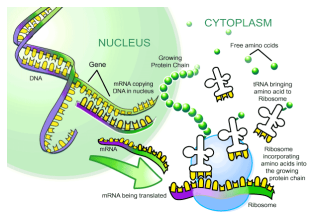
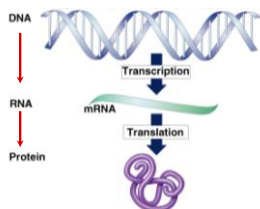


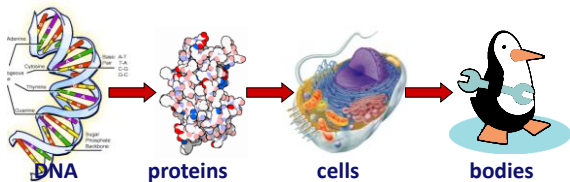
From Gene to Protein



How Genes Work

What do genes code for?

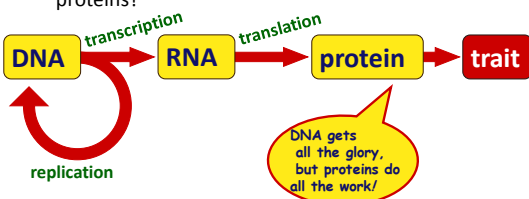
- **How does DNA code for cells & bodies?**
 - ◆ **how are cells and bodies made from the instructions in DNA**



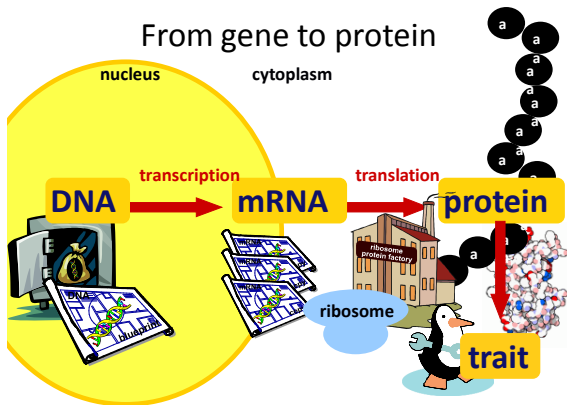
The “Central Dogma”

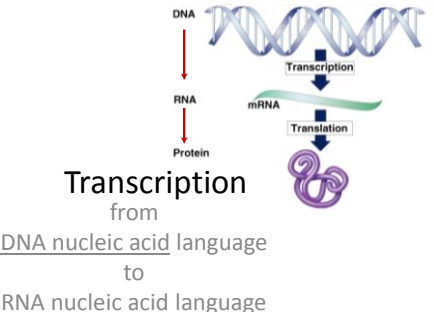


- Flow of genetic information in a cell
 - How do we move information from DNA to proteins?



From gene to protein



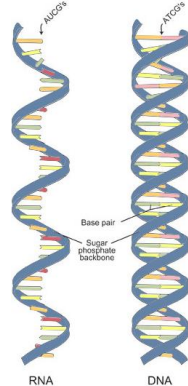


Transcription
 from
DNA nucleic acid language
 to
RNA nucleic acid language

2007-2008

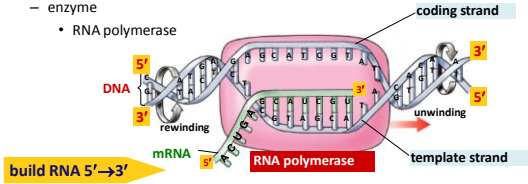
RNA

- ribose sugar
- N-bases
 - uracil instead of thymine
 - U : A
 - C : G
- single stranded
- lots of RNAs
 - mRNA, tRNA, rRNA, siRNA...



