

Problem One

A) i) Complete the following table. Assume that

- the reading is from left to right
- the columns represent transcriptional and translational alignments

A						A						DNA double helix
	A						G	C	T			
		G									A	mRNA transcribed
										C		Appropriate tRNA anticodon
			Trp (W)									Amino acids incorporated into protein

ii) Label 5' and 3' ends of DNA and RNA, as well as the amino and carboxyl ends of proteins.

B) Consider the following segment of DNA:

5' – GGCTACGTA – 3'

3' – CCGATGCAT – 5'

1) Assume that the top strand is the template strand used by the RNA polymerase.

i) Write the RNA transcript (5' → 3', from left to right).

ii) Write the corresponding amino acid chain and label its amino and carboxyl ends.

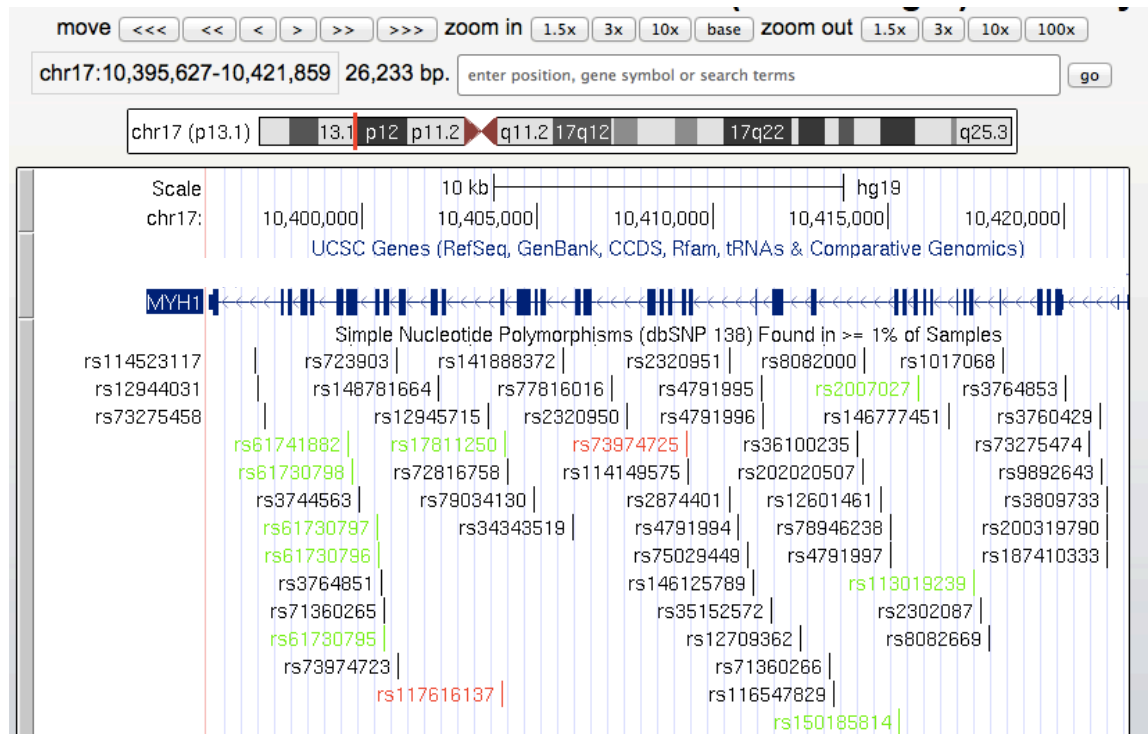
2) Now assume that the bottom strand is the template strand.
Repeat part (i) and (ii)

C) Write all six possible reading frames from 5' to 3' (left to right) of the following sequence:

5' --- GAGCACTGCGCAATA --- 3'

Problem Two

A) Consider the following screen shot.



i) What is the name of the genome browser from which this figure was taken?_____.

ii) What is the name of the gene that is shown in the panel? _____.

iii) What is the locus of the gene? _____.

iv) There are ____ exons and ____ introns in this gene.

v) Where is the 5' end of this gene (on left or right side of the browser)

-----.

vi) On the above figure, label the 5' and 3' UTR.

vii) Consider “rs723903” in the genome browser panel.

a) What does “rs” stand for?

b) Why are the rs ids colored in red, green and black?

