From DNA to Proteins: The Multiple Levels of Regulation

23 talks presented by many of the world's leading experts

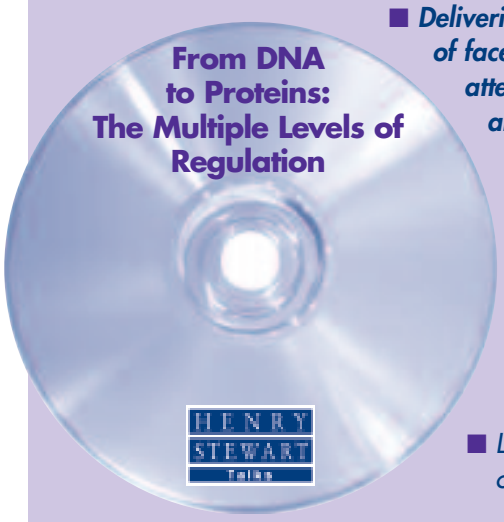
For all those wishing to be briefed on the latest developments in the study and understanding of gene regulation and expression

including

Molecular Biologists, Cell Biologists, Biochemists, Geneticists, Structural Biologists, Microbiologists and Immunologists, whether in Pharmaceutical Development, Biotechnology, Clinical Research or Academic Institutions

Topics covered:

Chromatin architecture – Nucleosome dynamics – DNA replication – Transcription – Intron Splicing – mRNA modifications – mRNA surveillance – miRNA – RNA editing – Nuclear organization – Protein synthesis, elongation, folding and destruction – Gene and protein microarrays – Global gene expression



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Series Editor:

Prof. Panagiotis A. Tsonis, Leonard A. Mann Chair in the Sciences, Department of Biology, University of Dayton, USA

HENRY STEWART Talks

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Prof. Walter Englander
Prof. Joachim Frank
Prof. Alfred Goldberg
Prof. Steve Hajduk
Prof. Michael Hampsey
Prof. Jeffrey Hansen
Dr. Trey Ideker
Prof. Roger Kornberg
Prof. Patrick Linder
Prof. James Manley
Prof. Lynne Maquat
Prof. Timothy Nilsen
Prof. Smita Patel
Prof. Anna Marie Pyle
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Dr. Frank Slack
Prof. David Spector
Dr. Craig Tomlinson
Prof. Panagiotis Tsonis
Prof. Jonathan Widom

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From DNA to Proteins: The Multiple Levels of Regulation

Introduction

1. Overview of Gene Regulation

Prof. Panagiotis Tsonis, University of Dayton, USA

General ideas behind DNA association with: histones, replication, transcription, splicing, RNA modifications, protein synthesis and death and global gene expression analysis

Chromatin and DNA

2. Chromatin Architecture and Alterations in the Control of Gene Regulation

Prof. Jeffrey Hansen, Colorado State University, USA

The chromatin environment – Hierarchical organization of chromatin fibers within interphase chromosomes – Milestone experiments that linked chromatin architecture and gene expression – Proteins and processes that influence both chromatin fiber architecture and gene expression – Core histone N-terminal tail domains – Core histone sequence variants – Linker histones – Heterochromatin proteins – Histone post-translational modifications – The structurally dynamic nature of the genome *in vivo* and its relation to gene expression

3. Nucleosome Dynamics and Remodeling

Prof. Jonathan Widom, Northwestern University, USA

Chromatin composition – Nucleosome structure and function – Dynamic properties inherent to nucleosomes – Invasion of nucleosomes by gene regulatory proteins – DNA binding proteins and enzymes – ATP dependent remodeling factors – Nucleosome relocation

