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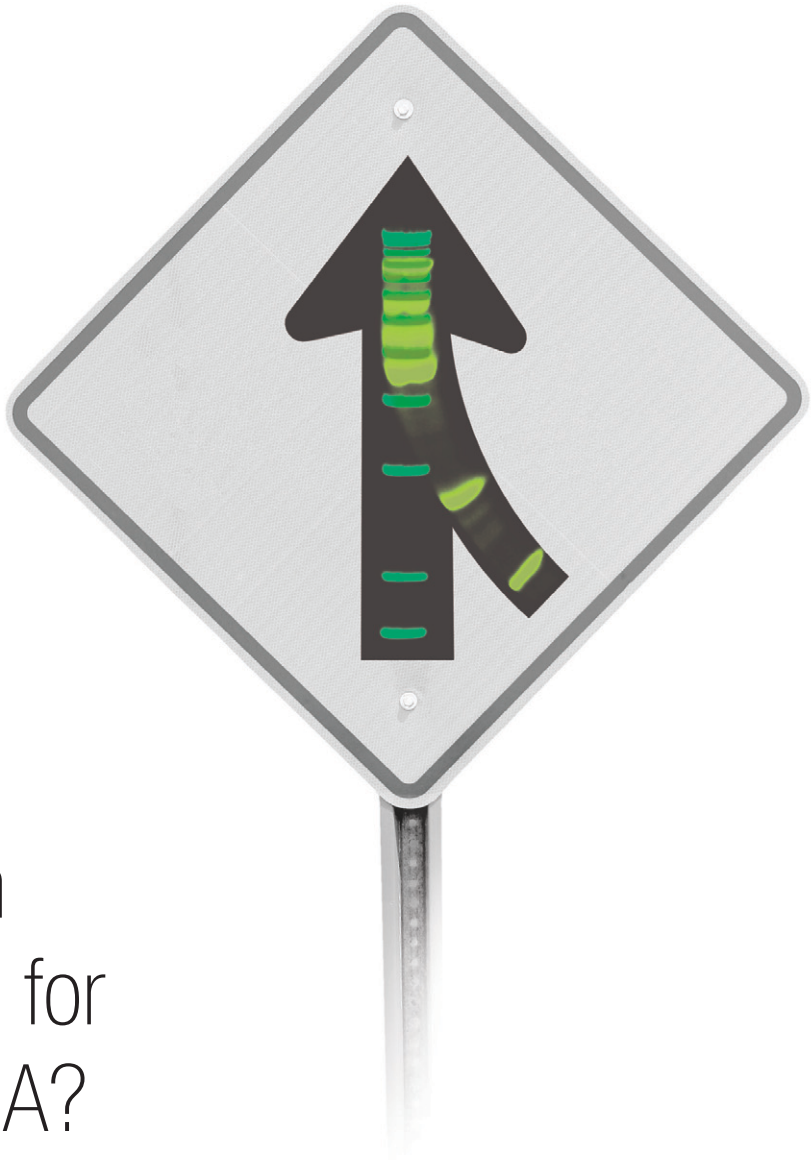

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A*STAR Investigatorships aim to support and promote early independent career development of the next generation of world leaders in scientific research. Applicants should have obtained their PhD not more than 48 months prior to the application date, and should have already demonstrated a strong ability and creativity in research. Applicants with MD-PhD should be in their last year of, or have completed their clinical specialty training at the time of application.

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- Discovery of Biomolecular Mechanisms using Theoretical Approaches
- Drug and Gene Delivery
- Epigenetic Regulation of Gene Expression
- Epithelial Biology
- Metabolic Medicine
- Molecular and Cellular Human Immunology
- Neuroscience
- Pharmaceuticals Synthesis and Nanobiotechnology
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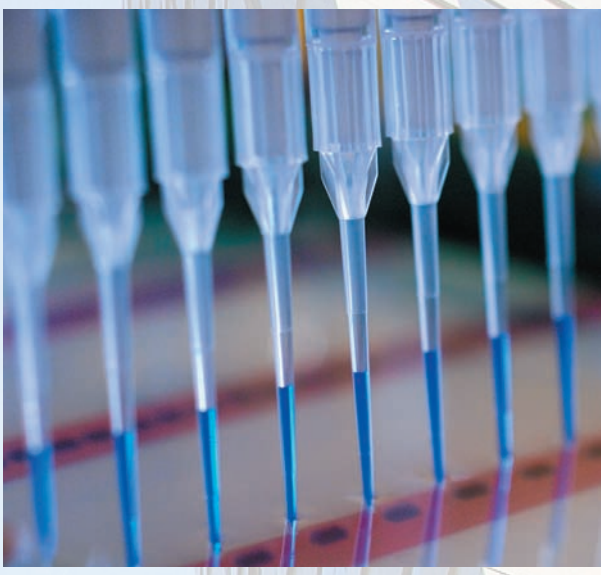
- **Professor Alex Matter**
  Chief Executive Officer, Experimental Therapeutics Centre (ETC), A*STAR



Up to ten shortlisted candidates will be invited to Singapore for interviews and a review based on a scientific presentation, expected to be held in September 2009.

