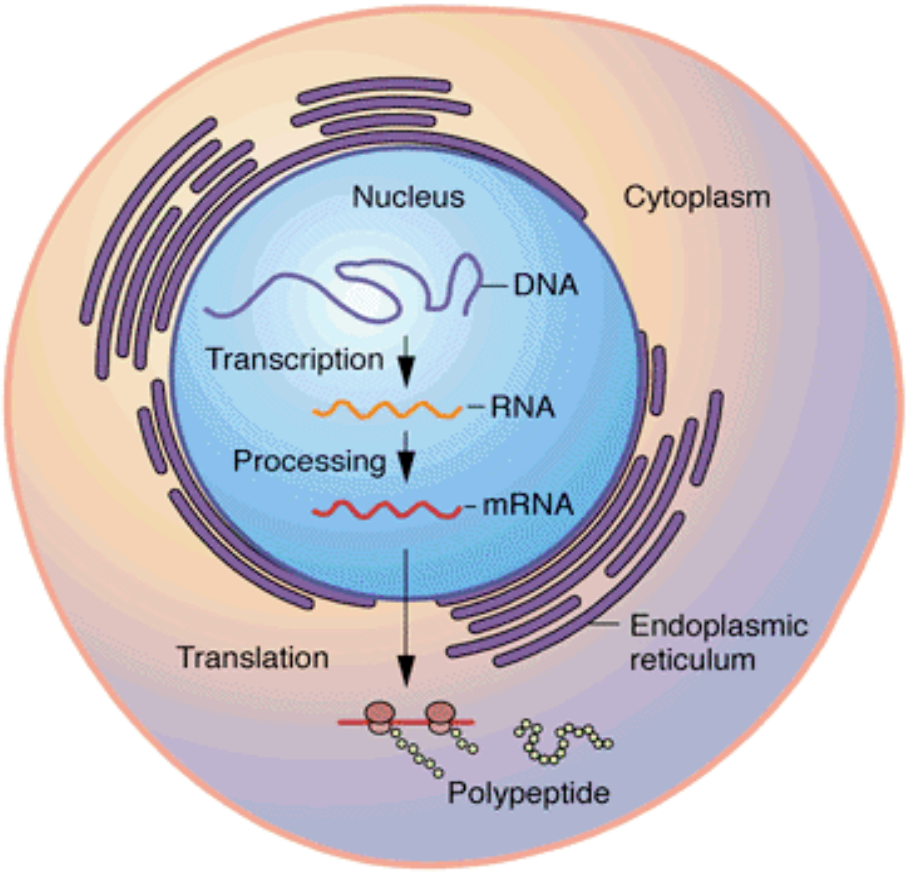
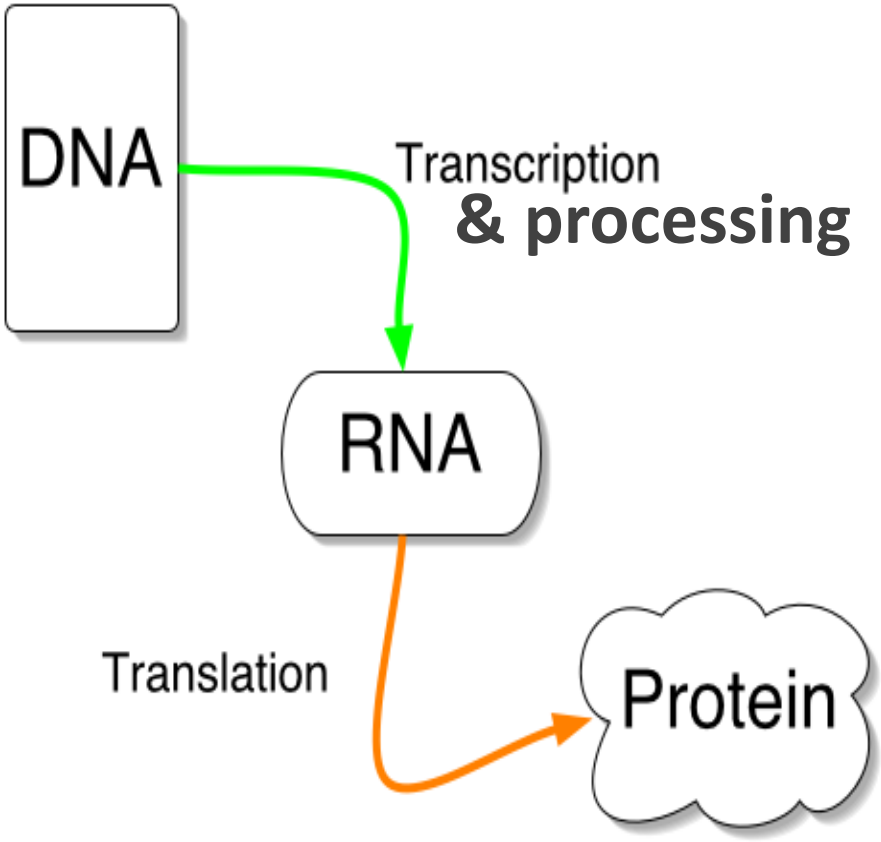
Course organization

- **Introduction (Week 1-2)**
  - Course introduction
  - A brief introduction to molecular biology
  - A brief introduction to sequence comparison
- **Part I: Algorithms for Sequence Analysis (Week 1 - 8)**
  - Chapter 1-3, Models and theories
    - » Probability theory and Statistics (Week 2)
    - » Algorithm complexity analysis (Week 3)
    - » Classic algorithms (Week 4)
  - Chapter 4. Sequence alignment (week 6)
  - Chapter 5. Hidden Markov Models (week 7）
  - Chapter 6. Multiple sequence alignment (week 8)
- **Part II: Algorithms for Network Biology (Week 9 - 16)**
  - Chapter 7. Omics landscape (week 9)
  - Chapter 8. Microarrays, Clustering and Classification (week 10)
  - Chapter 9. Computational Interpretation of Proteomics (week 11)
  - Chapter 10. Network and Pathways (week 12,13)
  - Chapter 11. Introduction to Bayesian Analysis (week 14,15)
  - Chapter 12. Bayesian networks (week 16)

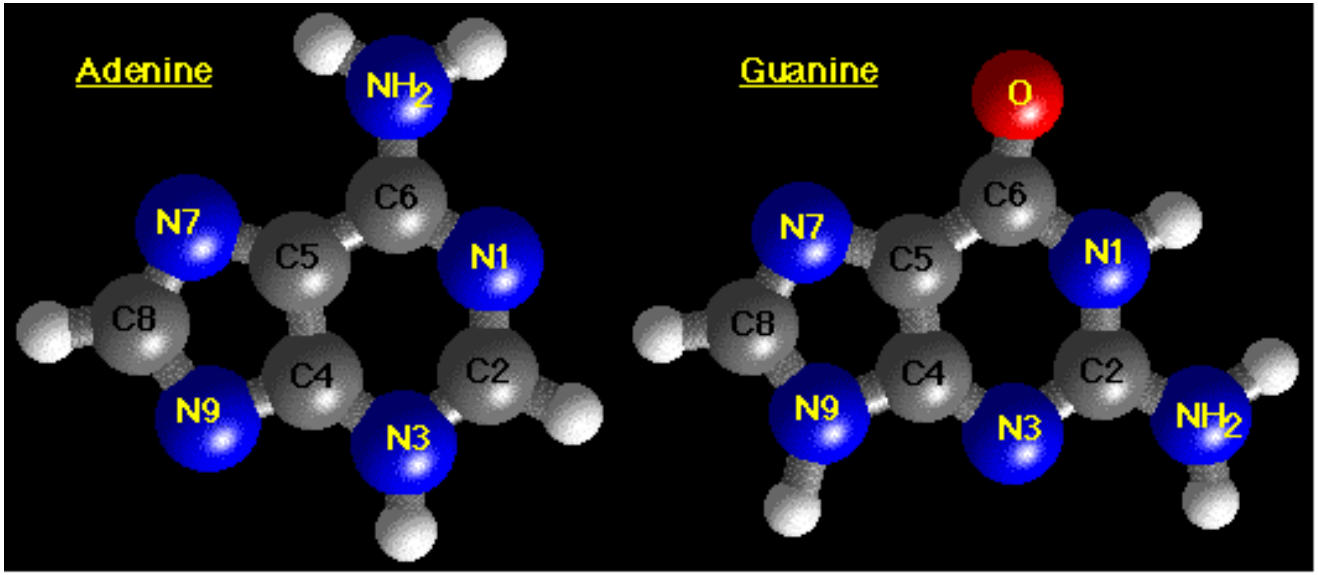
A brief introduction to Molecular Biology

