MCDB 3500 Final

Fall, 2004

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

Student ID KEY

Name

Q1_____

Q2_____

Q3_____

Q4_____

Q5_____

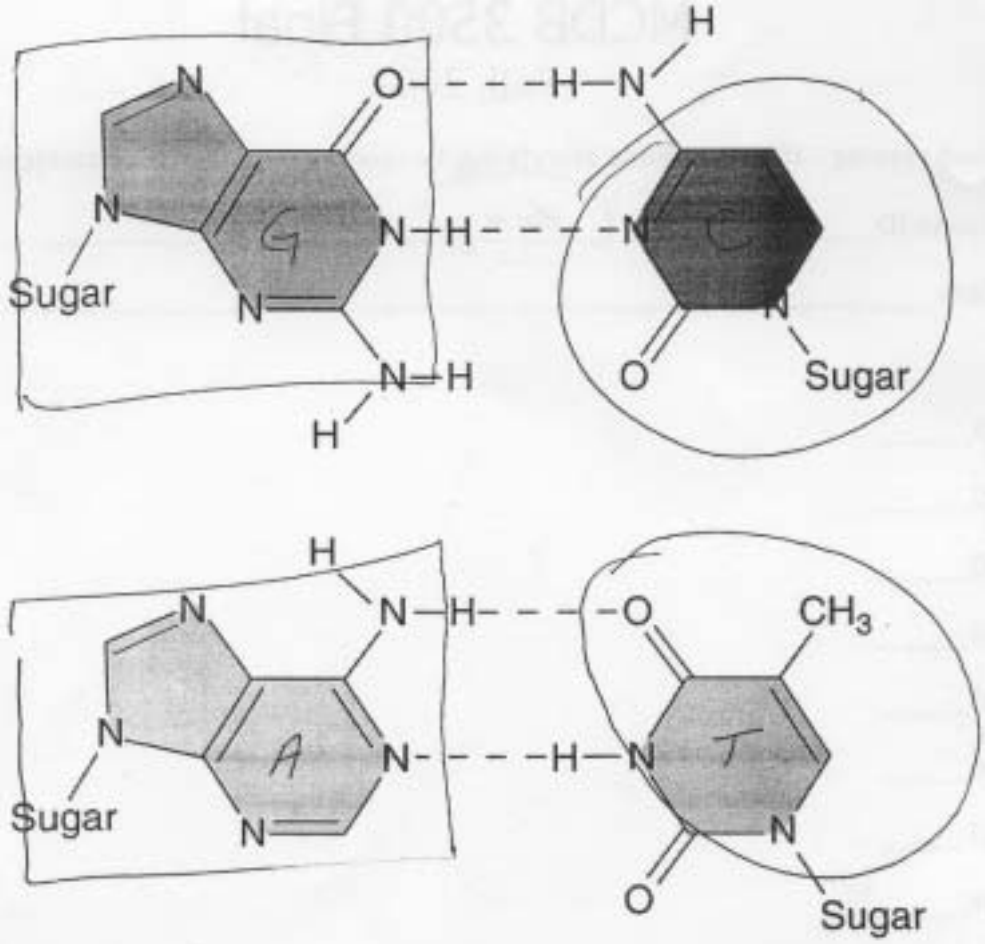
Q6_____

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.

