

Computational Biophysics: Algorithms to Applications (CS61060)

Instructor: Pralay Mitra
Email: pralay@cse.iitkgp.ac.in

Course Details

- TA
 - Purnima Gautam (purnimagautam94[at]gmail[dot]com)
 - Shruti Agrawal (shrutiag23@kgpian.iitkgp.ac.in)
 - Suman Kumar Bera (skbera4@kgpian.iitkgp.ac.in)
- Lecture Hours
 - Mon (12:00 -12:55); Tue (10:00-11:55); Thu (08:00-08:55)
- Evaluation
 - TA Evaluation 30
 - Mid Semester 30
 - End Semester 40

Lecture notes and materials

- Will be uploaded at

<https://moodlecse.iitkgp.ac.in/moodle/>

Login to CSE Moodle. Join to the course

CBP_2024S as Student with enrolment key CBP2024S

Course Coverage

Bioinformatics Topics:

1. Sequence alignment and comparison
2. Secondary structure prediction
3. Structure alignment
4. Protein folding
5. Protein docking
6. Protein Design

PCB Topics:

1. Protein and DNA structure

CS Topics:

1. Dynamic programming
2. Sequencing and Strings
3. Molecular surface
4. Simulation techniques
5. Relevant topics from ML and DL

Tutorials:

1. Databases and their usages
2. PDB file format
3. Rasmol, Pymol;
4. NW, SW, BLAST
5. PSIPred/PSSPred, DSSP, STRIDE
6. NACCESS
7. TM-align, TM-Score
8. Folding and Docking software

References

- **Text Book:**

1. Neil C. Jones and Pavel A. Pevzner. An Introduction to Bioinformatics Algorithms.
2. Gary D. Stormo. Introduction to Protein-DNA Interactions: Structure, Thermodynamics, and Bioinformatics.
3. Bruce R. Donald. Algorithms in Structural Molecular Biology (Computational Molecular Biology).
4. Dan Gusfield. Algorithms on Strings, Trees and Sequences

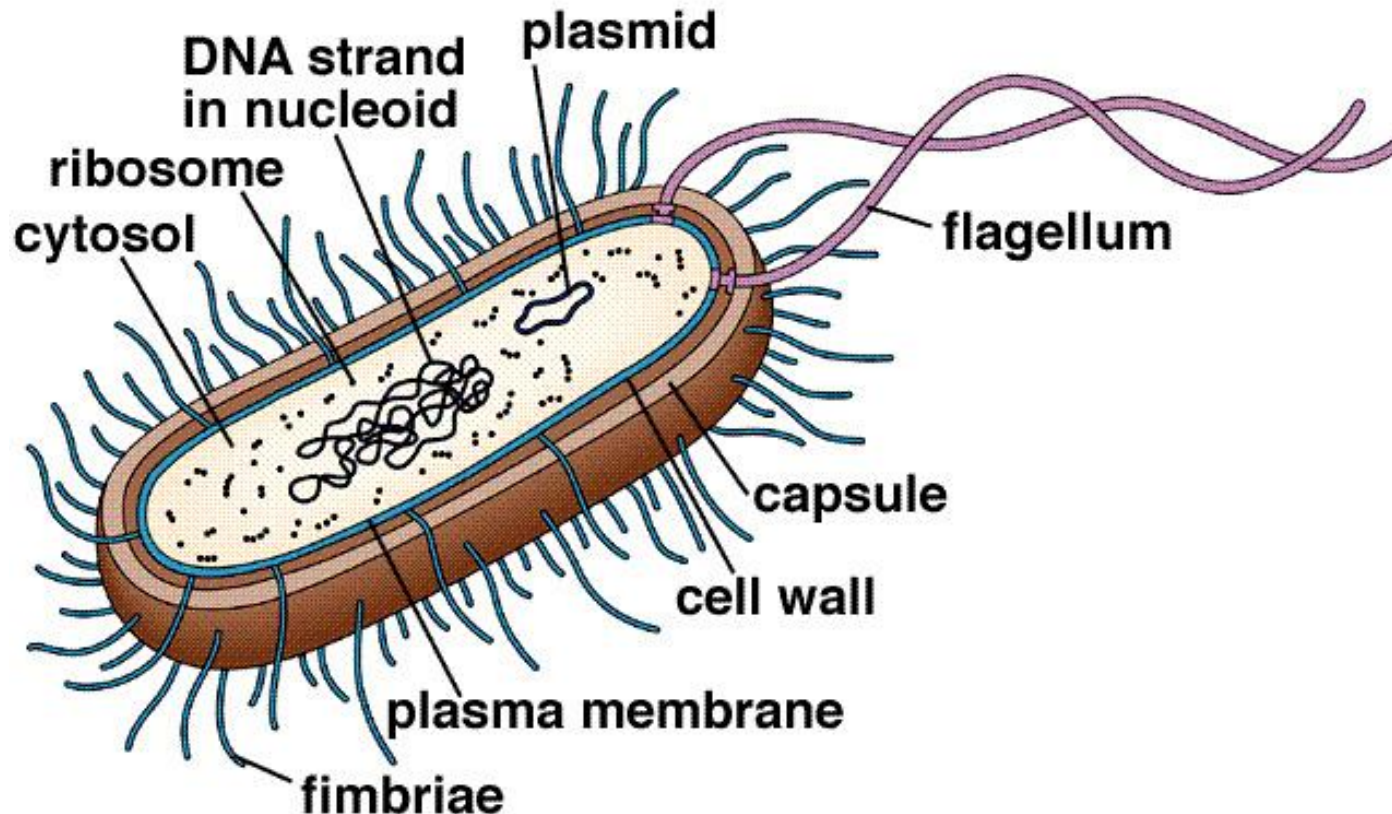
- **Literature:**

1. Christopher M. Dobson, Andrej Sali, Martin Karplus. (1998) Protein Folding: A Perspective from Theory and Experiment. *Angewandte Chemie International Edition* 37(7):868-893.
2. Inbal Halperin, Buyong Ma, Haim Wolfson, Ruth Nussinov. (2002) Principles of docking: An overview of search algorithms and a guide to scoring functions. *Proteins: Structure, Function, and Bioinformatics* 47(4):409-443.
3. Joan-Emma Shea and Charles L Brooks III. (2001). From Folding Theories To Folding Proteins: A Review and Assessment of Simulation Studies of Protein Folding and Unfolding. *Annual Review of Physical Chemistry* 52:499-535.
4. Literature will be provided from time to time.

