In *The Strongest Boy*’s title essay, Reilly tells the story of a German newborn whose strangely muscled physique is due to a frame shift mutation in the aforementioned muscle inhibitor, myostatin. As a result, his 7-month-old thighs look like those of a miniscule Lance Armstrong. His mother, a heterozygote and professional athlete, already has hidden him from public view, shielding him from scrutiny undue a boy who is, for all his extraordinary muscle mass, just a boy. This wise decision would be applauded by the Harvard political philosopher Michael Sandel, whose brief work *The Case against Perfection* attempts to articulate why we might find Reilly’s brave new world so distasteful.

Sandel believes genetic enhancement has the potential to capitalize on our insecurities. His discussion of the rise of off-label prescriptions of human growth hormone show that parents may jeopardize their children’s health and safety to help them fit some fantasy of normal. For Sandel, what should scare us most about genetic enhancement of human beings is that this practice is an extension — a mutation, if you will — of a pre-existing desire to cure, embellish, and fix ourselves into people who are less vulnerable to disease, more competitive, and better overall. Genetic technologies may allow those with the means to act out our neuroses — that our children should be the fastest, tallest, and smartest — which society should not systematically enable, lest we forget about unconditional love and acceptance of one’s neighbor, differences and all.

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_The Strongest Boy_ by Peter Reilly, Houghton Mifflin Harcourt; 2008, 192 pp. $21.99, Hardcover. ISBN: 039572271X.

**Won For All: How the Drosophila Genome Was Sequenced.** By Michael Ashburner. Woodbury, New York: Cold Spring Harbor Laboratory Press; 2006, 100 pp. $19.95, Hardcover. ISBN: 978-0879698027.

_Won For All: How the Drosophila Genome Was Sequenced_ is a personal narrative about a very important time in genomics by an equally important person — Michael Ashburner, a Drosophilist at the University of Cambridge. The time is a two-year period from 1998 to March 2000, and the topic is the collaborative genome sequencing of the fruit fly _Drosophila melanogaster_. Ashburner takes the reader on his personal journey surrounding the events that followed the announcement by Celera Genomics (a giant biotechnology company) that it would sequence the _Drosophila_ genome using a shotgun sequencing strategy as a test run to sequence the human genome. The result of this announcement is the eventual unprecedented international collaboration between academia and biotechnology involving 60 scientists. The book focuses on the differing approaches of the two camps — specifically, free open access to the genome data generated, a cause led by the author himself, vs. more restricted commercial access favored by Celera.

The author does an excellent job portraying this central tussle within an academic and biotech partnership. Using a very informal, fast-paced, and flowing writing style reflective of the rants and raves at the time of the project, the author manages to recreate his personal struggles during this time, resulting in _Won for All_ reading as a diary as opposed to a piece of science reporting. Indeed, the author describes this book as a form of self-therapy. This unrestricted reporting style gives the science and the scientists involved in the project a human face, putting on display the raw emotions involved when one is dedicated and passionate about science. Outstanding character sketches by renowned artist Lewis Miller further help this cause.

Readers in search of more technical information and the history of _Drosophila_ as a model organism beyond the social interactions among the scientists involved need not look any further than the book itself. Indeed, the postscripts by Scott Hawley and Ethan Bier, plus the generous footnotes throughout the main text, address these areas and underline the relevance of the _Drosophila_ sequencing project to the success of all subsequent sequencing projects.
All in all, *Won for All* is for the general reader and should interest anyone wanting a glimpse into modern science with an intimate look at the politics, ethics, principles, theory, and advancement that make science what it is today.

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*Genomics, Proteomics and Bioinformatics*. By A. Malcolm Campbell and Laurie J. Heyer. 2nd edition. San Francisco: Benjamin Cummings; 2006, 464 pp. $98.80 Paperback. ISBN: 978-0805382198.

*Genomics, Proteomics and Bioinformatics* is a guided tour to the new world of -omics. In contrast with most other books on the subject, the work by Campbell and Heyer invites the reader to walk the walk by following a problem-based approach. The descriptive chapters are logically constructed and carefully blended with the case studies, resulting in stimulating and scientifically enriching reading — it is Dr. House on paper.

The sequencing of the human genome and the boom in high-throughput methodology led to the foundation of genomics and modern systems biology. In parallel, increased availability of reliable and fast electronic communication made large quantities of data available to the global scientific community. The need to develop competences in the critical analysis and interpretation of these large scale data sets became pivotal in many fields of biomedical sciences. This book is ideal for all people interested in joining the -omics revolution and who need a solid starting point. The text is definitely more accessible for the scientists familiar with the data and methodology, but its high readability also makes it appropriate for colleagues with clinical background. Beginning researchers and those already at an advanced stage will be pleasantly surprised that one single book adequately tackles the major foundations of both genomics and proteomics. Typically, the genome is not even discussed in the same volume as the proteome, not to mention the integration of both.

The book is divided in three parts. The first deals with the aspects of genome sequence, specifically, its acquisition and analysis. The reader will become familiarized with the essential notions of human genetics and the tools used in the generation of -omics data. Loaded with this basic and technical knowledge, the reader is then invited to take an overview of several model organisms (prokaryotes, yeast, mammals), culminating in a chapter discussing the variability of the human genome. The second part of the book is dedicated to gene expression. It describes the methodology of expression microarray analysis and its application and ends with a chapter fully devoted to proteomics. Finally, the third part approaches systems biology, attempting to integrate data from several dimensions (genomic, proteomic, etc.). Here, the most exciting aspects of the -omics revolution are given attention: single-gene circuits, a.k.a. regulation of gene expression, gene networks and network regulation. In summary, *Genomics, Proteomics and Bioinformatics* is a recommended read for those looking for a guide to the rapidly evolving fields of genomics and proteomics.

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*Genomics and Evolution of Microbial Eukaryotes*. Edited by Laura A. Katz and Debashish Bhattacharya. New York: Oxford University Press; 2008, 256 pp. $60 Paperback. ISBN: 978-0199229055.

In *Genomics and Evolution of Microbial Eukaryotes*, editors Laura Katz and Debashish Bhattacharya guide the reader through an introductory overview of the vast world of pro-