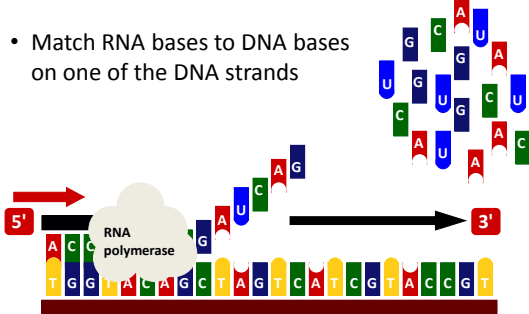
Transcription

- Making mRNA
 - transcribed DNA strand = template strand
 - untranscribed DNA strand = coding strand
 - same sequence as RNA
 - synthesis of complementary RNA strand
 - transcription bubble
 - enzyme
 - RNA polymerase



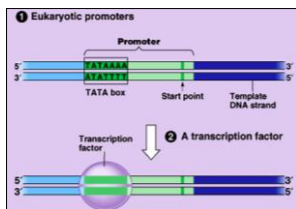
Matching bases of DNA & RNA

- Match RNA bases to DNA bases on one of the DNA strands



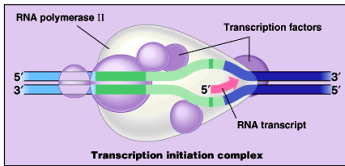
Which gene is read?

- Promoter region
 - binding site before beginning of gene
 - TATA box binding site
 - binding site for RNA polymerase & transcription factors
- Enhancer region
 - binding site far upstream of gene
 - turns transcription on HIGH



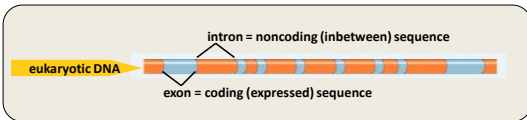
Transcription Factors

- Initiation complex
 - transcription factors bind to promoter region
 - suite of proteins which bind to DNA
 - turn on or off transcription
 - trigger the binding of RNA polymerase to DNA



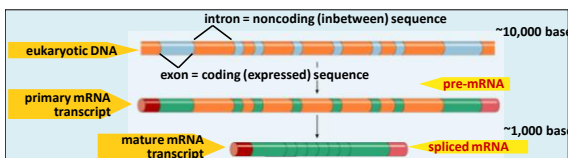
Eukaryotic genes have junk!

- Eukaryotic genes are not continuous
 - exons = the real gene
 - expressed / coding DNA
 - introns = the junk
 - inbetween sequence



mRNA splicing

- Post-transcriptional processing
 - eukaryotic mRNA needs work after transcription
 - primary transcript = pre-mRNA
 - mRNA splicing
 - edit out introns
 - make mature mRNA transcript



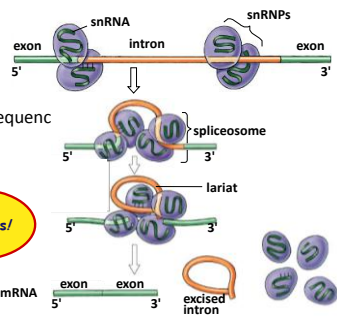
Splicing must be accurate

- No room for mistakes!
 - a single base added or lost throws off the reading frame

<p>AUGCGGCTATGGGUCCGAUAAGGGCCAU AUGCGGUCCGAUAAGGGCCAU AUG CGG UCC GAU AAG GGC CAU Met Arg Ser Asp Lys Gly His</p>
<p>AUGCGGCTATGGGUCCGAUAAGGGCCAU AUGCGGGUCCGAUAAGGGCCAU AUG CGG GUC CGA UAA GGG CCA U Met Arg Val Arg STOP</p>

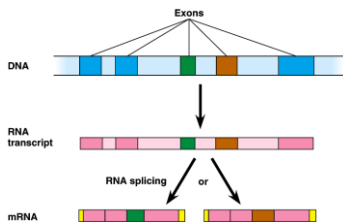
RNA splicing enzymes

- snRNPs
 - small nuclear RNA
- Spliceosome
 - several snRNPs
 - recognize splice site sequenc
 - cut & paste gene