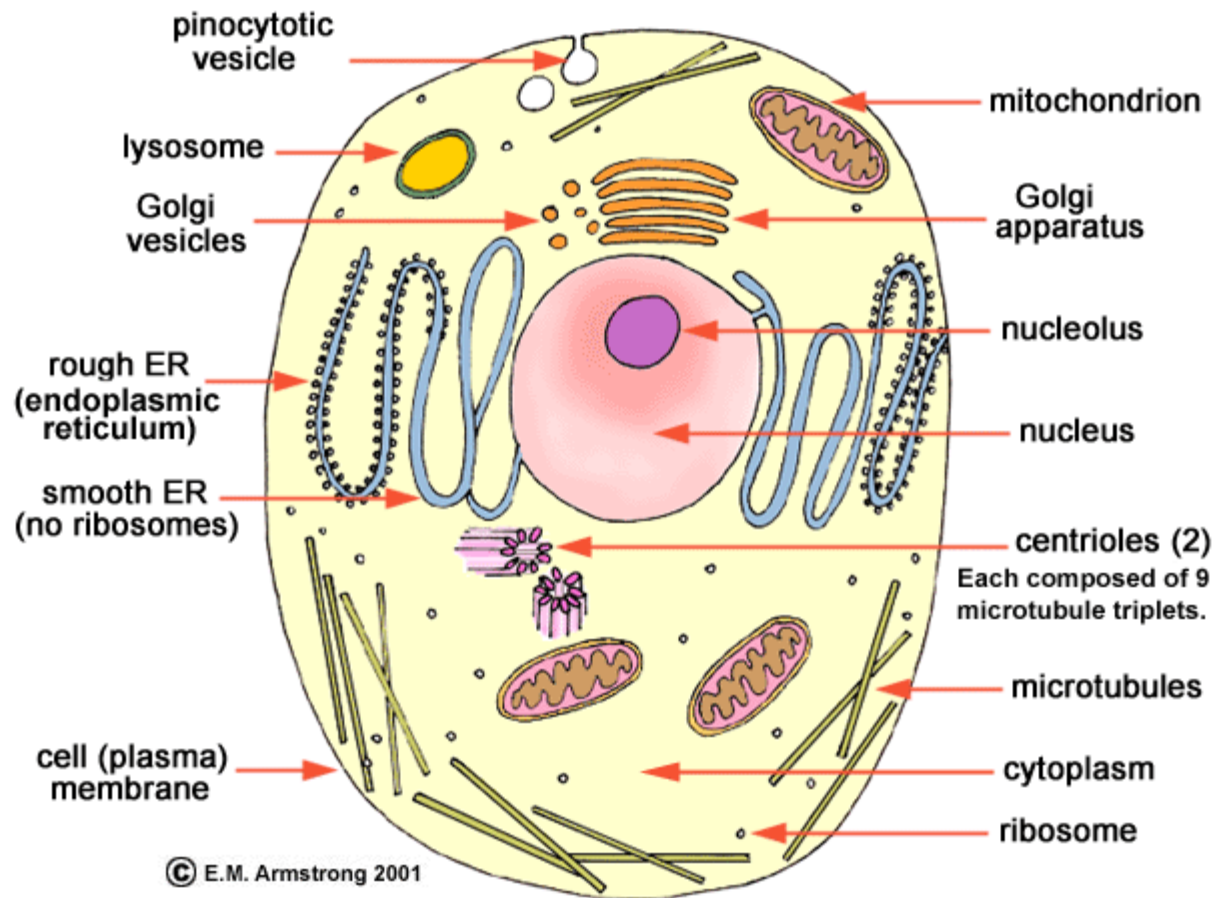
Prokaryotic Cell

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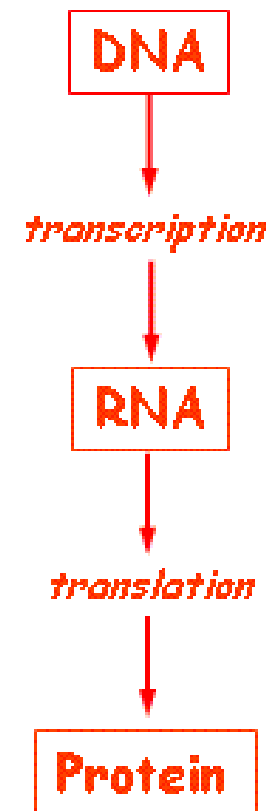
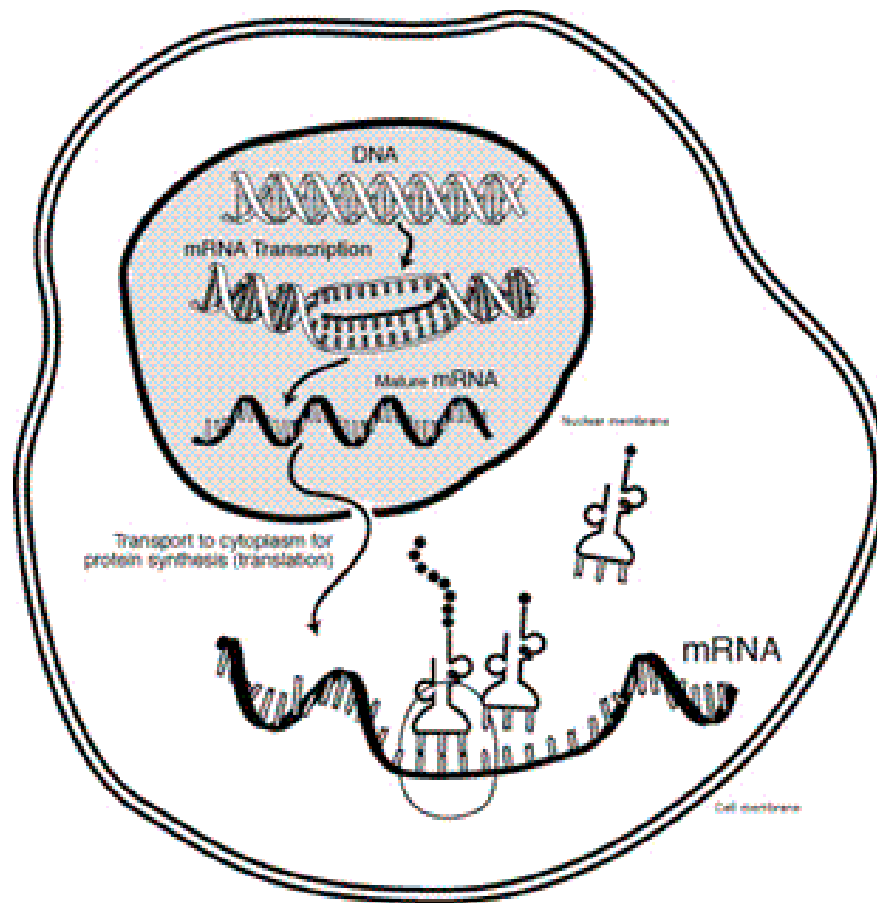
Generalized structure of a prokaryote