4. DNA Replication

Prof. Smita Patel, University of Medicine and Dentistry of New Jersey, USA

Chemical composition of DNA – Chargaff's rule – DNA structure – Base pairing – Semi-conservative DNA replication – Mechanism of DNA replication – Semi-discontinuous DNA replication – DNA replication is catalyzed by the cooperative action of a number of proteins: what we know – DNA polymerase structure – Structure of phage T7 DNA polymerase – Chemical reaction catalyzed by DNA polymerases – Metal ions play an essential role in DNA synthesis – DNA synthesis has to be efficient and accurate – Rates of correct and incorrect nucleotide addition – How are errors corrected? – Fidelity: exonuclease activity – Fidelity of DNA synthesis – Processivity of the DNA polymerase – Processivity factors – DNA unwinding: helicase protein – Mechanism of double helical DNA strand separation – Mechanism of ATPase and DNA translocation – Helicase functions in conjunction with the DNA polymerase – Synergy between the replication proteins in catalyzing DNA replication – Primers for DNA replication – Properties of the DNA primase

Transcription

5. Eukaryotic-Like Enhancer Dependent Transcription in Bacteria

Prof. Martin Buck, Imperial College London, UK

Understanding the origins of nucleotide driven conformational change – Molecular motors powered by ATP – ATPases belonging to the AAA protein family – PspF from *E.coli* – Phage shock genes – ATP transition state analogue ADPAlF – X-ray crystallographic structural analysis – Initiation of conformational changes – Role of structural changes in sigma54 subunit – Formation of open promoter complexes – Changes in DNA binding properties of sigma54

6. Mechanisms of Transcription: The Eukaryotic Pre-Initiation Complex

Prof. Michael Hampsey, University of Medicine and Dentistry of New Jersey, USA

Overview of RNA polymerase II transcription – Core promoter elements – Proximal promoters – Enhancers and silencers – General transcription factors – Activators and repressors – Coactivator complexes – RNA polymerase II structure and function – Mechanisms of transcription initiation – Steroid hormone receptors – Coactivator complexes, including mediator and TFIID – Chromatin remodellers including SWI/SNF – Covalent histone modifiers, including histone acetyltransferases, methyltransferases and deacetylases

7. Mechanisms of Transcription and Function of RNA Polymerase in Eukaryotes

Prof. Roger Kornberg, Stanford University School of Medicine, USA

Chromatin remodeling for transcription – The RNA polymerase II transcription machinery – Mediator of transcriptional regulation – Atomic structure of RNA polymerase II and of a transcribing complex – Structural basis of ribonucleotide addition and transcript elongation – Structure of a complete pre-initiation complex

RNA

8. Intron Splicing of Pre-mRNA: The Spliceosome

Prof. Timothy Nilsen, The Center for RNA Molecular Biology, Case Western Reserve University School of Medicine, USA

Recognition of splice junction sequences by components of the spliceosome – Spliceosome assembly, catalysis and disassembly – Roles of snRNPs as well as non-snRNP components – RNA dependent ATPases – Splicing in creating multiple mRNAs

9. Splicing of Group I and II Introns

Prof. Anna Marie Pyle, Howard Hughes Medical Institute, Yale University, USA

Different classes of introns – Autocatalytic group I and group II introns – Discovery of self-splicing – Converting a self-splicing RNA into a multiple-turnover enzyme – The "tetrahymena ribozyme" and discovery of RNA catalysis – New insights into molecular recognition of RNA – Group I intron structure and catalytic mechanism – Group I intron applications – Group II introns and the big picture – Discovery of self-splicing by group II introns – Chemical mechanism of group II intron reactions – Catalytic engines for driving eukaryotic evolution – Explaining specificity of group II ribozymes – Group II intron ribozymes as model systems for RNA folding – Group II ribozymes as model systems for RNA tertiary structure – Nucleotide analog interference mapping – Current map of important atoms – Nucleotide analog interference suppression – Lambda-lambda interaction – 3D model of ai5gamma intron – Group II introns as tools and therapeutics

