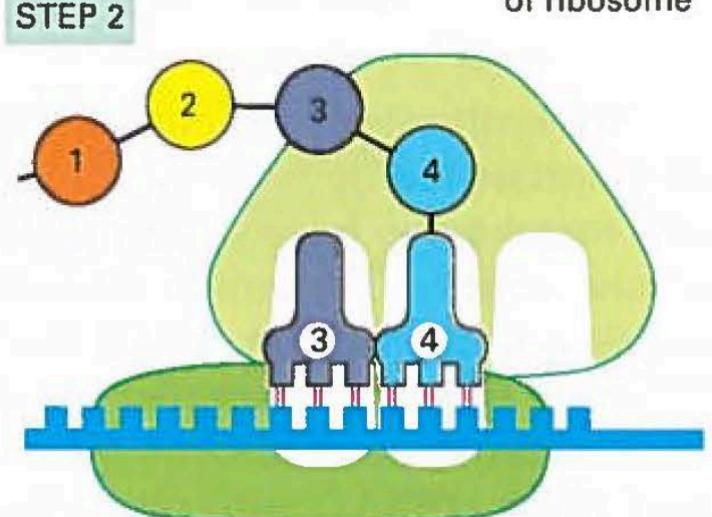
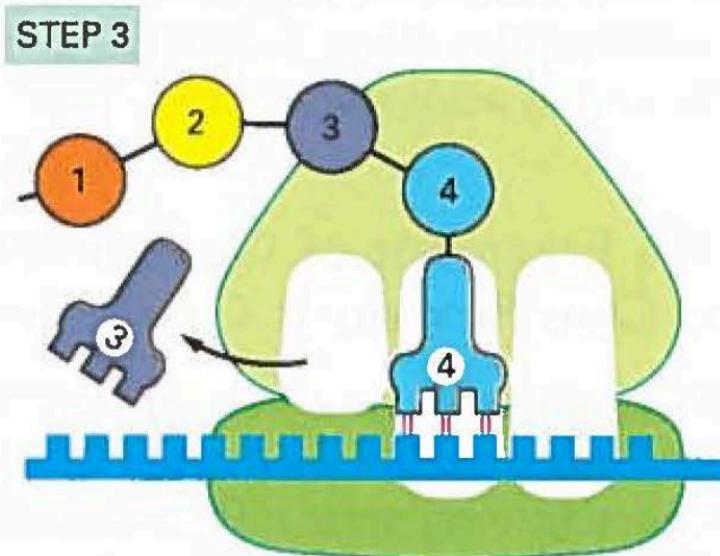
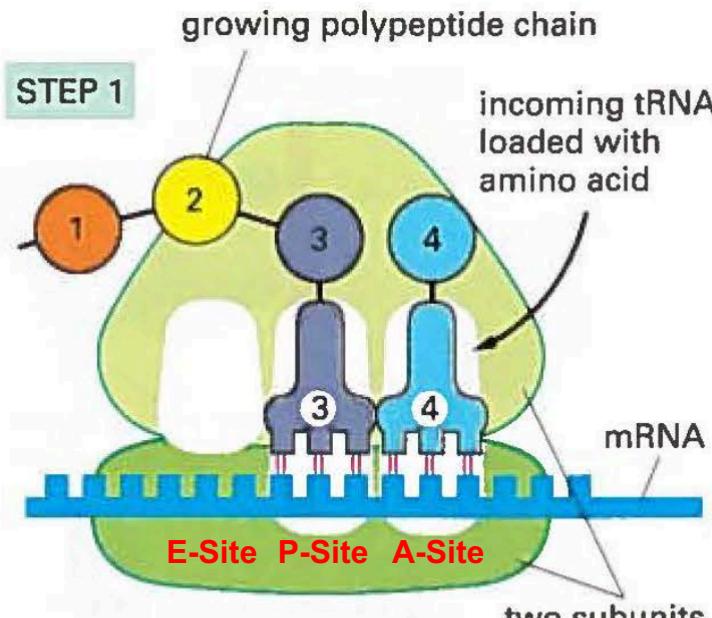


Figure 1-10, Alberts et. al.,
Molecular Biology of the Cell (eReserves)

HW3: Programming the Central Dogma

- A DNA sequence (a string).
- The *strand* the gene appears on (a string). If the string is '+', then the DNA is from the positive strand. If the string is '-', then the DNA is from the reverse complement (negative) strand.
- A list of exon start coordinates (a list of integers).
- A list of intron start coordinates (a list of integers).