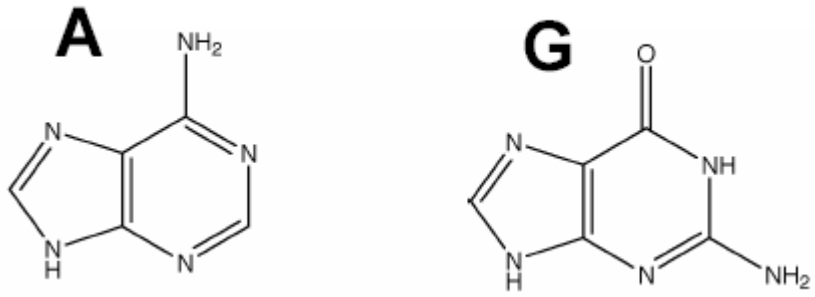
Central dogma



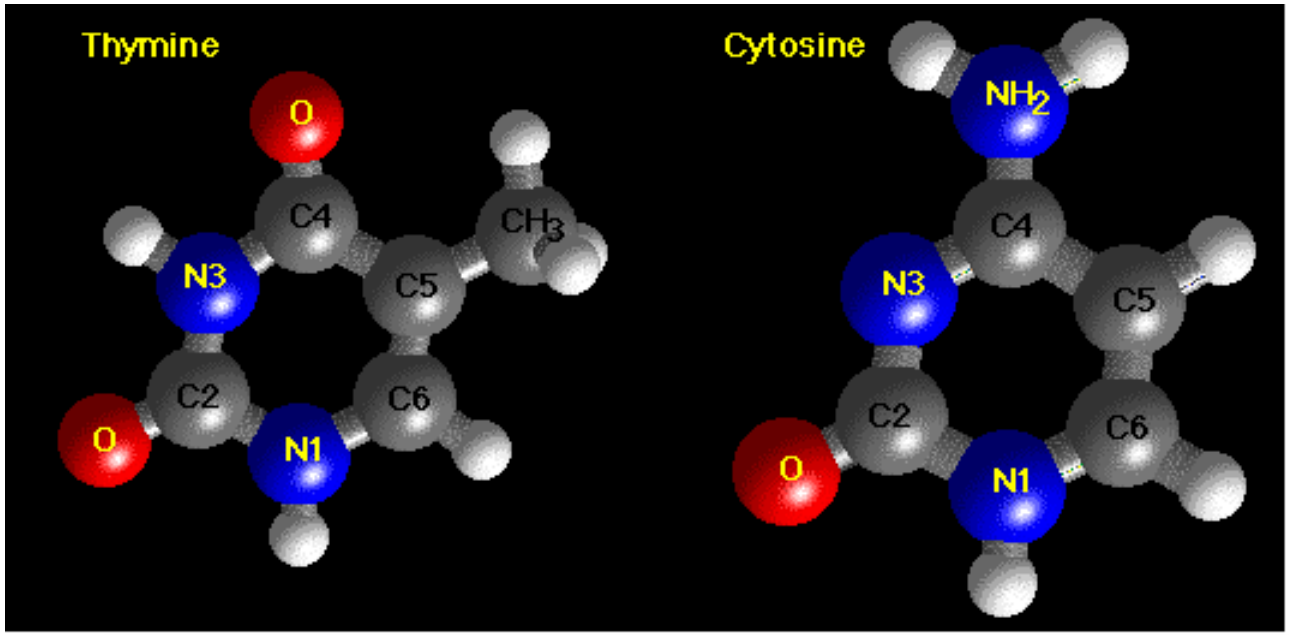


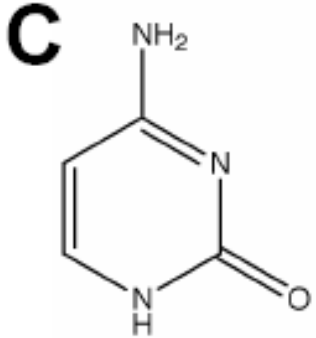
Structure of A and G

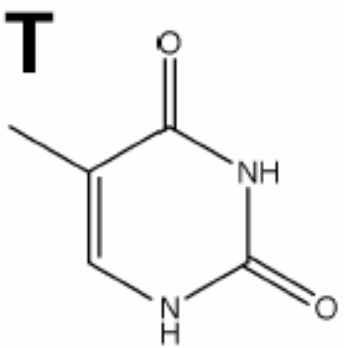


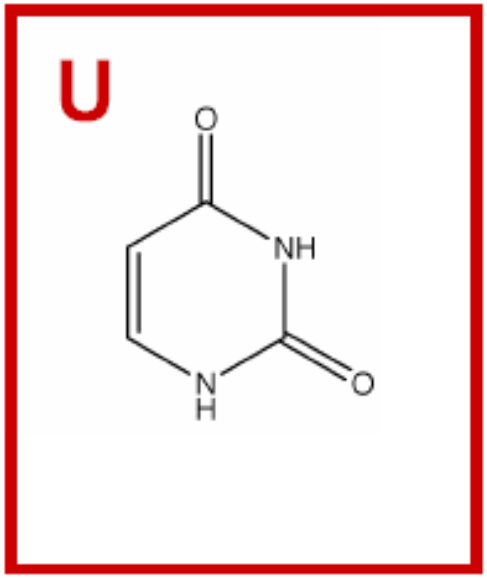


Structure of C and T

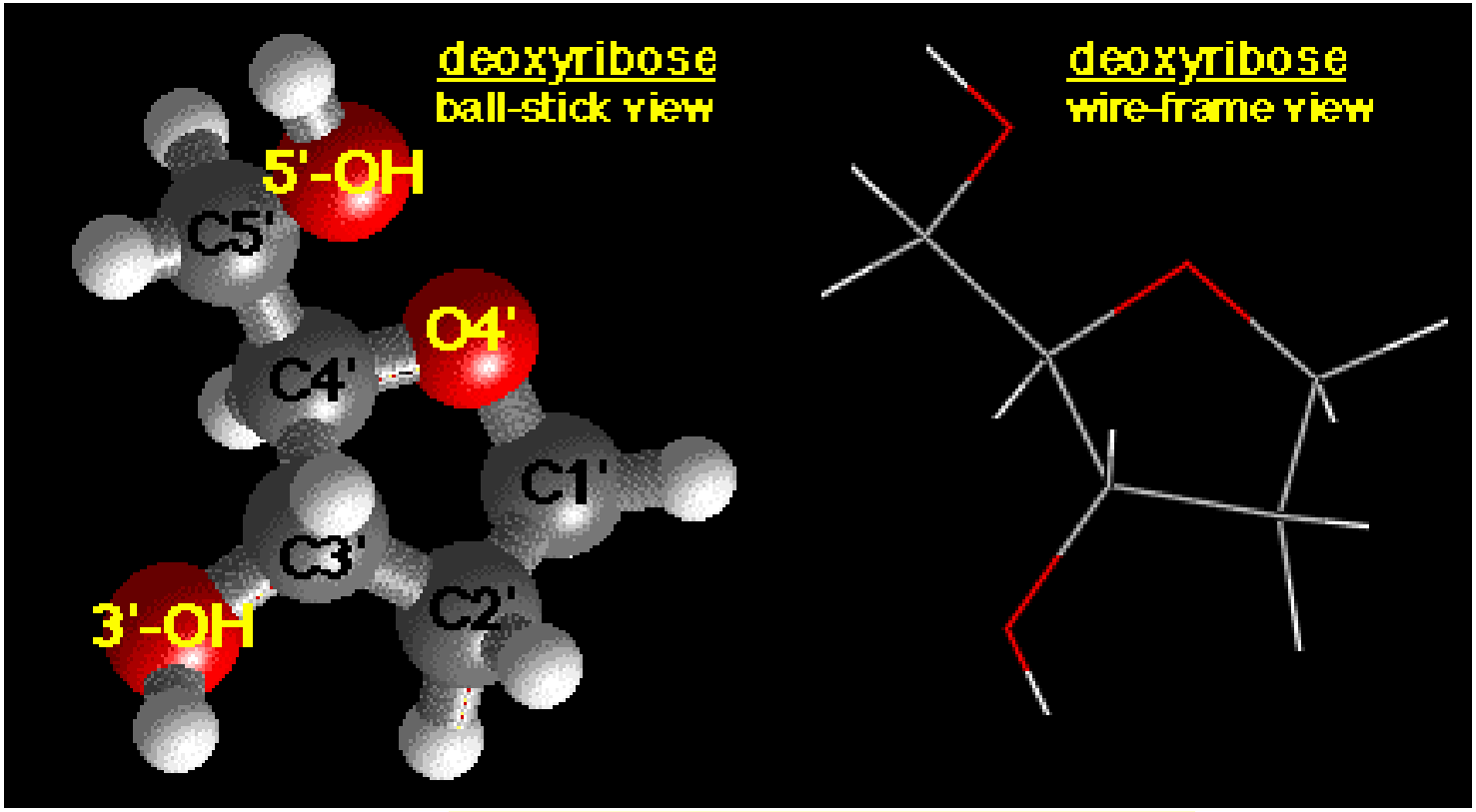




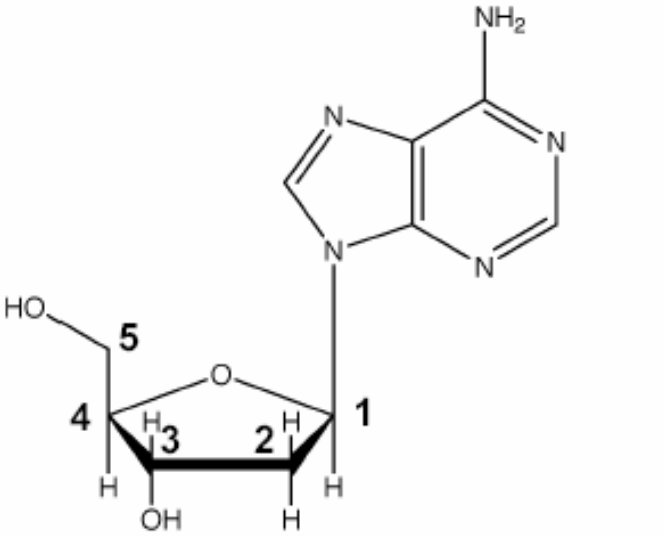




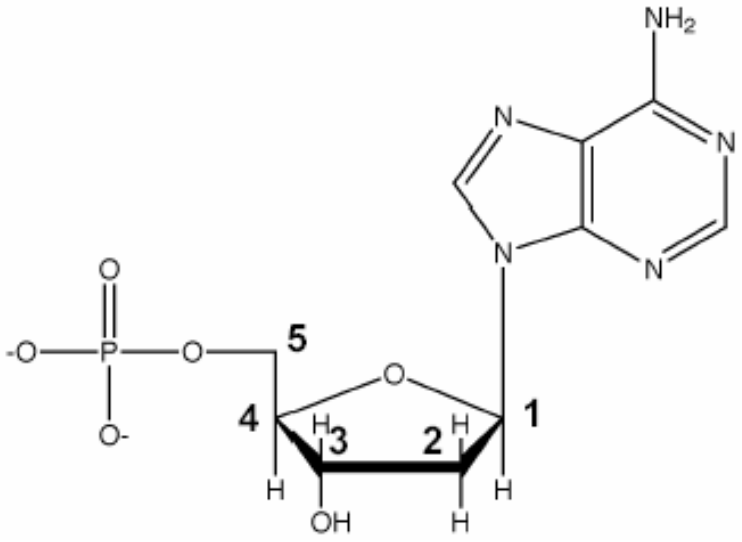
Structure of deoxyribose



Nucleoside and Nucleotide

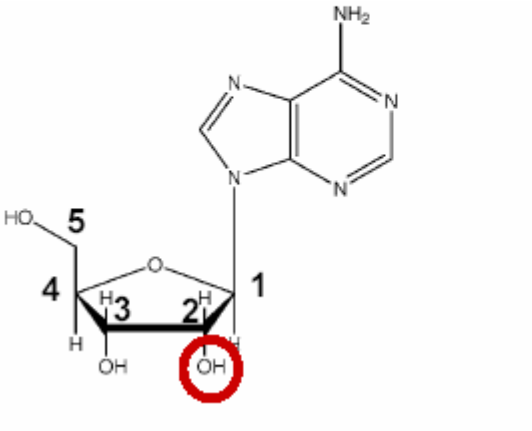


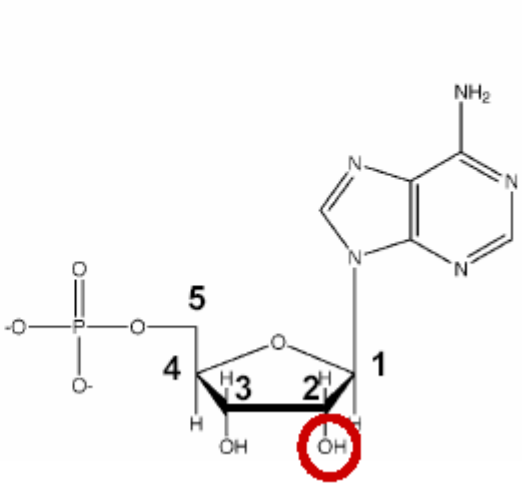
Nucleoside



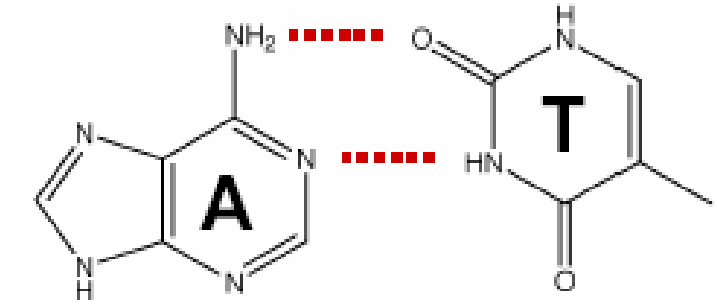
Nucleotide

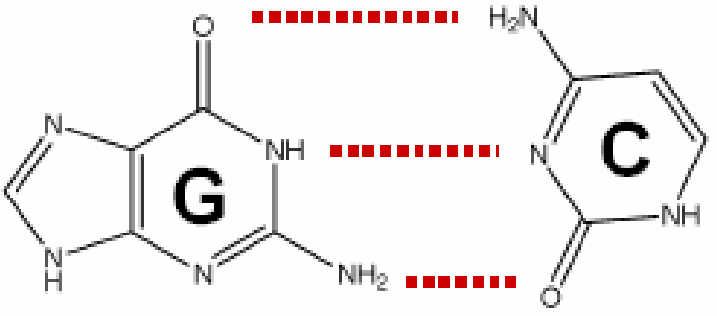