Eukaryotic Cell



Central Dogma of Molecular Biology



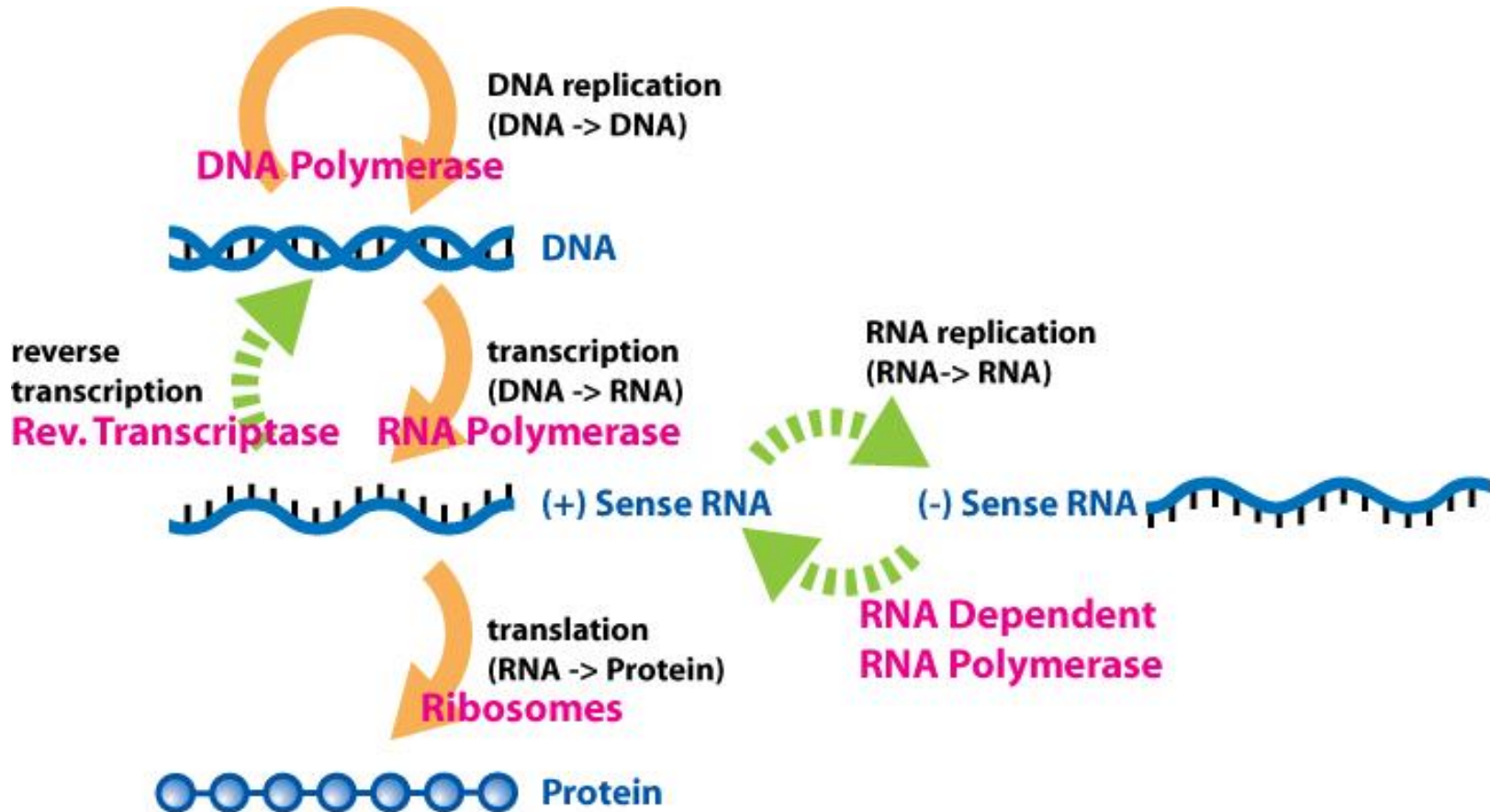
General transfers of biological sequential information

General	Special	Unknown
DNA → DNA	RNA → DNA	protein → DNA
DNA → RNA	RNA → RNA	protein → RNA
RNA → protein	DNA → protein	protein → protein

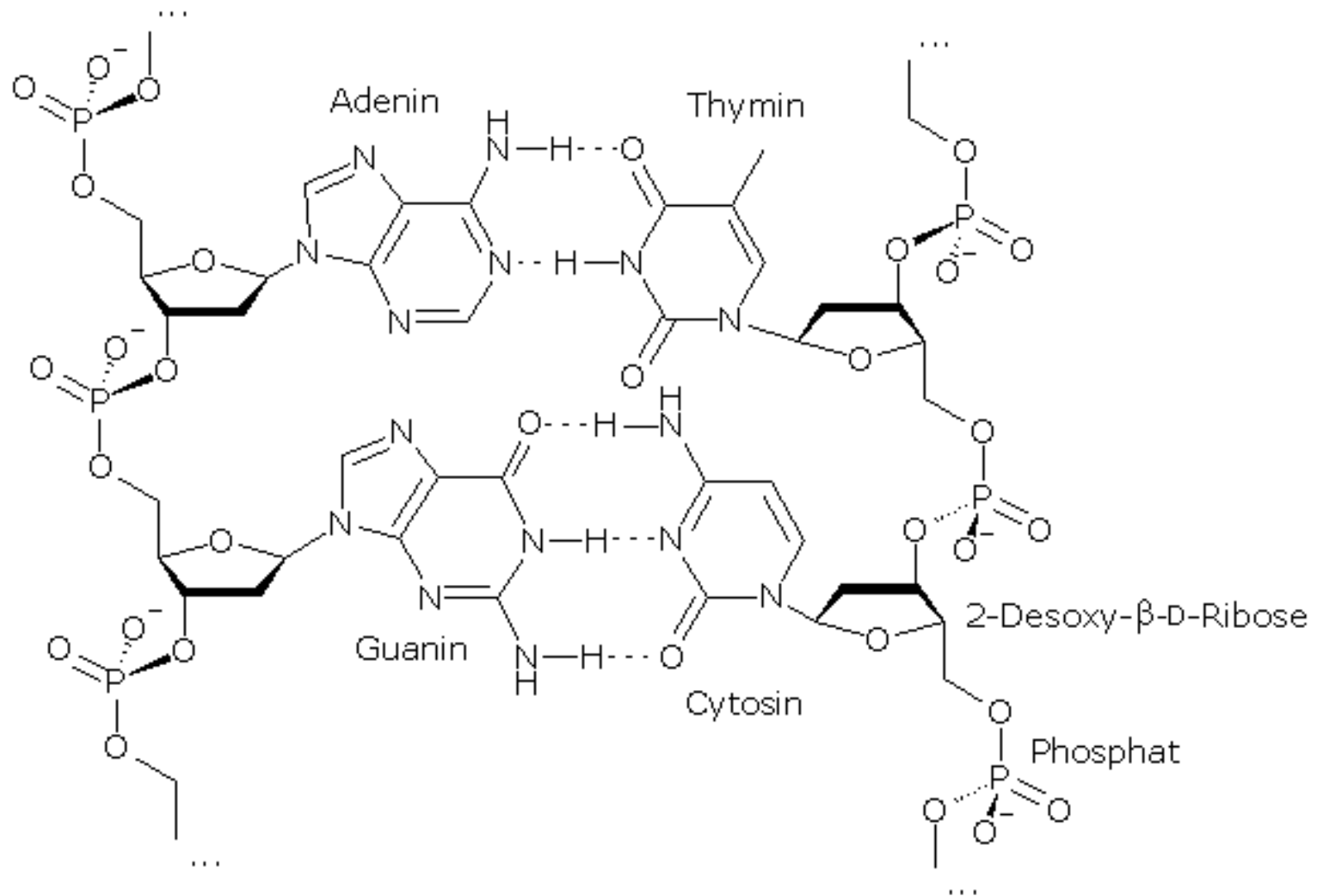
General transfers of biological sequential information

