Preface

The discovery of Epstein-Barr virus (EBV) by Epstein, Achong, and Barr, reported in 1964 (*Lancet* **1**:702–703), was stimulated by Denis Burkitt's recognition of a novel African childhood lymphoma and his postulation that an infectious agent was involved in the tumor's etiology (*Nature* **194:**232–234, 1962). Since then, molecular and cellular biological and computational technologies have progressed by leaps and bounds. The advent of recombinant DNA technology opened the possibilities of genetic research more than most would have realized. Not only have the molecular tools permitted the analyses of viral mechanisms, but, importantly, they have formed the basis for discerning viral presence and, subsequently, viral involvement in an increasing number of diseases. Though in every field of science the search for further knowledge is likely to be a limitless phenomenon, the distinct goal in EBV research, namely, to gain sufficient insight into the viral–host interaction to be able to intercept the pathogenic process, is beginning to be realized.

Epstein-Barr virus research has effectively entered the postgenomic era that began with the sequencing of the first strains, cloned in the mid to late 1980s. Owing to the lack of a productive lytic system, for many years the difficulty in manipulating the viral genome virtually surpassed that of manipulating the mammalian genome. These difficulties have now largely been resolved and the use of recombinant and mini viral genomes demonstrate the continuing power of mutant analysis. Though a wealth of information on viral action has been amassed over the years, this has nevertheless been predictably dwarfed by the new questions it is possible to pose. This is evidenced by the number of laboratories working on EBV and reflected in the success of the International Association for Research on EBV and Associated Diseases and its biennial meetings (http://www.med.ic.ac.uk/ebv/home.htm). Information concerning viral infection, latency, immunogenicity, and immune evasion are being integrated into a holistic understanding of viral pathogenesis. Moreover, the decades of research on EBV provide by example a fast track for research work on newly identified, related viruses such as Kaposi's sarcoma–associated herpesvirus/human herpesvirus 8 (HHV8).

Seminal molecular techniques have opened avenues of research and several, such as Southern blotting, first described in 1975 (detailed in many variant forms in this volume), continue to yield highly informative data. With the advent of the polymerase chain reaction method in the late 1980s, assay sensitivity and detection of nucleic acids are no longer barriers to study, and new applications continue to emerge. The ability to harness homologous recombination and select for the desired products, which initiated the continuing explosion in analyzing genetic function in higher organisms by virtue of gene deletion or manipulation, has also been applied to EBV. Recently, sophisticated techniques for genomic, transcript, and proteomic comparative analyses are blooming, for which high-quality sample preparation is a prerequisite. Though these applications are not necessarily described herein, the underlying protocols for sample preparation are covered in several chapters.

All the protocols an EBV researcher could desire cannot possibly be covered in one single volume; however, we have endeavored to include many of the principal methods used and described by experts. Moreover, most of these protocols can be applied directly, or easily adapted, to address questions in fields of molecular biological research unrelated to EBV studies.

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