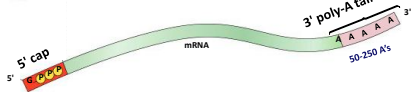
Alternative splicing

- Alternative mRNAs produced from same gene
 - when is an intron not an intron...
 - different segments treated as exons

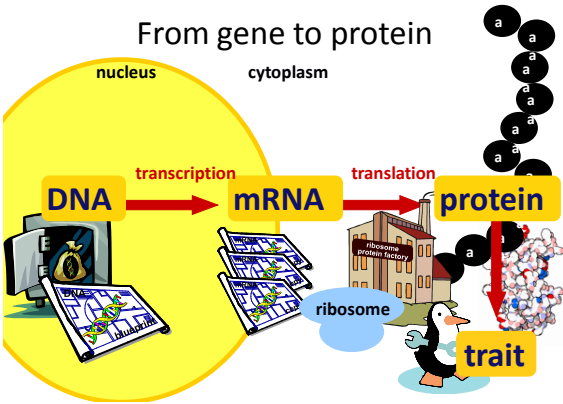


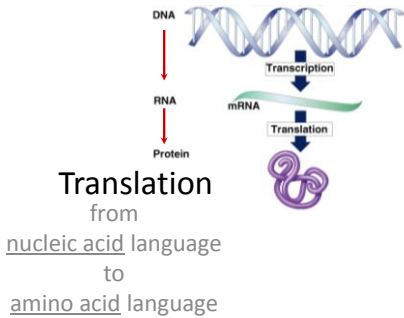
More post-transcriptional processing

- Need to protect mRNA on its trip from nucleus to cytoplasm
 - enzymes in cytoplasm attack mRNA
 - protect the ends of the molecule
 - add 5' GTP/Methylated cap
 - add poly-A tail
 - longer tail, mRNA lasts longer: produces more protein

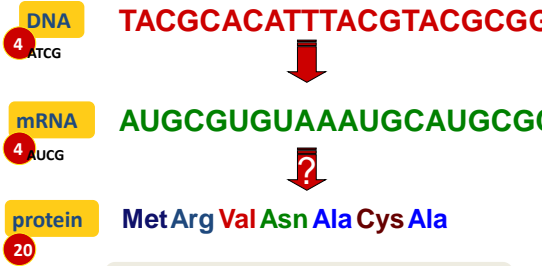


From gene to protein



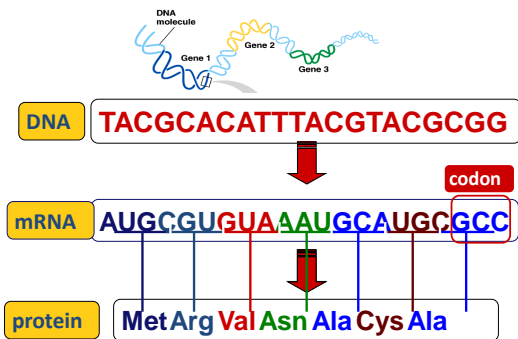


How does mRNA code for proteins?



How can you code for 20 amino acids with only 4 nucleotide bases (A,U,G,C)?

mRNA codes for proteins in triplets



Cracking the code

1960 | 1968
Nirenberg & Khorana

- Crick
 - determined 3-letter (triplet) **codon** system
- WHYDIDTHEREDBATEATTHEFATRAT**
- Nirenberg (47) & Khorana (17)
 - ◆ determined mRNA–amino acid match
 - ◆ added fabricated mRNA to test tube of ribosomes, tRNA & amino acids
 - created artificial UUUUU... mRNA
 - found that UUU coded for **phenylalanine**

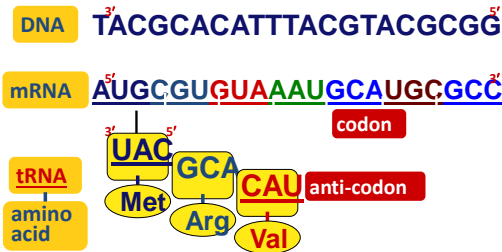
The code

- Code for **ALL** life!
 - strongest support for a common origin for all life
- Code is redundant
 - several codons for each amino acid
 - 3rd base “wobble”