10. mRNA Modifications: PolyA Addition

Prof. James Manley, Columbia University, USA

Polyadenylation of mRNA precursors – The polyadenylation machinery – A surprising complexity in PAP – Hyperphosphorylation by MPF inhibits PAP activity – Gld-2 in cytoplasmic polyadenylation in oocytes – The polyadenylation machinery – CPSF-73 is the 3′ processing endonuclease – CPSF-73 is absent in cytoplasmic polyadenylation – CstF protein interactions – Regulation of gene expression by alternative polyadenylation – The C-terminal domain of RNAPII – The CTD can stimulate 3′ cleavage *in vitro* – CPSF links transcription and 3′ end formation – RNA15 crosslinks to promoters – Polyadenylation and links to other cellular processes – CstF-50 – BRCA1 – BARD1 – BRCA associated ring domain protein – Why does BARD1 inhibit 3′ processing? – DNA damage inhibits 3′ processing – How does BARD1 inhibit 3′ processing? – BRCA1/BARD1 target RNAPII for ubiquitination – Many factors constitute the mRNA 3′ end formation machinery

11. mRNA Modifications: Capping

Prof. Aaron Shatkin, University of Medicine and Dentistry of New Jersey and the Center for Advanced Biotechnology and Medicine, USA

Modification of mRNA 5′ends by addition of a m7G cap structure – Capping for viability – Conservation in yeast to humans – Structure of caps and capping enzymes – Mechanism of cap synthesis – Protein-protein interactions that link capping to events in transcription, transport and translation – siRNA knockdown experiments

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12. RNA Surveillance

Prof. Lynne Maquat, University of Rochester School of Medicine and Dentistry, USA

Three core Upf NMD factors – Exon junction complexes (EJCs) – Upf1 – Mechanism of NMD – Activation of EJC-bound Upf1 – Role of NMD in downregulating spliced mRNAs to eliminate truncated proteins – NMD downregulating functional protein isoforms – Restriction to newly synthesized mRNAs during a pioneer round of translation – Cap Binding Protein (CBP) heterodimer CBP80-CBP20 – Eukaryotic translation initiation factor (eIF) 4E and steady state mRNA – Role of CBP80 in enhancing efficiency of NMD by promoting the interaction of Upf1 with EJC-bound Upf2 – Staufen (Stau)1-mediated mRNA decay (SMD) – Double-stranded RNA binding protein Stau1 – Mechanism of action of SMD

13. Regulation by miRNA

Dr. Frank Slack, Yale University, USA

miRNAs as endogenous small RNA regulators – Biogenesis of miRNAs – miRNAs and siRNAs – Mechanism of action of miRNAs – Targets of miRNAs – Biological roles for miRNAs – Roles for miRNAs in cancer

14. RNA Editing: Changing the Code in Plants, Animals and Parasites

Prof. Stephen Hajduk, The Marine Biological Laboratory, Woods Hole, and Brown University, USA

Diversity of RNA editing – Nucleotide deaminase reactions – Enzyme mediated cascades – Small guiding RNA – Alternative RNA editing

15. Nuclear Organization and Gene Expression

Prof. David Spector, Cold Spring Harbor Laboratory, USA

Spatial and temporal aspects of gene expression – Current understanding of the organization of the eukaryotic cell nucleus – How this organization impacts on gene expression – Development of a cell system to visualize a transcription site and its mRNA and protein products directly in living cells – Evaluating spatial and temporal changes in chromatin structure, mRNA synthesis and factor association/disassociation during the transition from an inactive to an active state – Understanding the *in vivo* dynamics of gene expression – Elucidating spatial and/or temporal alterations that occur in cells associated with various disease states

Proteins

16. An Overview of Protein Synthesis

Prof. Joachim Frank, University at Albany and Howard Hughes Medical Institute, Wadsworth Center, USA

