# Chapter 24

The lecture notes for this chapter will be briefer than those of previous chapters. More than in those chapters, these notes are going to simply point out highlights that you should pay close attention to. Finally, the notes below will concentrate on the "chemistry" of the cell. That is to say, things such as molecular structure and reactivity.

24.1 <u>Heredity and the Cell</u>

This chapter will concern it self with two macromolecules (polymers) with attached nucleic acids: deoxyribonucleic acid (DNA) and ribonucleic acid (RNA). The former contains all of the information necessary to create a living entity. To put it most briefly, one type of RNA is created directly from part of a DNA molecule and, through a series of steps involving several types of RNA, it creates enzymes. These are the catalysts that cause nearly all of the reactions in a cell to occur.

24.2 <u>Structure of Nuclei Acids</u>

There are some terms and structures you will need to become familiar with. First, at a very basic level DNA and RNA share the same structure.
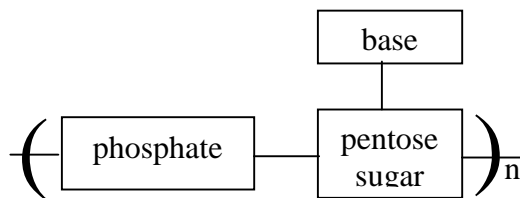
There are two significant structural differences between DNA and RNA. The first is DNA employs deoxyribose in its backbone, while RNA incorporates ribose into its background. The second major difference is that for DNA the four pendant bases are adenine, thymine, guanine,

and cytosine, while RNA substitutes uracil for thymine. You aren't responsible for the structures of the individual bases, but you should remember which bases are associated with which nucleic acid. The base always attaches at the aldol carbon. You should know the difference between ribose and deoxyribose.

These species are called nucleic *acids* because the phosphate groups have one –OH left after the backbone forms and this hydroxy group is acidic. As you already know, DNA consists of two strands wrapped around each other like braids (called a double helix). They are hooked together by pairs of bases hydrogen bonded to one another (Figure 24.5, p. 673). In particular it is worth remembering that each base can hydrogen bond effectively to only one other base, thus they <u>always</u> appear paired along the double helix. Guanine always pairs with cytosine (C-T) and adenine always pairs with thymine (DNA, A-T) or uracil (RNA, A-U). Thus, the strands are said to be *complimentary*.

One final note: Since the bases along the strands each bind to its complement on the other strand, one would be tempted to say this was the strongest interaction between the two strands. In fact, it is a hydrophobic interaction. The bases are hydrophobic and turn inward to avoid water. This gives rise to the twisting of the strands. While your book doesn't say this, my guess is that the complimentary bases come about for two reasons. First is that it maximizes hydrogen bonding and hence stability of the double helix. The second is that this mechanism results in a minimum of transcription errors and this is crucial to the health of an organism.

Finally, one tends to think of the DNA as being one continuous string of useful information. While this may well be true, at the present time it appears that there are sections with no useful information that are place holders. Some of this seems pretty logical. You'd expect a spacer between the code to make hemoglobin and the code to make collagen. What's interesting is that

there are spacers in the middle of the code to make nearly all proteins. Why this is so is still a mystery.

24.3 Ribonucleic Acids

There are several different types of RNA and each has a unique function. What is of primary importance to us here is how one creates a protein from a nucleic acid. As we have already seen, nucleic acids and proteins share no common elements. This naturally gives rise to the question "How can the former create the latter?"

We begin with a basic bit of math. There are twenty standard amino acids used to make proteins, so the RNA must be able to select from among them at each linkage. If only one base was necessary for the selection we could only choose between 4 amino acids (one for each different base). If two consecutive bases (along the backbone) were used, we could chose between a maximum of 16 amino acids (there are 16 different pairings of the 4 bases [AA, AU, AG, AC, UA, UU, … (the ordering of the pairs matters)]), while 3 consecutive bases would allow for 64 different amino acids. Since we only need 20 using 3 consecutive bases (called an *anticodon*) also provides for multiple combinations to signify the same amino acid. A look at Table 24.1 (p. 681) shows that for many amino acids the identity of the third base doesn't affect the amino acid selected. Thus an error at this site will not result in a defective protein. This redundancy provides some genetic protection to us when proteins are synthesized. A *codon* is similar to an anticodon except that it is used create the anticodon. An anticodon is generated by determining the complimentary base for each base on the codon, then listing them in reverse order.

Finally a protein is synthesized by taking the amino acids designated by the anticodon and polymerizing them into a single molecule in the order the anticodons appear on the transfer RNA.

The rest of this chapter is written such that I don't believe I can much to it here.

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