RNA Structure



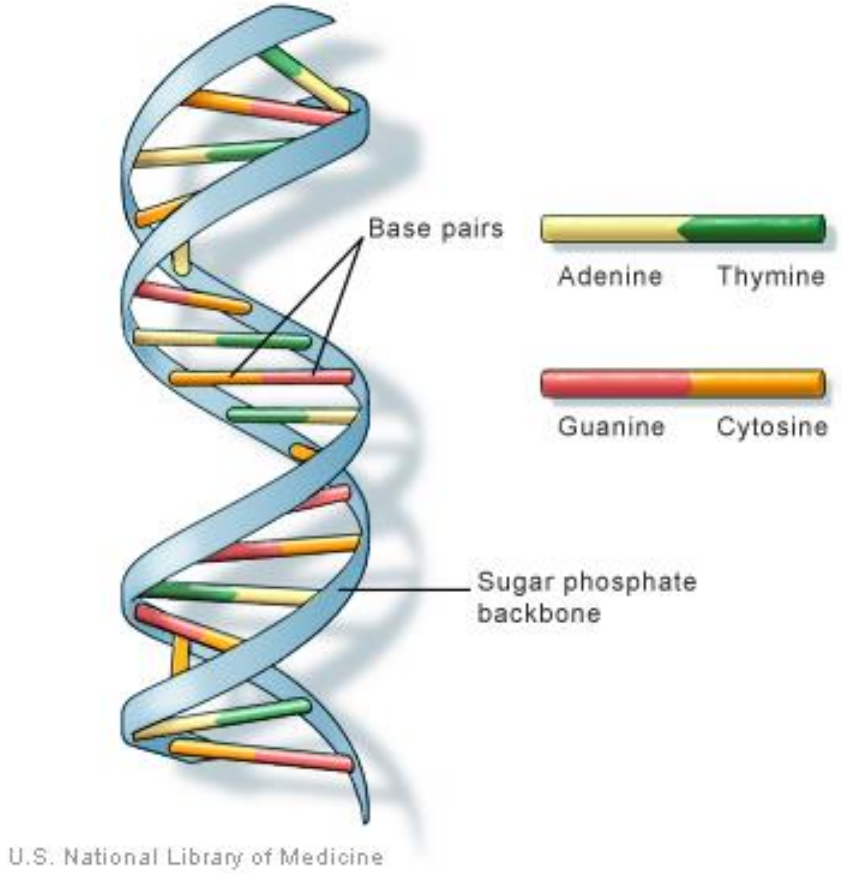


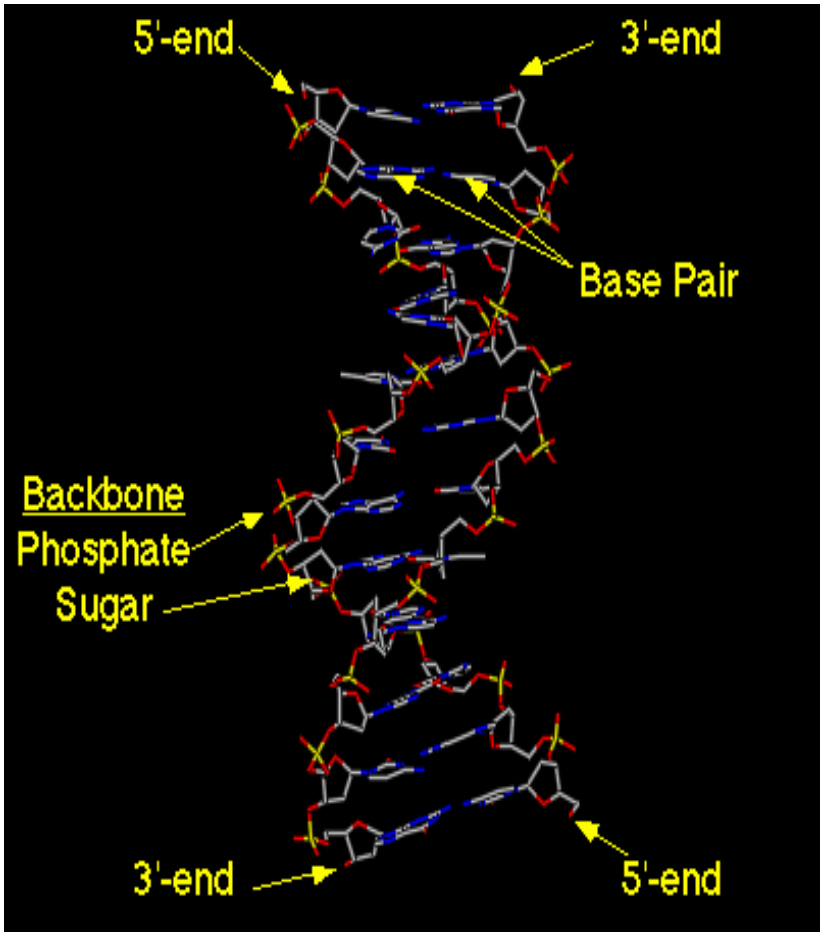
Base pair





Double helix structure





Quiz

1. A DNA strain with 10 nucleotides can form 4^{10} different sequences.

2. In a DNA molecular, the percentage of base A is 38%, then the percentage of base C and G in total is : （C）

A. 76%　　B. 62%

C. 24%　　D. 12%

3. In a DNA strain, A: C: T: G=l: 2: 3: 4, then in its complimentary strain , A: C: T: G is （B）

A. l: 2: 3: 4

B. 3: 4: l: 2

C. 4: 3: 2: 1

D. 1: 3: 2: 4

4、In a DNA strain，(A+G)/(T+C)=0.4. The corresponding percentages in its complimentary strain and the whole DNA molecular are （ B ）

