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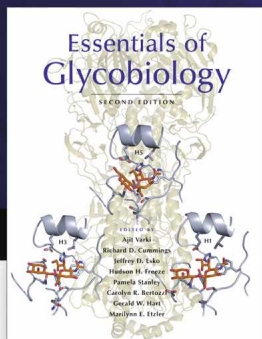
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Published in October 2008, 784 pp., illus., glossary, study guide, index

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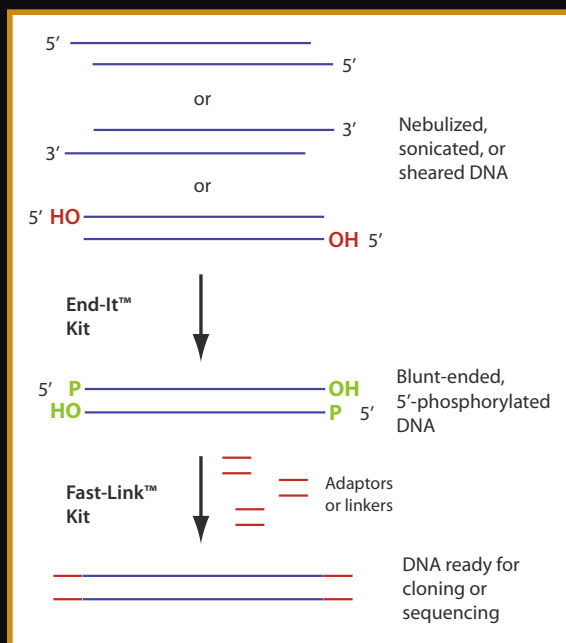
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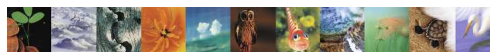
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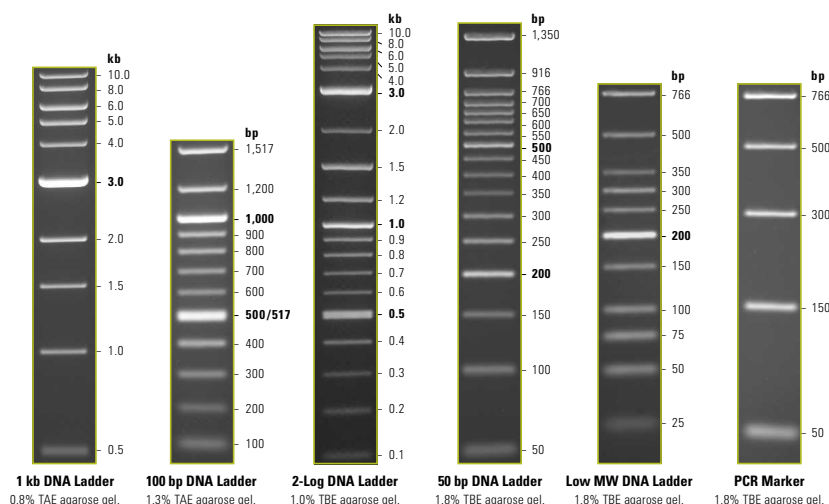
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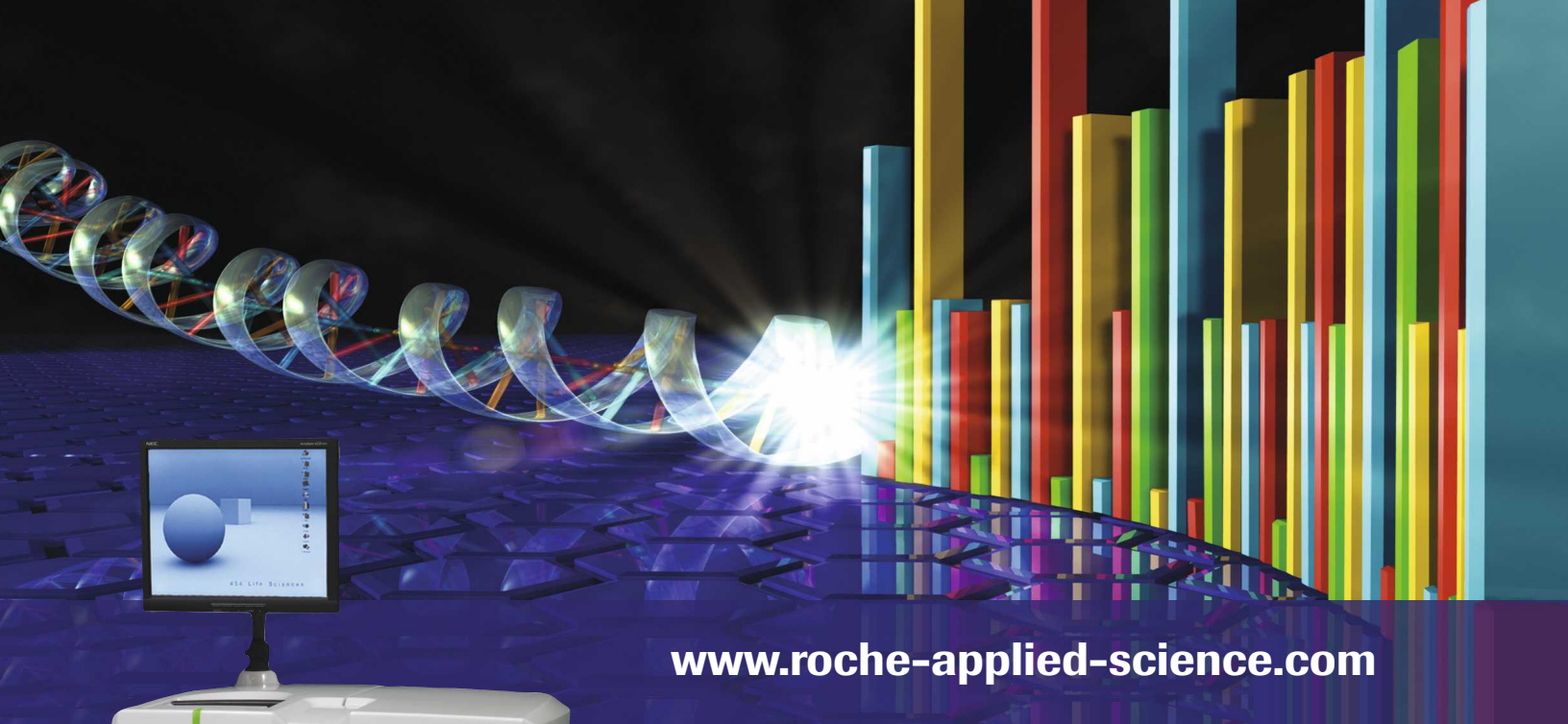


