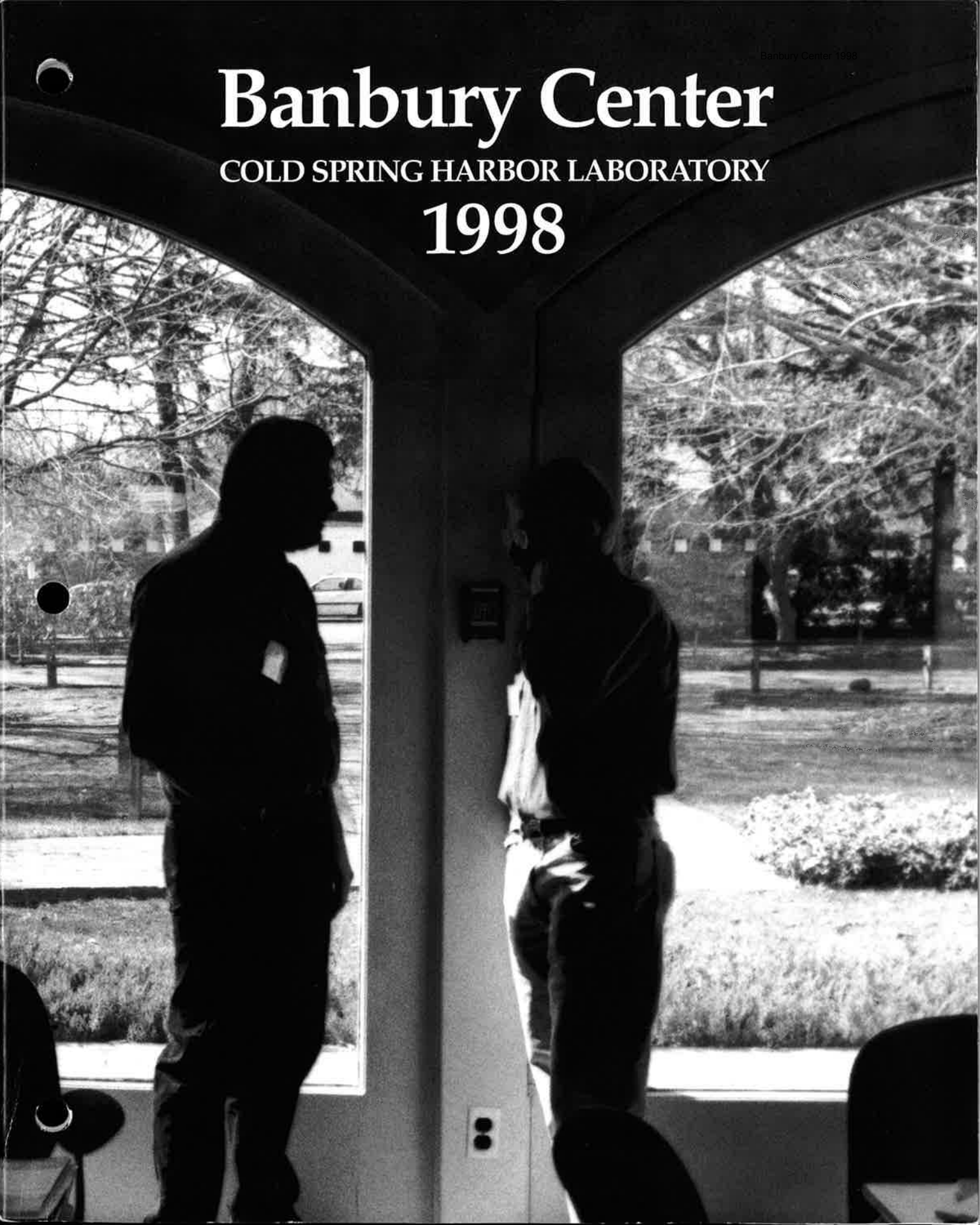
Banbury Center

COLD SPRING HARBOR LABORATORY

1998



BANBURY CENTER DIRECTOR'S REPORT

This was the 22nd year in which scientists from all over the world made their way to the beautiful estate that Charles Robertson so generously gave to Cold Spring Harbor Laboratory. And this year they made their way here in record numbers to participate in a record number of meetings. The Center was also used for meetings by Laboratory scientists and local community groups as well as for courses, so that no fewer than 40 events took place here.

Summary of Meetings and Participants

This was, indeed, a record year of 19 science meetings, 8 meetings for Laboratory-related purposes, 8 occasions when the Center was used for special meetings by local community groups, and the annual 5 neurobiology courses. There were 601 participants in the science meetings alone, of whom 474 were from the United States. Although, as usual, California, Maryland, Massachusetts, and New York accounted for more than 50% of these scientists, participants were drawn from no fewer than 36 states; 75 scientists came from Europe and our most distant visitors were from Japan and Australia. The Corporate Sponsors sent 75 scientists to the Center, and 41 scientists from other companies were invited participants.

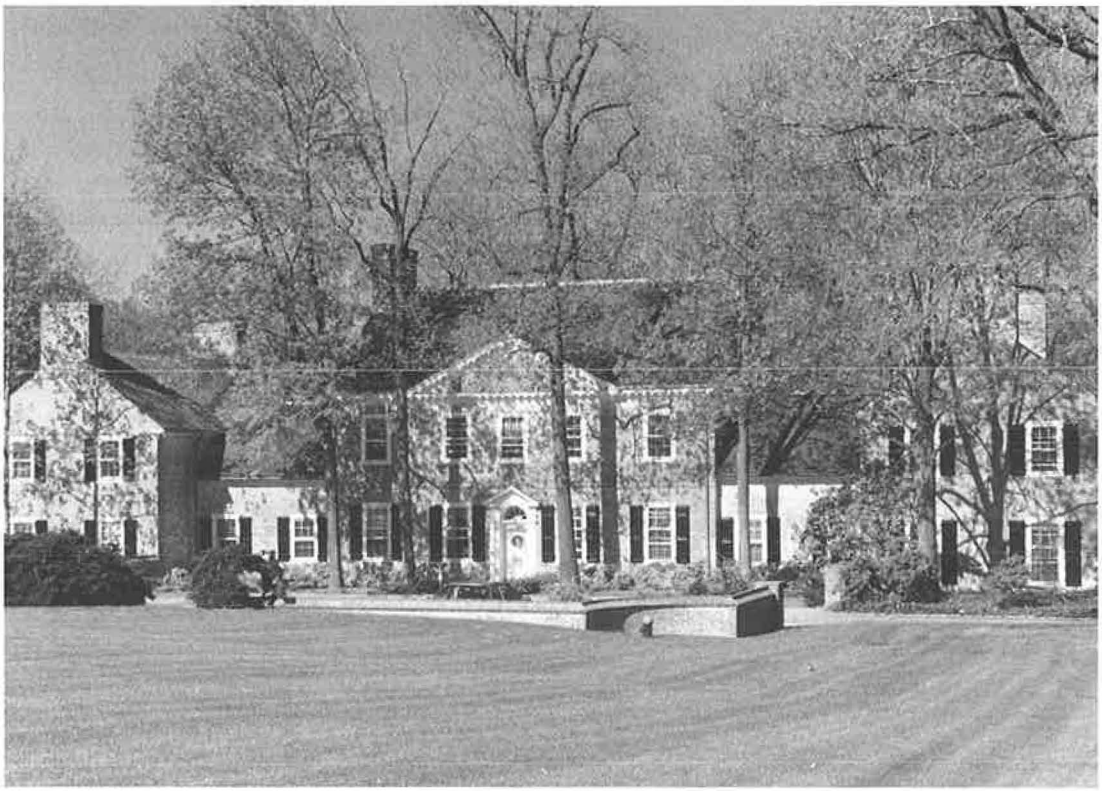
Human Genetic Disorders

We continue to hold meetings dealing with human genetic disorders and disorders in which there is likely to be a strong genetic component. Three of these meetings were designed to review critically specific research and provide guidance on what should be done next. *Superoxide Dismutase and Motor Neuron Disease* examined what is known of the role of superoxide dismutase in cells, its mechanism of action, and how it relates to cell death, and, most importantly, how useful the various animal models of ALS are for understanding the pathology of ALS and for testing therapeutic agents.

Therapeutic agents are not yet available for the treatment of Duchenne muscular dystrophy but major research is under way to exploit the fact that the muscle protein utrophin may be able to substitute for the dystrophin that is missing or nonfunctional in Duchenne muscular dystrophy. The key is to find a small molecule that will turn on the utrophin gene and that can be administered easily to patients. In *Muscle Gene Regulation and Its Therapeutic Potential*—the second in a series of meetings on this subject—we brought together experts from around the world to discuss what is known about the control of muscle gene expression. We were looking for common or special mechanisms that might provide clues as to how to turn on the utrophin gene and what sorts of molecules might work.

The third of these meetings—*Critical Issues in Marfan Research*—dealt with a very important strategic issue in all cases where advances have been made in the understanding of the genetic basis of a human disorder, namely, how to use that genetic knowledge to benefit patients. Thus, this meeting discussed not only continuing laboratory research, especially in mouse models, but also what clinically based research is needed and how new information can be used for diagnosis. Finally, there was discussion of research priorities and how collaborations might be set up to promote research.

Two other meetings in this group covered disorders where there is considerable molecular knowledge of both the genes involved and the systems affected. Because of this, researchers in these fields can begin to make rational, data-based choices of possible therapeutics. *The Molecular Basis of Asthma: Fundamental Processes with Potential Genetic and Therapeutic Targets* was particularly interesting in beginning to integrate all that is known about immunological mechanisms in asthma with the knowledge coming from the genetic analysis of the components of these systems.



Robertson House provides housing accommodations at Banbury Center.

The Molecular Physiology of Weight Regulation and Obesity meeting was equally interesting and exciting. Energy regulation has long been a field of research in physiology, but a revolution occurred some years ago when the first gene involved in obesity—leptin—was cloned. This has led to a remarkable synthesis of findings in genetics, endocrinology, and neuroendocrinology. The workshop explored what is known of leptin and its neuroendocrine control as well as the role of other molecules such as those derived from POMC (pro-opiomelanocortin).

Horse Genetics

At the same time that sequencing the human genome is forging ahead, programs have been established to do the same with animals of agricultural importance. The targeted livestock include cattle, sheep, chickens, and pigs, but one livestock animal that has not received the largesse of substantial funding is the horse. This is unfortunate not least because horses are interesting genetic animals in their own right and, through the horse-racing industry, an important economic force. The Banbury Center meeting on horse genetics was inspired by the claim that thoroughbred performance has not improved in recent years and that this failure may have a genetic basis. However, *Horse Genomics and the Genetics of Factors Affecting Horse Performance* went far beyond that one topic: It provided an occasion for evaluating the current state of horse genetics, for establishing collaborations, and for determined discussions on the future of horse genomics.

Genomics

Complete genome sequences are known for many bacteria, for parasites and yeast, and even for *Caenorhabditis elegans*, a multicellular organism. But all these millions of nucleotides are of little use unless we can identify the genes they contain and find out what the genes do. We held three techni-

cal meetings dealing with these questions, and the first was *Full-length cDNA Cloning: A Workshop on Problems and Solutions*. cDNA clones are made from mRNA that carries information from genes to sites of protein synthesis. They are very useful, representing as they do just genes without all of the sequences in chromosomal DNA that do not code for protein. Unfortunately, it is not easy to make complete cDNA clones or to make copies of all the mRNAs in a cell. Participants critically reviewed the current status of cDNA cloning and tried to identify new strategies for improving cloning. There was also a very interesting discussion of intellectual property rights that affect this work.