A、0.4 &0.6　　B、2.5&1

Genome

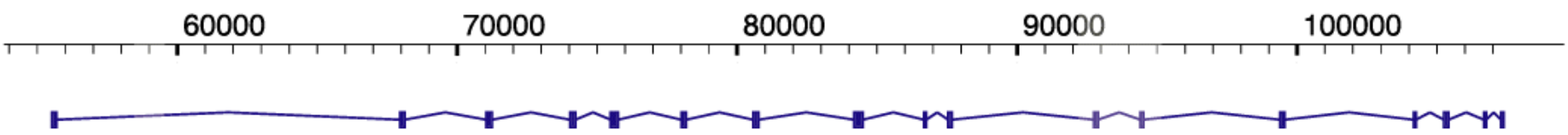
- The hereditary info present in every cell

Organisms	Base pairs	Genes
Mycoplasma genitalium	580,073	483
MimiVirus	1,200,000	1,260
Escherichia coli	4,639,221	4,290
Saccharomyces cerevisiae	12,495,682	5,726
Caenorhabditis elegans	~100 x 10^6	19,820
Arabidopsis thaliana	~115 x 10^6	25,498
Drosophila melanogaster	~122x 10^6	13,472
Human	3.3 x 10^9	~20,000

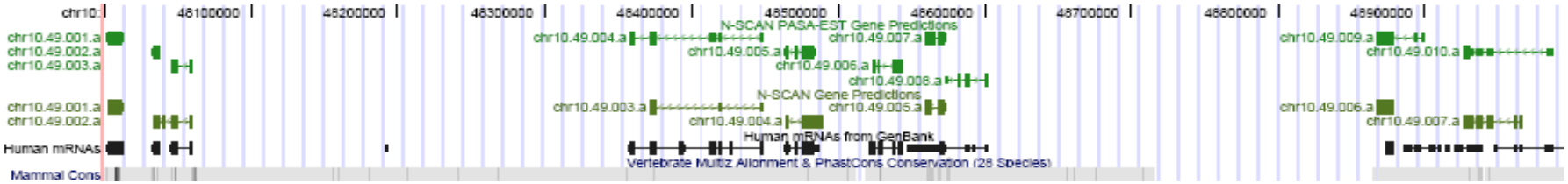
In a Mammalian Genome

- **Only about 1% for protein coding**
- **Mammalian genomes are large**
  - 8,000 km of 10pt type