*Extra print statements
are encouraged!*

```
Dataset: testPos
DNA: CCCATGGTCGGGGGGGGGGAGTCCATAACCC
Num exons: 2
strand: +
RNA (from file): AUGGUCAGUCAUAA
peptide (from file): MVSP*
```

Read and print Information
about the Input

```
Computed mRNA: AUGGUCAGUCAUAA
mRNA matches!
```

transcribe() function (returns mRNA)

```
Computed Peptide: MVSP*
Peptide matches!
```

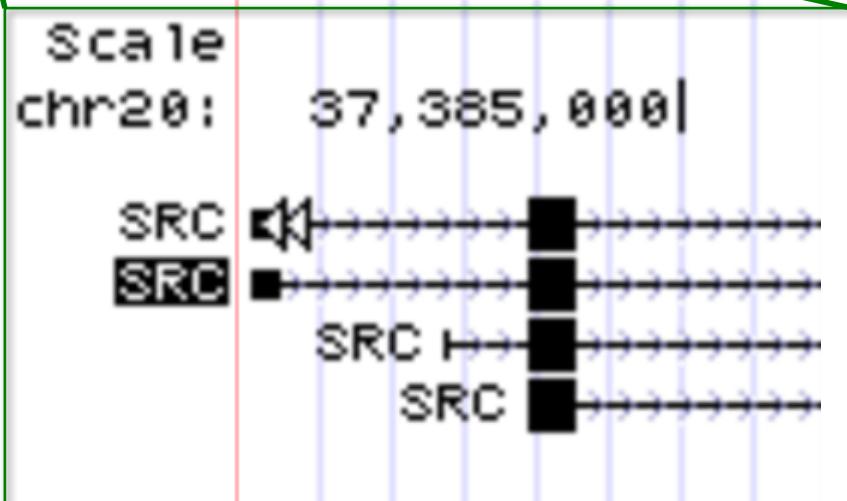
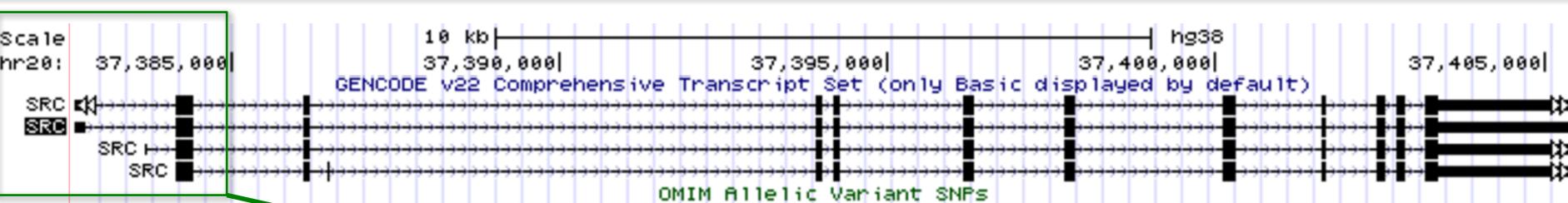
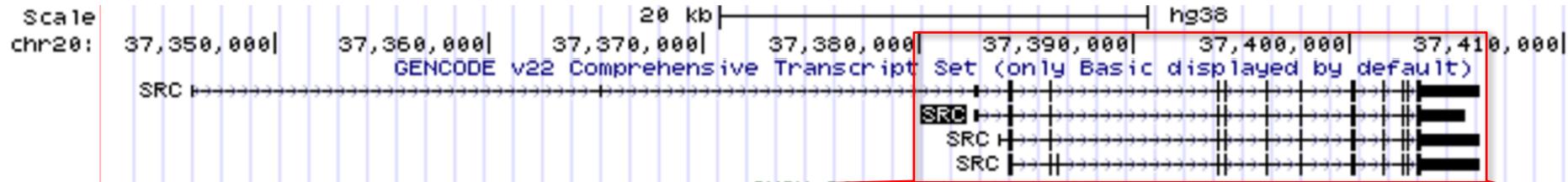
translate() function (returns peptide)