Finding human disease genes using mapping techniques has been very successful for disorders where one gene is involved. But it becomes increasingly difficult to do such mapping when several or even many genes may contribute to a disorder. *Large-scale Discovery and Genetic Applications of SNPs* was an in-depth look at single nucleotide polymorphisms, a relatively new tool for doing such mapping. Enthusiasts believe that SNPs will make it possible to find genes involved in complicated disorders, and although there have been some successes (e.g., in diabetes), much still needs to understood about how many SNPs will be needed, how they are to be found, and the theoretical basis for their use.

Finally, finding all of the genes in an organism will be of little use unless we can determine what they do. This has become a critical issue for those organisms for which the complete sequence is known (e.g., yeast). Beyond identifying the functions of genes, we also need to know how sets of genes interact in the life of the cell. Techniques are being developed to do this and *The Genome and Experimental Biology* reviewed a wide variety of approaches, especially those based on chip technology. One consequence of genomic-based research is that data are going to be produced at a very high rate. There was discussion of how to cope with this flood of information, which became very lively when it turned to the physicists' strategy of E-mail publishing.

Infectious Diseases

Banbury Center has long had an interest in Lyme disease and in the use of vaccines to combat infectious diseases. Our series of Lyme disease meetings shows how research in this area has changed—we now have the complete genomic sequence of *Borrelia burgdorferi*. The meeting this year dealt with a more prosaic topic but one of tremendous importance—*Laboratory Methods for the Diagnosis of Lyme Disease*. The meeting reviewed the various tests currently being used, including those based on immunological methods and those based on detecting spirochete DNA or RNA. In addition, there was considerable discussion of factors affecting the reliability of these tests. The meeting concluded with an overview of the key issues and how they might be tackled.

The goal of the Albert B. Sabin Vaccine Institute is to promote the use of vaccines. One obstacle in doing this—a problem common to many fields—is the difficulty of moving from research findings to applications in the "real world." Here, economic, social, and political factors come into play in ways not so evident in the laboratory. *From Bench to Bedside: A Colloquium on Translational Vaccine Control* was a case-based review of these problems and drew on a wide variety of vaccine developments, including vaccines directed against measles, influenza, viral hepatitis, Lyme disease, and even cancer.

Coping with Stress

It is not only human beings that feel stress. In fact, our cells lead very stressful lives and a complex metabolic system has evolved to help them cope. *Integrating Cellular Stress Responses* reviewed how cells detect and respond to a variety of stresses: heat, starvation, hypoxia, and poisoning by heavy metals, for example. The participants discussed the extent to which these challenges initiate the same or similar responses and how these responses evolved. Here is a case where the chip technology referred to above can be used to monitor all the changes in gene expression that go on in a yeast cell when it is stressed.

Our experience with boiling eggs demonstrates the effect of heat on proteins: It produces irreversible changes. And yet there are bacteria and other organisms that flourish in the boiling hot springs of Yellowstone Park or around the "black smoker" vents in the deepest oceans. How they are able to

survive there was the topic of *Biochemistry at 100°C: How Are Enzymes and Their Substrates Stabilized?* The participants came from a wide variety of backgrounds including chemistry, biophysics, biochemistry, and evolutionary biology. The former dealt with the mechanisms by which life goes on at these high temperatures and the latter discussed the controversial questions of whether these organisms are "primitive" and what they can tell us about the origins of life. We were honored to have Stanley Miller, who carried out seminal experiments on the origin of life more than 40 years ago, participate in the meeting.

The Art of Science—State and Federal Judges

The Federal Judicial Center serves as the agency for research and continuing education for judges in the federal court system. In addition, its Interjudicial Affairs Office is charged with serving as an information clearinghouse for the Center's research and education programs with state judicial systems. These two functions come together in the *Basic Issues in Science* seminars that we hold here at Banbury Center. These are not intended to give specific information on scientific issues as they come before the courts, but rather to give state and federal judges a flavor of how scientists think and carry out their research. Thus, our program includes history and philosophy of science, as well as an education in genetics. We try also to cover contemporary issues—this year, for example, Lee Silver came to Banbury to discuss human cloning.

Genetics Learning on the Web

Banbury Center and the DNA Learning Center are collaborating on a very exciting project to provide a genetics text for the lay public and high school students on the World Wide Web. Although many examples of genetics sites exist on the Web, Dave Micklos and I believe that none of them provides the information at the appropriate level or in a manner that does not intimidate. The Josiah Macy, Jr. Foundation agreed and has provided funding to support the project. Part of this funding is for workshops at Banbury Center to explore how such a site might be designed and made and to assess our progress. Thus, the meeting *Genes, Teens, and the World Wide Web* brought together science educators, Web designers, science writers, and Web scientists. We were especially pleased that Bruce Alberts, President of the National Academy of Sciences, was able to participate. He has made improving science education a major goal of the Academy.

Eugenics Source Materials on the Web

Banbury Center is also collaborating with the DNA Learning Center on another project exploiting the power of the Web to deliver information and materials that would otherwise be inaccessible. Our project, funded by the National Human Genome Research Institute, will make available to teachers, researchers, and the general public up to 1000 images on eugenics. This material is currently stored in archives in academic institutions and only a very small amount has been published in books and journals. An advisory group is helping us prepare this site and providing us with guidance about how to annotate and provide context for the materials. It is a very mixed group, including historians, geneticists, and ethicists. The group met here in September to review what we had collected and to discuss the guidelines for display. For example, should all names and other identifiers be removed? Can this be done without compromising the data? We will now go on to produce some sample pages for further review.

The J.P. Morgan/Cold Spring Harbor Laboratory Executives' Seminar

When this series of meetings began in 1986, there can have been no expectation of their remarkable success. Indeed, this year, the acceptance rate was so high that we became worried that our participants would be flowing out of the door. The meeting was remarkable also for the range of physical

dimensions covered. Entitled *Imaging from Molecules to Brains*, we began with atomic force microscopy of molecules, moved through X-ray crystallography and tracking molecules in cells, to imaging the living human brain at work on various tasks. The topic was chosen in part because of the Laboratory's increasing interest in imaging, and Leemor Joshua-Tor, David Spector, and Karel Svoboda described their work. We are very grateful to David Deming and J.P. Morgan for their continuing support of this extraordinary event.

Other Meetings

On several occasions, scientists from the Laboratory used the Center for small meetings. In addition, we are happy to make the Center available on a limited basis for use by local community groups, as the pressure of our schedule permits. In 1998, such groups included the Lloyd Harbor Conservation Board, Holiday House, and Huntington Hospital Board of Trustees.

Funding

The Corporate Sponsor Program, now in its 15th year, continues to provide funding for six Banbury Center meetings. The participating companies make good use of their spaces at Banbury Center, sending 46 scientists to our meetings. Foundation support of meetings was especially strong in 1998 with no fewer than eight foundations coming to Banbury: the ALS Foundation, the William Theodore Denslow Foundation, the Dorothy Russell Havermeyer Foundation, the National Marfan Foundation, the Merck Genome Research Institute, the Oxnard Foundation, the Albert B. Sabin Vaccine Institute, Shriners Hospitals for Children, and the Swartz Initiative for Computational Neuroscience. Federal funding came from the Federal Judicial Center; the National Heart, Lung, and Blood Institute; the National Human Genome Research Institute; and the National Institute of Allergy and Infectious Diseases. Company support for Banbury Center meetings comes for specific meetings as well as through the

Banbury Conference Center

Corporate Sponsor Program. In 1998, Glaxo Wellcome, Inc.; Immunetics; Research Genetics, Inc.; SmithKline Beecham Pharmaceuticals; and Tularik Inc. provided funding for meetings.

Other News

The most significant change to Banbury Center is the addition of the Meier House to the estate. Immediately across from the Conference Room, this house belonged to Dr. Walter and Mrs. Anne Meier, who was one of the daughters of Charles and Marie Robertson. The house has been refurbished and will provide extra accommodation for our participants. This means that the capacity of the Conference Room is now matched by the accommodation in Sammis Hall and Robertson and Meier Houses and we will not need to ferry people to and from the main Laboratory campus.

A very welcome improvement in 1998 was the upgrade of our Internet connection to a T1 line. The Web has become our primary source of information, and although 10 years ago, the fax machine revolutionized communications with organizers and participants, the impact of E-mail is far, far greater. The increased speed of the T1 line is much appreciated by participants as well, especially for genomics-related meetings where Internet access is a sine qua non of research and presentations.

Acknowledgments

It is not easy coping with over 600 scientists, and Banbury Center could not possibly sustain such a high level of activity without the energy and commitment of many people. First and foremost, Bea Toliver and Ellie Sidorenko manage the Center, dealing with all that is needed to keep things running smoothly, while Katya Davey looks after Robertson House. In addition, Bea Toliver administers the Corporate Sponsor Program that provides support for all Laboratory meetings. The surroundings of the Center make a major contribution to the ambience of the meetings, and Chris McEvoy and Andy Sauer work hard to maintain the beauty of our environment. Participants much appreciate the food at Banbury Center meetings and Jim Hope and his staff continue to meet high standards. The demand for audiovisual equipment becomes increasingly complex as computers join the traditional slide and overhead projectors. The AV team handles it all. Finally, Art Brings and his Staff in Facilities and Housekeeping look after us all year round.

Jan Witkowski

MEETINGS

Neurocomputational Strategies: From Synapses to Behavior

February 1–4

FUNDED BY **The Swartz Initiative for Computational Neuroscience**

ARRANGED BY **R. Malinow,** Cold Spring Harbor Laboratory
T. Sejnowski, The Salk Institute for Biological Studies

SESSION 1: Cellular and Molecular Mechanisms Underlying Synaptic Signaling, Synaptic Plasticity, and Axonal Pathfinding
Chairperson: T. Sejnowski, The Salk Institute for Biological Studies, San Diego, California

M. Poo, University of California, San Diego, La Jolla: Long-range propagation of LTP and LTD in neural networks.
G.J. Goodhill, Georgetown University Medical Center, Washington, D.C.: Theoretical modeling of axon guidance.
D. Willshaw, University of Edinburgh, Scotland: Competitive influences in the development of nerve connections.
R. Malinow, Cold Spring Harbor Laboratory: Silent synapses in plasticity.
Z.F. Mainen, Cold Spring Harbor Laboratory: Increase in functional AMPA receptors during LTP.
T. Bonhoeffer, Max-Planck Institute for Psychiatry, Munchen, Germany: Specificity of synaptic enhancement in the hippocampus.

SESSION 2: Spike Coding in Axons and Spike Decoding in Dendrites
Chairperson: R. Malinow, Cold Spring Harbor Laboratory

M. Wilson, University of California, Davis: The smallest unit of synaptic transmission.
K. Svoboda, Cold Spring Harbor Laboratory: Dendritic function in neocortex in vivo.
F. Gabbiani, California Institute of Technology, Pasadena: Multiplying with neurons.
D. Johnston, Baylor College of Medicine, Houston, Texas: Dendritic computations.
G.M. Shepherd, Yale University School of Medicine, New Haven, Connecticut: Action potential propagation in dendrites—Its significance for information processing in the olfactory system.
I. Segev, Hebrew University, Jerusalem, Israel: The noisy neuron.

P. Konig, T. Sejnowski, N. Kopell, A. Destexhe, K. Svoboda

SESSION 3: Thalamocortical Interactions and Short-term Synaptic Plasticity
Chairperson: R.E. Shrock, State University of New York, Stony Brook

S.M. Sherman, State University of New York, Stony Brook: Functional organization of thalamus and thalamocortical interactions.
A. Destexhe, Laval University, Quebec, Canada: How corticothalatic feedback and intrathalatic inhibition cooperate to synchronize oscillations over large cortical territories.
P.R. Adams, State University of New York, Stony Brook: The thalamocortical algorithm.
D.A. McCormick, Yale University School of Medicine, New Haven, Connecticut: Network and computational implications of short- and long-term changes in thalamic and cortical activity.
M.V. Tsodyks, Weizmann Institute of Science, Rehovot, Israel: Dynamics of neocortical circuits—Models and experiments.
L.F. Abbott, Brandeis University, Waltham, Massachusetts: The role of short-term synaptic plasticity in cortical processing.