General	Special	Unknown
DNA \rightarrow DNA (DNA replication)	RNA \rightarrow DNA (reverse transcription)	protein \rightarrow DNA
DNA \rightarrow RNA (transcription)	RNA \rightarrow RNA (RNA replication)	protein \rightarrow RNA
RNA \rightarrow protein (translation)	DNA \rightarrow protein (direct translation)	protein \rightarrow protein

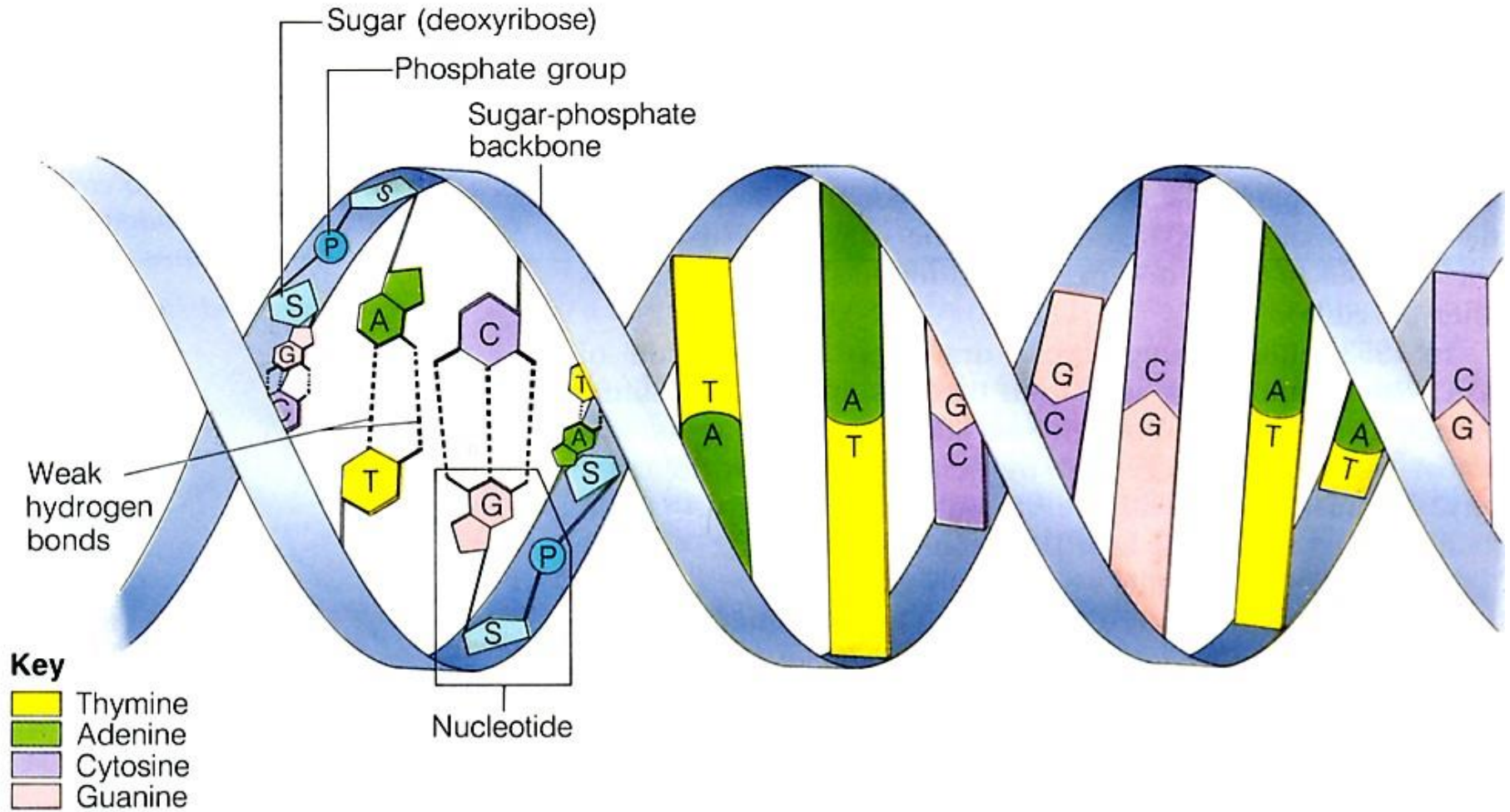
Central Dogma with Enzymes



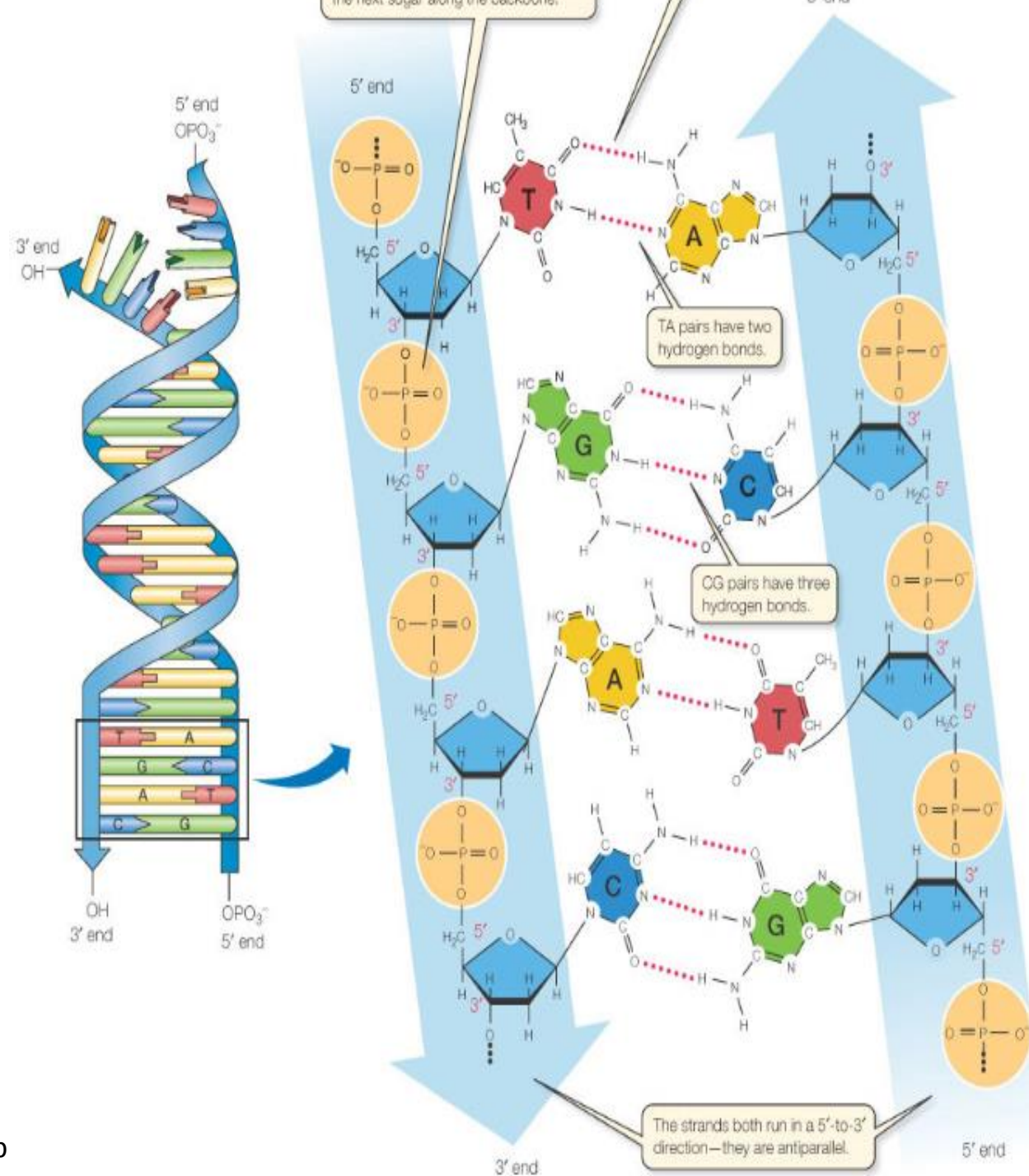
DNA Structure



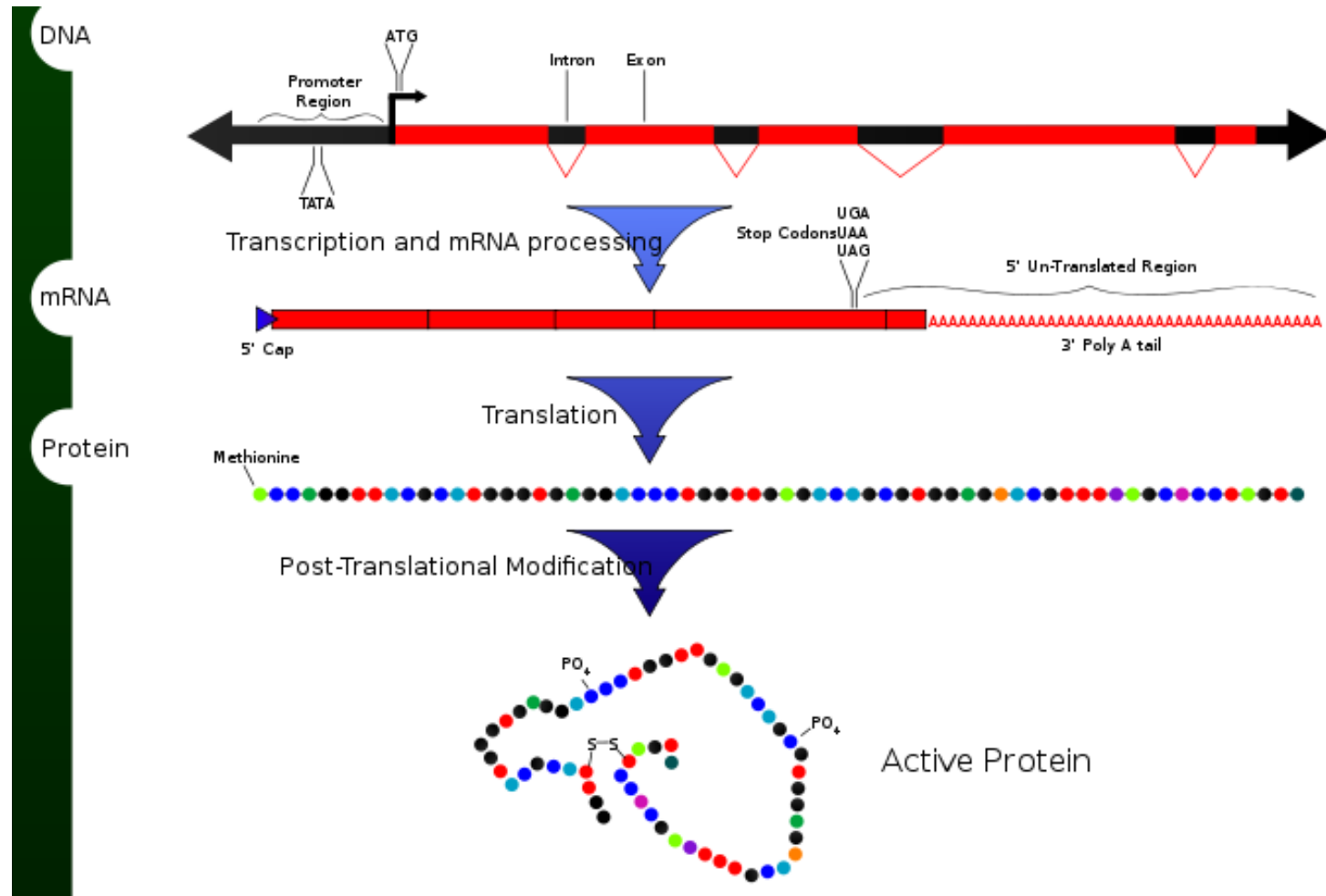
DNA Structure