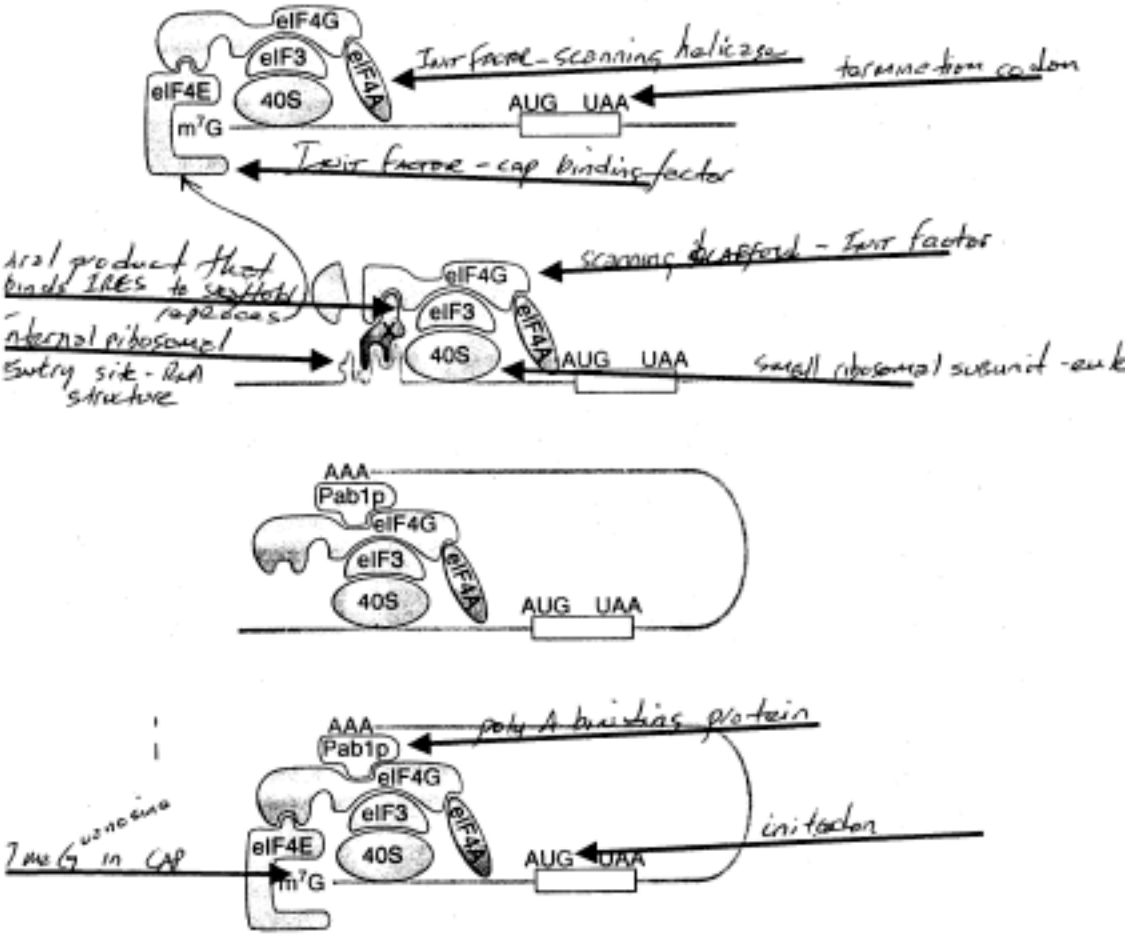
Circle the pyrimidines.

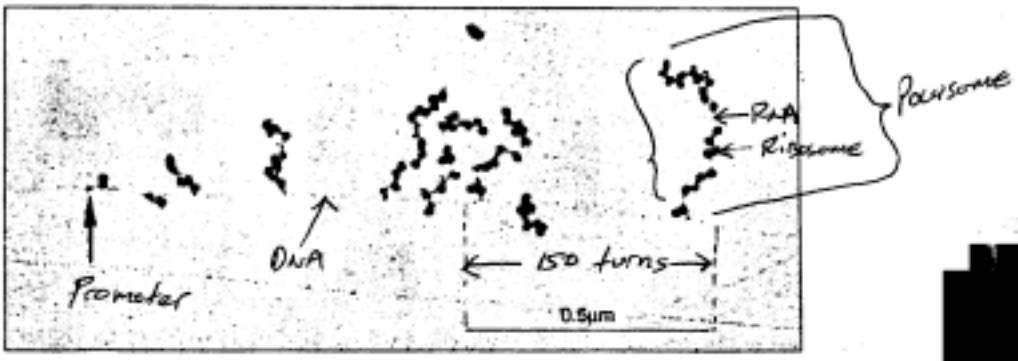
Box around the purines.