SESSION 4: Mechanisms for Response Properties and Synchronization of Cortical Neurons
Chairperson: P.R. Adams, State University of New York, Stony Brook

D.L. Ferster, Northwestern University, Evanston, Illinois: Assembly of receptive fields in cat visual cortex.
K.D. Miller, University of California, San Francisco: Ocularly matched, contrast-invariant orientation tuning in cat V1: Development and mature circuitry.
G.G. Turrigiano, Brandeis University, Waltham, Massachusetts: Activity-dependent scaling of synaptic strengths in neocortical networks.
P. Konig, Institute for Neuroinformatics, Zurich, Switzerland: Is synchronization of neuronal activity relevant for behavior?
R.D. Traub, Birmingham University School of Medicine, United Kingdom: Synaptic plasticity induced by 40 Hz oscillations.
N. Kopell, Boston University, Massachusetts: Mechanisms for synchronization (and desynchronization) in networks of neurons.
R.E. Shrock, State University of New York, Stony Brook: Synaptic plasticity in neural networks modeling brain function.

SESSION 5: Neural Assemblies and Neural Population Codes
Chairperson: L.F. Abbott, Brandeis University, Waltham, Massachusetts

D. Horn, Tel Aviv University, Israel: Memory maintenance via neuronal regulation.
D.W. Tank, Bell Laboratories, Lucent Technologies, Murray Hill, New Jersey: Cellular and circuit mechanisms of persistent neural activity.
W.B. Kristan, University of California, San Diego: Population codes for directed behaviors in simple nervous systems.
T. Sejnowski, The Salk Institute for Biological Studies, San Diego, California: Limits on the accuracy of population codes.

SESSION 6: Whither Computational Neuroscience?
Discussion Leader: T. Sejnowski, The Salk Institute for Biological Studies, San Diego, California

Superoxide Dismutase and Motor Neuron Disease

February 22–25

FUNDED BY **Amyotrophic Lateral Sclerosis Association**

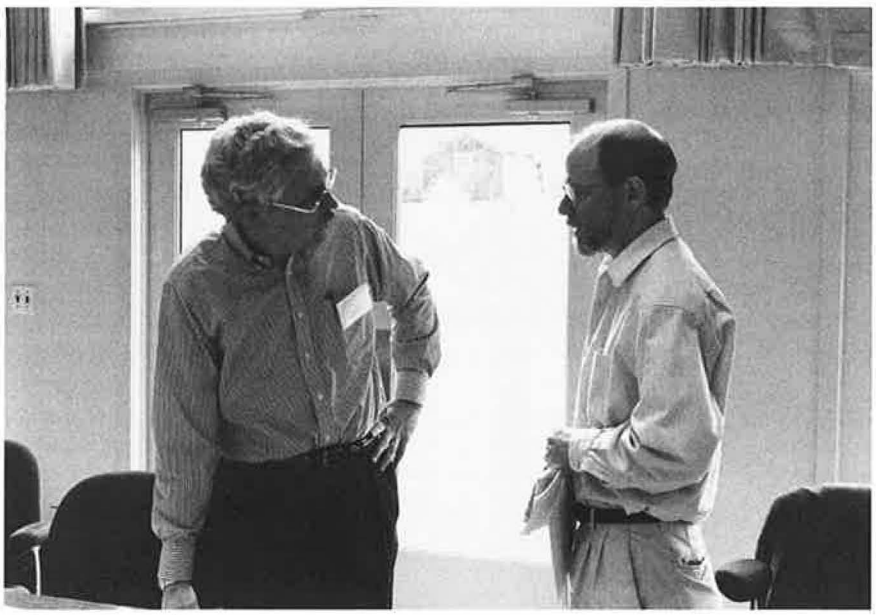
ARRANGED BY **R.H. Brown,** Massachusetts General Hospital
R. Horvitz, Massachusetts Institute of Technology

SESSION 1: Superoxide Dismutase—Structure and Related Issues
Chairperson: R.H. Brown, Massachusetts General Hospital, Charlestown

R.H. Brown, Massachusetts General Hospital, Charlestown: Introduction to ALS and SOD1—WT and mutant.
I. Fridovich, Duke University Medical Center, Durham, North Carolina: A superoxide-dependent proxidase activity of the H48Q variant.
L.J. Hayward, Massachusetts General Hospital-East, Boston: Introduction to ALS and SOD1—WT and mutant.
P.J. Hart, University of California, Los Angeles: Atomic structure of human SOD and effect of FALS mutations on this structure.
V.S. Culotta, Johns Hopkins University, School of Hygiene and Public Health, Baltimore, Maryland: The role of copper chaperone for superoxide dismutase.

SESSION 2: Superoxide Dismutase—Catalytic and Noncatalytic Mechanisms
Chairperson: J.S. Valentine, University of California, Los Angeles

J.S. Valentine, University of California, Los Angeles: The abnormal copper chemistry of ALS-mutant CuZnSODs.
E.R. Stadtman, National Heart, Lung, and Blood Institute, NIH, Bethesda, Maryland: Increased peroxidation.
M.B. Yim, National Heart, Lung, and Blood Institute, NIH, Bethesda, Maryland: Increased peroxidation.
J.P. Crow, University of Alabama at Birmingham: Aberrant metal binding by SOD mutants and possible functional consequences.
M.F. Beal, Massachusetts General Hospital, Boston: Oxidative pathology in ALS.
C. Kunst, Eleanor Roosevelt Institute, Denver, Colorado: Aberrant protein binding.
A.L. Goldberg, Harvard Medical School, Boston, Massachusetts: Selective degradation of abnormal proteins—Proteasome inhibitors and protection against cell damage.
K.J. Davies, University of Southern California, Los Angeles: Protein aggregation/recycling.



R. Brown, R. Horvitz

SESSION 3: Superoxide Dismutase—Cell Death Activation
Chairperson: H.R. Horvitz, HHMI, Massachusetts Institute of Technology, Cambridge

H.R. Horvitz, HHMI, Massachusetts Institute of Technology, Cambridge: Overview of programmed cell death.
C.M. Troy, College of Physicians & Surgeons of Columbia University, New York: Caspase specificity in different models of neuronal cell death.
R.P. Roos, University of Chicago, Illinois: Mechanisms of FALS-associated neuronal death and rescue.
D.A. Figlewicz, University of Rochester Medical Center, New York: Pathways of cell death in mutant–SOD-expressing spinal motor neurons.
R.M. Friedlander, Massachusetts General Hospital, Boston: Mechanisms and modulation of the ICE cell death cascade.
S. Przedborski, Columbia University, New York: (1) Programmed cell death. (2) Oxidative stress.
D.E. Bredesen, The Burnham Research Institute, La Jolla, California: Protein abnormalities in motor neuron diseases.

SESSION 4: Animal Models for ALS and Other Neurodegenerative Diseases
Chairperson: D. Cleveland, University of California, San Diego, La Jolla

M. Gurney, Pharmacia and Upjohn, Kalamazoo, Michigan: Excess in vivo free radical production in FALS transgenic mice.
D. Cleveland, University of California, San Diego, La Jolla: Mechanism of FALS-linked SOD1 mutant-mediated disease in mice.
D.L. Price, The Johns Hopkins University School of Medicine, Baltimore, Maryland: Models of ALS and other neurodegenerative disorders.
J.P. Phillips, University of Guelph, Ontario, Canada: Targeted expression of normal and FALS human SOD in motor neurons of wild-type and SOD-Null mutants of *Drosophila*.
S.W. Davies, University College London, United Kingdom: Neuronal intranuclear inclusions and trinucleotide repeat disease.

SESSION 5: Non-SOD1 ALS and Other Neurodegenerative Diseases
Chairperson: K.H. Fischbeck, University of Pennsylvania Medical School, Philadelphia

R.H. Brown, Massachusetts General Hospital, Charlestown: Other ALS genes.
K.H. Fischbeck, University of Pennsylvania Medical School, Philadelphia: Spinal and bulbar muscular atrophy (Kennedy's disease).
A.H.M. Burghes, Ohio State University, Columbus: Spinal muscular atrophy/SMN.

SESSION 6: General discussion: Future Research

Participants during meeting break.

Horse Genomics and the Genetics of Factors Affecting Horse Performance

March 8–11

FUNDED BY **The Dorothy Russell Havemeyer Foundation, Inc.**

ARRANGED BY **D. Antczak,** Cornell University
E. Bailey, University of Kentucky

SESSION 1: Background
Chairperson: W.R. Allen, University of Cambridge, United Kingdom

D.F. Antczak, Cornell University, Ithaca, New York and E.F. Bailey, University of Kentucky, Lexington: Introduction.
E.G. Cothran, University of Kentucky, Lexington: Genetic variability in the horse.

SESSION 2: Determinants of Performance
Chairperson: E.F. Bailey, University of Kentucky, Lexington

J.R. Rooney, Queenstown, Maryland: Structural and functional conformation and lameness.
S.G. Kamerling, Louisiana State University, Baton Rouge: Equine performance: Tests and targets.
T. Ivers, Equine Racing Systems, Inc. Washougal, Washington: Nongenetic factors in racehorse performance.

SESSION 3: Performance: What It Is: How To Measure It
Chairperson: D.F. Antczak, Cornell University, Ithaca, New York

E.P. Cunningham, Trinity College, Dublin, Ireland: Estimates of heritability and genetic gain in thoroughbreds.

COMMENTARIES

J. Leimbach, West Chester, Pennsylvania: Signs of inbreeding depression in the thoroughbred. Pedigree analysis. Mapping on full-sibling horse reference families.
A. Porter, Alan Porter Pedigree Research, Lynbrook, New York: The way the racing/breeding community recognizes the leading performers (the social divide—stakes winners and the rest).

J. Witkowski, E. Bailey, D. Antczak

SESSION 4: Horse Genomics

A. Chakravarti, Case Western Reserve University, Cleveland, Ohio: Problems and strategies of complex trait analysis.
A.T. Bowling, University of California, Davis: Synteny map.
M. Binns, Animal Health Trust, Suffolk, United Kingdom: Mapping on full-sibling horse reference families.
E.F. Bailey, University of Kentucky, Lexington: Status of the International Gene Mapping Workshop for the Horse: Completion of Phase I.
L.C. Skow, Texas A&M University College of Veterinary Medicine, College Station: Development of anchored type II markers in the horse map.

SESSION 5: Horse Genetics
Chairperson: S.J. O'Brien, National Cancer Institute, Frederick, Maryland

D.F. Antczak, Cornell University, Ithaca, New York: The maternal grandsire effect: Does it exist, and could it be caused by genomic imprinting.
E.P. Cunningham, Trinity College, Dublin, Ireland: Inbreeding and fertility in thoroughbreds.
S. Ohno, City of Hope, Duarte, California: The rule of mitochondrial inheritance dictates Eclipse and Matchem (two foundation sires of the racing thoroughbred) shared the identical mitochondrial sequence.
S. Valberg, University of Minnesota, St. Paul: Clinical application of equine genetics to neuromuscular disorders.
J. Mickelson, University of Minnesota, St. Paul: Genetic basis of the overo lethal white foal syndrome.
L.D. Van Vleck, University of Nebraska, Lincoln: Issues involved with improving quantitative traits such as racing ability.