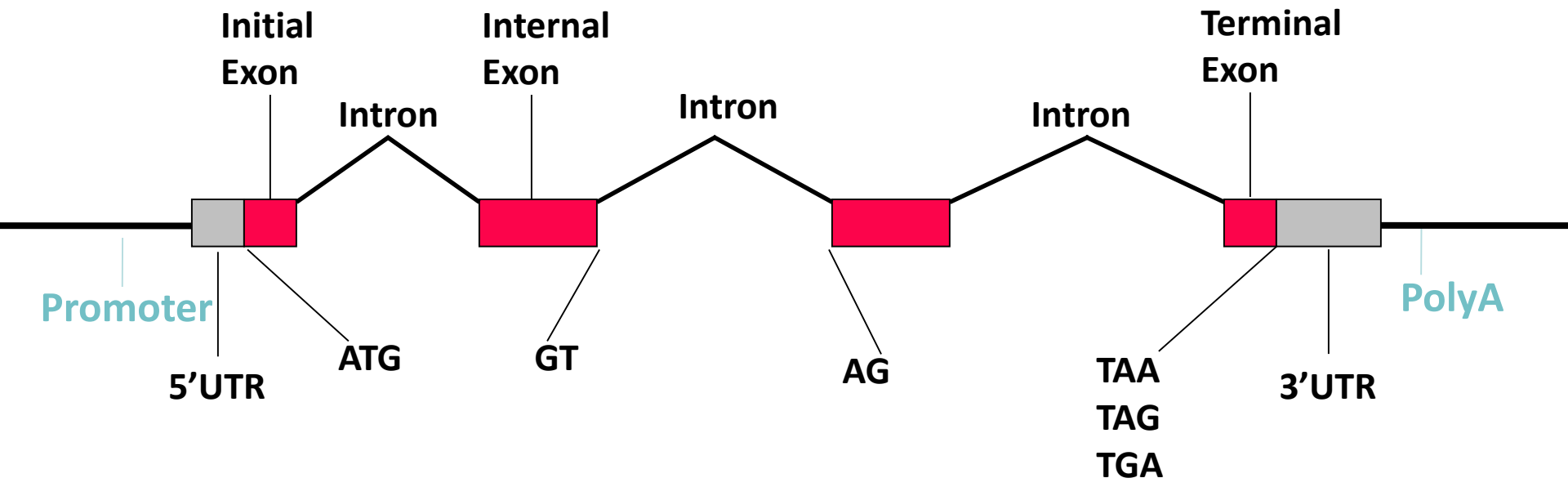
A Typical Human Gene Structure



Genes in a Genome



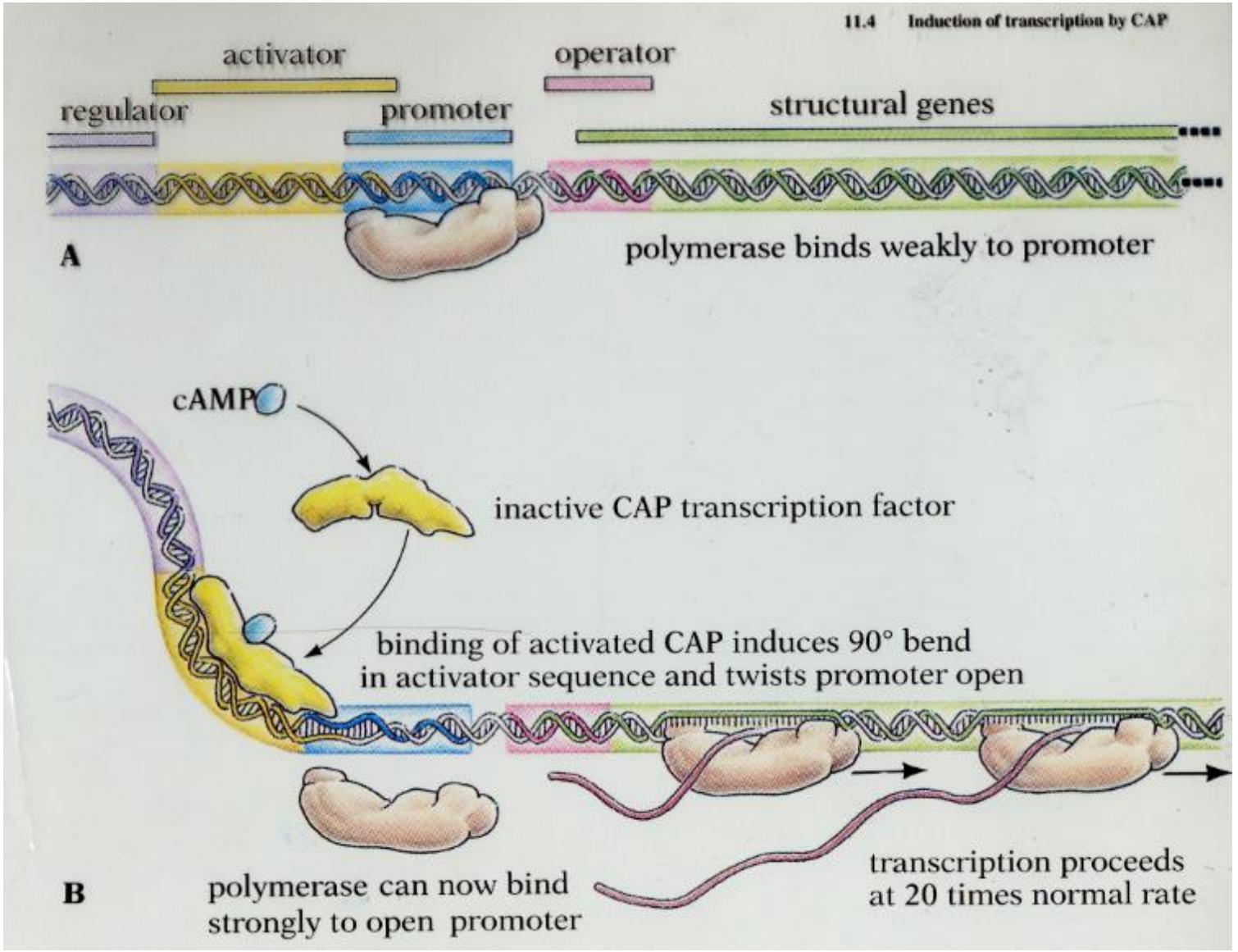
Gene Structure



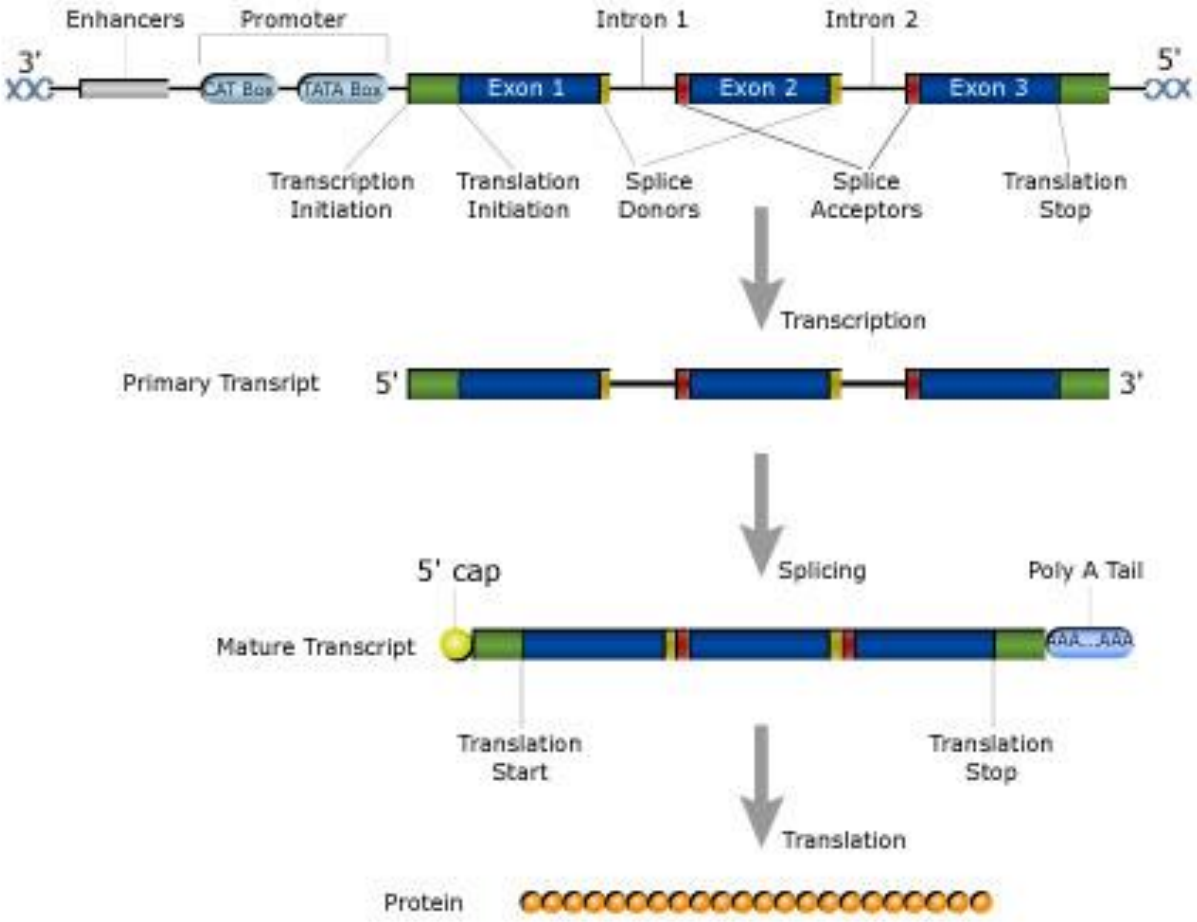
Gene Structure

- Transcribed 5’ to 3’
- Promoter region and transcription factor binding sites precede 5’
- Transcribed region includes 5’ and 3’ untranslated regions
- In eukaryotes, most genes also include introns, spliced out before export from nucleus, hence before translation