Applications close on 31 May 2009.

Applicants are requested to submit their CVs, including 3 letters of reference from academic referees, and a 5-page research proposal (1 hard copy and 1 soft copy) to:

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SINGAPORE
Agency for Science, Technology and Research

The ExactSTART™ Platform for Transcript Discovery and Profiling: A Process for Tagging Any RNA Species in Less Than 1 Day without Gel Purification

Introduction

The ExactSTART™ Platform* technology enables the user to selectively "tag" the exact 5′ nucleotide of any RNA species—such as mRNA, uncapped primary transcripts, miRNA and other small noncoding RNA—in a total RNA preparation. The tagged RNAs are converted to 5′- and 3′-end-tagged, double-stranded cDNA in less than 1 day, using a simple process that does not require gel purification.

- Discover and profile both coding and noncoding transcripts.
- Prepare template for a variety of applications, such as next-gen sequencing (RNA-seq), cloned libraries, RT-PCR, RACE, etc.
- Accurately map sites of transcription initiation and polyadenylation.
- Preserve the transcript's directional information.

Methods Overview

A general overview of the ExactSTART transcript tagging and amplification process is shown (Fig. 1) and summarized as follows:

1. Treat a total RNA or size-selected RNA sample with a discrete set of RNA modifying enzymes (Table 1) to generate substrates for tagging.
2. Ligate a tagging sequence specific for the downstream application to the exact 5′ nucleotide of the desired RNA.
3. Reverse-transcribe the tagged RNA into cDNA that is now tagged at both ends.

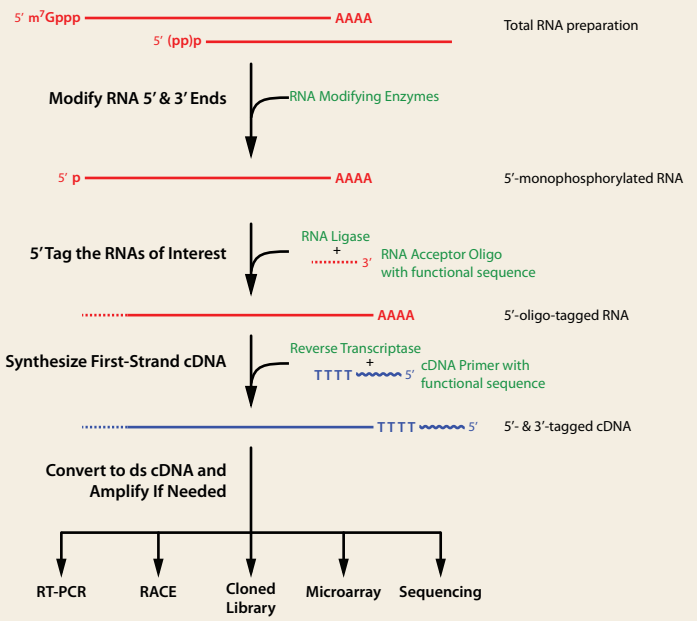


Figure 1. Overview of the ExactSTART™ transcript discovery and analysis process. The actual RNA modifying enzymes used (Table 1) and their order of use is dictated by the RNA species that you wish to tag. The tagging sequence included in the RNA Acceptor Oligo and the cDNA Primer is dependent on the intended downstream application.

Table 1. The ExactSTART™ Platform of transcriptome discovery and profiling tools uses a select group of RNA modifying enzymes with strict enzymatic specificity. Shaded enzymes are unique to EPICENTRE.