SESSION 6: Genetics In Other Species
Chairperson: S. Ohno, City of Hope, Duarte, California

S.J. O'Brien, National Cancer Institute, Frederick, Maryland: Comparative genomics in mammals.
S.C. Heath, Rockefeller University, New York: Linkage analysis for large complex pedigrees.
M. Neff, University of California, Berkeley: From cottage industry to community: Canine molecular genetics.

SESSION 7: Future Developments—Scientific and Policy
Discussion Leaders: D.F. Antczak, Cornell University, Ithaca, New York, and **E.F. Bailey,** University of Kentucky, Lexington

Presentation during a meeting.

Full-length cDNA Cloning: A Workshop on Problems and Solutions

March 22-25

FUNDED BY **The Merck Genome Research Institute, National Cancer Institute, and Research Genetics, Inc.**

ARRANGED BY **M.B. Soares,** University of Iowa
P. Carninci, RIKEN, Ibaraki, Japan

SESSION 1: Meeting Overview and Discussion of Issues

M.B. Soares, University of Iowa, Iowa City: Meeting overview.

SESSION 2: Quality Assessment of Full-length cDNA Libraries
Chairperson: P. Carninci, RIKEN, Ibaraki, Japan

C. Auffray, Genetique Moleculaire et Biologie du Development, Villejuif, France: Generating and analyzing full-length cDNA clones for muscle and brain-specific transcripts.
R.A. Gibbs, Baylor College of Medicine, Houston, Texas: Sequencing and sequence analysis of full-length cDNAs.
M.A. Marra, Washington University School of Medicine, St. Louis, Missouri: Sequencing and sequence analysis of full-length cDNAs.

SESSION 3: Synthesis and Selection of Full-length cDNAs I
Chairperson: W. Szybalski, University of Wisconsin Medical School, Madison

M.B. Soares, University of Iowa, Iowa City: Introductory overview.
J. Jessee, Life Technologies, Inc., Rockville, Maryland: New reverse transcriptases for cDNA synthesis.
P. Carninci, RIKEN, Ibaraki, Japan: First-strand synthesis of cDNAs by thermoactivated reverse transcriptase.
C. Schneider, National Laboratory CIB, Trieste, Italy: Strategies to select full-length cDNA copies for cloning.
J. Pelletier, McGill University, Montreal, Canada: Affinity selection of full-length cDNA: RNA product.
P. Carninci, RIKEN, Ibaraki, Japan: Full-length cDNA selection by biotinylated cap trapper.
M. Lovett, University of Texas Southwestern Medical Center, Dallas: CAP trapping as a full-length cDNA methodology.
S. Sugano, The University of Tokyo, Japan: Oligo-capping method and its use in construction of full-length cDNA libraries.
S. Kato, Sagami Chemical Research Center, Sagamihara-shi, Japan: Synthesis of full-length cDNA using a DNA-RNA oligo capping method.
N. Nomura, Kazusa DNA Research Institute, Chiba, Japan: Complete sequencing of 610 human nearly full-length cDNA clones which correspond to long transcripts.
D.B. Krizman, National Cancer Institute, Bethesda, Maryland: Analysis of transcript size from various sources of RNA.
G.G. Lennon, Gene Logic, Inc. Columbia, Maryland: Imagene: Clustering of ESTs and full-length clones.

C. Schneider, M. Soares

SESSION 4: Synthesis and Selection of Full-length cDNAs II
Chairperson: S. Weissman, Yale University School of Medicine, New Haven, Connecticut

L. Stubbs, Lawrence Livermore National Laboratory, California: Constructing libraries with large inserts using size-selected mouse cDNA.

M.B. Soares, University of Iowa, Iowa City: cDNA synthesis and cloning from size-fractionated mRNA.

SESSION 5: Critical Issues Pertaining to Cloning and Amplification of Full-length cDNAs: From Single Cells to Bulk Tissues I
Chairperson: S. Weissman, Yale University School of Medicine, New Haven, Connecticut

W. Szybalski, University of Wisconsin Medical School, Madison: Introductory overview.

K.W. Beisel, Boys Town National Research Hospital, Omaha, Nebraska: Construction of cDNA libraries from single cells.

D.B. Krizman, National Cancer Institute, Bethesda, Maryland: Construction of cDNA libraries from a few thousand cells derived from microdissected tissues.

M. McClelland, Sidney Kimmel Cancer Center, San Diego, California: Critical issues pertaining to PCR amplification of full-length cDNAs.

F.S. Hagen, Icogen Corporation, Redmond, Washington: Full-length representative cDNA libraries.

M. Metzker, Merck Genome Research Institute, West Point, Pennsylvania: Full-length cloning and sequencing at Merck.

SESSION 6: Critical Issues Pertaining to Cloning and Amplification of Full-length cDNAs: From Single Cells to Bulk Tissues II
Chairperson: R.A. Gibbs, Baylor College of Medicine, Houston, Texas

W. Szybalski, University of Wisconsin Medical School, Madison: Development of conditionally amplifiable pBAC vectors for cloning of full-length cDNAs.

M.B. Soares, University of Iowa, Iowa City: Full-length normalized libraries. Are they needed? Can they be constructed with existing methods?

V. Prasad, Albert Einstein College of Medicine, Bronx, New York: Factors affecting processivity and fidelity of RT.

S. Weissman, Yale University School of Medicine, New Haven, Connecticut: cDNA display from small numbers of hematopoietic cells.

S. Wiemann, German Cancer Research Center, Heidelberg: Identification and characterization of full-length cDNA.

SESSION 7: Toward the Development of a Unigene Set of Full-length cDNAs
Chairperson: R.A. Gibbs, Baylor College of Medicine, Houston, Texas

J.R. Hudson, Research Genetics, Inc., Huntsville, Alabama: Clone distribution, availability, and intellectual property.

SESSION 8: Revisiting the Critical Issues: Critical Overview, Coordination, and Future Planning
Chairperson: M. Boguski, National Center for Biotechnology Information, NLM, Bethesda, Maryland

S. Weissman, Yale University School of Medicine, New Haven, Connecticut: A critical overview.

M.J. Finley Austin, Merck Genome Research Institute, West Point, Pennsylvania: Coordination among different public and private institutions.

R.L. Strausberg, National Cancer Institute, Bethesda, Maryland: The Cancer Genome Anatomy Project: Coordination challenges. What have we learned from CGAP that could facilitate this project?

E.A. Feingold, National Human Genome Research Institute, Bethesda, Maryland: Role of NHGRI.

N. Nomura, Kazusa DNA Research Institute, Japan: Proposal for cDNA symposiums in Kazusa.

Round Table Discussion on Funding Interests/Opportunities

The Molecular Basis of Asthma: Fundamental Processes with Potential Genetic and Therapeutic Targets

March 29–April 1

FUNDED BY **The William Theodore Denslow Foundation, with additional support from the National Heart, Lung, and Blood Institute, NIH, Tularik, Inc., and private contributions**

ARRANGED BY **J.M. Drazen,** Brigham and Women's Hospital
S.B. Liggett, University of Cincinnati College of Medicine

Goals of Conference:
S.B. Liggett, University of Cincinnati College of Medicine

SESSION 1: Interlukin 5
Chairperson: C.J. Sanderson, TVW Telethon Institute for Child Health Research, Perth, Australia

J. Tavernier, University of Gent Faculty of Medicine, Belgium: Expression and activation of the IL-5 receptor: The close relationship between agonism and antagonism.
A.E.I. Proudfoot, Glaxo Wellcome Research & Development SA, Geneva, Switzerland: Structure-function studies of the IL-5/IL-5R interaction.
P.S. Foster, John Curtin School of Medical Research, Canberra, Australia: IL-5 and allergic airways disease as assessed in IL-5 knockout mice.
C.J. Sanderson, TVW Telethon Institute For Child Health Research, Perth, Australia: IL-5 production.
R.W. Egan, Schering-Plough Research Institute, Kenilworth, New Jersey: Biology of IL-5 blockade.

P. Foster, M. Rothenberg, L. Glimcher

SESSION 2: IL-4 and the TH2 Phenotype-basic Immunobiology
Chairperson: L.H. Glimcher, Harvard School of Public Health, Boston, Massachusetts

L.H. Glimcher, Harvard School of Public Health, Boston, Massachusetts: Transcriptional regulation of IL-4 gene expression.
W.E. Paul, National Institutes of Health, Bethesda, Maryland: IL-4 signaling mechanisms with regard to TH commitment.
R.M. Locksley, University of California, San Francisco: In vivo origins of TH2 cells in murine parasitic infestation.
R.L. Coffman, DNAX Research Institute of Molecular and Cellular Biology, Palo Alto, California: T cell development in murine models of allergic disease.
G.K. Khurana Hershey, Children's Hospital Medical Center, Cincinnati, Ohio: Biology of the R576 IL-4 receptor allele: A gain-of-function variant.

SESSION 3: Polymorphisms of Target Genes in Asthma
Chairperson: S.B. Liggett, University of Cincinnati College of Medicine, Ohio

N.J. Schork, Case Western Reserve University, Cleveland, Ohio: Analysis of target gene variations in complex diseases.
M.T. Boyce-Jacino, Molecular Tool, Inc., Baltimore, Maryland: Methods of rapid detection of polymorphisms.
J.M. Drazen, Brigham and Women's Hospital, Boston, Massachusetts: Genetic variants of 5-lipoxygenase.
S.M. Prescott, University of Utah, Salt Lake City: Platelet activating factor acetylhydrolase gene variation.
S.B. Liggett, University of Cincinnati College of Medicine, Ohio: Polymorphisms of the β-adrenergic receptor.

SESSION 4: Chemokines
Chairperson: J. Oppenheim, NCI-Frederick Cancer Research and Development Center, Maryland

T.J. Williams, National Heart and Lung Institute, London, United Kingdom: Regulation of eotaxin.
M.E. Rothenberg, Children's Hospital Medical Center, Cincinnati, Ohio: Control of eosinophil trafficking by chemokines.
D.M. Center, Boston University School of Medicine, Massachusetts: Regulation of $CD4^+$ T-cell accumulation and activation in the lung by IL-16.
J.A. Elias, Yale University School of Medicine, New Haven, Connecticut: Transgenic modeling: Lessons from IL-11 and IL-16 mice.
N.W. Lukacs, University of Michigan Medical School, Ann Arbor: Role of chemokines on leukocyte recruitment, airway reactivity and lymphokine profiles.
J. Oppenheim, NCI-Frederick Cancer Research and Development Center, Maryland: Chemokine-induced neutrophil release of immunoadjuvants: Defensins and cathepsin G.

SESSION 5: IgE Function and Regulation
Chairperson: S.J. Galli, Beth Israel Deaconess Medical Center, Boston, Massachusetts

S.J. Galli, Beth Israel Deaconess Medical Center, Boston, Massachusetts: Role of mast cells and IgE- and FαRI-dependent amplification and positive feedback mechanisms.
J.V. Ravetch, The Rockefeller University, New York: FCαRII-dependent regulation of the allergic response.
K.J. Moore, Millennium Pharmaceuticals Inc., Cambridge, Massachusetts: Analysis of the defective IgE response in a mouse inbred strain.
J.-P. Kinet, Beth Israel Deaconess Medical Center, Boston, Massachusetts: Positive and negative regulation of signaling via the FαRI.

Critical Issues in Marfan Research

April 17–19

FUNDED BY **National Marfan Foundation, with additional support from Shriners Hospitals for Children**

ARRANGED BY **P. Byers,** University of Washington School of Medicine
R.B. Devereux, New York Hospital/Cornell Medical Center
H.C. Dietz, The Johns Hopkins Hospital
Uta Francke, HHMI, Stanford University Medical Center
R.E. Pyeritz, Allegheny University of the Health Sciences
F. Ramirez, Mount Sinai School of Medicine
L.Y. Sakai, Shriners Hospital for Children

SESSION 1: Clinical Research in Marfan Syndrome and Related Disorders
Chairperson: R.E. Pyeritz, Allegheny University of the Health Sciences, Pittsburgh, Pennsylvania

R.E. Pyeritz, Allegheny University of the Health Sciences, Pittsburgh, Pennsylvania: Introduction and overview.