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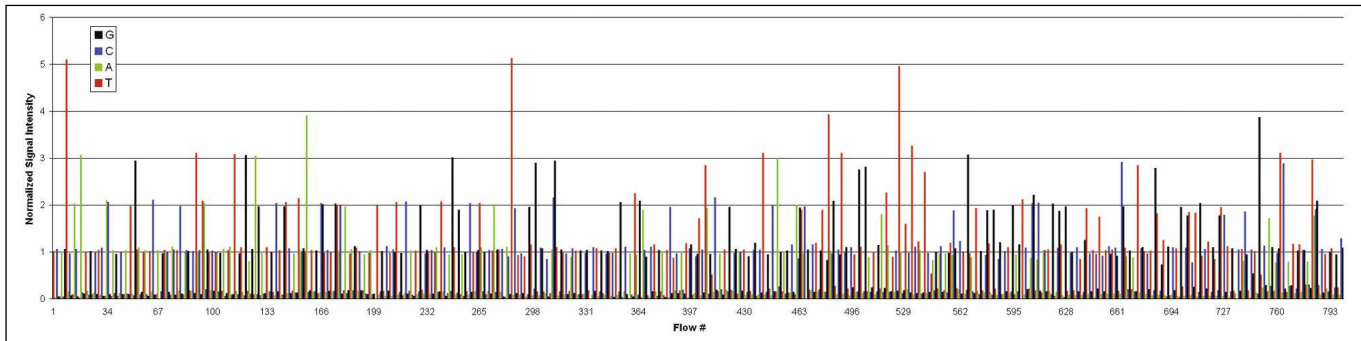
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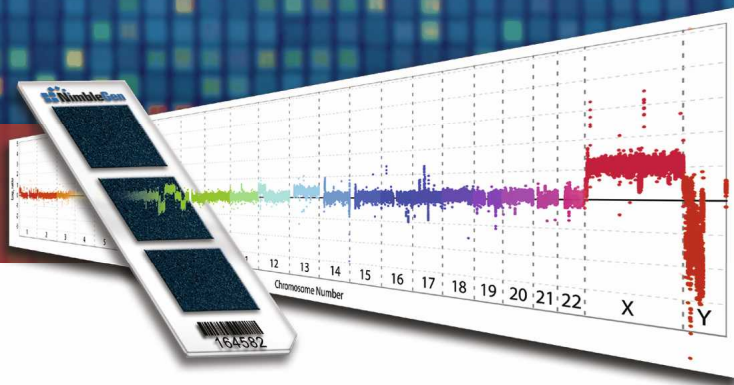
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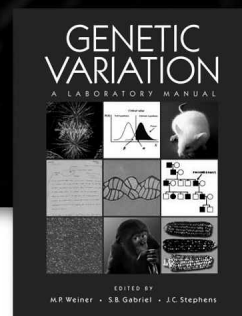
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GENETIC VARIATION