Identify an error or omission in the drawings above

3rd 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 nt pairs/turn = 36 Å 150 turns = 5400 Angstroms = 5.1×10^{-7} M = 0.5 μ

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

IN THE LABELLED POLYSOME, THERE ARE

~ 22 RIBOSOMES

&

~ 350 TURNS OF TEMPLATE DNA,

∴ ~3675 nt OF RNA PRODUCT

$\frac{3675}{22} = 168$ nt/ribosome

So the existing bar is way close to 150 turns 1575 nt pai

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?

\# codons → 1×3×6×2 = 36 sequences

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

Codons { 5' UC U/C/A/G 3', AG U/C } → Anticodons { 5' GGA / UGA 3', GCU } There is no unique anticodon sequence

Write down all amino acid sequences that could result from the translation of the repeating mRNA $(GAC)_n$?

GACGACGACGACG } 3 different homopeptide sequences
Asp - Asp - Asp - Asp
Thr - Thr - Thr
Arg - Arg - Arg

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

If S/D ← 8-12nt → AUG, it's an initiator & gets fMet. Otherwise, AUG = Met.

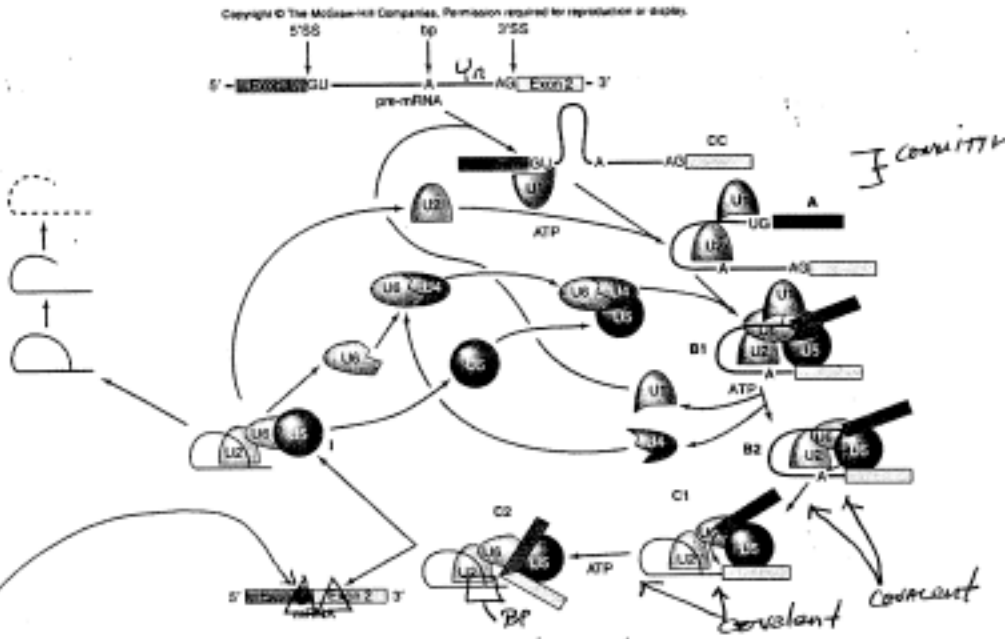
Name two tRNAs that might be easily mutated to become nonsense suppressors of UGA stop.

UG U/C → UGA STOP (Cys)
CGA → UGA STOP (Arg)
} The mutation happens in tRNA anticodon sequence, but we can just look at codons & get the same answer.