Brief Reports

D.M. Alcorn, Stanford University Medical Center, California
A.C. Braverman, Washington University School of Medicine, St. Louis, Missouri
P. Byers, University of Washington School of Medicine, Seattle
H.C. Dietz, The Johns Hopkins Hospital, Baltimore, Maryland
D.M. Milewicz, University of Texas Medical School at Houston
S.D. Shapiro, Washington University School of Medicine, St. Louis, Missouri

SESSION 2: Lessons from Animal Models
Chairperson: F. Ramirez, Mount Sinai School of Medicine, New York

F. Ramirez, Mount Sinai School of Medicine, New York: Introduction.
H.C. Dietz, The Johns Hopkins Hospital, Baltimore, Maryland: Vascular pathogenesis of MFS and mice.
S.D. Shapiro, Washington University School of Medicine, St. Louis, Missouri: Metalloproteinases which degrade elastic fibers.
P. Carmeliet, KU Leuven, Belgium: Proteinases and aneurysm formation.
H.C. Dietz, The Johns Hopkins Hospital, Baltimore, Maryland: Phenotypic variability in MFS and mice.
R. Akhurst, Onyx Pharmaceuticals, Richmond, California: Identification of modifiers in mice.

P. Byers, R. Akhurst, D. Rifkin, L. Sakai

SESSION 3: Molecular Diagnostics and Databases

A. Diagnostic Issues—Clinical

All participants: Revisit the clinical diagnostic criteria for MFS—experience using the Ghent criteria.
R. Pyeritz, D.M. Milewicz, P. Byers, H.C. Dietz: Define MFS/CCA overlap syndromes.
All participants: Clinical subtypes or continuum?

B. Diagnostic Issues—Laboratory

M. Godfrey, University of Nebraska Medical Center, Omaha, H.C. Dietz: Immunofluorescence with FBN1 antibodies.
D.M. Milewicz: ^{35}Cys pulse-chase studies.

All participants: MFAPS, LTBPS screening methods.
C. Boileau, H.C. Dietz, R. Pyeritz: FBN1.
D.M. Milewicz: FBN2.
M. Godfrey: LTBP2.

C. Database Issues

P. Byers, R. Pyeritz: NMF-supported clinical database.
C. Boileau, INSERM-Clinique Maurice Lamy, Paris, France: Marfan database.
H.C. Dietz: Consortium database.

D. Discussion of Research Priorities and Possible Collaborations

SESSION 4: Summaries and General Discussion
Chairperson: P. Byers, University of Washington School of Medicine, Seattle

R.E. Pyeritz, Allegheny University of the Health Sciences, Pittsburgh, Pennsylvania
F. Ramirez, Mount Sinai School of Medicine, New York

General Discussion
Moderator: P. Byers, University of Washington School of Medicine, Seattle

Coffee break

Muscle Gene Regulation and Its Therapeutic Potential

April 26–29

FUNDED BY **Oxnard Foundation**

ARRANGED BY **K.E. Davies,** University of Oxford
S.D. Hauschka, University of Washington
D. Helfman, Cold Spring Harbor Laboratory
P.W.J. Rigby, MRC National Institute for Medical Research

SESSION 1: Muscle Transcription
Chairperson: P.W.J. Rigby, MRC National Institute for Medical Research, London, United Kingdom

K.E. Davies, University of Oxford, United Kingdom: Introduction to Utrophin Project.
J.D. Haley, OSI Pharmaceuticals, Inc. Uniondale, New York: Searching for small molecules to regulate gene expression.
W. Herr, Cold Spring Harbor Laboratory: Introduction to general transcription factors.
O. Pourquie, Developmental Biology Institute of Marseilles, France: Evidence for a molecular clock linked to somitogenesis.
C.P. Emerson, University of Pennsylvania School of Medicine, Philadelphia: Developmental regulation of MyoD.

SESSION 2: Muscle Gene Regulation I
Chairperson: K.E. Davies, University of Oxford, United Kingdom

M. Buckingham, Institut Pasteur, Paris, France: Myf-5.
P.W.J. Rigby, MRC National Institute for Medical Research, London, United Kingdom: Regulation of Myf-5.
H.H. Arnold, University of Braunschweig, Germany: Control of the Myf-5 gene.
S.F. Konieczny, Purdue University, West Lafayette, Indiana: Positive and negative regulators of myogenesis.
L. Kedes, University of Southern California, Los Angeles: Conformation and acetylation control of MyoD activity.
M. Buckingham, Institut Pasteur, Paris, France: Attaining in vivo levels of muscle gene transcription.

J. Rafael, K. Davies

SESSION 3: Muscle Gene Regulation II
Chairperson: S.D. Hauschka, University of Washington, Seattle

S.J. Tapscott, Fred Hutchinson Cancer Research Center, Seattle, Washington: Expression of genes in native chromatin in skeletal muscle cells.
C.P. Ordahl, University of California, San Francisco: Transcriptional repression and activation via MCAT elements.
P. Maire, INSERM, Paris, France: Characterization of MEF3 proteins and their role in controlling muscle gene expression.
N. Rosenthal, Massachusetts General Hospital-East, Charlestown: The molecular basis of muscle cell diversity.
M.A. Rudnicki, McMaster University, Ontario, Canada: Regulations of myogenic determination and differentiation.
J. Robbins, Children's Hospital Research Foundation, Cincinnati, Ohio: Control of muscle protein levels during transgenic overexpression.

SESSION 4: Muscle Gene Regulation III
Chairperson: D. Helfman, Cold Spring Harbor Laboratory

S.D. Hauschka, University of Washington, Seattle: Are there new muscle gene control elements and transcription factors still to be discovered?
R.J. Schwartz, Baylor College of Medicine, Houston, Texas: Regulation of muscle gene activity.
M. Antoniou, UMDS, Guy's Hospital, London, United Kingdom: The value of locus control regions in integrating and nonintegrating gene therapy vectors.
L. Schaeffer, Pasteur Institute, Paris, France: Implication of a multisubunit Ets-related transcription factor in synaptic expression of the nicotinic acetylcholine receptor.
S. Burden, Skirball Institute, New York University Medical Center: Neuregulin-activated gene expression.
A. Buonanno, National Institute of Child Health and Human Development, Bethesda, Maryland: Activity-dependent and fiber-type-specific regulation of muscle genes.

SESSION 5: Implications for Therapies
Chairperson: T.A. Partridge, Imperial College School of Medicine, London, United Kingdom

B. Jasmin, University of Ottawa, Ontario, Canada: Regulation of utrophin gene expression in skeletal muscle cells.
J.M. Tinsley, University of Oxford, United Kingdom: Multifunctional analysis of utrophin transgenes in mouse models.
J.M. Leiden, The University of Chicago, Illinois: Gene transfer into skeletal and cardiac muscle in vivo.
G. Cossu, University of Rome La Sapienza, Italy: Nonsomitic myogenic progenitors.
J.S. Chamberlain, University of Michigan Medical School, Ann Arbor: Development of muscle-specific adenoviral vectors.

Roundup/General Discussion
Moderator: T.A. Partridge, Imperial College School of Medicine, London, United Kingdom

Cocktails at Robinson House

Laboratory Methods for the Diagnosis of Lyme Disease

August 30–September 2

FUNDED BY **National Institute of Allergy and Infectious Diseases, NIH, Centers for Disease Control and Prevention, and ORD, with additional support from Immunetics and SmithKline Beecham Pharmaceuticals**

ARRANGED BY **P. Baker,** National Institute of Allergy and Infectious Diseases, NIH

SESSION 1: ELISA and Western Blot Assays
Chairperson: B.J. Luft, State University of New York, Stony Brook

A.C. Steere, New England Medical Center, Boston, Massachusetts: Prospective evaluation of two-tiered testing in early Lyme disease.
M. Aguero-Rosenfeld, Westchester County Medical Center, Valhalla, New York: Critique of recommended two-tiered testing.
M.E. Schriefer, Centers for Disease Control and Prevention, Ft. Collins, Colorado: Can two-tiered testing do any better?
J. Glass, Brook Biotechnologies, Inc., Stony Brook, New York: Use of recombinant antigens in diagnosis.
A. de Silva, Yale University School of Medicine, New Haven, Connecticut: Differential *Borrelia burgdorferi* gene expression: Applications in serodiagnosis.
B.J.B. Johnson, Centers for Disease Control and Prevention, Fort Collins, Colorado: Evaluation of recombinant antigens.
A.E. Levin, Immunetics, Inc., Cambridge, Massachusetts: Neural network interpretation of Lyme Western blots: Human versus Deep Green.
F.C. Cabello, Viro Dynamics, New York: Potential use of BmpC, a *Borrelia burgdorferi* protein of the 39 kD family, as a reagent in diagnosis of Lyme disease.

SESSION 2: Nucleic-acid-based Approaches and Applications I
Chairperson: J.L. Goodman, University of Minnesota, Minneapolis

J.L. Goodman, University of Minnesota, Minneapolis: PCR in *Borrelia burgdorferi* infection: Principles, practice, and critical review.
G.P. Wormser, Westchester County Medical Center, Valhalla, New York: PCR and the culturing of *Borrelia burgdorferi*.

SESSION 3: Nucleic-acid-based Approaches and Applications II
Chairperson: J.L. Goodman, University of Minnesota, Minneapolis

I. Schwartz, New York Medical College, Valhalla, New York: Mining the *Borrelia burgdorferi* genome sequence for improved diagnostic targets.
A.C. Steere, New England Medical Center, Boston, Massachusetts: New strategies for improved diagnosis.

SESSION 4: Other Approaches for Diagnosis
Co-Chairpersons: A.G. Barbour, University of California, Irvine and **A.C. Steere,** New England Medical Center, Boston, Massachusetts

E.A. Davidson, Georgetown University School of Medicine, Washington, D.C.: Rapid detection and early diagnosis.
M.S. Klempner, Tufts-New England Medical Center, Boston, Massachusetts: Matrix metalloproteinases in the cerebrospinal fluid of patients with Lyme disease.
P.K. Coyle, State University of New York, Stony Brook: Antigen-capture and immune.
S.E. Schutzer, UMDNJ-New Jersey Medical School, Newark: Immune complex analysis for the diagnosis of early and active Lyme disease.
A.G. Barbour, University of California, Irvine: Bacteriocidal assays.
S. Lesley, Promega Corporation, Madison, Wisconsin: Use of phage display to isolate biotinylated detection reagents.

SESSION 5: Evaluating the Influence of Coinfection and Other Factors
Co-Chairpersons: G.P. Wormser, Westchester County Medical Center, Valhalla, New York and **A. Weinstein,** George Washington University Medical Center, Washington, D.C.

G.P. Wormser, Westchester County Medical Center, Valhalla, New York: Addressing coinfection.
J.W. IJdo, Yale University School of Medicine, New Haven, Connecticut: Serologic diagnosis of human granulocytic ehrlichiosis.
D.T. Dennis, Centers for Disease Control and Prevention, Ft. Collins, Colorado: Evaluating testing in primary care practice.
R.R. Porwancher, Infectious Disease Consultants, P.C., Trenton, New Jersey: A probabilistic approach to the diagnosis of Lyme disease.

