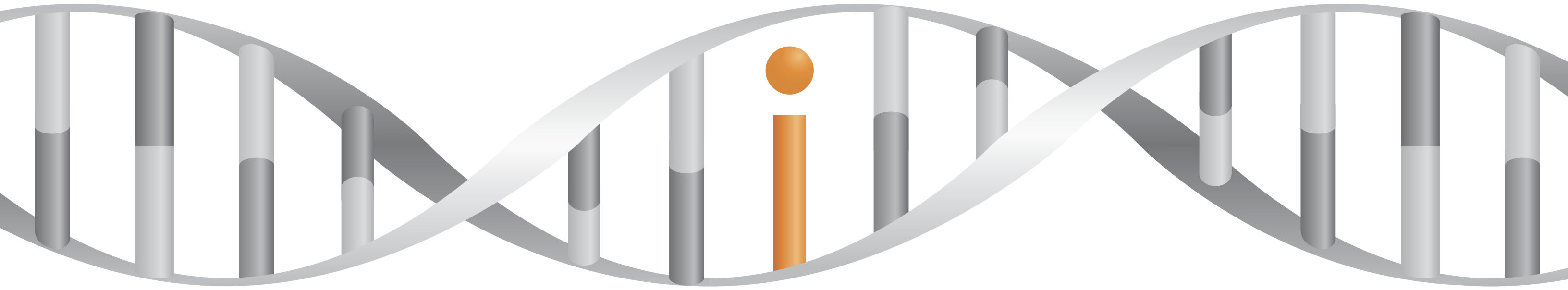

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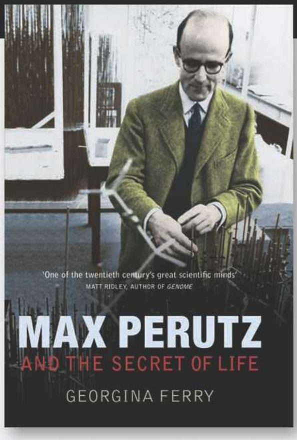

> "In science, truth always wins."
> —Max Perutz

By Georgina Ferry

Few scientists have thought more deeply about the nature of their calling and its impact on humanity than Max Perutz (1914-2002). Born in Vienna, Jewish by descent, lapsed Catholic by religion, he came to Cambridge in 1936, to join the lab of the legendary Communist thinker J.D. Bernal. There he began to explore the structures of the molecules that hold the secret of life. In 1940, he was interned and deported to Canada as an enemy alien, only to be brought back and set to work on a bizarre top secret war project. In 1947, he founded the small research group in which Francis Crick and James Watson discovered the structure of DNA: under his leadership it grew to become the world-famous Laboratory for Molecular Biology. Max himself explored the protein hemoglobin and his work, which won him a Nobel Prize in 1962, launched a new era of medicine, heralding today's astonishing advances in the genetic basis of disease.

Max Perutz's story, wonderfully told by Georgina Ferry, brims with life. It has the zest of an adventure novel and is full of extraordinary characters. Max was demanding, passionate and driven but also humorous, compassionate and loving. Small in stature, he became a fearless mountain climber; drawing on his own experience as a refugee, he argued fearlessly for human rights; he could be ruthless but had a talent for friendship. An articulate and engaging advocate of science, he found new problems to engage his imagination until weeks before he died aged 88.

About the author: Georgina Ferry is a former staff editor on *New Scientist*, and contributor to BBC Radio 4's *Science Now*. Her books include the acclaimed biography *Dorothy Hodgkin: A Life* (1998); *The Common Thread* (2002, with Sir John Sulston) and *A Computer Called LEO* (2003). She lives in Oxford.

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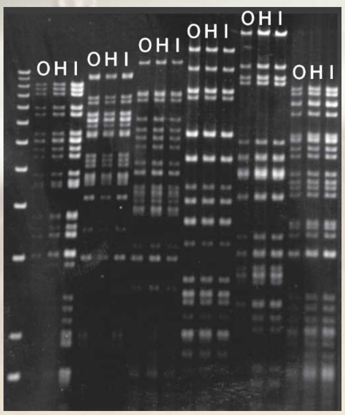

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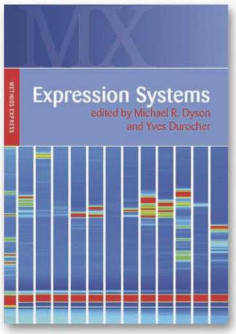

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The book takes the reader through how to make an informed choice of appropriate system, taking into account the protein target, the time involved, the ultimate use of the expressed protein, and the laboratory equipment required. It also provides step-by-step methods for each system. In addition, the book describes the optimisation of expression strategies, expression engineering using ribosome display, and how to select protein variants with improved expression.

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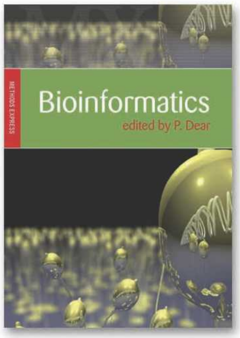

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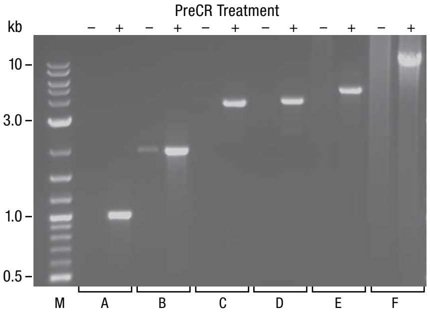

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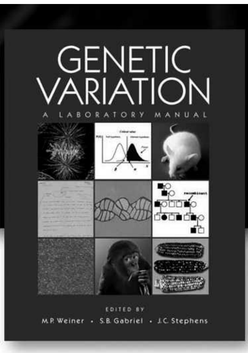
GENETIC VARIATION

A Laboratory Manual



Edited by Michael P. Weiner, *RainDance Technologies, Inc., Guilford, Connecticut*;
Stacey B. Gabriel, *The Broad Institute, Massachusetts Institute of Technology, Cambridge,*
and J. Claiborne Stephens, *Motif BioSciences, New York*

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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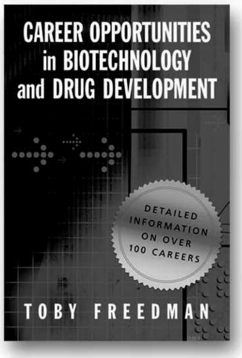

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The Department of Biostatistics at Harvard School of Public Health (HSPH), is seeking an outstanding candidate for a tenure-track faculty position in Bioinformatics/Computational Biology at the level of Assistant or Associate Professor. The successful candidate would join an active group at HSPH developing novel computational and statistical methods, and conduct collaborative research with clinical and basic scientists at Harvard University and its affiliated medical centers. She/he is expected to play a vital leadership role in expanding the quantitative science research and educational programs at HSPH in bioinformatics and computational biology and its related fields. Candidates should have doctoral degree and a demonstrated record of achievement; candidates in all areas of computational biology, bioinformatics and statistical science are encouraged to apply. Please send a letter of application, including a statement of current and future research interests, a curriculum vitae, sample publications, and the names of three referees to the address below. Applicants should ask their three referees to write independently to this address.

Computational Biology Junior Faculty Search Committee
Department of Biostatistics
Harvard School of Public Health
655 Huntington Avenue, 4th Floor
Boston, MA 02115

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