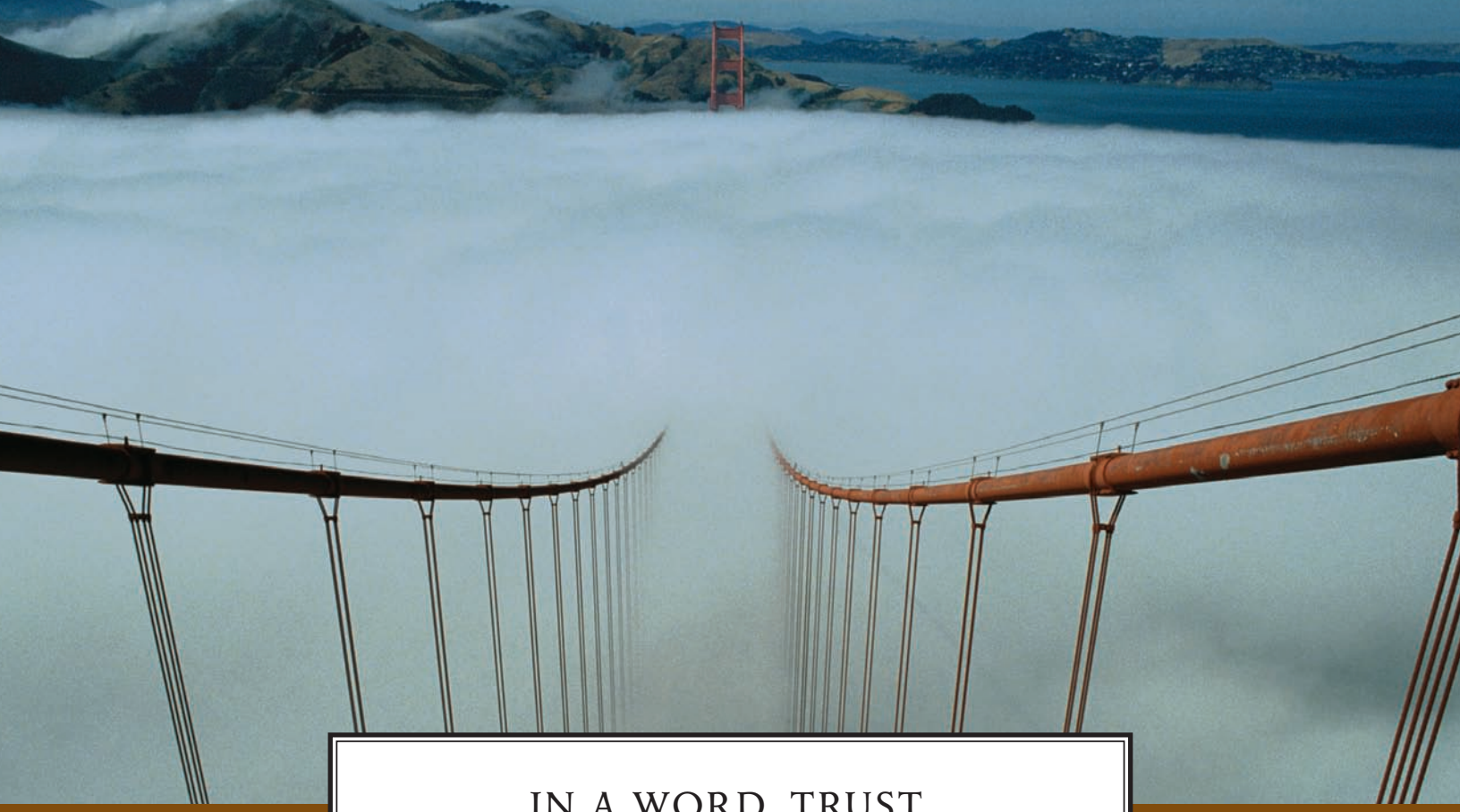
	RNA Modifying Enzyme	RNA Substrate(s) End-Product	Comments
5′ End	RNA 5′ Polyphosphatase*	5′ pppN—— 3′ → 5′ pN—— 3′	Removes γ, β phosphates from RNA with 5′-triphosphorylated end.
5′ End	Tobacco Acid Pyrophosphatase (TAP)	5′ m7GpppN—— 3′ → 5′ pN—— 3′ 5′ pppN—— 3′ → 5′ pN—— 3′	Removes the 5′ cap structure from 5′-capped RNA. Also removes γ, β phosphates from RNA with a 5′-triphosphorylated end.
5′ End	Terminator™ 5′-Phosphate*-Dependent Exonuclease	5′ pN—— 3′ → NMPs	Degrades RNA with a 5′-mono-phophorylated end.
5′ End	APex™ Heat-Labile Alkaline Phosphatase	5′ pN—— 3′ → 5′ HO—— 3′ 5′ pppN—— 3′ → 5′ HO—— 3′	Removes terminal phosphates from RNA.
5′ End	Polynucleotide Kinase (PNK)	5′ HO—— 3′ → 5′ pN—— 3′ 5′ ——Np 3′ → 5′ ——OH 3′	Adds a phosphate to the 5′-hydroxyl end of RNA. Also removes 3′ phosphate.
3′ End	Poly(A) Polymerase	5′ ——OH 3′ → 5′ ——AAAA 3′	Adds a poly(A) tail to the 3′-hydroxyl end of RNA.
	RNA Ligase	5′——OH 3′ (acceptor) + 5′ pN—— 3′ (donor) ↓ 5′ ——— 3′	Joins RNA with 5′ monophosphate to RNA with a 3′ hydroxyl.

