Summary slide:

RNA processing: 5' & 3' modification and splicing of beta globin gene



-5' Cap (adding 7 methyl guanos ine) stabilizes mRNA, allows ribosome binding.

-3'Poly A stabilizes mRNA and promotes its export to cytoplasm.

-Each intron has a 5' splice donor and a 3' splice acceptor site.

-Introns can be alternatively spl iced out.

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Schematic of an mRNA transcript



-Transcript shown is *nascent* or spliced. Circle one.

- -Label the 5' and 3' ends of the transcript.
- -Show the direction in which the transcript is made using an arrow.

-How many mature mRNA transcripts can result from this transcript (Assume all introns are removed)?
4: (E1+E2+E3+E4), (E1+E4), (E1+E3+E4), (E1+E2+E4)
-Give the length (in kb) of each mature transcript.
4kb, 2kb 3kb, 2.9kb

Summary slide: From Gene to protein



5'<u>CGGUCCCGGUA</u>AUG/AAU/GUG/UGC/UGA<u>CCGAUC3</u>'

Name a sequence that is a part of nascent but NOT mature mRNA? (Think of what gets spliced out) *Introns*

Name a sequence that is a part of gene but NOT transcribed mRNA? (Think of regulatory regions) *Promoters and/ or enhancers*

Underline the corresponding 5'UTR. (The 3'UTR is underlined. Think of the region prior to the start codon)

Box the open reading frame (ORF) & separate each codon by "/". (Think of the region prior to the start and stop codon)

Write the corresponding protein $(N \rightarrow C; use thegenetic code chart)N- Met-Asn-Val-Cys-C$

tRNA and mRNA binding during translation

Label the 5' and 3' ends of mRNA in the drawing (The binding is anti-parallel and complementary)

Which amino acid will this tRNA be charged with? (Take a look at the codon chart)



For the prokaryotic gene below, and bottom strand as template

5 ' ACATGCATGTGTGCAAATAA3 ' 3 ' TGTACGTACACACGTTTATT5 '

Write the corresponding RNA, indicating each codon (RNA sequence = non-template strand, 5' to 3', codon = base triplets) 5 'ACAUGC AUG UGU GCA AAU AA3 '

Write the corresponding protein ($N \rightarrow C$; use the genetic code chart) *N-Met-His-Val-Cys-Lys-C*

Write the corresponding anti-codon sequence for 2nd amino acid. (RNA sequence = non-template strand, 5' to 3', codon = base triplets) 5'-ACA-3'

The tRNA works as an adaptor molecule. Explain. (Think what does tRNA bind to) It binds to both mRNA and amino acids. It translates the information in mRNA to make the protein For the prokaryotic gene below, and bottom strand as template

5 ' ACATGAAATTTGGGCTGTAA3 ' 3 ' TGTACTTTAAACCCGACATT5 '

Write the corresponding RNA and shade the ORF 5' ACAUGAAAUUUGGGCUGUAA3'

Write the corresponding protein and label its N and C ends N-Met-Lys-Phe-Gly-Leu-C

Write the corresponding anti-codon sequence for 1st amino acid.

5'-CAU-3'

DNA POINT MUTATIONS

WILD TYPE	_					
DNA (coding/non-templat	tel 'ATG	CCC	GGG	TTA	GGG3′	Reading frame
(template)	3'TAC	GGG	CCC	AAT	CCC5 ′	
mRNA	5'AUG	CCC	GGG	UUA	GGG3′	
Protein	N-Met	Pro	Gly	Leu	Gly-C	
FRAME SHIFT mutation			←			
DNA (coding)	5 ' ATG	CCC	GGG	TTA	GGG3 '	delete
(template)	3'TAC	<mark>G</mark> GG	CCC	AAT	CCC5 ′	
mRNA	5 ' AUG	CCG	GGU	UAG	GG . 3 ′	
Protein	N-Met	Pro	Gly	STO	P - C	

SILENT mutation codes for the SAME amino acid					
			L	A inst	ead of C in mRNA
DNA (coding/non-template)	5'ATG	CCA	GGG	TTA	GGG3′
(template)	3' TAC	GGT	CCC	AAT	CCC5 ′
mRNA	5 ' AUG	CCA	GGG	UUA	GGG3′
Protein	N-Met	Pro	Gly	Leu	Gly-C

MIS-SENSE mutation codes for a DIFFERENT amino acid

	G instead of U in mRNA			
DNA (coding)	5'ATG CCC GGG GTA GGG3'			
(template)	3'TAC GGG CCC CAT CCC5'			
mRNA	5'AUG CCC GGG GUA GGG3'			
Protein	N-Met Pro Arg Val Gly-C			

If the gene sequence is mutated (<u>red and underlined</u>) and <u>bottom</u> <u>strand is template</u>



Write the new corresponding RNA, indicating each codon (RNA sequence = non-template strand) 5-AUGAAUGUGUGA-3'

Write the new corresponding protein N-Met-Asp-Val-C

Identify the type of point mutation *Non-sense*

If the gene sequence is mutated (red), bottom strand as template



Write the new corresponding RNA, and indicate codons

5' AUGAAUAGUGUGC......3'

Write the new corresponding protein

N-Met-Asp-Ser-Val.....-C

Identify the type of point mutation *Missense*

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