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■ INTRODUCTION

There are some 3000000000 base pairs (bp) making up human genomic DNA within a haploid cell. If that DNA is isolated from such a cell, it will weigh approximately 0.0000000000015 grams (g). To amplify a specific segment of that purified DNA using the polymerase chain reaction (PCR), 0.00000000001 moles (M) of each of two primers can be added to a reaction that can produce, following some 30 cycles of the PCR, over 1000000000 copies of the target gene.

On a day-to-day basis, molecular biologists work with extremes of numbers far outside the experience of conventional life. To allow them to more easily cope with calculations involving extraordinary values, two shorthand methods have been adopted that bring both enormous and infinitesimal quantities back into the realm of manageability. These methods use scientific notation and metric prefixes. They require the use of exponents and an understanding of significant digits.

1.1 SIGNIFICANT DIGITS

Certain techniques in molecular biology, as in other disciplines of science, rely on types of instrumentation capable of providing precise measurements. An indication of the level of precision is given by the number of digits expressed in the instrument's readout. The numerals of a measurement representing actual limits of precision are referred to as **significant digits**.

Although a zero can be as legitimate a value as the integers one through nine, significant digits are usually nonzero numerals. Without information on how a measurement was made or on the precision of the instrument used to make it, zeros to the left of the decimal point trailing one or more nonzero numerals are assumed not to be significant. For example, in stating that the human genome is 3000000000 bp in length, the only significant digit in the number is the 3. The nine zeros are not significant. Likewise, zeros to the right of the decimal point preceding a set of nonzero numerals are assumed not to be significant. If we determine that the DNA within a