

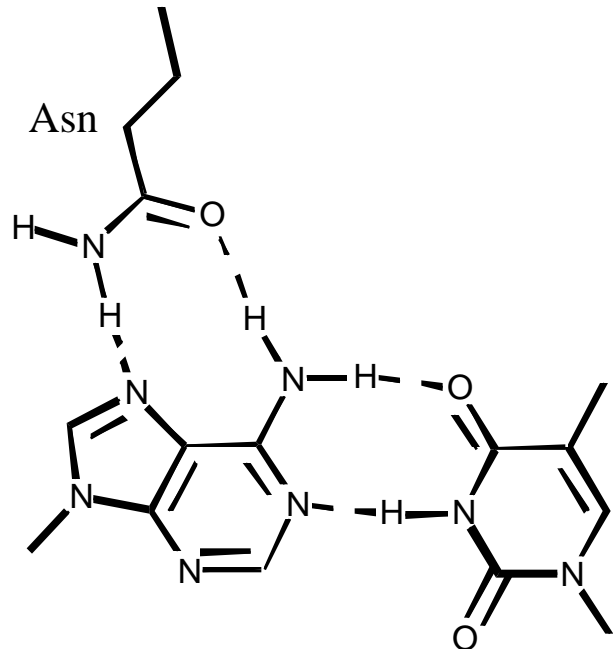
1. Use the structures on the attached sheet as trace-through templates (put the template sheet under your answer sheet to help you draw to scale).

a) Draw an **AT** base pair

See below

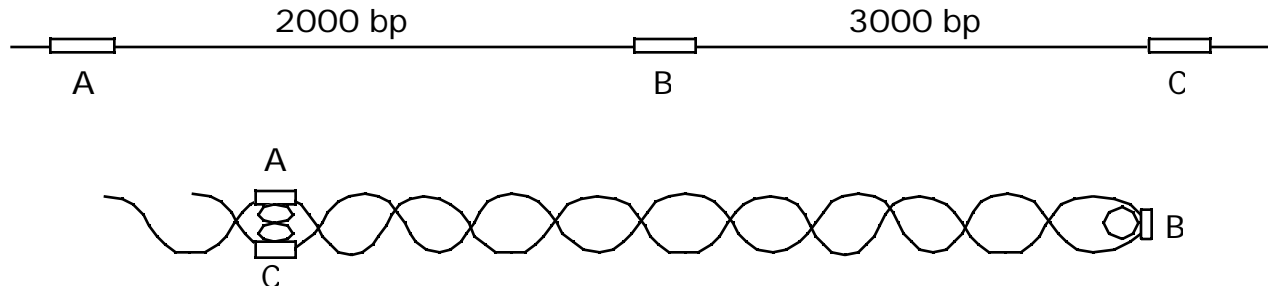
b) If you were designing a protein to **specifically** recognize an AT base pair through major groove contacts, which **one** of the amino acids on the template sheet would you use at the binding site? Explain why your choice is the **best** and draw a structure to illustrate your explanation (remember to consider reasonable hydrogen bond lengths and angles)

As shown at right, only Asn can form TWO simultaneous, good distance/angle hydrogen bonds with an AT base pair. This is much better than any interaction which would only provide one hydrogen bond, because of the benefits of cooperativity. Note the hint to look in the *major* groove.



2. For the sequence of DNA shown below, in some organism's genome, explain how binding of two different proteins to sites B and C might activate an enzyme bound to DNA at site A.

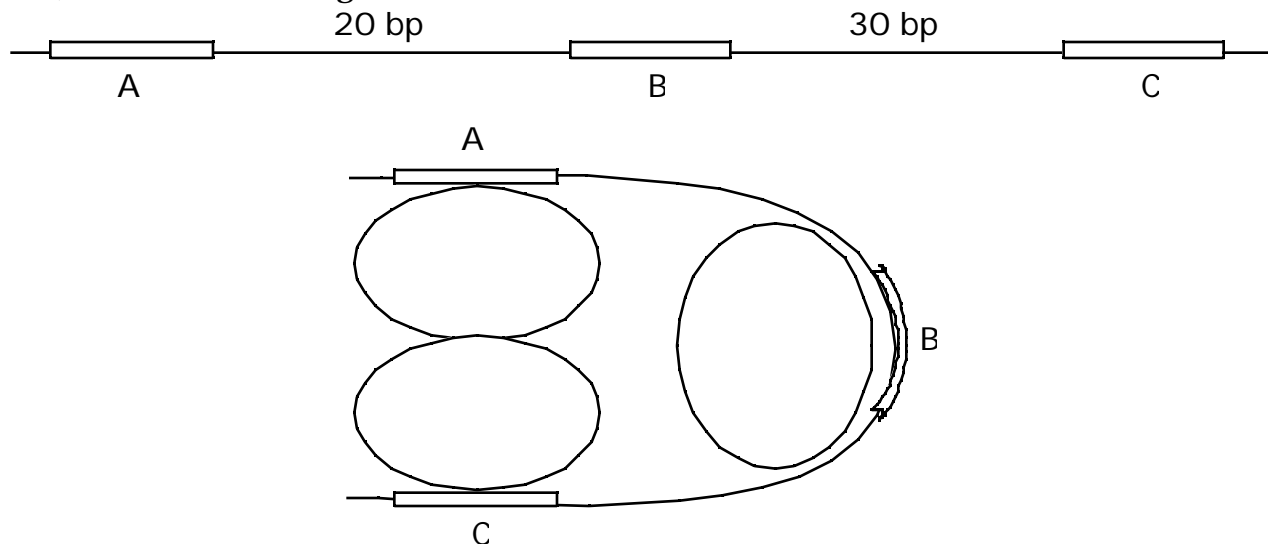
a) For the following situation:



As shown above, communication over this very long distance is achievable by **supercoiling** (a single line in the picture above represents a DNA *duplex*). As discussed in class, binding of a protein to site B can influence supercoiling (not *create* it), such that sites A and C are close. This would allow proteins bound to sites A and C to interact directly, with A activating C.

We saw nice examples of this in the MCB seminar by Pat Higgins on October 17.

b) For the following situation:



This is much shorter distance over which to mediate interactions. Supercoiling won't work. However, simple **bending** of the DNA, induced by a protein bound to site B, can act to bring proteins bound at sites A and C closer together, allowing activation of C by A.

