The study of the structure and functioning of a living cell at the molecular level uses a significant number of physics concepts. Since the interior of a cell is mainly water, we can imagine it as a vast sea of molecules continually in motion, colliding with one another with various amounts of kinetic energy. One of the ways these molecules can interact with each other is through electrostatic attraction.

The many processes that occur within the cell are now understood to be the result of random (thermal) molecular motion plus ordering due to Coulomb’s law. We can use these basic ideas to analyze some of the cellular processes involving macromolecules. Remember that the picture given here is a simplified model based on accepted physical theories and many experimental results.

The genetic information that is passed on from generation to generation in all living objects is contained in the chromosomes, which are made up of genes. Each gene contains the information needed to produce a particular type of protein. The genetic information contained in a gene is built into the principle molecule of a chromosome, DNA (deoxyribonucleic acid). A DNA molecule consists of a long chain of many small molecules known as nucleotide bases. There are only four types of bases: adenine (A), cytosine (C), guanine (G), and thymine (T).

The DNA in a chromosome generally consists of two long DNA chains wrapped about one another in the shape of a double helix. In the figure on the following page, one can see that the two strands are held together by electrostatic forces. We see that an A on one strand is always opposite a T on the other strand; similarly a G is always opposite a C. This happens because of the shape of the four molecules A, T, C and G are such that a T only fits closely into an A, and a G into a C. Only in the case of this close proximity of the charged portions is the electrostatic force great enough to hold them together even for a short time, forming what are often referred to as weak bonds (indicated by the dotted lines in the figures). The electrostatic force between A and T, and between C and G, exists because these molecules have charged parts due to some electrons in each molecule spending more time orbiting one atom than another. For example, the electron normally on the H atom of adenine (in the H₂N molecule) spends some of its time orbiting the adjacent N atom, so the N has a net negative charge and the H a positive charge. What the other bases see is a positive charge as the H is at the end of
the A molecule. This H⁺ atom of adenine is then attracted to the O⁻ atom of thymine. Notice that there are two such bonds between A and T and three between C and G.

We can use this basic model to also explain how DNA replicates. The two strands of DNA separate (with the help of enzymes, which also operate via the electrostatic force), leaving the charge parts of the bases exposed. Without going into the details of how replication starts, let’s see how the correct order of bases occurs by focusing our attention on one exposed base. Say this is a G. There are many unattached nucleotide bases of all four kinds moving about the cell, but only a C will attach to the G. Now, on the opposite strand of the original or old DNA we left a C base exposed (it was attached to the G in the original double helix). This C will eventually bond to a new G, forming another new helix. In this way we go from one double helix to two new ones.

This replication process is incredibly effective with an error rate on the order of 1 in $10^4$. This means that for every 10,000 base pairs, only 1 will be a mismatch. (In reality, certain enzymes serve as “proofreaders” and can reduce this error rate even further, say to 1 in $10^5$).

Let’s try a simple calculation to get a feel for the forces involved in holding the two strands of DNA together in a double helix. Assume that the net average charge on H₂N, NH₂ and NH is +0.2e, and on O and N is −0.4e. Also, assume that the atoms that form the weak bonds in each base are 1.5 x $10^{-10}$ m apart from the atoms in the opposite base. (The H₂N in A is 1.5 x $10^{-10}$ m away from the O in thymine.) First, estimate the net force between a thymine and an adenine; and between a cytosine and guanine. Next, estimate the total force for a DNA double helix containing $10^5$ pairs of such bases.