SESSION 6: Overview and Panel Discussion
Chairperson: D.J. Gubler, Centers for Disease Control and Prevention, Ft. Collins, Colorado

Panel Members: J.L. Goodman, G.P. Wormser, A.G. Barbour, B.J. Luft, A.C. Steere

Image Archive on the American Eugenics Movement Editorial Advisory Panel Workshop

September 20–22

FUNDED BY **National Human Genome Research Institute, NIH**

ARRANGED BY **D. Micklos,** DNA Learning Center, Cold Spring Harbor Laboratory
J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

SESSION 1: Introduction and Overview

D. Micklos, DNA Learning Center, Cold Spring Harbor Laboratory, and J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory: Introduction—Description of the project and summary of what has been done, review of the functions of the EAP as defined in the grant application, and review of important issues as identified by the NIH Review Panels.

SESSION 2: Round Table Discussion

An opportunity for each participant to raise other issues based on their professional and personal perspectives and making a list of key points to be kept in mind during the meeting.

SESSION 3: "Focus" Talks

M.L. Levitt, The American Philosophical Society, Philadelphia, Pennsylvania: The American Philosophical Society and the Project.

E.J.Thompson, National Human Genome Research Institute, Bethesda, Maryland: Privacy and confidentiality—A view from NHGRI.

P. Reilly, Shriver Center for Mental Retardation, Waltham, Massachusetts: Privacy and confidentiality—A geneticist's view.

H. Friedlander, Brooklyn College/City University of New York, Brooklyn: A historian's view.

SESSION 4: Review Selected Images

Examine selected images in the light of the morning's discussions, with particular reference to: themes, keywords, privacy, context.

Tour of Laboratory and DNA Learning Center; Review Macy Foundation *DNA from the Beginning* Project

SESSION 5: Review Images

Examine as many examples as possible, with particular reference to interest, coverage of themes, technical quality.

SESSION 6: Summary

An opportunity for critical review of the meeting, suggestions for the next stage of the project, date and goals of next meeting.

Gathering outside the Banbury Conference Center.

Y Chromosome in Disease and Evolution

October 13–16

FUNDED BY **Cold Spring Harbor Laboratory Corporate Sponsor Program**

ARRANGED BY **H. Cooke,** University of Edinburgh

SESSION 1

J.A. Marshall Graves, La Trobe University, Melbourne, Australia: Evolution of the mammalian Y chromosome, spermatogenesis and sex determining genes.

D.S. Guttman, University of Chicago, Illinois: An X-linked gene with a degenerate Y-linked homolog in the dioecious plant *Silene latifolic*.

M. Mitchell, INSERM, Marseilles, France: The organization of genes on the mouse Y chromosome.

J. Schmidtke, Institute of Human Genetics, Hannover, Germany: Evolution of TSPY and related genes.

S.C. Maxson, University of Connecticut, Storrs: The mouse Y chromosome and behavior.

SESSION 2

P.S. Burgoyne, National Institute for Medical Research, London, United Kingdom: The multiple-copy Y-gene families Rbm and Ssty in the mouse.

Y.-F.C. Lau, University of California, San Francisco: Expression of Y chromosome genes in human prostate cancers.

W.R. Rice, University of California, Santa Cruz: Evolutionary decay of the Y sex chromosome.

B. Charlesworth, University of Edinburgh, United Kingdom: The population genetics of Y chromosome evolution.

D.C. Page, HHMI, Whitehead Institute for Medical Research, Cambridge, Massachusetts: The fall and rise of the human Y chromosome.

SESSION 3

G.A. Rappold, Institute of Human Genetics, Heidelberg, Germany: SHOX—A pseudoautosomal gene involved in growth and development.

W. Schempp, Universitat Freiburg, Germany: Fiber-FISH mapping of DAZ, RBM, and CDY gene family members within deletion interval 6 of the human Y chromosome.

W.-H. Li, University of Texas, Houston: Male-driven evolution of DNA sequences in mammals.

H. Cooke, University of Edinburgh, United Kingdom: Lack of detectable differences in function between DAZ and Dazl.

M.F. Hammer, University of Arizona, Tucson: Evolutionary history of the human Y chromosome.

P. Burgoyne, S. Maxson, E. Simpson

SESSION 4

M.A. Jobling, University of Leicester, United Kingdom: Identification and dating of Y chromosomal lineages, and the influence of selection on Y haplotypes.
E.E. Eichler, Case Western Reserve University, Cleveland, Ohio: Pericentromeric gene duplications and the complex architecture of the human genome.
B.D. McKee, University of Tennessee, Knoxville: Role of gene conversion in maintenance of sequence homogeneity in Su (Ste) and rDNA clusters of *D. melanogaster* X and Y chromosomes.
S. Henikoff, HHMI, Fred Hutchinson Cancer Research Center, Seattle, Washington: Evolution and utility of satellite repeats.
P.A. Underhill, Stanford University, California: Y chromosome SNP halotype diversity.
C.E. Bishop, Baylor College of Medicine, Houston, Texas: Sequencing the mouse Y chromosome.

SESSION 5

E.M. Simpson, The Jackson Laboratory, Bar Harbor, Maine: Toward a physical map of the mouse Y chromosome: Enrichment, sizing, and cloning by bivariate flow cytometry.
D. Vollrath, Stanford University, California: DNA sequence diversity of the human Y chromosome.
S.R. Haynes, National Institute of Child Health and Human Development, NIH, Bethesda, Maryland: Rb97D, a *Drosophila* RNA-binding protein that associates with a specific region of the Y chromosome in spermatocytes.
M. Steinemann, Henrich Heine Universitat Dusseldorf, Germany: *Drosophila miranda:* A model system for Y chromosome evolution and differential gene activity.
P.H. Yen, University of California, Los Angeles, Torrance: Deletion interval 6 of the human Y chromosome: Spermatogenesis genes and large repeats.
J.A. Marshall Graves, La Trobe University, Melbourne, Australia: Meeting overview.

Participants outdoors discussing the meeting during a break.

The Molecular Physiology of Weight Regulation and Obesity

October 18–21

FUNDED BY **Cold Spring Harbor Laboratory Corporate Sponsor Program**

ARRANGED BY **R. Cone,** Oregon Health Sciences University
J.S. Flier, Beth Israel Deaconess Medical Center

Goals of the Conference:
J.S. Flier, Beth Israel Deaconess Medical Center, Boston, Massachusetts

SESSION 1: Leptin
Chairperson: R. Cone, Oregon Health Sciences University, Portland

J.M. Friedman, HHMI, The Rockefeller University, New York: Leptin and the neural circuits regulating weight.
J.S. Flier, Beth Israel Deaconess Medical Center, Boston, Massachusetts: Leptin and the regulation of neuroendocrine function.
R.A. Steiner, University of Washington, Seattle: Leptin as a neuroendocrine signal to the reproductive system.
J.L. Cameron, Oregon Regional Primate Research Center, Beaverton: Neural control of food intake in nonhuman primates: Comparison with rodent species.
M.W. Schwartz, Puget Sound VA Health Care System, Seattle, Washington: Leptin, hypothalamic neuropeptides, and energy homeostasis.

SESSION 2: Central Regulation of Energy Balance I
Chairperson: M.W. Schwartz, Puget Sound VA Health Care System, Seattle, Washington

J.K. Elmquist, Beth Israel Deaconess Medical Center, Boston, Massachusetts: Linking mediobasal and lateral hypothalamic feeding centers in the rodent and human brain.
R. Palmiter, HHMI, University of Washington, Seattle: Role of NPY and dopamine in regulation of feeding behavior.
G. Barsh, Stanford University School of Medicine, California: Genetics and biochemistry of endogenous

M. Yanagiswa

melanocortin receptor antagonists.
K.L. Stark, Amgen, Inc., Thousand Oaks, California: AGRP and the control of feeding.
B.E. Levin, VA Medical Center, East Orange, New Jersey: Neuropeptides and the defense of body weight set-point in diet-induced obesity.

SESSION 3: Central Regulation of Energy Balance II
Chairperson: L. Van der Ploeg, Merck Research Laboratories, Rahway, New Jersey

R. Cone, Oregon Health Sciences University, Portland: Melanocortins and energy balance.
K. Gudmundsson, Children's Hospital, Boston, Massachusetts: CRH-leptin interactions.
P.J. Larsen, Novo-Nordisk, Maalov, Denmark: Hypothalamic CART: A new anorectic peptide regulated by leptin.
E. Maratos-Flier, Joslin Diabetes Center, Harvard Medical School, Boston, Massachusetts: Melanin concentrating hormone.
M. Yanagisawa, HHMI, University of Texas Southwestern Medical Center, Dallas: Orexins: Novel lateral hypothalamic neuropeptides that regulate feeding behavior.

SESSION 4: GLP-1/Energy Expenditure
Chairperson: J.M. Friedman, HHMI, The Rockefeller University, New York

S. Bloom, Hammersmith Hospital, London, United Kingdom: GLP-1 and body weight regulation.
D. Drucker, The Toronto Hospital, Canada: Essential neuroendocrine role of GLP-1 in vivo.
M.L. Reitman, National Institutes of Health, Bethesda, Maryland: Role of adipose tissue in metabolic regulation: Lessons from a no-fat mouse.
B. Spiegelman, Dana-Farber Cancer Institute, Boston, Massachusetts: PGC1: A transcriptional regulator of energy dissipation.
G.S. McKnight, University of Washington, Seattle: Role of PKA IIB isoform in weight regulation.

SESSION 5: Genetics of Obesity
Chairperson: J.S. Flier, Beth Israel Deaconess Medical Center, Boston, Massachusetts

J. Naggert, The Jackson Laboratory, Bar Harbor, Maine: Fat and tub.
R.L. Leibel, Columbia University, New York: Molecular physiology of human obesity.
C. Bouchard, Laval University, Ste-Foy, Quebec, Canada: Genetics of human obesity.
A.G. Comuzzie, Southwest Foundation for Biomedical Research, San Antonio, Texas: Genome scanning for obesity genes in humans.
S. O'Rahilly, Addenbrooke's Hospital, Cambridge, United Kingdom: Genetics of early-onset obesity in humans.
A. Gruters-Kieslich, Humboldt University, Berlin, Germany: POMC defects in human obesity.

J.P. Morgan & Co. Incorporated/Cold Spring Harbor Laboratory Executive Conference on Imaging: From Molecules to Brains

October 23–25

ARRANGED BY **J.D. Watson,** Cold Spring Harbor Laboratory
J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

SESSION 1

J.D. Watson, Cold Spring Harbor Laboratory: Welcoming remarks.
C. Bustamante, University of California, Berkeley: Seeing molecules—The scanning force microscope in biology.

SESSION 2

P. Sigler, HHMI, Yale University, New Haven, Connecticut: Proofreading and editing protein folding—Imaging the final step in gene expression.
R. Tsien, HHMI, University of California, San Diego: Fluorescent sensors of intracellular signal transduction—Applications to pharmaceutical screening.
M. Ellisman, National Center for Microscopy and Imaging Research, University of California, San Diego: Cellular and subcellular components of nervous systems—3-D microscopy.

SESSION 3

B. Stillman, Cold Spring Harbor Laboratory: Introduction—Imaging at Cold Spring Harbor Laboratory
K. Svoboda, Cold Spring Harbor Laboratory: Two-photon Imaging.
D. Spector, Cold Spring Harbor Laboratory: Imaging RNA processing in cells.

SESSION 4

B. Rosen, MGHG-NMR Center, Harvard Medical School, Cambridge, Massachusetts: Functional imaging of the working brain.
J. Gabrieli, Stanford University, California: Imaging memory in the brain.
J.D. Watson, Cold Spring Harbor Laboratory: Closing remarks.