Compare to sequences

HW3: Organization of the program

- Download the file from Moodle and open it in Sublime
`HW3-for-pythontutor.py`
- You don't need to run it (no need to open Terminal)
- Follow as we visualize the execution in
`pythontutor.com`

The Data: SRC Gene



Data From Genome Browser

- DNA string (slice of chromosome)
- Strand = '+'
- Exon/Intron Start Positions shifted to index into DNA string.

HW3: Programming the Central Dogma

- A DNA sequence (a string).
- The *strand* the gene appears on (a string). If the string is '+', then the DNA is from the positive strand. If the string is '-', then the DNA is from the reverse complement (negative) strand.
- A list of exon start coordinates (a list of integers).
- A list of intron start coordinates (a list of integers).

*Extra print statements
are encouraged!*

Dataset: testPos

DNA: CCCATGGTCGGGGGGGGGGAGTCCATAACCC

Num
str
RNA
pep

Lastly...make your program
work for genes on the
negative strand ("")

Computed mRNA: AUGGUCAGUCCAUAA
mRNA matches!

Computed Peptide: MVSP*
Peptide matches!

Compare to sequences

Read and print Information
about the Input

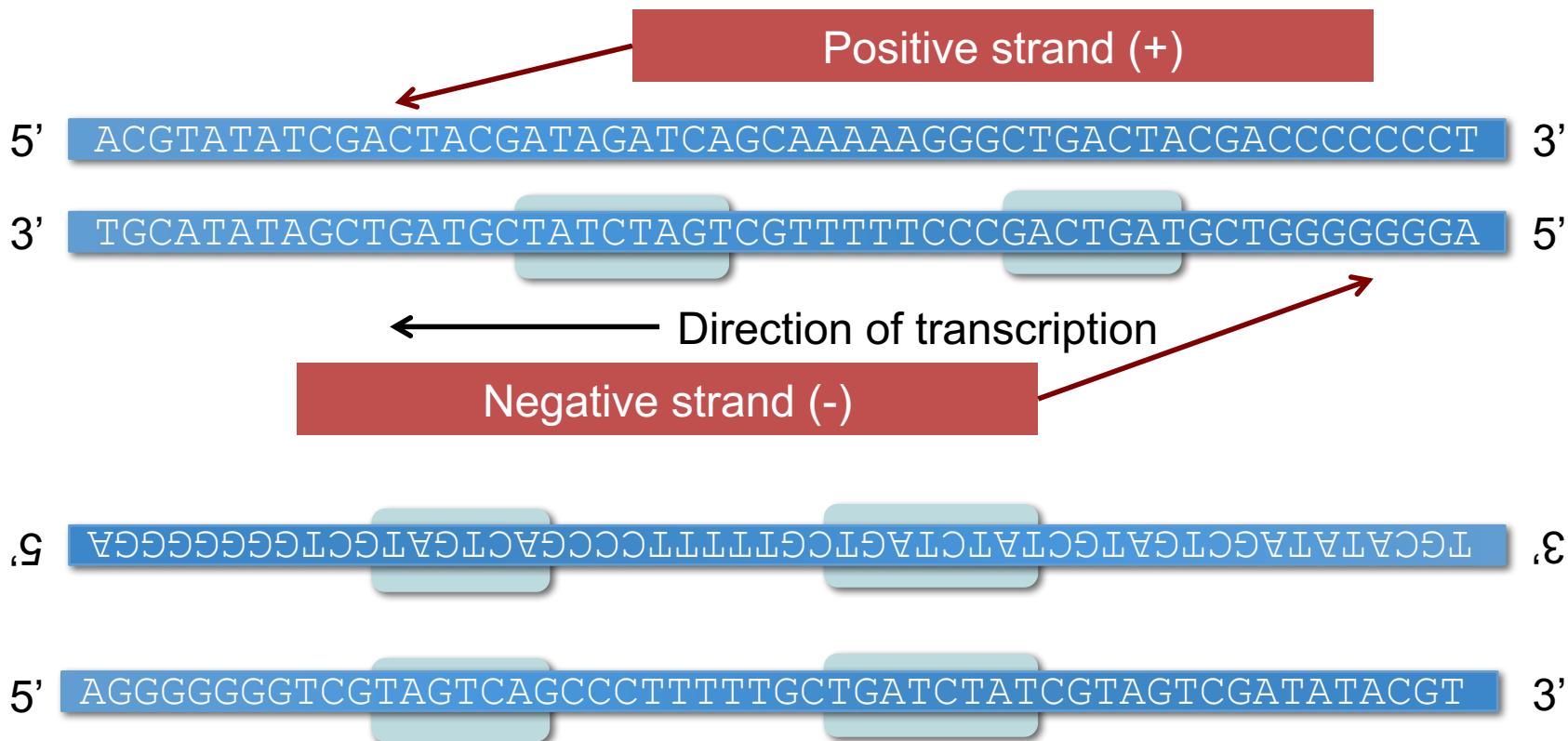
transcribe() function (returns mRNA)