Composition of the ribosome – Principle of translation – The four phases of translation – Structure and function of small and large ribosomal subunits – Role of elongation factors – The paths of messenger RNA, transfer RNA and the nascent polypeptide – Elongation cycle and binding positions of elongation factors – Decoding, peptidyl transfer and translocation – Phylogenetic conservation of ribosomal architecture

17. Initiation of Protein Synthesis

Prof. Patrick Linder, University of Geneva, Switzerland

Main steps in translation initiation – Control of translation – Initiation factor modification – Competitive interactions for translational control – General versus gene-specific control

18. Elongation of Protein Synthesis: Structural Basis of the Process of Decoding

Prof. Marina Rodnina, Institute of Physical Biochemistry, University of Witten, Germany

Fidelity in biological processes – Elongation step of protein synthesis – Ribosome structures – Errors in protein synthesis – The decoding problem – Kinetic proof-reading – Kinetic model of tRNA selection – Role of induced fit in tRNA selection – Recognition of codon-anticodon complexes by the 30S ribosomal subunit – Local and global conformational changes of the 30S subunit – Interactions of tRNA during decoding – Active role of tRNA – Accommodation of tRNA in the A site

19. Elongation of Protein Synthesis: Structural Basis of the Peptide Bond

Prof. Marina Rodnina, Institute of Physical Biochemistry, University of Witten, Germany

The ribosome – Chemistry of peptide bond formation – Structure of the peptidyl transferase center of the ribosome – Structures of the catalytic subunit with reaction substrates and transition state analogs – Induced fit in peptide bond formation and peptidyl-tRNA hydrolysis – Reaction pathways of catalyzed and uncatalyzed reactions – pH dependence of catalysis – Entropic catalysis – Role of active site residues – Importance of 2′ OH of A76 of the tRNA in the P site – The mechanism of peptide bond formation

20. Protein Folding

Prof. Walter Englander, University of Pennsylvania, USA

Challenges to studying protein folding – Methods based on hydrogen exchange (HX) – Foldon units – Step-wise assembly – Building the native protein – Error-dependent misfolding steps – Role of chaperone molecules – Other roles for Foldon behavior

21. Mechanisms and Regulation of Protein Degradation in Cells

Prof. Alfred Goldberg, Harvard Medical School, USA

Protein levels in cells are regulated by their rates of synthesis and degradation – Regulatory proteins are rapidly degraded by the ubiquitin-proteasome pathway – Examples include many oncogenes, transcription factors and cyclins which control progress through the cell cycle – NFkB activation in disease depends on degradation of the inhibitor, IkB – Misfolded or mutant proteins are rapidly degraded – Neurodegenerative and protein folding diseases – Two major proteolytic pathways exist in mammalian cells – Many acid hydrolases exist in lysosomes – Endocytosed proteins and those in autophagic vacuoles are degraded in lysosomes – The ubiquitin-proteasome pathway – 3D structure of ubiquitin – Formation of the isopeptide bonds during ubiquitin conjugation to proteins – The ubiquitin-proteasome pathway – Proteasome function is linked to ATP hydrolysis – Proteasomes unfold proteins and translocate them into 20S particles – Three types of peptidase sites – Proposed mechanism of proteasome inhibitors – Therapeutic applications of proteasome inhibitors – Two systems for protein breakdown function in the two pathways for antigen presentation – Changes in proteasome subunits induced by interferon – Steps involved in generating antigenic peptides

Understanding Global Gene Expression

22. Gene and Protein Microarrays: Tools for Gene Discovery and Function

Dr. Craig Tomlinson, Dartmouth Hitchcock Medical Center, Dartmouth College, USA

High-throughput methods to examine global gene expression – Understanding interactions in a given cell, tissue and organism under normal and disease state conditions – Application of high throughput methods used in genomics and proteomics – Use of DNA and protein microarrays for gene discovery and function – Background information and terminology used in genomics and proteomics – How DNA and protein microarrays are carried out – Predicted future direction of genomics and proteomics microarray technologies