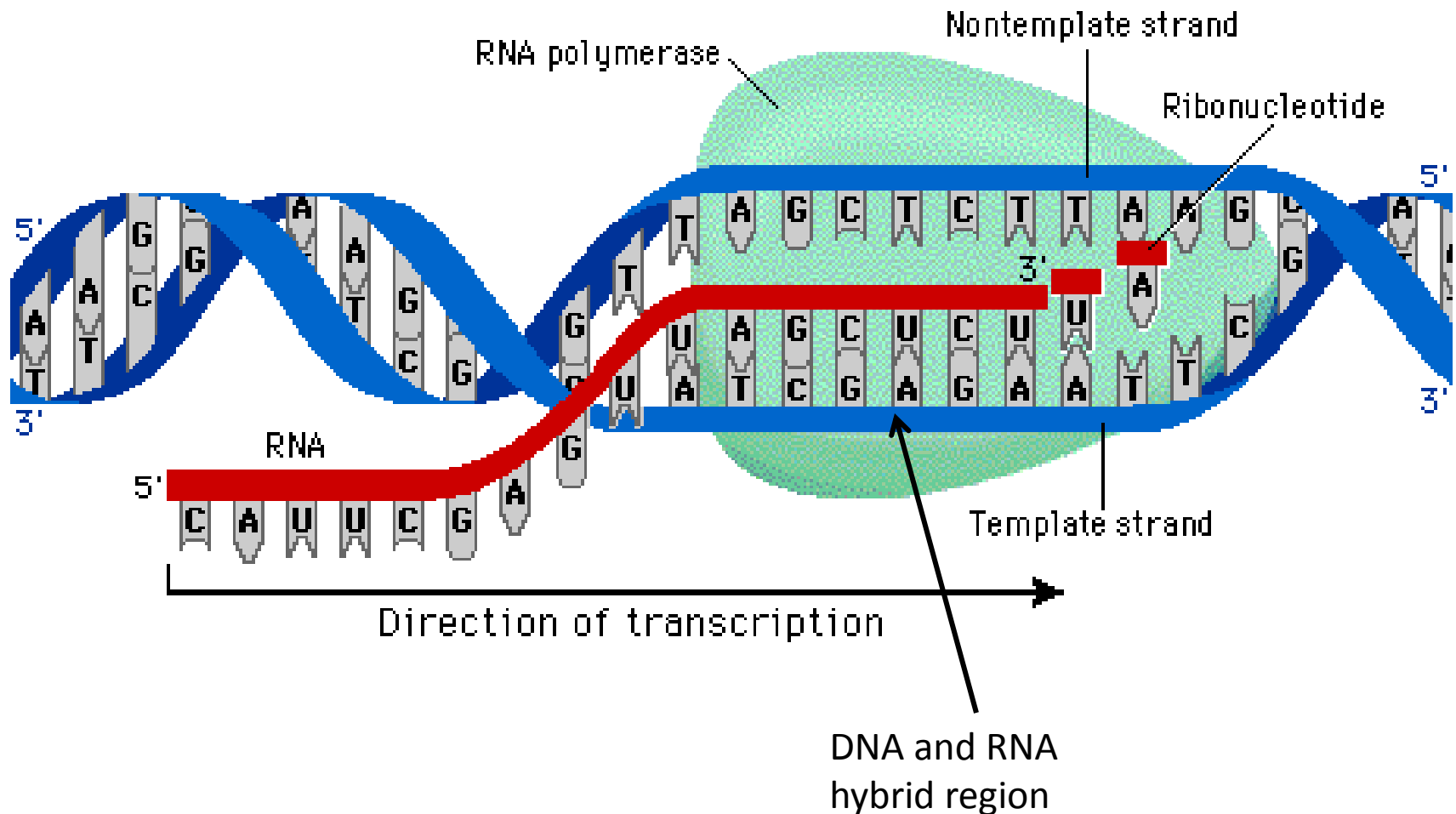
DNA Structure



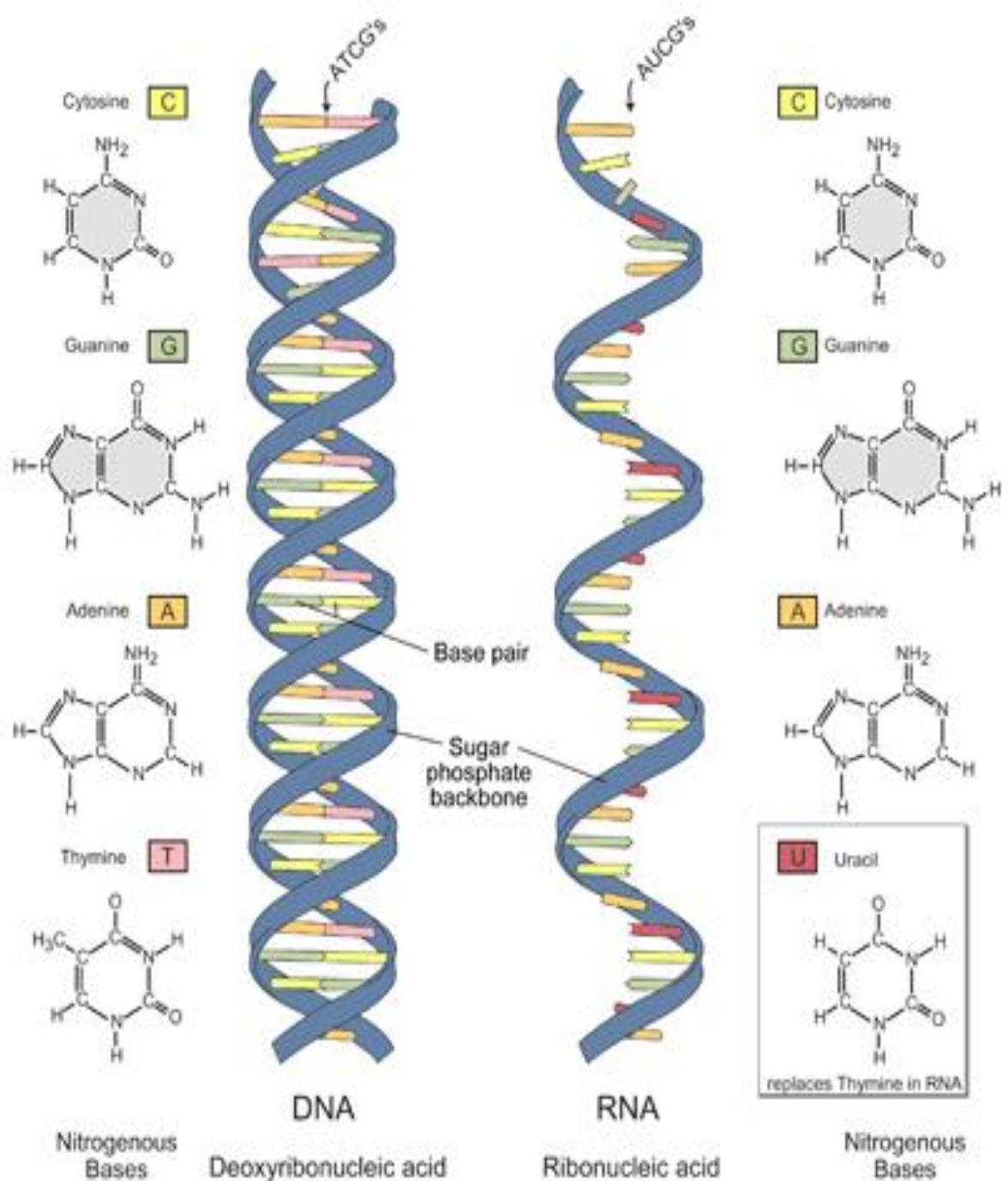
Central Dogma of Molecular Biology: Eukaryotic Model



Transcription

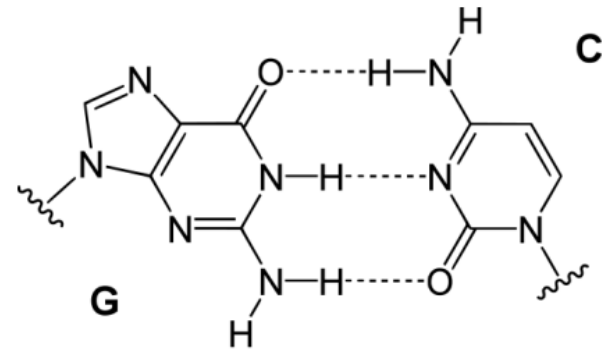
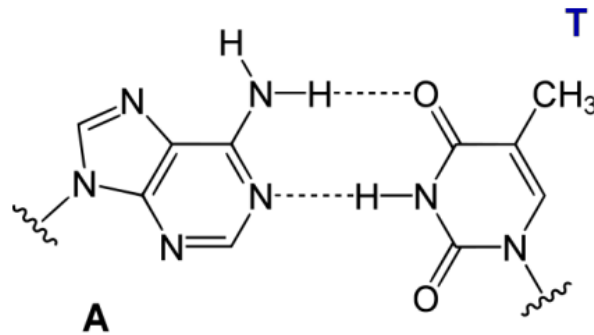