translate() function (returns peptide)

The Reverse Complement Strand

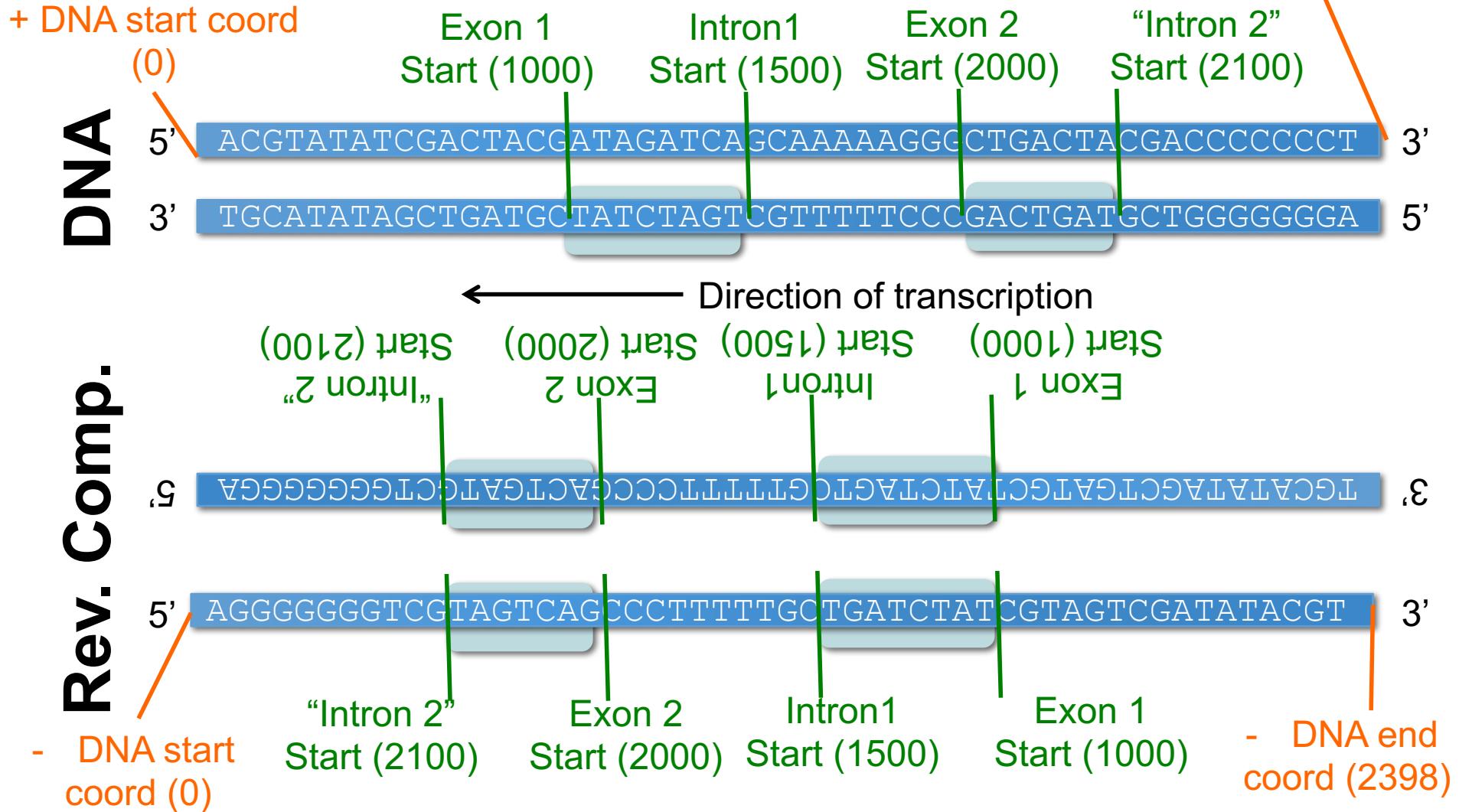
DNA

Rev. Comp.

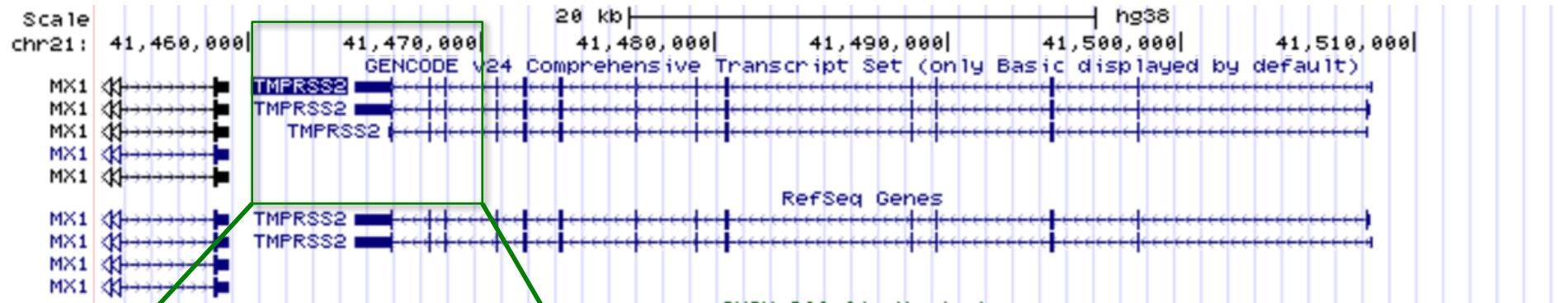


Sequences are always reported
in the 5' to 3' direction.

BUT, the coordinates are always relative to the forward strand! (this is very, very annoying)



The Data: TMPRSS2 Gene



- ## Data From Genome Browser
- DNA string (slice of chromosome)
 - Strand = '+'
 - Exon/Intron Start Positions shifted to index into DNA string.

Upcoming Schedule

Week 1	
Anna Office Hours 11a—12pm Wed/Thurs	Lecture, HW2 Due, HW3 Out
Tues 2/2/16	Tues Lab: Reverse Complement Function
Tues 2/7/16	12p-1p: <i>ES-Bio Faculty Candidate Talk</i>
Mina Dojo Hours (8-10pm Thurs)	Lecture
Fri 2/12/16	2/9 12p-1p: <i>ES-Bio Faculty Candidate Talk</i>
Elaine Dojo Hours (7-9pm Tues)	Lecture, Internal HW3.1 Deadline
Sun 2/13	Lecture, Internal HW3.2 Deadline
Mon 2/14	Tues Lab: Rosalind Tutorial
Rose Dojo Hours (8-10pm Thurs)	Lecture
Mon 2/17	Lecture, HW3 Due

HW1 Back
(Email?)

Obtain
Textbook