23. Networks and Global Gene Expression

Dr. Trey Ideker, University of California San Diego, USA

A paradigm shift: from databases of protein sequences to protein interactions – Technologies for measuring interactions – Chromatin immunoprecipitation (ChIP) – Yeast Two Hybrid (Y2H) technology – Mass spectrometry based approaches – Methods for querying protein networks with gene expression profiles – Systematic validation of protein network models using gene deletions – Cytoscape open-source software for network modeling and visualization – Methods for network comparison across species – Application to discover conserved protein complexes among the networks of yeast, worm, fly and Plasmodium – Methods for querying protein networks to explain genetic (synthetic lethal) interactions – Future directions: how network queries will enable systems biology

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Speaker Biographies

Speaker Biographies

Prof. Martin Buck, Imperial College London, UK

Martin Buck gained his BSc in Biochemistry at Bedford College, University of London, before taking a PhD at the National Institute for Medical Research where he studied transfer RNA modification in pathogenic *E.coli*, under conditions of iron-restricted growth. Continuing this interest, he joined Prof. Bruce Ames' laboratory, University of California at Berkeley as a postdoc and in 1983 he joined the nitrogen fixation laboratory at the University of Sussex, under the direction of Prof. John Postgate, where he studied the determinants of prosthetic group binding in the nitrogenase of *Klebsiella* bacteria. In 1994 he moved to Imperial College London and continued working on the control of RNA polymerase by enhancer binding transcriptional activator proteins.

Prof. Walter Englander, University of Pennsylvania, USA

Walter Englander received his BS in physics and maths at the University of Maryland. He then went on to receive a MS and a PhD in Biophysics at the University of Pittsburgh. Having been previously Professor of Biochemistry and Biophysics at the University of Pennsylvania, he is now Jacob Gershon-Cohen Professor of Medical Science. Dr. Englander is a member of the National Academy of Sciences, USA, an honorary fellow of the Biophysical Society and of the AAAS. Dr. Englander is the world's leading authority on the hydrogen exchange of proteins and nucleic acids. Methods newly devised in Dr. Englander's laboratory are being used by his group and others to study and explain how proteins fold.

Prof. Joachim Frank, University at Albany and Howard Hughes Medical Institute, Wadsworth Center, USA

Joachim Frank received his BS and Masters in physics at the University of Freiburg and University of Munich, respectively. He obtained his PhD from the Technical University of Munich. He received an appointment at the Wadsworth Center as a Senior Research Scientist and joined the Department of Biomedical Sciences at the University at Albany. Dr. Frank is an investigator of the Howard Hughes Medical Institute and a fellow of the AAAS and the Biophysical Society. In 2005 he gave the National Lecture at the Biophysical Society Meeting. Dr. Frank is known for his development of single-particle reconstruction methods to investigate the structure and dynamics of macromolecular assemblies and for applications of these methods in the study of ribosomal function, which has advanced the understanding of translation.

Prof. Alfred Goldberg, Harvard Medical School, USA

Alfred Goldberg has been associated with Harvard during his entire academic career: he earned his AB in 1963 and his PhD in 1968 and was appointed an Assistant Professor at Harvard Medical School in 1969, immediately following one year as an Instructor. Dr. Goldberg has been a Professor at Harvard Medical School since 1977. The Goldberg lab is attempting to understand why the cell's machinery destroys only damaged proteins, leaving normal proteins untouched. They are also studying how protein breakdown is important in the body's immune defences, why the destruction process goes into high gear in certain disease states such as cancer and how this excessive destruction can be controlled.