DNA vs RNA

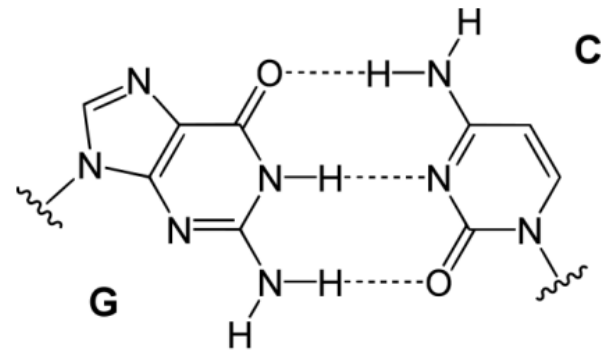
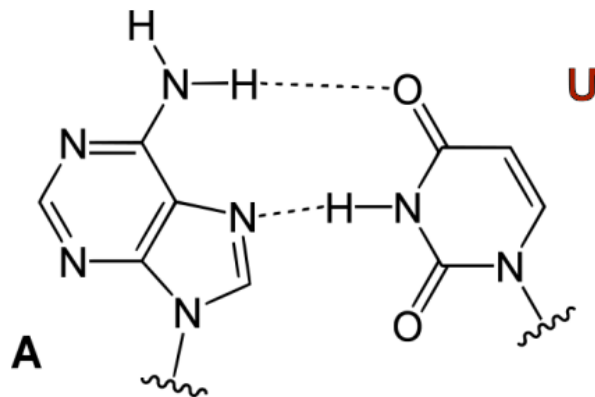


