

## Speakers

**Patrick O. Brown, Ph.D., M.D.**

Howard Hughes Medical Institute  
and Department of Biochemistry  
Stanford University School of Medicine  
Stanford, California 94305-5428  
USA

- 1976 University of Chicago, B.A., with honors, Major: Chemistry
- 1980 University of Chicago, Ph.D. in Biochemistry
- 1981 University of Chicago, M.D., with honors
- 1982–1985 Resident in Pediatrics, Children's Memorial Hospital; Chicago, Illinois
- 1985–1988 Postdoctoral fellow, Department of Microbiology and Immunology, University of California
- 1988–1994 Assistant Professor, Departments of Pediatrics and Biochemistry, Stanford University School of Medicine
- 1988–1997 Assistant Investigator, Howard Hughes Medical Institute
- 1995–present Associate Professor, Department of Biochemistry, Stanford University School of Medicine
- 1997–present Associate Investigator, Howard Hughes Medical Institute

**Observing the living genome**

Following the static descriptions of genomes provided by physical mapping and sequencing, dynamic pictures of the living genome are now beginning to emerge. Diverse features of the living genome are accessible to observation using DNA microarrays. Much of the information encoded in the genome is devoted not to specifying the structure of proteins and RNA encoded by structural genes, but rather to controlling precisely when, where and in what amount genes are expressed. Indeed, the variation in each gene's expression is not only much richer than the allelic variation in its sequence, but also much more accessible to comprehensive examination on a genomic scale. The richness of the information represented in the variation in each gene's expression provides the basis for richly detailed and informative genomic maps, of a new kind. The geography represented in these maps reveals functional relationships among genes, reflecting the deep logical connection between the function of each gene and its program of expression. The maps also reveal connections between characteristic genome-wide patterns of expression and the identity, location, environment, physiological milieu, history and health of cells and tissues, reflecting the transduction of these diverse inputs by the regulatory networks that govern the expression program of the genome. In addition to variation in abundance of each gene's transcripts, variation in their translation rates and their sub-cellular localization can be observed on a genomic scale. And many other characteristics of the living genome are now accessible to observation, including its replication, recombination, and the distribution of proteins across chromosomes. Integrating these diverse new molecular pictures of genomes and organisms, and understanding the biology they reveal, is an ongoing challenge.