Prof. Stephen Hajduk, The Marine Biological Laboratory, Woods Hole, and Brown University, USA

Stephen Hajduk received his BS from the University of Georgia and his PhD from the University of Glasgow. He was a visiting NATO and EMBO scholar at the University of Amsterdam and a Rockefeller Foundation postdoctoral fellow at Johns Hopkins University. He was a Professor in the Department of Biochemistry and Molecular Genetics at the University of Alabama at Birmingham. Dr. Hajduk is a Burroughs Wellcome Scholar in Molecular Parasitology and a Fogarty International Scholar. Dr. Hajduk is a leading authority on RNA editing and the molecular biology of parasitic diseases and his laboratory has played a major role in elucidating the components of the editing machinery and the function of this novel form of RNA processing.

Prof. Michael Hampsey, University of Medicine and Dentistry of New Jersey, USA

Michael Hampsey earned his BS degree in chemistry at the State University of New York at Geneseo and PhD in biochemistry at Purdue University. Following postdoctoral training in yeast genetics at the University of Rochester Medical Center, he was on the faculty at Louisiana State University Health Sciences Center in Shreveport. He is currently Professor of Biochemistry at the University of Medicine and Dentistry of New Jersey and member of the UMDNJ – Master Educators Guild. His research group studies mechanisms of transcription initiation and reinitiation in yeast.

Prof. Jeffrey Hansen, Colorado State University, USA

Jeffrey Hansen is a Professor in the Department of Biochemistry and Molecular Biology at Colorado State University. He obtained his PhD in biochemistry from the University of Wisconsin-Madison in 1986, and was an NIH postdoctoral fellow at Oregon State University from 1987-1990. He spent 12 years on the faculty of the University of Texas Health Science Center at San Antonio prior to moving to Colorado State University in 2003. Over the last decade he has helped pioneer the use of analytical ultracentrifugation for studying complex macromolecular assemblages in solution. His research program focuses on biochemical and biophysical characterization of genome architecture.

Dr. Trey Ideker, University of California San Diego, USA

Trey Ideker received bachelors and masters degrees from MIT in Electrical Engineering and Computer Science. Encouraged by developments in the Human Genome Project, he became interested in applying methods from computer science and engineering to the understanding of biological systems. He obtained a PhD in Molecular Biotechnology at the University of Washington and at the Institute for Systems Biology. Dr. Ideker is currently Assistant Professor in the Department of Bioengineering at UC San Diego and was recently chosen as one of the Technology Review's most innovative scientists under the age of 35. He is on the advisory board of Genstruct and the BioCyc Project and was a Bioinformatics Lecturer for ISTR Inc.

Prof. Roger Kornberg, Stanford University School of Medicine, USA

Roger Kornberg obtained his PhD in Chemistry from Stanford University and then moved to the MRC Laboratory Cambridge, UK. He became Assistant Professor of Biological Chemistry at Harvard Medical School. Since 1978 he has been Professor of Structural Biology and Medicine at Stanford University School of Medicine. He has received numerous awards including the Massry Prize (shared with M. Grunstein and D. Allis) and the Sloan Prize. Prof. Kornberg is Editor of the Annual Review of Biochemistry. His current work focuses on discovery of the molecular machines involved in transcription, reconstitution of the process with purified components, structure determination of the transcription machinery, structure-function relationships in chromatin and the natural DNA template for transcription.

Prof. Patrick Linder, University of Geneva, Switzerland

Patrick Linder was born in 1954 and received his PhD at the University of Geneva on the control of plasmid replication in *Escherichia coli*. After postdoctoral work in Gif sur Yvette on nucleo-mitochondrial interaction in the budding yeast *Saccharomyces cerevisiae*, Dr. Linder was project leader at the Biozentrum of the University in Basel. It was during this time that he started to work on RNA helicases and translation initiation. Since then, Dr. Linder has been attached to this fascinating and central problem of the cellular life.