1st Q: any U'N'U/C will do. (box drawn around UUU, UUC)

Second position

First position (5'-end)	U	C	A	G	Third position (3'-end)
U	UUU Phe	UCU Ser	UAU Tyr	UGU Cys	U
	UUC Phe	UCC Ser	UAC Tyr	UGC Cys	C
	UUA Leu	UCA Ser	UAA STOP	UGA STOP	A
	UUG Leu	UCG Ser	UAG STOP	UGG Trp	G
C	CUU Leu	CCU Pro	CAU His	CGU Arg	U
	CUC Leu	CCC Pro	CAC His	CGC Arg	C
	CUA Leu	CCA Pro	CAA Gln	CGA Arg	A
	CUG Leu	CCG Pro	CAG Gln	CGG Arg	G
A	AUU Ile	ACU Thr	AAU Asn	AGU Ser	U
	AUC Ile	ACC Thr	AAC Asn	AGC Ser	C
	AUA Ile	ACA Thr	AAA Lys	AGA Arg	A
	AUG Met	ACG Thr	AAG Lys	AGG Arg	G
G	GUU Val	GCU Ala	GAU Asp	GGU Gly	U
	GUC Val	GCC Ala	GAC Asp	GGC Gly	C
	GUA Val	GCA Ala	GAA Glu	GGA Gly	A
	GUG Val	GCG Ala	GAG Glu	GGG Gly	G



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.

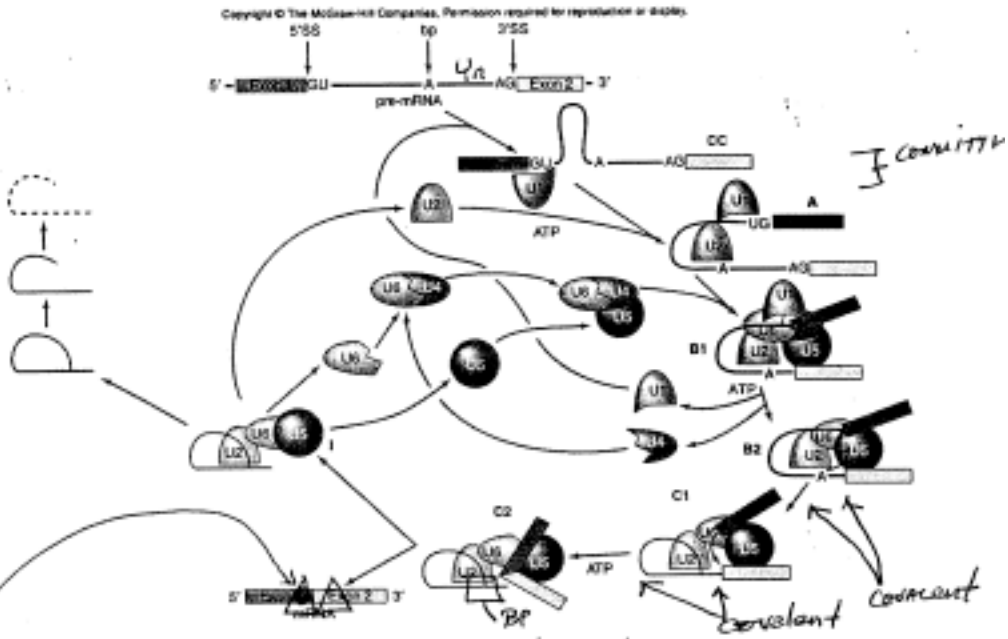
Put the expression "Y_n" beside the polypyrimidine sequence.

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 snRNP

The role of the ATP used in this process is TO POWER CONFORMATIONAL CHANGE

Put a filled circle (●) at the position of an exon junction complex.



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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 RNA POL.

Attenuation controls gene expression by changing THE PROBABILITY OF EARLY RNA POL 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 PRODUCTS OF UNIQUE LENGTH. LABELING BOTH STRANDS WOULD CONFUSE LENGTH

A eukaryotic promoter without a TATA box can still work by
1 BINDING THE INITIATOR 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.