Won for All: How the Drosophila Genome Was Sequenced. Michael Ashburner. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press, 2006, 107 pp., $19.95, hardcover. ISBN 0-87969-802-0.

In this slim volume, the well-known *Drosophila* expert Michael Ashburner provides a very personal account of the events surrounding the annotation of the sequence of the genome of the small fly, *Drosophila melanogaster*. The book, written in the style of a "nonfiction novel", is amusing, insightful, and, at times, irreverent. The author's liberal use of footnotes provides not only a bibliography, but also timely explanations of acronyms, clarification of the Latin names of all animals that stray into the text, advice on restaurants, and identification of the key players who, more often than not, are referred to only by their the first names (Jim, Gene, Craig, Gerry, Suzi, Uncle Syd, et al.).

The narrative covers the 2-year period from May 1998 to March 2000 and exploits the author's central position in the annotation of the sequence of the *Drosophila* genome. The text is illustrated by Lewis Miller's portraits of many of the scientists involved in this story.

In 1995, publicly funded groups in the United States and Europe set out to sequence *Drosophila*. However, the entry of Celera Genomics into this field in 1998, and their announcement that they would sequence this genome using the shotgun sequencing strategy as a warm-up for sequencing of the human genome, caused considerable consternation. The outcome was a collaboration between academia and Celera Genomics. The text unfolds an insider's view of this collaboration, which culminated in an intense 2-week effort (the "jamboree") by 60 dedicated scientists gathered at Celera Genomics in Gaithersburg, Maryland, in November 1999. The tensions between the open-access mindset of academics and the restricted-access strategies of the commercial world are exposed.

The style is refreshing and fast-paced, relating the story in a brief 4 chapters. An epilogue by R Scott Hawley and an afterword by Ethan Brier provide perspective on the importance of this sequencing saga, which would turn out to be a prelude to the much anticipated announcement of the draft sequence of the human genome in February 2001.

Sequencing of nucleic acids underscores modern day genetics and molecular diagnostics. The origins of this important technology have been captured in the Smithsonian videohistory collection, available at http://www.si.edu/archives/ihd/videocatalog/9549.htm. This book provides another view of the history of sequencing as told by a key participant in the annotation of the genome of an organism that is an important model system.

Larry J. Kricka

Hospital of the
University of Pennsylvania
Philadelphia, PA

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Proteins of the Cerebrospinal Fluid: Analysis and Interpretation in the Diagnosis and Treatment of Neurological Disease, Second Edition. Edward J. Thompson. London: Elsevier Academic Press, 2005, 332 pp., $149.95, hardcover. ISBN 0-12-369369-1.

With a comprehensive collection of references spanning the period from 1950 to 1988, the first edition of this book documented the roots of protein analysis in cerebrospinal fluid (CSF). In this new edition, which has 220 new references, the author emphasizes qualitative electrophoresis methods in CSF analysis and describes their clinical relevance, particularly for diagnosis of multiple sclerosis, which historically has been closely associated with the development of CSF analysis. In several chapters, the author describes blood–CSF barrier models, sources of CSF proteins, and qualitative differences between serum- and brain-derived protein species. The appendix offers technical details of methods such as isoelectric focusing for detection of oligoclonal IgG bands. A cross-index of references helps the reader locate details of the different topics and protein species described.

Like the previous edition, this updated version presents different approaches to protein data interpretation (in particular, IgG concentrations) to differentiate between brain- and blood-derived protein fractions in CSF. Unfortunately, the author still focuses on the older models of blood–CSF barrier function ("serum leak"), while struggling with the models derived from current understanding of biophysics and protein dynamics. For example, the empirical fit of the largest set of patient data ever published in the field, supported by the only biophysically derived theory explaining barrier function for blood-derived proteins as well as the dynamics of brain-derived proteins, is described as "mathematical manipulation to try to make sense". Corresponding references are cited, but this new concept, which is relevant for normal and pathologic CSF, is not at all integrated into the text. The obvious deficits in biophysics terminology (filtration is used instead of diffusion, as are nonbiophysical terms such as "percentage transfer" gaining central relevance) lead to many wrong descriptions and conclusions, particularly in regard to blood–CSF barrier selectivity and CSF flow-related dynamics of brain proteins. As a result, sophisticated discussion of analytical approaches, such as laboratory-supported differential diagnosis based on disease-related quantitative analysis of immunoglobulin response patterns (www.horeiber.de), is precluded, and the book's relevance is limited.

Thus, the wording in the subtitle of the 2nd edition, "Analysis and Interpretation . . .", may be misleading, whereas the subtitle of the first edition, "A Biochemical Approach", would still hold. Nonetheless, this book is a relevant introduction to the origins of CSF protein analysis. Detailed information about diagnostically relevant proteins and the history of their evaluation are presented with a satisfying, competent descrip-