B) Consider the alignment on the following page obtained upon blasting a query sequence against the protein sequences of GenBank at NCBI. The actual file was edited and some entries were removed.

Range 1: 1 to 208 Graphics						▼ Next Match ▲ Previous Match	
Score	Expect	Method	Identities		Positives	Gaps	
412 bits(1058)	7e-152	Compositional matrix adjust.	□/210()		□/210()	□/210()	
Query 1		MDLSALRVEEVQNVINAMQKILECPICLELIKEPVSTKCDHIFCKFCMLKLLNQKKGPSQ				60	
Sbjct 1		MDLSA+RVEEVQNVINAMQKILECPICLELIKEPVSTKCDHIFCKFCMLKLLNQKKGPSQ				60	
Query 61		CPLCKNDITKRSLOESTRFSQVVEELLKIIICAFQLDTGLEYANSYNFAKKENNSPEHLKD				120	
Sbjct 61		CPLCKNDITKRSLOESTRFSQVVEELLKIIICAFQLDTGL ANSYNFAKKENNSPEHLKD				118	
Query 121		EVSIIQSMGYRNRKRLQSEPNPSLQETSLSVQLSNLGTVRTLRQRIQPQKTSVYI				180	
Sbjct 119		EVSIIQSMGYRNRKRLQSEPNPSLQETS SVQLSNLGTVRTLRQRIQPQK SVYI				178	
Query 181		ELGSDSSEDTVNKATYCSVGDQELLQITPQ	210				
Sbjct 179		ELGSDSSEDTVNKATYCSVGDQELLQITPQ	208				

- i) What is the name of the program was used to generate this pairwise sequence alignment? Be as specific as possible.
- ii) What is the probability that the similarity between the query and the hit occurred only by chance? Why?
- iii) The second line in the figure has three blanks (boxes); the first after “Identities”, the second is “Positives”, and the third is “Gaps”. Fill in the blanks by putting the missing numbers on the figure.
- iv) i) What is the purpose of the middle row (between Query and Sbjct) in the alignment?

C) Consider the following GenBank entry. The actual file was edited to fit in one page. There are 2 occurrences of “CDS”. Note that the characters of the two “/translation” sequences were removed.

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LOCUS      DQ926871                334 bp    mRNA    linear    MAM 11-
OCT-2006 DEFINITION  Felis catus BCL2 (BCL2) mRNA, partial cds.
ACCESSION  DQ926871
VERSION    DQ926871.1  GI:115607125
KEYWORDS   .
SOURCE     Felis catus (domestic cat)
.....
FEATURES             Location/Qualifiers
     source           1..334
                     /organism="Felis catus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9685"
     gene            <1..>334
                     /gene="BCL2"
     CDS              <1..>334
                     /gene="BCL2"
                     /codon_start=3
                     /product="BCL2"
                     /translation="....."
ORIGIN
1  ggggacgctt tgccacggtg gtggaggagc tcttcagga tggagtgaac tgggggagga
61 ttgtggcctt ctttgagttc ggtggggtca tgtgtgtgga gacgctcaac cgagagatgt
121 cgcccctggt ggacaacatc gccctgtgga tgactgagta cctgaaccgg cacctgcaca
     .....
301 gggccttgcat caccctgggt gcctatctgg gccca

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- i) What does CDS stand for? _____.
- ii) What type of sequence is this record showing?_____.
- iii) Consider the “CDS”. Give the second and third characters of “/translation”. Show all your work.