Prof. James Manley, Columbia University, USA

James Manley is a major leader in studies of the mechanisms and regulation of gene expression. He pioneered the use of cell-free systems to dissect critical steps in the synthesis and processing of mRNA. His discoveries have contributed to our understanding of RNA transcription, splicing and polyadenylation. He received his PhD in Molecular Biology from SUNY. He was made Assistant Professor in the Department of Biological Sciences at Columbia University in 1980, Julian Clarence Levi Professor of Life Sciences in 1995 and was Chairman of the Department of Biological Sciences until 2001. Dr. Manley has published extensively, has received an NIH MERIT Award and is an ISI Highly Cited Researcher. He is currently the Editor for Molecular and Cellular Biology.

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Speaker Biographies

Prof. Lynne Maquat, University of Rochester School of Medicine and Dentistry, USA

Lynne Maquat received a BS degree from the University of Connecticut-Storrs and PhD from the University of Wisconsin-Madison. After postdoctoral training at the McArdle Laboratory for Cancer Research, she joined the faculty of the Department of Human Genetics at Roswell Park Cancer Institute in Buffalo. There she expanded her studies of NMD to include additional types of anemias. She is currently Professor of Biochemistry and Biophysics at the University of Rochester School of Medicine and Dentistry. Recent work has identified and characterized the pioneer translation initiation complex and Staufen1-mediated mRNA decay. She is currently President of the RNA Society. She is on numerous editorial boards including RNA, in the Faculty of 1000 and was formerly chair of the NIH CDF-1 study section.

Prof. Timothy Nilsen, The Center for RNA Molecular Biology, Case Western Reserve University School of Medicine, USA

Timothy Nilsen's principal research interest is in the mechanism of pre-mRNA splicing, with particular emphasis on the process of splice site recognition in higher eukaryotes and trans-splicing, an unusual splicing reaction that occurs in certain lower eukaryotes. He holds a PhD from SUNY Albany and serves as Editor-in-Chief of the scientific journal, RNA.

Prof. Smita Patel, University of Medicine and Dentistry of New Jersey, USA

Dr. Smita Patel, Professor in the Department of Biochemistry at the UMDNJ-Robert Wood Johnson Medical School in New Jersey, received her PhD in Chemistry from Tufts University. She obtained postdoctoral training in Prof. Kenneth Johnson's lab at the Pennsylvania State University where she studied the kinetic pathway and fidelity of DNA synthesis by T7 DNA polymerase using transient state kinetic approaches. The research in her laboratory is focused on understanding the mechanisms of enzymes involved in DNA replication and transcription. Her work has focused on elucidating the nucleic acid unwinding mechanisms of DNA and RNA helicases from phage T7 and hepatitis C virus. She studies the mechanisms and regulation of transcription initiation in phage and mitochondrial RNA polymerases using transient state kinetic approaches.

Prof. Anna Marie Pyle, Howard Hughes Medical Institute, Yale University, USA

Anna Marie Pyle received her PhD in Chemistry under the direction of Jacqueline K. Barton at Columbia University and went on to become Professor of Biochemistry and Molecular Biophysics there. She became Professor of Molecular Biophysics and Biochemistry at Yale University in 2002. Dr. Pyle has been named a Searle Scholar, a Beckman Young Investigator, an NSF National Young Investigator and an Irma T. Hirschl Career Scholar. Dr. Pyle uses the group II intron as a model system for studying ribozyme catalysis, RNA folding and RNA-protein interactions. She also studies the mechanisms of RNA helicase enzymes, which are molecular motors that unwind RNA and displace proteins from RNA binding sites. New computational approaches for analyzing properties of RNA have complemented this work.

Prof. Marina Rodnina, Institute of Physical Biochemistry, University of Witten, Germany

The group of Marina Rodnina has developed novel approaches to study the function of the ribosome as a macromolecular machine. They pioneered the use of kinetic and fluorescence methods in conjunction with quantitative biochemistry to solve the mechanisms of translation. Marina Rodnina has over 80 publications in her research area. Since 2004 she has been an elected member of the European Molecular Biology Organization. Her current interests are focused on the dynamics of the ribosome and translation factors and implementing the knowledge gained from studies of ribosome movements for developing new nanomachines.

