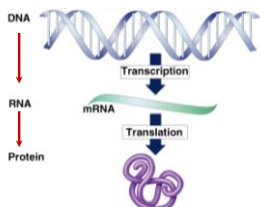
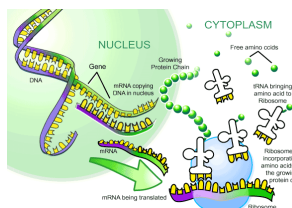


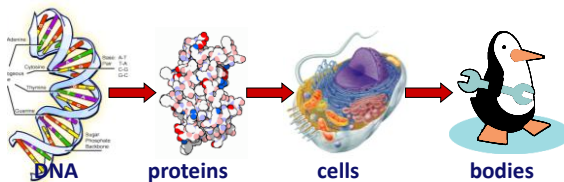
### From Gene to Protein



### How Genes Work

### What do genes code for?

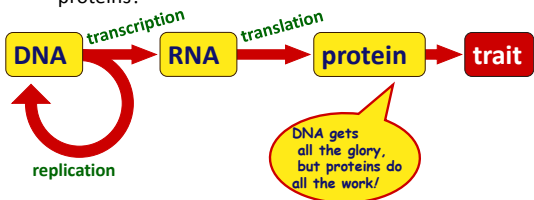
- How does DNA code for cells & bodies?
  - how are cells and bodies made from the instructions in DNA



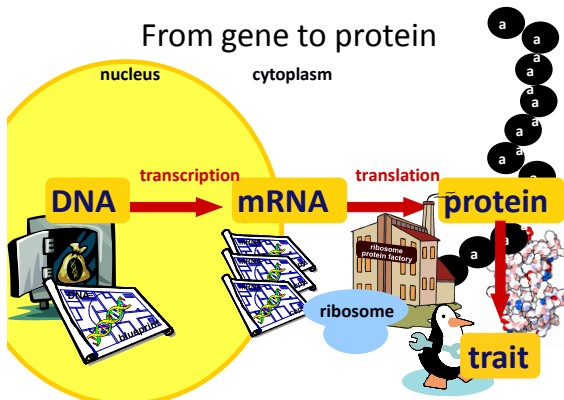
### The "Central Dogma"



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

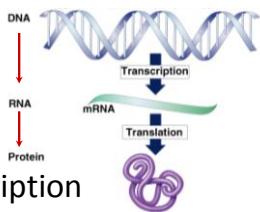


### From gene to protein



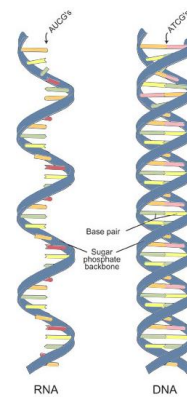
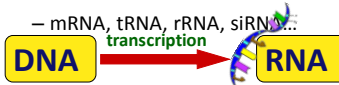
### Transcription

from DNA nucleic acid language to RNA nucleic acid language



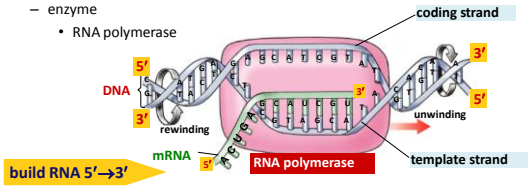
### RNA

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



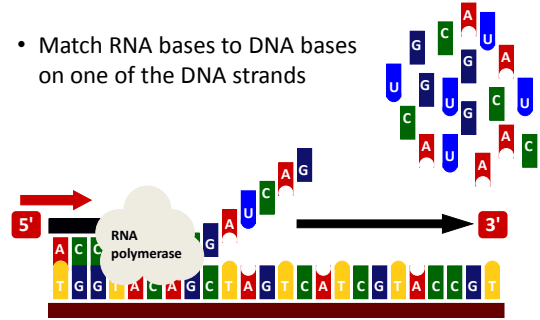
## Transcription

- 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



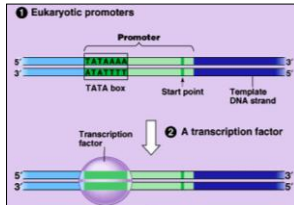
## Matching bases of DNA & RNA

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



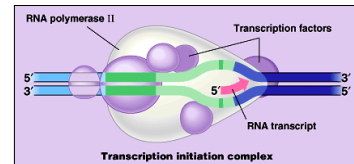
## Which gene is read?

- 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



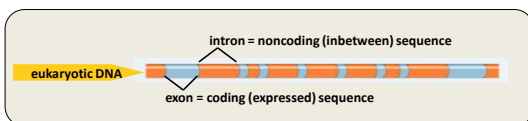
## Transcription Factors

- 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



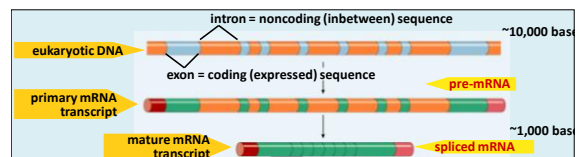
## Eukaryotic genes have junk!