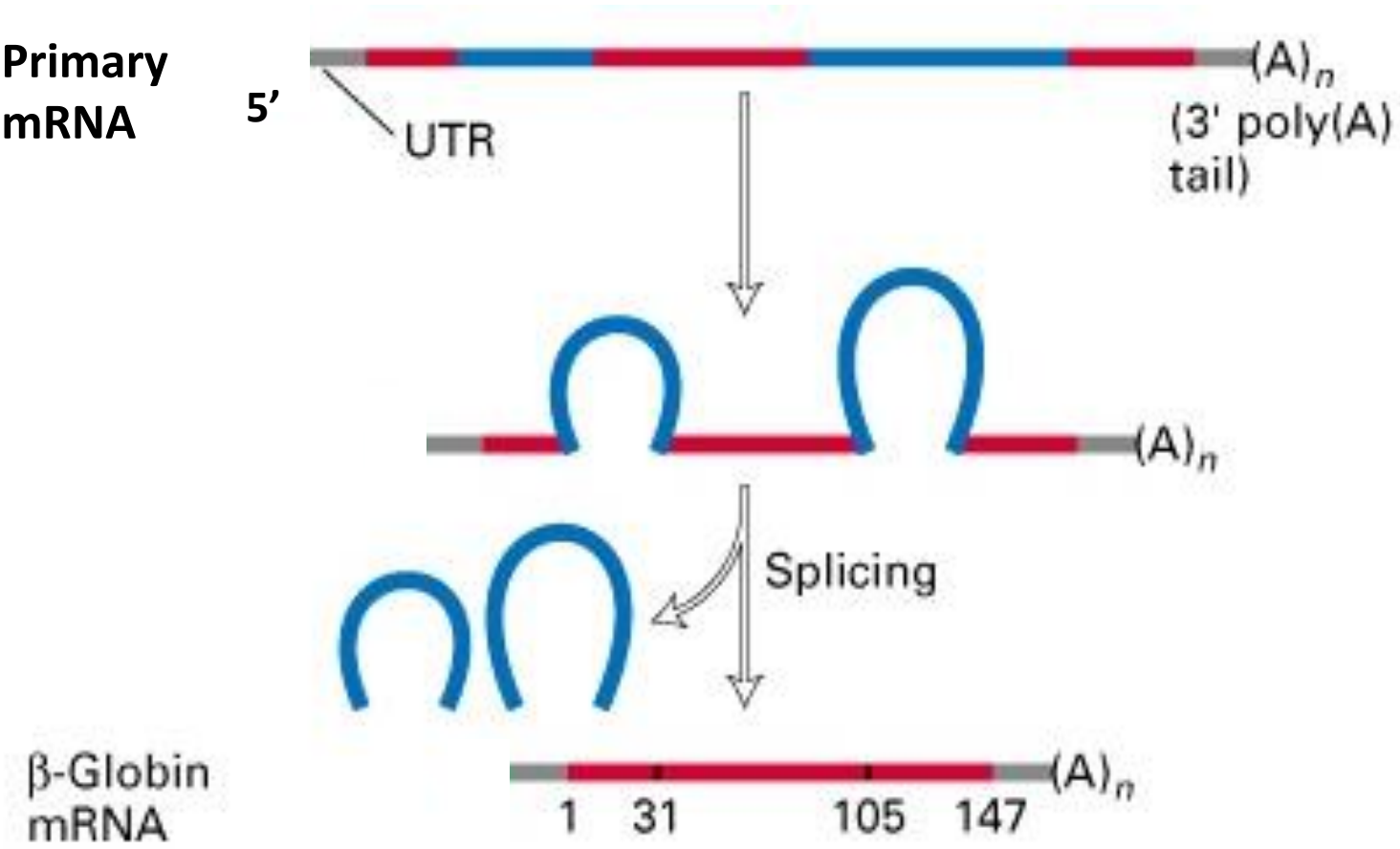
Transcription



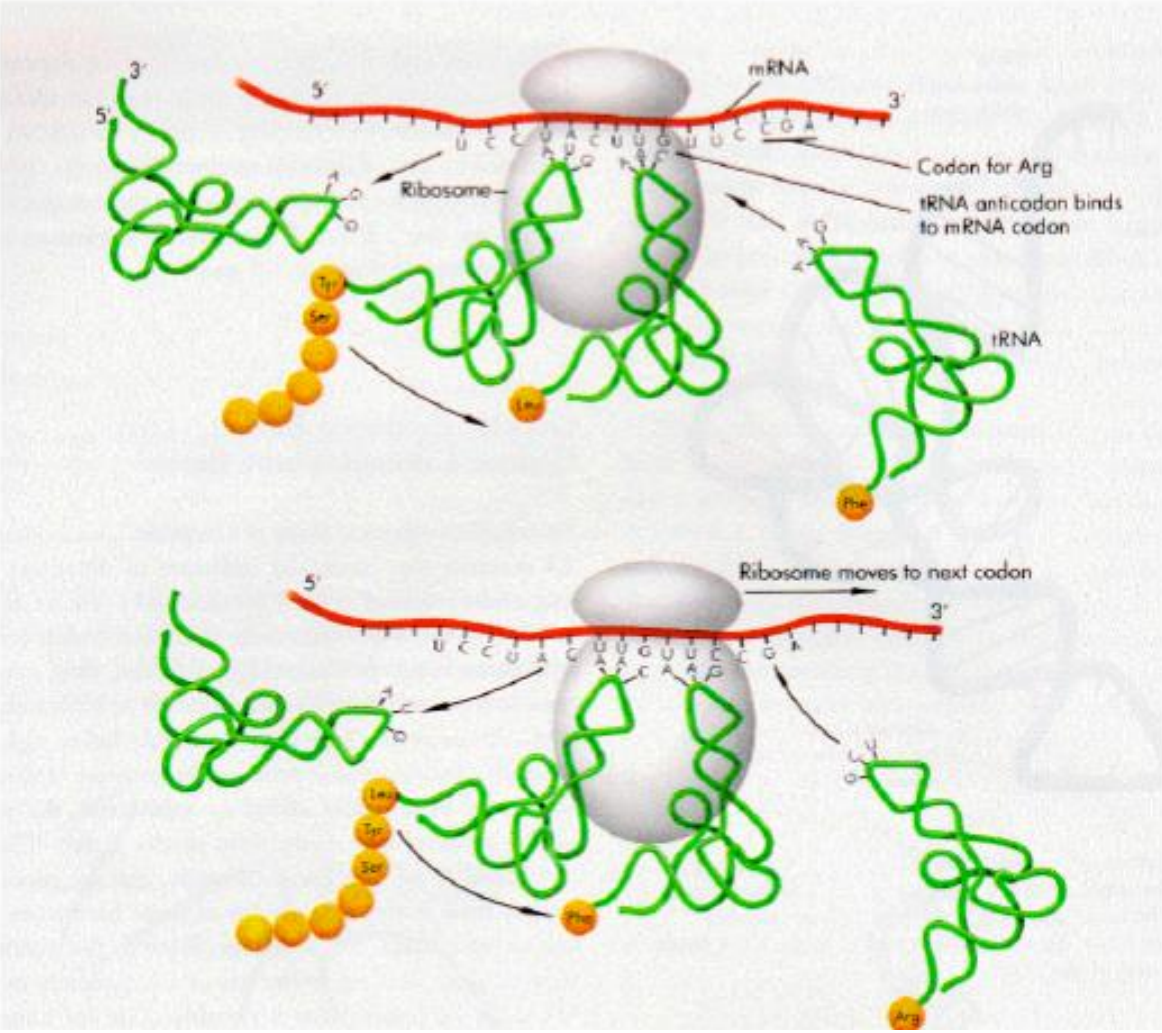
splice


Enhancers
Promoter
Intron 1
Intron 2
3'
5'
CAT Box
TATA Box
Exon 1
Exon 2
Exon 3
Transcription Initiation
Translation Initiation
Splice Donors
Splice Acceptors
Translation Stop
Transcription
Primary Transript
5'
3'
5' cap
Splicing
Poly A Tail
Mature Transcript
AAA...AAA
Translation Start
Translation Stop
Translation
Protein

RNA Processing



Translation



http://bioweb.uwlax.edu/GenWeb/Molecular/Theory/Translation/translation.htm

Genetic code （Codons）

First Position	Second Position				Third Position
	U	**C**	**A**	**G**	
U	Phe (F)	Ser (S)	Tyr (Y)	Cys (C)	**U**
	Phe (F)	Ser (S)	Tyr (Y)	Cys (C)	**C**
