

**Quiz 1 (key)**  
**PL S/MCB/MIC 340**  
**9/17/02**  
**(20 points)**

Following a series of gene-cloning experiments, you have obtained the sequence of your favorite gene (YFG) from the mouse genome as indicated below. Besides the sequence of YFG, you have also obtained its exact position of transcription start (denoted by the underlined nucleotide) using the mRNA sequence coded by the gene. Your data indicate that YFG does not contain an intron. Using the following sequence: (1) indicate the longest mRNA sequence possibly coded by this gene; (2) show the typical post-transcriptional modifications and where they occur on the mature YFG mRNA sequence; (3) indicate the most likely position of transcription regulatory sequences for YFG; and (4) derive a peptide sequence for YFG protein. For all nucleic acid and polypeptide molecules, please indicate the orientation of the molecules using the appropriate end labels.

5' REGULAT SEQS

5' GAACCCTGGACGACTTGCAGAGCGGCTGGCGCAGTCATGGCGGACTACT

3' CTTGGGACCTGCTGAACGTCTCGCCGACCGCGTCAGTACCGCCTGATGA

5' CAP UGCAGAGCGGCUGGCGCAGUCAUGGCGGACUACU

N<sup>-</sup> M A D Y

GGAAGTCACAGCCAAAGAAATTCTGTGATTACTGCAAGTGCTGGATAGCAG  
 CCTTCAGTGTCGGTTTCTTTCCGACACTAATGACGTTTACGACCTATCGTC  
 GGAAGUCACAGCCAAAGAAAGGCUGUGAUUACUGCAAGUGCUGGAUAGCAG  
 W K S Q P K K F C D Y C K C W I A

ACAATAGGCCTAGTGTTGAATTTTCATTAGTTGCAG<sup>3'</sup>  
 TGTTATCCGGATCACAACCTTAAAGTAATCAACGTC<sup>5'</sup>  
 ACAAUAGGCCUAGUGUUGAAUUUCAUUAGUUGCAGaaaaaaa<sup>3'</sup>  
 D N R P S V E F H<sup>-C</sup> .

		Second base				
		U	C	A	G	
First base (5' end)	U	UUU	UCU	UAU	UGU	U
		UUC	UCC	UAC	UGC	C
		UUA	UCA	UAA Stop	UGA Stop	A
		UUG	UCG	UAG Stop	UGG Trp	G
C	C	CUU	CCU	CAU	CGU	U
		CUC	CCC	CAC	CGC	C
		CUA	CCA	CAA	CGA	A
		CUG	CCG	CAG	CGG	G
A	A	AUU	ACU	AAU	AGU	U
		AUC	ACC	AAC	AGC	C
		AUA	ACA	AAA	AGA	A
		AUG Met or start	ACG	AAG	AGG	G
G	G	GUU	GCU	GAU	GGU	U
		GUC	GCC	GAC	GGC	C
		GUA	GCA	GAA	GGA	A
		GUG	GCG	GAG	GGG	G

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