1. Explain how the following modifications of the chromatin structure effect the expression of the gene.

    a. DNA methylation- methylation of DNA causes the DNA to become more tightly packed to the histone, suppressing transcription. Methylation occurs to CpG islands, typically binds to the C. Methylation is also even along double strands. For every methyl group on one strand there is a methyl group on the other strand. You can also methylate the histones and have the same effect.

    b. Histone acetylation- Acetyl groups neutralize the positive charge on the tails of the histone making it less attracted to DNA. This decondenses the DNA allowing transcription to occur.

        Ex. Flowering in Arabidopsis plants- FLC (acetylated chromatin) prevents flowering. FLD produces a deacetylase enzyme that deacetylases FLC and allows flowering.

    c. Nucleosome repositioning- the histone slides along the DNA exposing different areas of the DNA allowing these regions to be accessible to proteins to permit expression or transcription.

2. Explain the following examples of controlling eukaryotic transcriptional initiation.

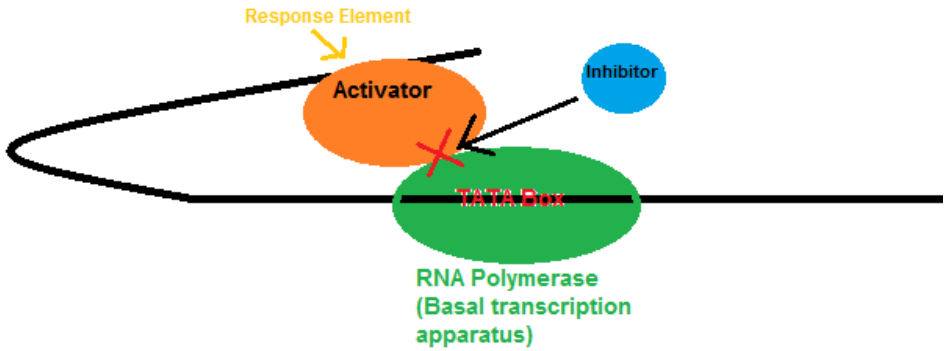
    a. Transcriptional Activators- stimulates transcription!!!! It does so by binding to the basal transcription apparatus (aka the polymerase).

        - Response Elements- are short sequences that typically contain consensus sequences. These are binding sites for transcriptional activators.

        Ex. GAL4-transcriptional activator in yeast. It binds to RNA polymerase and enhances transcription.

    b. Transcriptional Repressors- inhibit transcription. Are NOT like repressors in the operon (prokaryotes) instead compete with activators and suppress the activation.

        Ex. GAL80- a repressor that blocks GAL4 from activating transcription.



    c. Enhancers- enhance transcription. Typically lie within the regulatory promoter and loop around to interact with the promoter.

d. Insulators- block or insulate the effect of enhancers. Must lie between enhancer and promoter.

3. Explain the following examples of controlling eukaryotic gene regulation.

   a. RNA splicing-alternative splicing allows a pre-mRNA to be spliced in multiple ways, generating different proteins in different tissues or at different times in development.

      Ex. Sex determination in Drosophila- alternative splicing results in different sexes.

      Active Sxl gene→ sxl protein—splices→ tra mRNA → tra proteins→ female splice dsx→ Female fly

      Inactive sxl gene→no sxl protine→ no spliced tra mRNA→no tra protines→ male splice dsx → male fly

   b. RNA degradation- RNA is degraded quickly due to instability. This affects what genes are made into proteins.

      - What enzyme degrades cellular RNA? Ribonucleases

4. Explain the following examples of controlling eukaryotic gene regulation by RNA Interference.

   a. RNA cleavage using siRNA- Dicer cleaves dsDNA→produces siRNA (small interfearing)→RISC + siRNA complex pair with complementary sequence on mRNA →complex cleaves mRNA→ degrades RNA.
   b. Inhibition of translation using miRNA- Dicer cleaves dsRNA→ produces miRNA (micro)→ RISC+miRNA complex pair imperfectly with mRNA→ inhibition of translation.
   c. Transcriptional silencing using siRNA- miRNA+RISC complex pair imperfectly with DNA → attract methylating enzyme→ methylate histone or DNA→ more tightly packed DNA→ inhibit transcription.