	Leu (L)	Ser (S)	Stop	Stop	**A**
	Leu (L)	Ser (S)	Stop	Trp (W)	**G**
C	Leu (L)	Pro (P)	His (H)	Arg (R)	**U**
	Leu (L)	Pro (P)	His (H)	Arg (R)	**C**
	Leu (L)	Pro (P)	Gln (Q)	Arg (R)	**A**
	Leu (L)	Pro (P)	Gln (Q)	Arg (R)	**G**
A	Ile (I)	Thr (T)	Asn (N)	Ser (S)	**U**
	Ile (I)	Thr (T)	Asn (N)	Ser (S)	**C**
	Ile (I)	Thr (T)	Lys (K)	Arg (R)	**A**
	Met (M)	Thr (T)	Lys (K)	Arg (R)	**G**
G	Val (V)	Ala (A)	Asp (D)	Gly (G)	**U**
	Val (V)	Ala (A)	Asp (D)	Gly (G)	**C**
	Val (V)	Ala (A)	Glu (E)	Gly (G)	**A**
	Val (V)	Ala (A)	Glu (E)	Gly (G)	**G**

Six reading frames

- 5' 3'

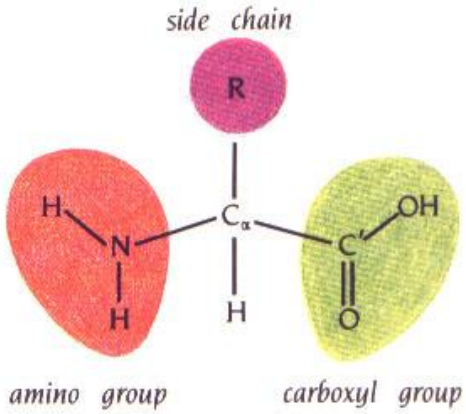
  atgcccaagctgaatagcgtagaggggttttca tcatttgaggacgatgtataa

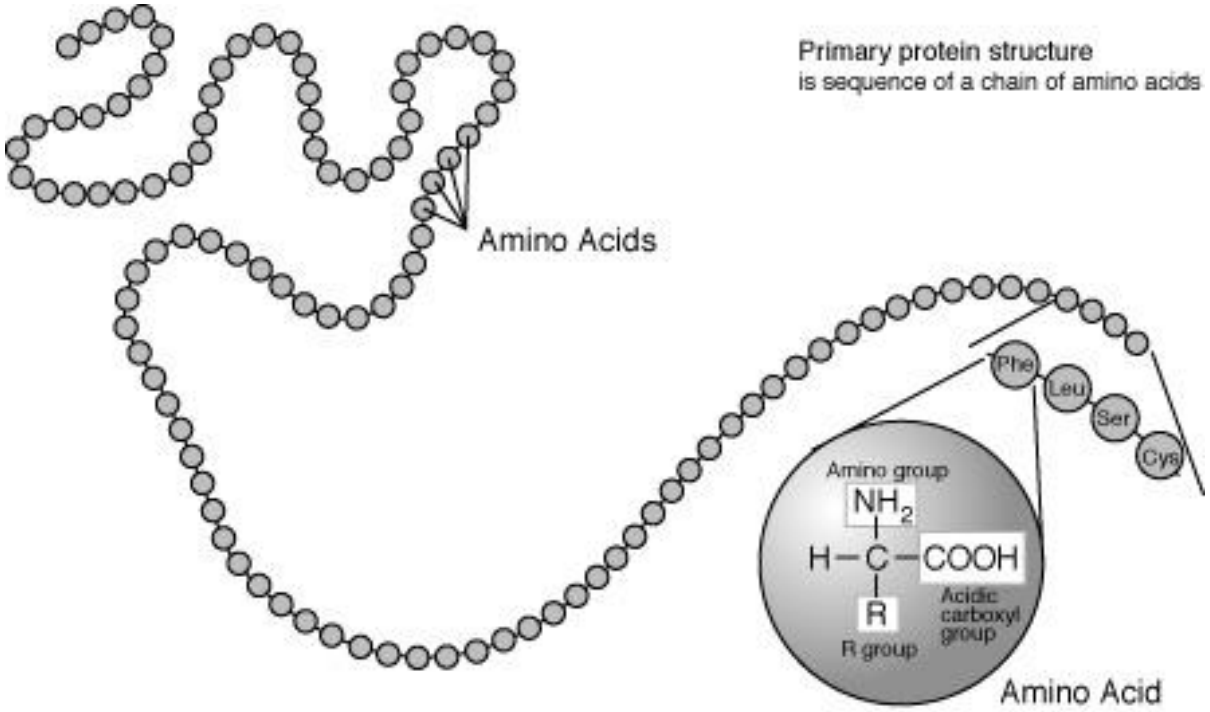
  - Atg..
  - Tgc..
  - Gcc..