Base Pairs

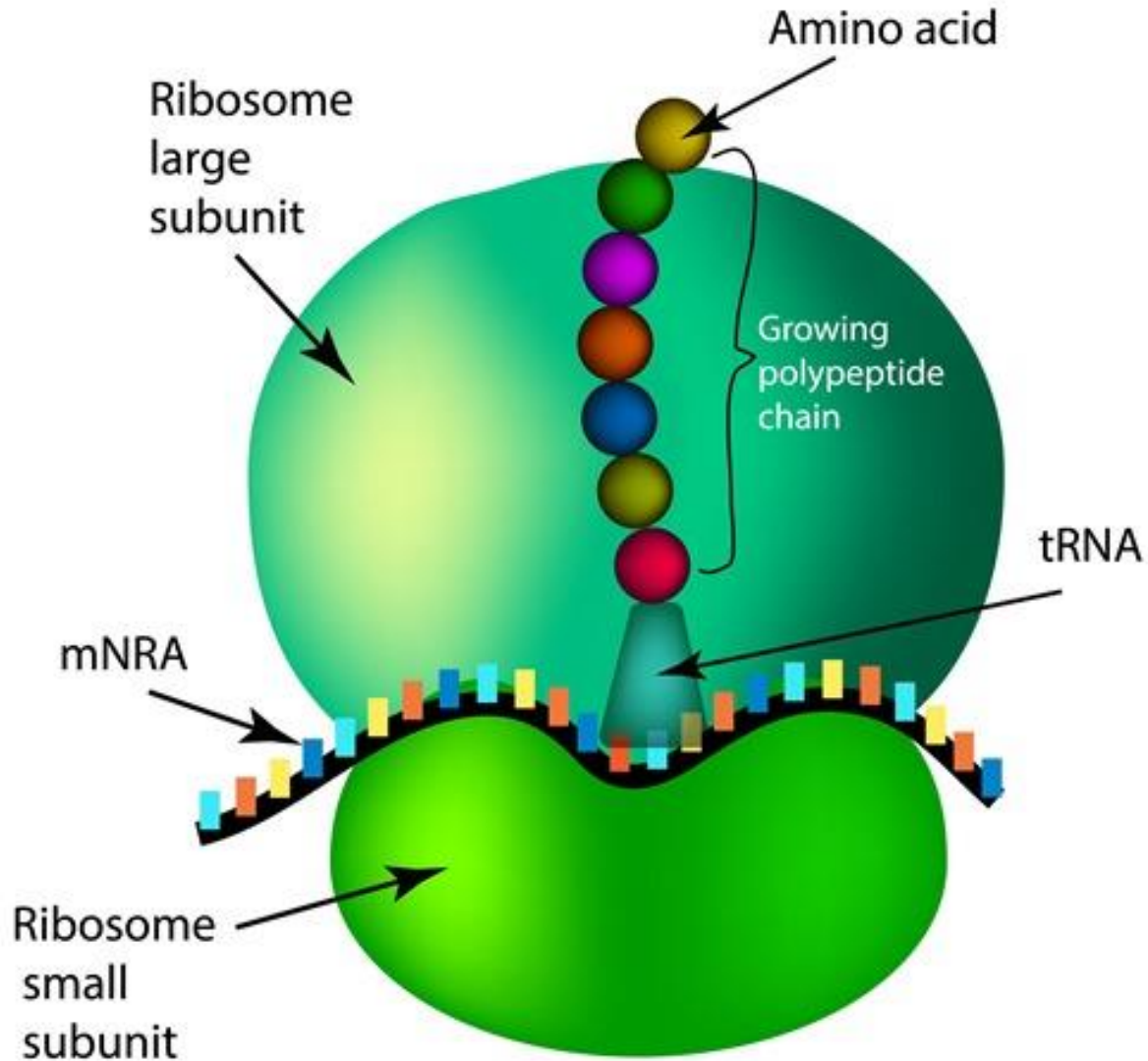
DNA



RNA



Ribosome

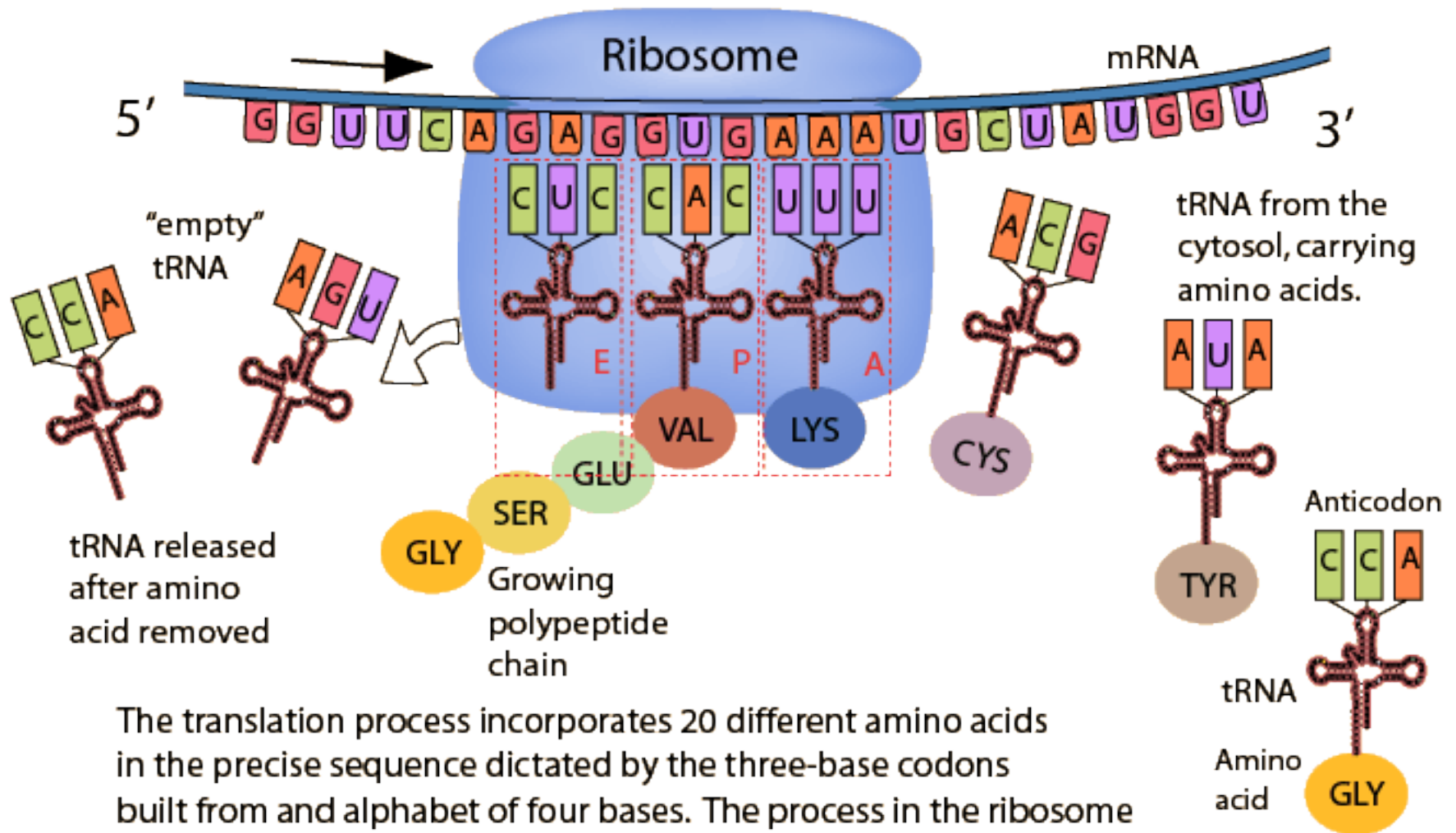


The diagram illustrates the process of translation. An mRNA strand with the sequence 5'-GGUUCAGAGGUGAAAUGGCUAUGGU-3' is being read by a ribosome. The ribosome has three sites: E (Exit), P (Peptidyl transfer), and A (Aminoacyl). tRNAs with anticodons CCA, AGU, CUC, CAC, UUU are shown. Amino acids GLY, SER, GLU, VAL, LYS, CYS, TYR are being added to the growing polypeptide chain. Labels include 'Ribosome', 'mRNA', '5'', '3'', 'empty tRNA', 'tRNA released after amino acid removed', 'Anticodon', and 'Amino acid'.

The translation process incorporates 20 different amino acids in the precise sequence dictated by the three-base codons built from an alphabet of four bases. The process in the ribosome

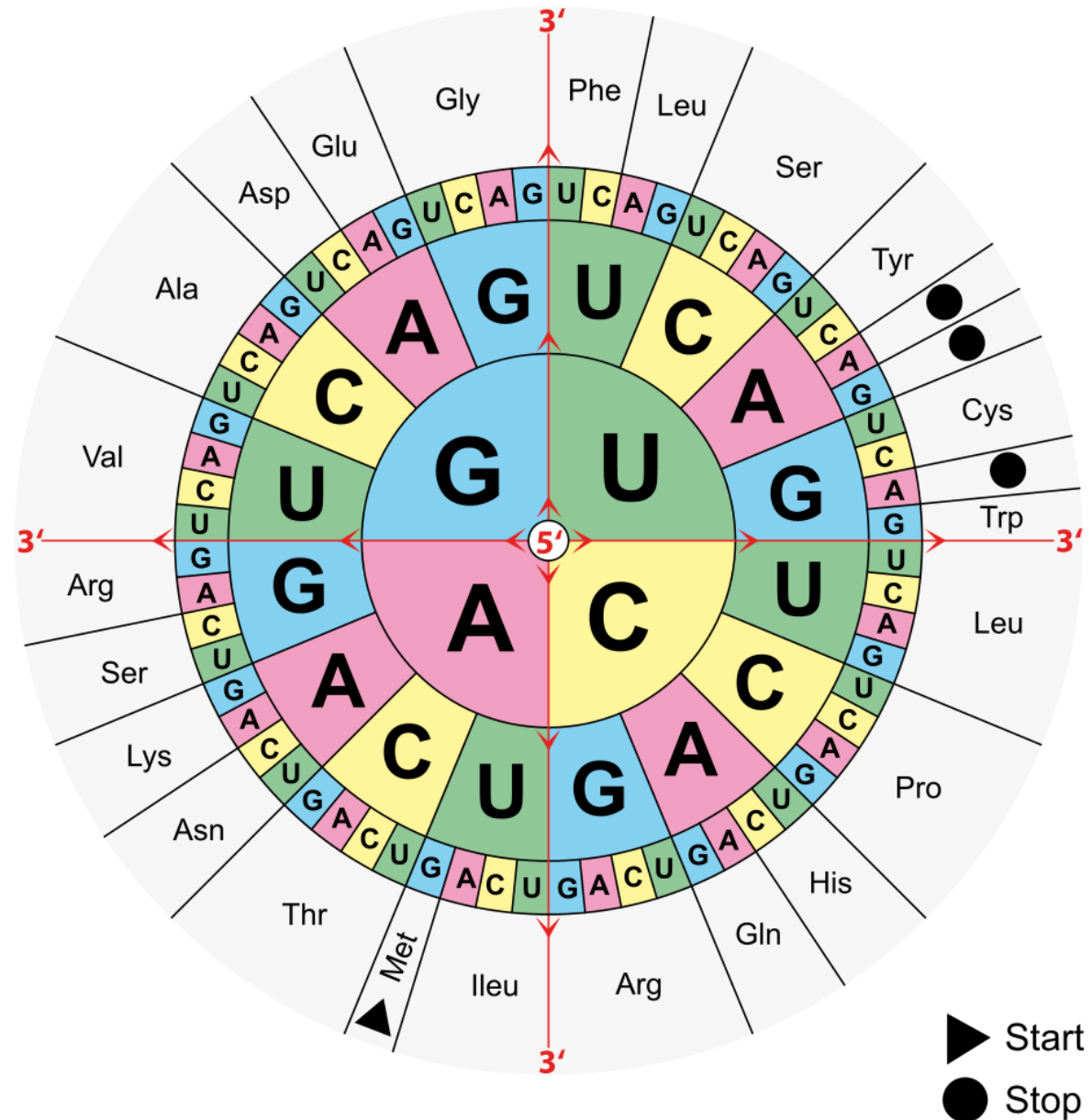
Source: <http://hyperphysics.phy-astr.gsu.edu/hbase/organic/imgorg/translation2.gif>

Translation



The translation process incorporates 20 different amino acids in the precise sequence dictated by the three-base codons built from an alphabet of four bases. The process in the ribosome builds the polypeptide chains that will become proteins.

CODON WHEEL



Amino Acids

Amino Acid	3-Letter Code	1-Letter Code
Alanine	Ala	A
Cysteine	Cys	C
Aspartic acid or aspartate	Asp	D
Glutamic acid or glutamate	Glu	E
Phenylalanine	Phe	F
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Lysine	Lys	K
Leucine	Leu	L
Methionine	Met	M
Asparagine	Asn	N
Proline	Pro	P
Glutamine	Gln	Q
Arginine	Arg	R
Serine	Ser	S
Threonine	Thr	T
Valine	Val	V
Tryptophan	Trp	W
Tyrosine	Tyr	Y

Protein Sequence