Prof. Aaron Shatkin, University of Medicine and Dentistry of New Jersey and the Center for Advanced Biotechnology and Medicine, USA

Aaron Shatkin majored in chemistry at Bowdoin College and trained at Rockefeller University in microbiology with E.L. Tatum. In 1986, he was appointed the director of the Center for Advanced Biotechnology and Medicine, jointly administered by Rutgers University, where he is Professor of Molecular Biology and by UMDNJ-Robert Wood Johnson Medical School where he is Professor of Molecular Genetics, Microbiology and Immunology. His lab's findings have provided many important insights into how gene expression is regulated in eukaryotic cells and viruses. He was the founding editor of Molecular and Cellular Biology and is the author of more than 200 scientific publications. He has received several honors including a DSc (Hon) from Bowdoin College and the 2003 Award for Distinguished Research in the Biomedical Sciences.

Dr. Frank Slack, Yale University, USA

Frank Slack received his BSc from the University of Cape Town, before completing his PhD in molecular biology at Tufts University School of Medicine. He started work on microRNAs as a postdoctoral fellow in Gary Ruvkun's laboratory at Harvard Medical School, where he co-discovered the second known microRNA, let-7. He is currently an Associate Professor in the Department of Molecular, Cellular and Developmental Biology at Yale University. His laboratory studies the roles of microRNAs and their targets in development and disease, particularly cancer.

Prof. David Spector, Cold Spring Harbor Laboratory, USA

David Spector received a PhD in Cell Biology at Rutgers University. He is currently a Professor at Cold Spring Harbor Laboratory (CSHL) and Head of the Gene Expression Program of the CSHL Cancer Center. He has published numerous papers in the area of nuclear organization and gene expression, as well as several laboratory manuals in the areas of basic microscopy and live cell imaging for CSHL Press.

Dr. Craig Tomlinson, Dartmouth Hitchcock Medical Center, Dartmouth College, USA

Craig Tomlinson is Assistant Professor of Medicine and Pharmacology & Toxicology at Dartmouth College. His research interests include the effects of *in utero* exposures of environmental toxicants on DNA methylation and global gene expression in the developing fetus, the interaction of the aryl hydrocarbon receptor and transforming growth factor-beta signaling pathways and the use of high throughput genomics as a tool to predict the outcome of gene-environment interactions.

Prof. Panagiotis Tsonis, University of Dayton, USA

Panagiotis Tsonis received his basic training in Greece and a Bachelor degree in Biology from Patras University. He completed his graduate studies at the Institute of Molecular Biology, Nagoya University, Japan, where he received both his MSc and PhD. After postdoctoral training at the Scripps Institute and the La Jolla Research Foundation he took his first academic appointment as an Assistant Professor of Molecular Biology at the University of Dayton and became full Professor in 1997. He currently holds the Mann Chair in the Sciences and is the Director of the Center for Tissue Regeneration and Engineering. The main goal of his research is to identify the molecular mechanisms of regeneration in amphibia and apply them to induce regeneration in mammals. Dr. Tsonis has published nearly 120 papers and 2 books.

Prof. Jonathan Widom, Northwestern University, USA

Jonathan Widom received his BA in Chemistry from Cornell University and his PhD in Biochemistry from Stanford University. He was a Jane Coffin Childs Postdoctoral Fellow with Sir Aaron Klug at the MRC Laboratory of Molecular Biology in Cambridge, UK. He then joined the faculty of the University of Illinois, Urbana-Champaign, with appointments in the Departments of Chemistry, Biochemistry and Biophysics and in the Beckman Institute. In 1991, he moved to Northwestern University, where he is now William and Gayle Cook Professor in the Department of Biochemistry, Molecular Biology and Cell Biology and Chemistry Department. His research investigates the biophysical chemistry of DNA and protein-DNA complexes, with a specific focus in the area of chromosome structure and gene regulation.

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