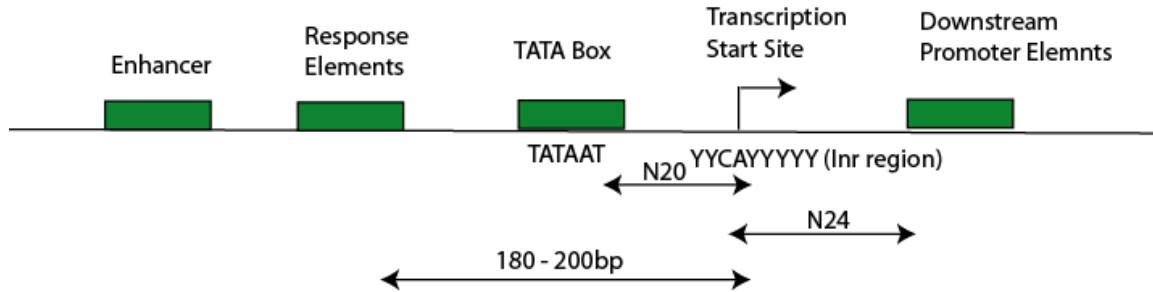


Name \_\_\_\_\_

**MBMB 451A Section 2 - Bartholomew  
Fall 2008 Exam II - KEY 10-23-08**

Answer the following question

1. Draw out the DNA elements of a typical eukaryotic mRNA gene that are required for both basal and activated transcription. Make sure to indicate besides their name, the position and distance from the start site of transcription and whether they are important for activated or basal level transcription. (9 pt)



The TATA box, INR, and DPE are involved in basal level transcription while the response elements and enhancer are required for activated transcription.

2. Describe the properties of the general transcription factors of RNA polymerase II. What enzymatic activities do some of the transcription factors possess and how do they facilitate transcription? Please provide an order of events or a flow chart. Describe TAFs and if they are involved in activated or basal transcription. (10 pt)

**Where indicated are worth 2 pts otherwise they are each 1 pt**

**TFIID:** binds to TATA box, contains TBP and TAFs, responsible for promoter binding. TBP alone can facilitate in the assembly of the transcription complex. TBP binds to the TATA box 2pts

**TFIIA:** maybe involved in activation and stabilizes TBP binding and may help counteract repressor proteins that actively displace TBP from DNA

**TFIIB:** involved in start site recognition, may also stabilize TBP-DNA interactions

**TFIIF:** Helicase activity, maybe involved in DNA melting, and helps bring RNA pol transcription complex. It promotes the association of TFIIIE with the preinitiation complex

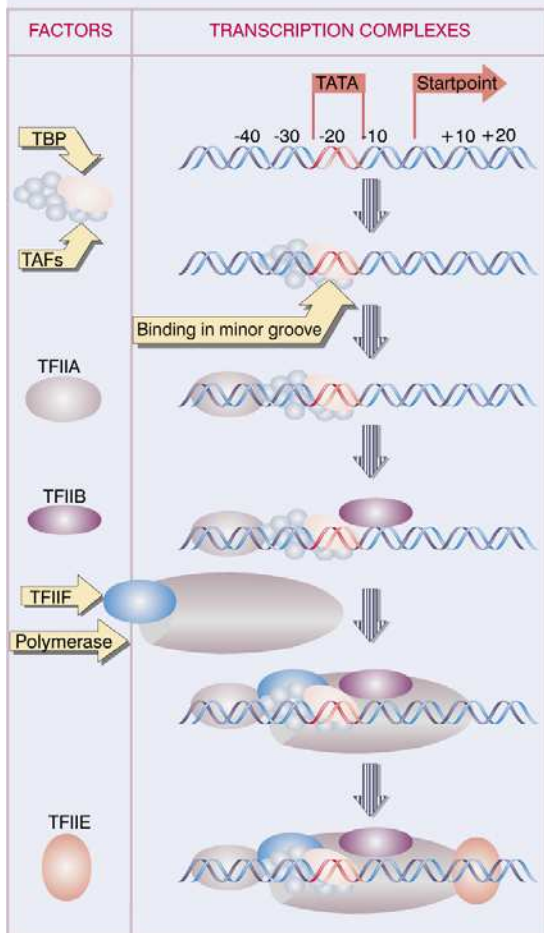
**TFIIIE:** along with TFIIH it is involved in promoter clearance,