A Laboratory Manual



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Genetic Variation: A Laboratory Manual is the first compendium of protocols specifically geared towards genetic variation studies, and includes thorough discussions on their applications for human and model organism studies. Intended for graduate students and professional scientists in clinical and research settings, it covers the complete spectrum of genetic variation—from SNPs and microsatellites to more complex DNA alterations, including copy number variation. Written and edited by leading scientists in the field, the early sections of the manual are devoted to study design and generating genotype data, the use of resources such as HapMap and dbSNP, as well as experimental, statistical, and bioinformatic approaches for analyzing the data. The final sections include descriptions of genetic variation in model organisms and discussions of recent insights into human genetic ancestry, forensics, and human variation.

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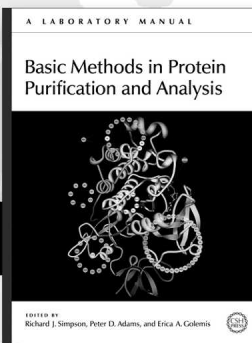
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A Laboratory Manual



Edited by Richard J. Simpson, *Joint ProteomicS Laboratory (JPSL) of the Ludwig Institute for Cancer Research* and the *Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia*, Peter D. Adams, *Fox Chase Cancer Center, Philadelphia*, and Erica A. Golemis, *Fox Chase Cancer Center, Philadelphia*

Understanding how proteins function is an essential part of many biological research endeavors. The complexity and sheer number of proteins in a cell are impediments to identifying proteins of interest or purifying proteins for function and structure analysis. Thus, reducing the complexity of a protein sample or in some cases purifying a protein to homogeneity is necessary. The latest manual in the Basic Methods series contains a collection of convenient and easy to use protein purification protocols along with a sampling of dependable methods for assessing protein–protein interactions. The protocols are supported by background information to assist researchers in understanding how the purification methods work and how to optimize and troubleshoot the methods.

The collection of essential methods found in *Basic Methods in Protein Purification and Analysis* is mainly drawn from the popular manuals *Proteins and Proteomics*, *Purifying Proteins for Proteomics*, and *Protein–Protein Interactions*, 2nd Ed. In addition to protocols for purification using gel electrophoresis and column chromatography, this book contains tested methods for preparing cellular and subcellular extracts—a critical and often neglected step in successful protein purification. Rounding out the manual are methods for characterizing protein–protein interactions, an extensive appendix of essential methods for quantifying protein concentration, stabilizing and storing proteins, concentrating proteins, and immunoblotting. Finally, there is a new chapter on a method complementary to gel electrophoresis and chromatography: *in silico* analysis of genomic and proteomic databases.

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