- **Start codon**
 - ◆ AUG
 - ◆ methionine
- **Stop codons**
 - ◆ UGA, UAA, UAG

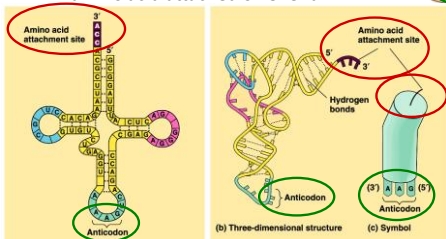
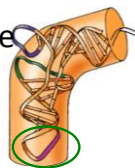
		Second base					
		U	C	A	G		
U	UUU	Phe	UCU	UAU	Tyr	UGU	Cys
	UUC		UCC	UAC	Ser	UGC	C
	UUA	Leu	UCA	UAA	Stop	UGA	Stop
	UUG		UCG	UAG	Stop	UGG	Trp
C	CUU		CCU	CAU	His	CGU	U
	CUC		CCC	CAC	Pro	CGC	Arg
	CUA	Leu	CCA	CAA	Gln	CGA	G
	CUG		CCG	CAG		CGG	
A	AUU	Ile	ACU	AAU	Asn	AGU	Ser
	AUC		ACC	AAC	Thr	AGC	
	AUA		ACA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

How are the codons matched to amino acids?



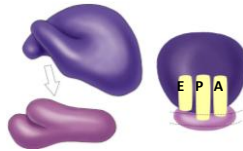
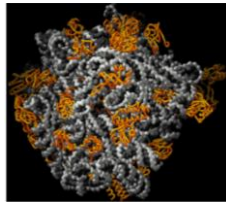
Transfer RNA structure

- “Clover leaf” structure
 - anticodon on “clover leaf” end
 - amino acid attached on 3' end



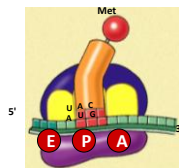
Ribosomes

- Facilitate coupling of tRNA anticodon to mRNA codon
- Structure
 - ribosomal RNA (rRNA) & proteins
 - 2 subunits
 - large
 - small



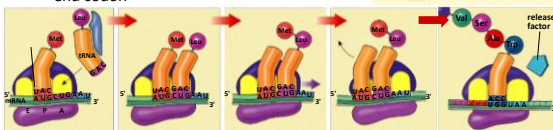
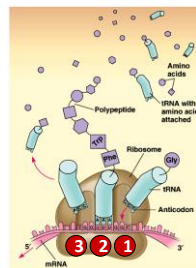
Ribosomes

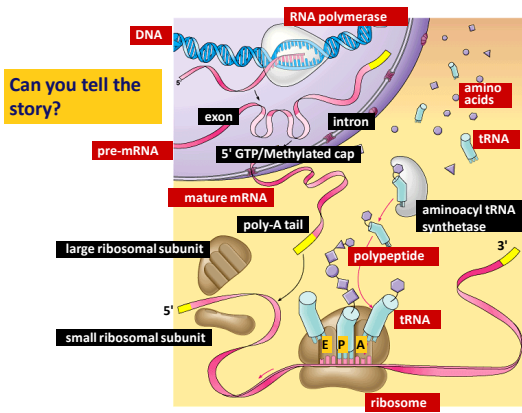
- A site (aminoacyl-tRNA site)
 - holds tRNA carrying next amino acid to be added to chain
- P site (peptidyl-tRNA site)
 - holds tRNA carrying growing polypeptide chain
- E site (exit site)
 - empty tRNA leaves ribosome from exit site



Building a polypeptide

- Initiation
 - brings together mRNA, ribosome subunits, initiator tRNA
- Elongation
 - adding amino acids based on codon sequence
- Termination
 - end codon





Can you tell the story?