H. Solomon, C. Bustamante

The Art of Judging: Perspectives of Science

October 27–30

FUNDED BY **The Federal Judicial Center, Judiciary Leadership Development Council, and Cold Spring Harbor Laboratory**

ARRANGED BY **J.G. Apple,** Federal Judicial Center, Washington, D.C.
J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

SESSION 1

D. Micklos, DNA Learning Center, Cold Spring Harbor Laboratory: Cold Spring Harbor Laboratory and its place in science.

SESSION 2

J. Maienschein, Arizona State University, Tempe: From Darwin to Dolly: Developments in the biological sciences in the 20th century.
L. Silver, Princeton University, New Jersey: Cloning: The biological and social implications of new science.

SESSION 3

D. Wilkinson, Princeton University, New Jersey: Life in an inhospitable universe.
S. Feinberg, Carnegie Mellon University, Pittsburgh, Pennsylvania: Statistics and probabilities in science.

SESSION 4

D. Wilkinson, Princeton University, New Jersey: New concepts of the universe.

SESSION 5

J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory: A look at the past.
J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory: DNA and the Human Genome Project.
Visit to DNA Learning Center and Cold Spring Harbor Laboratory
Tour Leader: J. Kruper, DNA Learning Center, Cold Spring Harbor Laboratory

SESSION 6

P. Reilly, Shriver Center for Mental Retardation, Waltham, Massachusetts: Social implications of genetic research.

SESSION 7

R. Shapiro, New York University, New York: Origins of life.
M. Gallo, Robert Wood Johnson Medical School, Piscataway, New Jersey: Toxicology, the environment, and risk assessment.

SESSION 8

J. Horgan, *Scientific American*, Washington, D.C.: Science in the 21st century.

Overhead slide projection presentation.

Integrating Cellular Stress Responses

November 1–4

FUNDED BY **Cold Spring Harbor Laboratory Corporate Sponsor Program**

ARRANGED BY **M.-J.H. Gething,** University of Melbourne
R.I. Morimoto, Northwestern University

SESSION 1
Chairperson: N.C. Jones, Imperial Cancer Research Fund, London, United Kingdom

R.I. Morimoto, Northwestern University, Evanston, Illinois: Introduction
J.A. King, Massachusetts Institute of Technology, Cambridge: How protein folding fails at higher temperatures.
T. Baker, Massachusetts Institute of Technology, Cambridge: Specificity determinants in the Clp/Hsp100 protein family.
R.I. Morimoto, Northwestern University, Evanston, Illinois: Protein homeostasis and the heat shock response.
J. Bardwell, University of Michigan, Ann Arbor: Heat shock proteins, beyond the chaperone paradigm.
P. Spellman, Stanford University School of Medicine, California: Examination of stress responses in yeast using DNA microarrays.

SESSION 2
Chairperson: J.A. King, Massachusetts Institute of Technology, Cambridge

S. Hultgren, Washington University, St. Louis, Missouri: Link between pilus biogenesis, pathogenesis, and host responses.
M.-J.H. Gething, University of Melbourne, Victoria, Australia: Unfolded protein and inositol starvation responses: Modulation by the cell integrity MAPK pathway.
N.C. Jones, Imperial Cancer Research Fund, London, United Kingdom: Gene regulation by stress-activated map kinases.
D. Ron, The Skirball Institute of Biomolecular Medicine, New York: CHOP and the ER stress response.

SESSION 3
Chairperson: D.R. Green, La Jolla Institute for Allergy and Immunology, California

U. Jakob, University of Michigan, Ann Arbor: Hsp33-A Redox-regulated molecular chaperone.
G.L. Semenza, Johns Hopkins Hospital, Baltimore, Maryland: Regulation of oxygen homeostasis by hypoxia-inducible factor 1.
C. Prives, Columbia University, New York: Signaling to the p53 tumor suppressor protein.
T.V. O'Halloran, Northwestern University, Evanston, Illinois: Managing heavy metal stress: Copper and zinc trafficking pathways.
W. Schaffner, Universitat Zurich, Switzerland: MTF-1, a mammalian zinc finger transcription factor, is required for correct response to heavy metal and oxidative stress.

SESSION 4
Chairperson: C. Prives, Columbia University, New York

D. Ingber, Children's Hospital Medical Center, Boston, Massachusetts: Cellular signal integrations.
D.L. Levens, National Cancer Institute, Bethesda, Maryland: How does DNA sense stress?
D.R. Green, La Jolla Institute for Allergy and Immunology, California: The apoptotic response to stress.
G.I. Evan, Imperial Cancer Research Fund, London, United Kingdom: Cytokines and oncogenes: Decisions for growth control.

SESSION 5
Chairperson: T. Baker, Massachusetts Institute of Technology, Cambridge

M.E. Feder, University of Chicago, Illinois: Organismal and evolutionary limits to inducible responses.
S.L. Rutherford, HHMI, University of Chicago, Illinois: Hsp90 as a capacitor of evolution.
M.-J.H. Gething, University of Melbourne, Victoria, Australia: Closing comments and summary.

Large-scale Discovery and Genetic Applications of SNPs

November 10–13

FUNDED BY **Glaxo Wellcome Inc. and the National Human Genome Research Institute, NIH**

ARRANGED BY **A. Chakravarti,** Case Western Reserve University
E. Lander, Whitehead Institute for Biomedical Research

SESSION 1: Genomic Variation
Chairperson: A. Chakravarti, Case Western Reserve University, Cleveland, Ohio

A. Chakravarti, Case Western Reserve University, Cleveland, Ohio: Introduction.
C.H. Langley, University of California, Davis: Lessons from SNP association studies in *Drosophila*.
M.E. Kreitman, University of Chicago, Illinois: Toward a DNA polymorphism database.
C.F. Aquadro, Cornell University, Ithaca, New York: DNA diversity and rates of recombination across the human genome.
R. Harding, John Radcliffe Hospital, Oxford, United Kingdom: Patterns of nucleotide diversity, recombination, and linkage disequilibrium in the beta-globin gene.
A.G. Clark, Pennsylvania State University, University Park: Fine-scale structure of linkage disequilibrium in LPL, ACE, and ApoE.

SESSION 2: Genome-wide Mapping and Association Studies
Chairperson: E.S. Lander, Whitehead Institute for Biomedical Research, Cambridge, Massachusetts

D. Cohen, Genset SA, Paris, France and Nicholas Schork, Case Western Reserve University, Cleveland, Ohio.
L. Kruglyak, Fred Hutchinson Cancer Research Center, Seattle, Washington: Prospects for the use of SNPs in whole-genome linkage disequilibrium mapping.
A. Chakravarti, Case Western Reserve University, Cleveland, Ohio: Quantitating genome sharing using SNPs.
A.J. Brookes, University of Uppsala, Sweden: Association study design based on SNPs: Optimizing chances of success.

D. Cox, A. Roses, J. Witkowski

SESSION 3: Current Status of SNP Discovery
Chairperson: D. Nickerson, University of Washington, Seattle

D.G. Wang, Bristol-Myers Squibb, Princeton, New Jersey: Large-scale identification, mapping, and genotyping of single-nucleotide polymorphisms.
P.-Y. Kwok, Washington University School of Medicine, St. Louis, Missouri: Strategies for SNP discovery and testing.
E. Lai, Glaxo Wellcome Inc., Research Triangle Park, North Carolina: Large-scale SNP identification.
J. Hacia, National Human Genome Research Institute, NIH, Bethesda, Maryland: Evolutionary sequence analysis of human SNP sites.
P.J. Oefner, Stanford University, California: Geographic distribution and frequency of SNPs.

SESSION 4: Future Technologies for SNP Discovery
Chairperson: D.R. Cox, Stanford University School of Medicine, California

L. Fors, Third Wave Technologies, Inc., Madison, Wisconsin: Scalable, high-throughput technology for SNP analysis directly from genomic DNA.
U. Landegren, University of Uppsala, Sweden: Strategies for high-throughput SNP analysis.
L.M. Smith, University of Wisconsin, Madison: Mass spectrometric analysis of genetic variations.
M.P. Weiner, Glaxo Wellcome, Inc., Research Triangle Park, North Carolina: SNP analysis using mobile solid support.
R. Lipshutz, Affymetrix, Santa Clara, California: Chips and SNPs.
C. Tynan, PE-Applied Biosystems, Foster City, California: High-density TaqMan arrays and "Zip Chips."

SESSION 5: Intellectual Property Issues
Chairperson: A.R. Williamson, London, United Kingdom

A.R. Williamson, London, United Kingdom: Introduction.
M. Freire, National Institutes of Health, Rockville, Maryland: NIH perspective on ESTs and SNPs intellectual property.
D.R. Cox, Stanford University School of Medicine, California: A high-resolution SNP map of the Human Genome.
R. Eisenberg, University of Michigan Law School, Ann Arbor: Competition between public and private research funding for SNP discovery.

SESSION 6: General Discussion and Summing Up
Chairpersons: A. Chakravarti, Case Western Reserve University, Cleveland, Ohio and **E.S. Lander,** Whitehead Institute for Biomedical Research, Cambridge, Massachusetts

Coffee break

Genes, Teens, and the World Wide Web

November 22–24

FUNDED BY **The Josiah Macy, Jr. Foundation**

ARRANGED BY **J. Kruper,** DNA Learning Center, Cold Spring Harbor Laboratory
D. Micklos, DNA Learning Center, Cold Spring Harbor Laboratory
J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

SESSION 1: Opening Remarks and Keynote Address I

J.D. Watson, Cold Spring Harbor Laboratory: Thirty years of biology publishing.
A. Kay, Walt Disney Imagineering, Glendale, California: Helping children learn.

SESSION 2: The Web in Biology Education and Publishing

N. Campbell, University of California, Riverside: The biology place: Using the Web to build investigative learning communities.
L.J. Chaput, Cogito Learning Media, Inc., San Francisco, California: Making cutting edge science accessible to students.
V.L. Ward, Genentech Access Excellence, South San Francisco, California: Preparing teachers for genomic biology.
R.J. Semper, The Exploratorium, San Francisco, California: Live@the Exploratorium: Communicating scientific discovery through webcasting.

SESSION 3: Keynote Address II

B.M. Alberts, National Academy of Sciences, Washington, D.C.: Why it's important to communicate biology.

SESSION 4: How Do We and How Should We Use the Web to Learn?

C. Marshall, Xerox Palo Alto Research Center, California: A reader's-eye view of the Web: Hypertext, annotation, collaboration, and the real world.
T.M. Kahn, Design Worlds for Learning, Inc., San Jose, California: Building virtual learning communities.
P. Greenspun, Massachusetts Institute of Technology, Cambridge: Building scalable online communities.
B. Berenfeld, The Concord Consortium, Massachusetts: Authentic science for kids: The global laboratory curriculum.

SESSION 5: Emerging Technologies and Opportunities

J. McEntyre, National Center for Biotechnology Information, NIH, Bethesda, Maryland: The Human Genome Project and opportunities to integrate research into education.
J. Kruper, DNA Learning Center, Cold Spring Harbor Laboratory: DNA from the beginning.
K. Jones, Magnet Interactive Studios, Washington, D.C.: PBS online: Bringing educational programming to the digital age.
T. Hass, Applications Development for Internet2, Ann Arbor, Michigan: High bandwidth and opportunities for learning.

The Genome and Experimental Biology

December 1–4

FUNDED BY **Cold Spring Harbor Laboratory Corporate Sponsor Program**

ARRANGED BY **P.O. Brown,** Stanford University
G.M. Rubin, University of California

SESSION 1: How Has the Genome Sequence Changed the Way We Look At Yeast?

G.N. Giaever, Stanford University School of Medicine, California: Drug-induced haploinsufficiency, drug target identification.
P. Spellman, Stanford University Medical Center, California: Identification of cell-cycle-regulated genes in yeast.
R.A. Young, Whitehead Institute for Biomedical Research, Cambridge, Massachusetts: Dissecting the regulatory circuitry of the yeast genome.
M. Martin, Rosetta Inpharmatics, Kirkland, Washington: Genomics and drug discovery.

