MCDB 3500 Final
Fall, 2004

Good evening - 150 min; closed everything, be succinct, ask about any ambiguity.

Student ID

Name

Q1

Q2

Q3

Q4

Q5

Q6

Q7

Q8

Σ ______ of 100

Four exam grade______
What, most likely, is the name of the “Sugar”?

Deoxyribose (to go with T)

Label the bases with their letter names.

Circle the pyrimidines.

Box around the purines.

Identify an error or omission in the drawings above

3' H-bond in G≡C pair missing.
Write on the arrows below with responsive, substantive definitions of the structure at the arrow’s point.
From what sort of creature were these molecules taken?  

*bacterium*

Label:

DNA  
RNA  
Ribosome  
Polysome  
Promoter

A length corresponding to 150 W/C turns (NB: 1 meter = $10^{10}$ Angstroms = $10^9$ nanometers, bases are 3.4 Ångstroms thick)

\[
10.5 \text{ nt pairs/turn} = 36 \AA \\
150 \text{ turns} = 5400 \text{ Angstroms} = 5.1 \times 10^{-7} \text{ m} = 0.051
\]

How many messenger RNA nucleotides per ribosome are there in a functioning message?

In the labelled Polysome, there are

\[
\begin{align*}
&\text{22 ribosomes} \\
&\text{350 turns of template DNA} \\
&\text{3675 nt of RNA Product}
\end{align*}
\]

\[
\frac{3675}{22} = 168 \text{ nt/ribosome}
\]

So the existing bar is very close to

1575 nt pair
In the coding table below, put a box around a set of codons read by a tRNA anticodon of sequence GNN (N = any nucleotide).

How many different mRNA sequences could code for the peptide Trp Ile Leu Cys?

\[ \# \text{ codons} = 1 \times 3 \times 6 \times 2 = 36 \text{ sequences} \]

Why can't the aaRS that puts serine on tRNA\textsuperscript{Ser} rely solely on the anticodon nucleotides of the tRNA to bind the correct subset of tRNAs?

Write down all amino acid sequences that could result from the translation of the repeating mRNA (GAC)\textsubscript{n}.

How does a bacterial cell distinguish between the message sequences AUG = methionine within a protein, and AUG = initiator amino acid?

Name two tRNAs that might be easily mutated to become nonsense suppressors of UGA stop.

![Codon Table]

<table>
<thead>
<tr>
<th>First position (5'-end)</th>
<th>Second position</th>
<th>Third position (3'-end)</th>
</tr>
</thead>
<tbody>
<tr>
<td>AUU</td>
<td>Phe</td>
<td>GUC</td>
</tr>
<tr>
<td>AUC</td>
<td>Ile</td>
<td>GCU</td>
</tr>
<tr>
<td>AUA</td>
<td>Leu</td>
<td>GCA</td>
</tr>
<tr>
<td>AUG</td>
<td>Met</td>
<td>GCG</td>
</tr>
<tr>
<td>CUA</td>
<td>Leu</td>
<td>CGU</td>
</tr>
<tr>
<td>CUG</td>
<td>Arg</td>
<td>CGG</td>
</tr>
<tr>
<td>CCA</td>
<td>Pro</td>
<td>CAC</td>
</tr>
<tr>
<td>CCC</td>
<td>Leu</td>
<td>CCG</td>
</tr>
<tr>
<td>CUU</td>
<td>Leu</td>
<td>CAU</td>
</tr>
<tr>
<td>UUA</td>
<td>Leu</td>
<td>UAA</td>
</tr>
<tr>
<td>UUG</td>
<td>Leu</td>
<td>UAG</td>
</tr>
</tbody>
</table>

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This process occurs in (kind of creature) **eukaryotes**.

The name of the process is **spliceosomal splicing**.

Draw arrows to the steps that modify covalent connections between RNA nucleotides.

Circle the step where "commitment" occurs.

Put a box around a branch point.

Put the expression "Y" beside the polypyrmidine sequence.

Put triangles around two positions where splicing enhancers often occur.

What is the catalytic element often thought to act like a group II RNA sequence? UB53

The role of the ATP used in this process is **to promote conformational change**

Put a filled circle (●) at the position of an exon junction complex.
This process occurs in (kind of creature) eukaryotes.

The name of the process is **spliceosomal splicing**.

Draw arrows to the steps that modify covalent connections between RNA nucleotides.

Circle the step where "commitment" occurs.

Put a box around a branch point.

Put the expression "Y_r" beside the polypyrimidine sequence.

Put triangles around two positions where splicing enhancers often occur.

What is the catalytic element often thought to act like a group II RNA sequence? U6 snRNA

The role of the ATP used in this process is to induce conformational change.

Put a filled circle (●) at the position of an exon junction complex.
A small molecule that turns on a set of bacterial genes is said to **induce** them.

A positive factor like CAP protein turns gene expression (on, off) **on** by **binding** to RNA pol.

Attenuation controls gene expression by changing **the polymerase ii for termination**.

RNA Pol II is strongly inhibited by the mushroom peptide **α-amanitin**.

RNA polymerase backtracking is useful for **error correction**.

Footprinting can only be done on individual strands of a doubled stranded DNA separately because you must have product of unique length. Labeling both strands would confuse length.

A eukaryotic promoter without a TATA box can still work by
1. **Binding** to the initiation with a TAF.
2. **Binding** to an enhancer - **binding** protein

A eukaryotic transcription activator often consists of separate protein domains that bind DNA and activate transcription or bind polymerase.

When we speak of a “histone code” we mean the **pattern of modifications on histone tails**.

An enzymatic activity found in TAF’s is **histone deacetylation / histone acetyl transfer**.
On the basis of the electron micrographs below, showing progressive times during the replication of a circular DNA, draw clear arrows to, and label the:

Origin
Terminus
Replication fork
Restriction site

Draw the DNA as it would appear in a hypothetical panel that follows panel 8.