**TFIIH:** has ATPase, helicase and kinase activity (CTD phosphorylation) and involved in DNA damage repair 2pts

TAFs are TBP associated factors. They control the activity of TBP and TFIID and are involved in **activated** transcription 2 pts

Name \_\_\_\_\_

**Figure 20.11** An initiation complex assembles at promoters for RNA polymerase II by an ordered sequence of association with transcription factors.



3. Explain what are a leucine zipper and a zinc finger. Highlight what amino acid sequence requirements exist and structural characteristics of these two protein motifs. (8 pts)

Leucine zipper – (1) dimerization domain, (2) contains leucine every 7<sup>th</sup> amino acid, (3) hydrophobic zipper comprised of leucines holds the two proteins together – forms a coiled-coil structure. Leucine zipper brings two DNA binding domains in close juxtaposition. 4 pts

Zinc fingers: (1) there are three types: (A) Cys2-His2 fingers: Cys-X2-4-Cys-X3-Phe-X5-Leu-X2-His-X-His, (B) Cys2-Cys2 fingers: Cys-X2-Cys-X13-Cys-X2-Cys, and (C) Binuclear Zn cluster example is Gal4. Either occurs as single units or in tandem with other Zn fingers. They bind to the major groove of DNA. Zn fingers are found in such TF such as TFIIIA, SP1, and steroid receptors. 4 pts

Name \_\_\_\_\_

4. Define what is a transcription coactivator and give an example of one such type of complex. (3 pt) How do these complexes help activate transcription? (4 pt)

- Coactivators are the protein that are required to bridge the promoter specific transcription factors to the general transcription factors so that activation can occur.
- Examples of these are TFIID (specifically the TAFs), mediator, SAGA (containing GCN5), CREB and so on.  
(3 points).
- Coactivators may work through covalent modification and in particular histone acetylation (i.e. SAGA).
- This means they may help the other transcription deal with the chromatin that maybe blocking out TFs or RNA Pol II.
- The other model is that they may help the two sets of TFs bind and stabilize of strengthen the recruitment of these factors to the DNA template.
- And the third option is they may cause a conformational change somewhere in the transcription machinery the promotes transcription.  
(each sentence is worth about 1 point)

5. Describe the structure of the nucleosome core particle in terms of its DNA and protein components and organization. (4 pt) How are nucleosome core particles used to form a 30 nm chromatin fiber and are there any additional factors required? (4 pt)

Four core histones: H3, H4, H2A, H2B      DNA – 147 bp of DNA  
DNA is wrapped 1.7 times around histone core, presence of histone tails and globular central domain.      4 pts

NCPs form a beads on a string like structure (10 nm fiber). The addition of linker histone H1 and moderate salt (~100 mM NaCl) promotes the folding of the 10 nm structure into either a solenoid or zig-zag structure. (Mg can also cause folding of the 10 nm fiber) 4 pts

6. List the different types of ATP-dependent chromatin remodeling complexes. (4 pt) How does ATP-dependent chromatin remodeling facilitate in transcription activation of only a particular subset of genes? (4 pt)

SWI/SNF, ISWI, CHD or Mi-2, and INO80 subfamilies      4 points

A pioneer transcription factor binds to its cognate binding site in the genomic DNA and recruits the chromatin remodeling complex to that particular site. The targeting of the complex by the transcription factor (like Gal4 or steroid receptor) makes it gene specific. The remodeling complex then reorganizes the chromatin in this region making it more accessible to the other transcription factors and RNA polymerase II. This therefore makes it possible to form a productive transcription initiation complex and likely chromatin remodeling also facilitates in the transcription complex being able to elongate through the chromatin template. (4 points)

Please write your answers on separate pieces of paper