SESSION 2: Comprehensive Genetic Surveys and Screens—Methods and Models

G.M. Rubin, University of California, Berkeley: Using genetics to analyze gene function in *Drosophila*.
E.H. Ruley, Vanderbilt Medical Center, Nashville, Tennessee: Genetic analysis of cultured cells and mice by tagged sequence mutagenesis.
B.J. Wold, California Institute of Technology, Pasadena: Challenges for functional genomics in the mouse: Single cell expression states and dispersed *cis*-regulatory elements.
L.I. Zon, HHMI, Children's Hospital, Boston, Massachusetts: Zebrafish genetics and human disease.

SESSION 3: Dealing with a Flood of Data: Understanding, Integrating, Publishing

M.B. Eisen, Stanford University School of Medicine, California: Exploring gene expression space.
D.J. Lipman, National Library of Medicine, Bethesda, Maryland: Computing discoveries in biology.
P.H. Ginsparg, Los Alamos National Laboratory, New Mexico: Knowledge network for physics?
M. Ashburner, European Bioinformatics Institute, Cambridge, United Kingdom: Integrating information across organisms—On the representation of information concerning gene functions in databases.

P. Brown, L. Zon, J.D. Watson

SESSION 4: Experimental Approaches with a "Genomic" Style

O. Kallioniemi, National Human Genome Research Institute, NIH, Bethesda, Maryland: Tissue microarrays for high-throughput molecular profiling.

M. Wigler, Cold Spring Harbor Laboratory: Representational approaches to genomic analysis.

J.S. Minden, Carnegie Mellon University, Pittsburgh, Pennsylvania: Difference gel electrophoresis: A rapid method for identifying proteosome changes.

T.S. Heuer, Massachusetts General Hospital, Boston: Functional screening of cDNA libraries with mRNA-protein fusions.

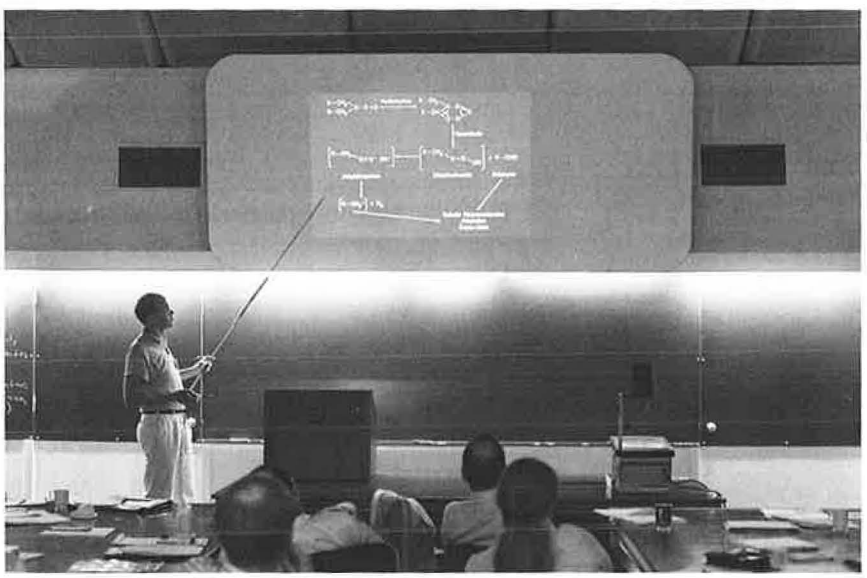
SESSION 5: Experimental Genomic Approaches to Understanding, Diagnosing, and Treating Human Disease

D. Gerhold, Merck & Company, West Point, Pennsylvania: A drug metabolism and safety gene-chip database; on silica to in silica.

L. Staudt, National Cancer Institute, NIH, Bethesda, Maryland: Genomic-scale views of gene expression in normal and malignant lymphocytes using the Lumphochip cDNA microarray.

L.T. Williams, Chiron Corporation, Emeryville, California: A high throughput gene expression study in cancer.

P.O. Brown, HHMI, Stanford University Medical School, California: The DNA microarray as a vehicle for genome exploration.



Making a presentation.

Biochemistry at 100°C: How Are Enzymes and Their Substrates Stabilized?

December 6–9

FUNDED BY **Cold Spring Harbor Laboratory Corporate Sponsor Program**

ARRANGED BY **M.W. Adams,** University of Georgia
R.M. Kelly, North Carolina State University

Welcoming Remarks:
J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

Goals of the Conference:
M.W. Adams, University of Georgia, Athens
Robert M. Kelly, North Carolina State University, Raleigh

SESSION 1: Origins, Environments and Organisms
Chairpersons: D.S. Clark, University of California, Berkeley and **F.T. Robb,** University of Maryland, Baltimore

S.L. Miller, University of California, La Jolla: A cold origin for life: Pros and cons.
J. Wiegel, University of Georgia, Athens: Thermal ranges of microbial growth.
M.W. Adams, University of Georgia, Athens: Hyperthermophilic metabolisms and pathways: Unusual or standard?
R.W. Kelly, North Carolina State University, Raleigh: Carbohydrate utilization by hyperthermophiles: What do the genome sequences tell us?

SESSION 2: Biochemistry
Chairperson: R. Jaenicke, University of Regensburg, Germany

H. Santos, Universidade Nova de Lisboa, Oeiras, Portugal: Organic solutes from hyperthermophiles: Stabilizing effects on enzymes.
J. Trent, NASA Ames Research Center, Moffett Field, California: Role of heat-shock proteins in vivo—Do hyperthermophilic enzymes need chaperones?
F.B. Perler, New England BioLabs, Inc., Beverly, Massachusetts: Protein splicing in hyperthermophiles.
G. Antranikian, Technical University, Hamburg, Germany: Hydrolytic enzymes from hyperthermophiles.
M.J. Danson, University of Bath, United Kingdom: Staying together—The importance of subunit interactions in enzyme hyperstability.

R. Jaenicke, F. Perler

SESSION 3: Protein Structure
Chairpersons: M.J. Danson, University of Bath, United Kingdom and **A. Karplus,** Cornell University, Ithaca, New York

R. Jaenicke, University of Regensburg, Germany: Stability and folding of hyperthermophilic proteins.
F.T. Robb, University of Maryland, Baltimore: Rational placement of mutations that enhance protein thermostability.
T. Oshima, Tokyo University of Pharmacy and Life Science, Japan: Stabilization of mesophilic enzymes by a combination of theoretical design and evolutionary molecular engineering.
J.G. Zeikus, Michigan State University, East Lansing: Molecular determinants for activity and stability of xylose isomerase, amylase, and alkaline phosphatase.
R. Sterner, University of Gottingen, Germany: How do (ba)8-barrel enzymes protect themselves and their thermolabile substrates at temperatures close to 100°C?

SESSION 4: Biophysical Approaches
Chairpersons: J.N. Reeve, Ohio State University, Columbus and **H. Santos,** Universidade Nova de Lisboa, Oeiras, Portugal

M. Rossi, University of Naples, Italy: Studies on molecular bases of the thermostability of the β-glycosidase from *Sulfolobus solfataricus*.
W. Englander, University of Pennsylvania, Philadelphia: Hydrogen exchange as a tool to assess protein stability.
G.N. La Mar, University of California, Davis: Solution NMR study of the novel molecular structure of the ferredoxin from *Pyrococcus furiosus*.
D.S. Clark, University of California, Berkeley: Pressure stabilization of proteins near 100°C: Implications for structure-function relationships.
J.W. Shriver, Southern Illinois University School of Medicine, Carbondale: Global analysis of the linkage of pH and salt concentration to protein folding: Application to core packing mutants of Sac7d and Sso7d.

SESSION 5: Genetics/Protein–DNA Interactions/Genomics
Chairperson: F.B. Perler, New England Biolabs, Inc., Beverly, Massachusetts

J.N. Reeve, Ohio State University, Columbus: Histone-fold stabilization.
P. Lopez-Garcia, Universite Paris-Sud, Orsay, France: Control of DNA superhelical changes during heat shock in hyperthermophilic Archaea.
K.M. Noll, University of Connecticut, Storrs: Recent developments in genetic transfer methods in *Thermotoga*.
D.W. Grogan, University of Cincinnati, Ohio: Genetic processes in thermophilic Archaea.
H.-P. Klenk, University of Gottingen, Germany: Extreme thermophilia: Ancient conserved feature or phylogenetic pitfall?

Participants discussing presentation.

From Bench to Bedside: Colloquium on Translational Vaccine Research

December 15–17

FUNDED BY **The Albert B. Sabin Vaccine Institute, Inc. at Georgetown University**

ARRANGED BY **H.B. Herscowitz,** Georgetown University
P.K. Russell, Potomac, Maryland

Introductory Remarks:
H.R. Shepherd, The Albert B. Sabin Vaccine Institute, Inc. at Georgetown University, Washington D.C.
P. Hotez, Yale University School of Medicine, New Haven, Connecticut
P.K. Russell, Potomac, Maryland

SESSION 1: Historical Perspective
Chairperson: P. Hotez, Yale University School of Medicine, New Haven, Connecticut

P. Hotez, Yale University School of Medicine, New Haven, Connecticut: Welcoming remarks.
R. Rabinovich, National Institute of Allergy and Infectious Diseases, NIH, Bethesda, Maryland: Setting the stage.

SESSION 2: Viral Vaccines
Chairperson: P. Hotez, Yale University School of Medicine, New Haven, Connecticut

D.E. Griffin, Johns Hopkins School of Public Health, Baltimore, Maryland: Issues in developing new measles vaccines.
J.L. Gerin, Georgetown University Medical Center, Rockville, Maryland: Vaccines for viral hepatitis.
A.R. Shaw, Merck Research Laboratories, West Point, Pennsylvania: Development of a live oral vaccine for rotavirus.
R.B. Belshe, St. Louis University School of Medicine, Missouri: Efficacy of live attenuated influenza vaccine given intranasally.

P. Hotez, J. Gerin, D. Sack

SESSION 3: Arthropod-borne Infection Vaccines
Chairperson: P. Hotez, Yale University School of Medicine, New Haven, Connecticut

W.R. Ballou, Walter Reed Army Institute of Research, Washington, D.C.: Malaria vaccines: Translational obstacles.
A.C. Steere, New England Medical Center, Boston, Massachusetts: Vaccination for Lyme disease with recombinant *Borrelia burgdorferi* OspA with adjuvant.
S. Hoffman, Naval Institute of Medical Research, Bethesda, Maryland: Translating genomic sequence data into vaccines: Malaria as a model system.
N. Kanesa-Thasan, Walter Reed Army Institute of Research, Washington, D.C.: Progress and problems in Dengue virus vaccine development.
P. Hotez, Yale University School of Medicine, New Haven, Connecticut: Approaches to vaccinating against Helminth infections.

SESSION 4: Bacterial Vaccines

M.M. Levine, University of Maryland School of Medicine, Baltimore: Attenuated *Salmonella typhi* as live vector vaccines expressing foreign antigens.
D.A. Sack, Johns Hopkins University, Baltimore, Maryland: Formulation issues with cholera vaccine: Making efficacious vaccines effective.

SESSION 5: Cancer Vaccines and Immunomodulators

J. Schlom, National Cancer Institute, NIH, Bethesda, Maryland: T-cell costimulation in vaccine design and development.
R. Bucala, The Picower Institute for Medical Research, Manhasset, New York: A novel circulating cell type with potent antigen presenting properties: basic and clinical studies.
M.M. Levine, University of Maryland School of Medicine, Baltimore, and P.K. Russell, Potomac, Maryland: Wrap up and discussion.

Robertson House Library

Banbury Center