- 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

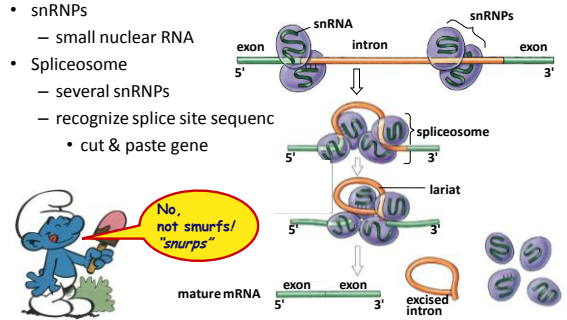


### Splicing must be accurate

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

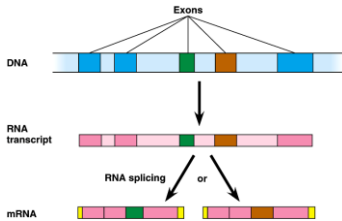


### RNA splicing enzymes



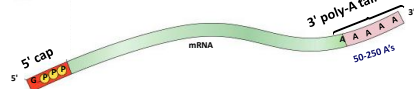
### Alternative splicing

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

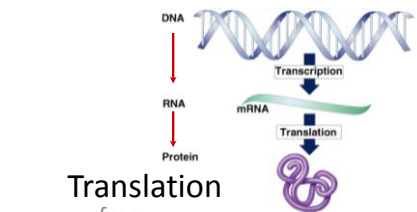
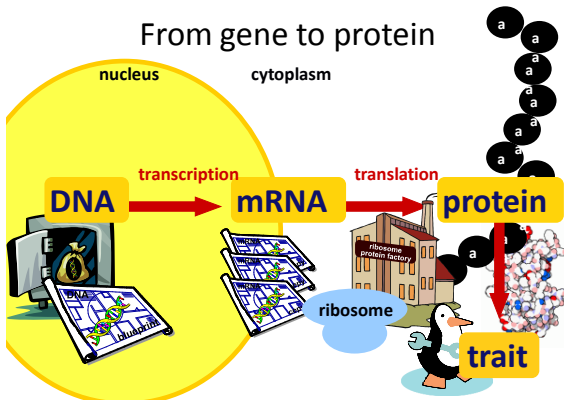


### More post-transcriptional processing

- 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

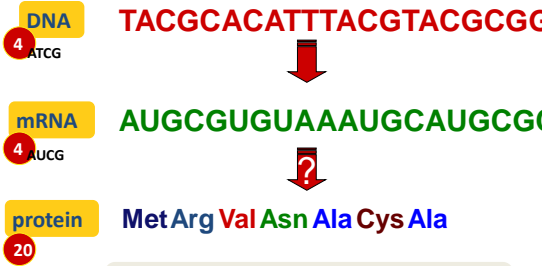


### From gene to protein



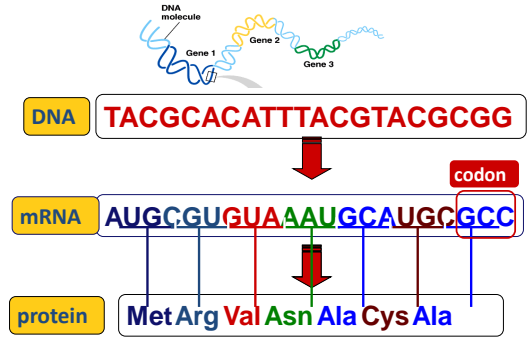
Translation  
 from  
nucleic acid language  
 to  
amino acid language

### 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
- **WHY DID THEY BATE AT THE FAT RAT**
- 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**

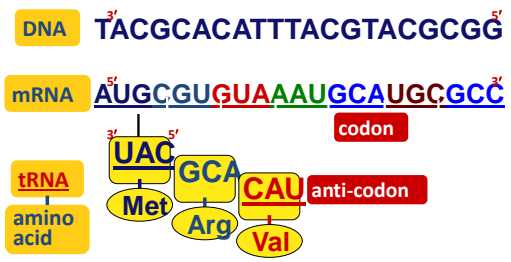
### The code

- 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

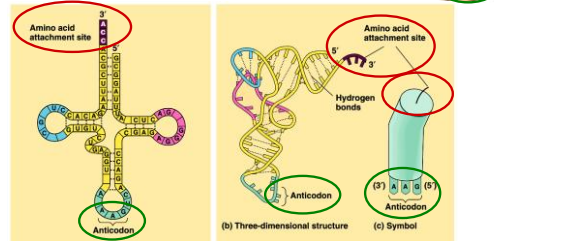
		Second base				
		U	C	A	G	
U	UUU	UCU	UAU	UGU	Cys	U
	UUC	UCC	UAC	UGC	Cys	C
	UUA	UCA	UAA	UGA	Stop	A
	UUG	UCG	UAG	UGG	Trp	G
C	CUU	CCU	CAU	CGU	U	C
	CUC	CCC	CAC	CGC	Arg	A
	CUA	CCA	CAA	CGA	Arg	G
	CUG	CCG	CAG	CGG	Arg	G
A	AUU	ACU	AAU	AGU	Ser	U
	AUC	ACC	AAC	AGC	Ser	C
	AUA	ACA	AAA	AGA	A	A
	AUG	ACG	AAG	AGG	Arg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

### How are the codons matched to amino acids?



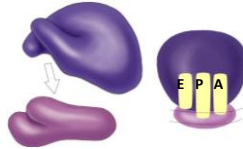
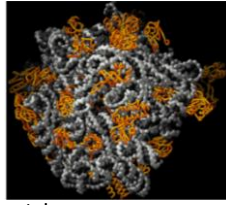
### Transfer RNA structure

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



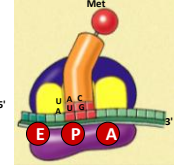
## Ribosomes

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



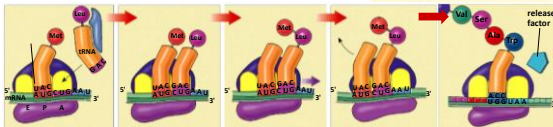
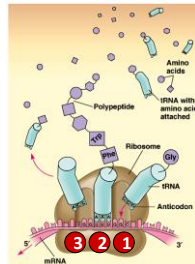
## Ribosomes

- 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?