  - 3 more reading frames on the reverse complement strand

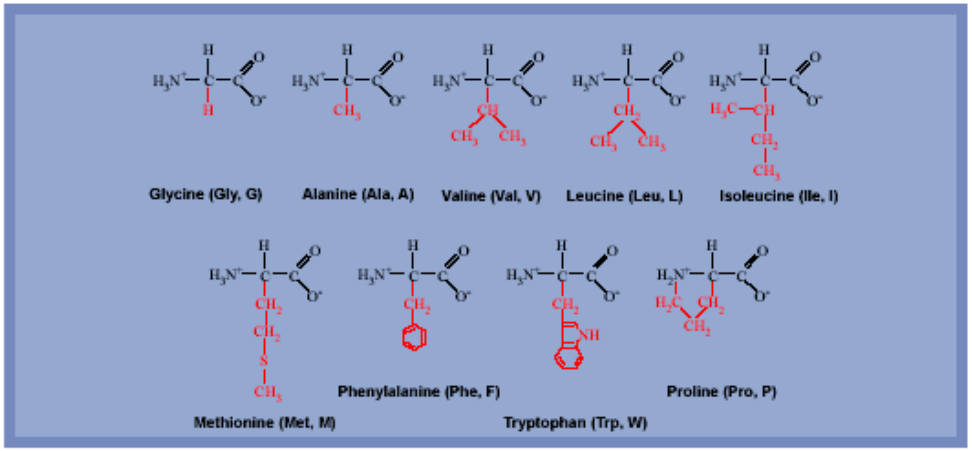
Protein

- **20 amino acids**

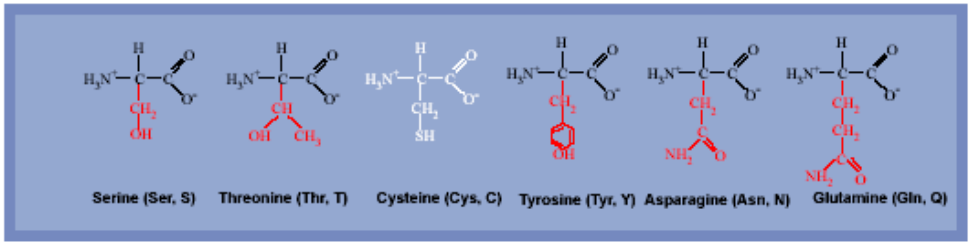




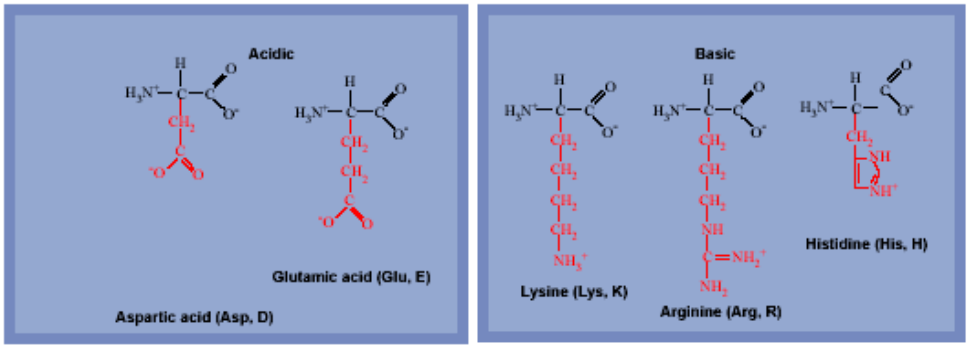
Nonpolar, Hydrophobic R-groups



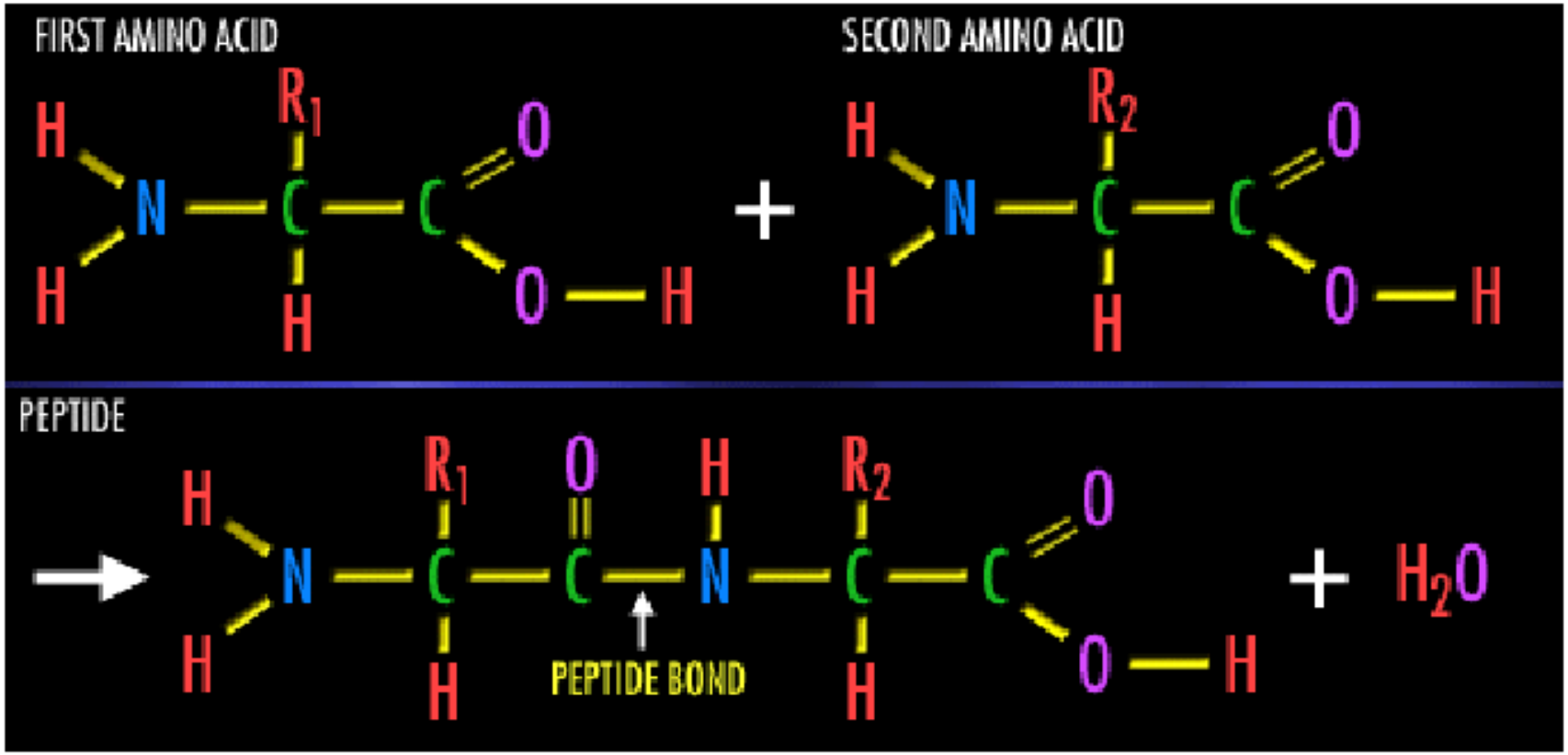
Polar, Hydrophillic R-groups



Electrically charged



Peptide


FIRST AMINO ACID
SECOND AMINO ACID
PEPTIDE
PEPTIDE BOND
H_2O

Protein Structure

primary structure
(amino acid sequence)

secondary structure
(α-helix)

tertiary structure
(folded individual peptide)

quaternary structure
(aggregation of two or more peptides)

Acknowledgement

- Most of the slides were from Dr. Qi Liu's course materials.