Current ExactSTART™ Kits

- ExactSTART™ End-Tagged Double-Strand cDNA Synthesis Kit for Small RNA
- ExactSTART™ Small RNA Cloning Kit
- ExactSTART™ Eukaryotic mRNA 5′ & 3′-RACE Kit
- ExactSTART™ Full-Length cDNA Library Cloning Kit

We invite you to visit www.EpiBio.com/exactstart/ to learn more about the ExactSTART Platform of products.

*Covered by issued and/or pending patents; see www.EpiBio.com/legal.



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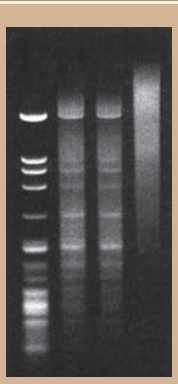

Ligation of blunt-ended HaeIII fragments of Lambda DNA using various amounts of T4 DNA Ligase (400,000 cohesive end units/ml) in a 20 µl reaction volume. Reactions were incubated for 30 minutes at 16°C.

Ligation of HindIII fragments (4-base overhang) of Lambda DNA using 1 cohesive end unit (1µl of 1:400 dilution) of T4 DNA Ligase. Reactions were incubated at 25°C.

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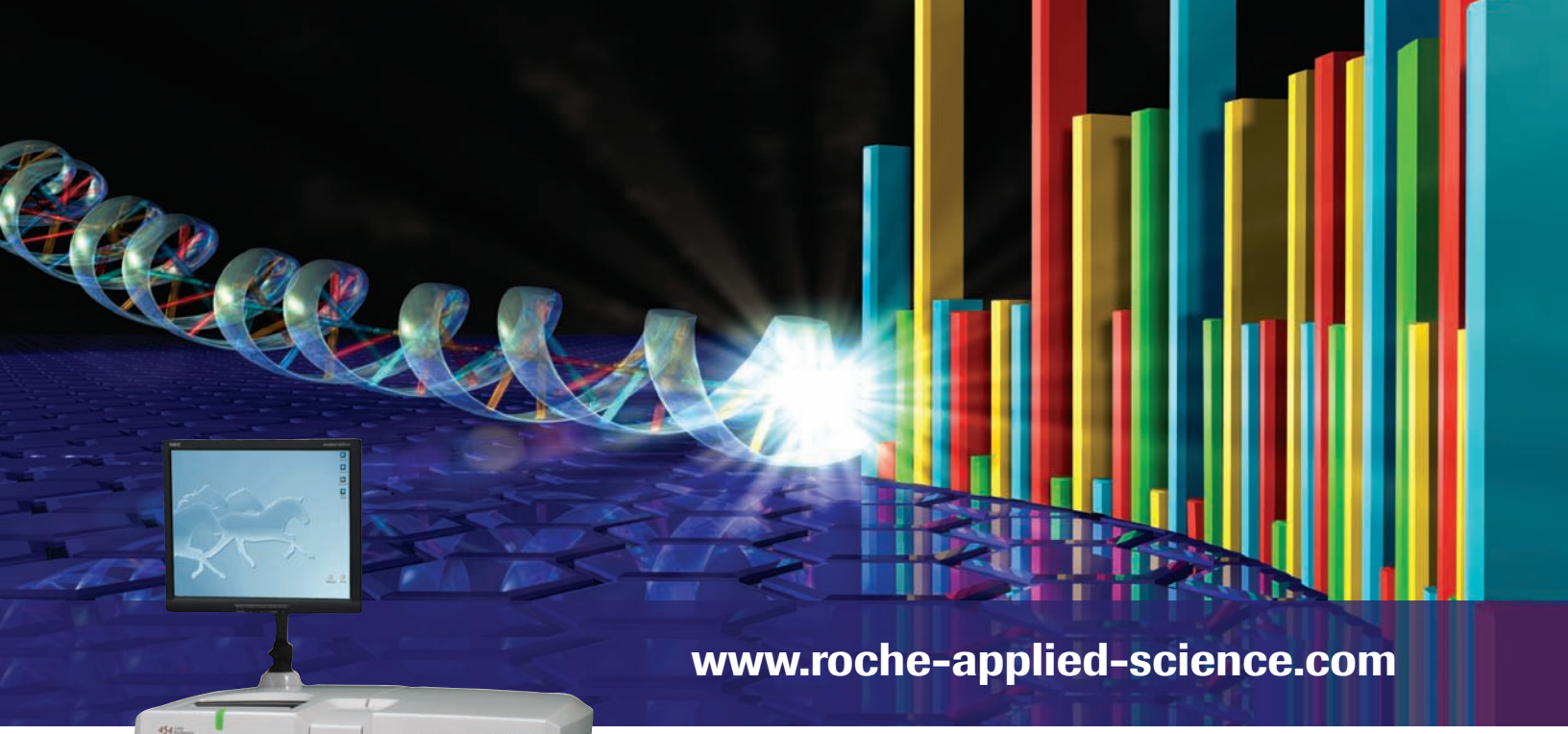

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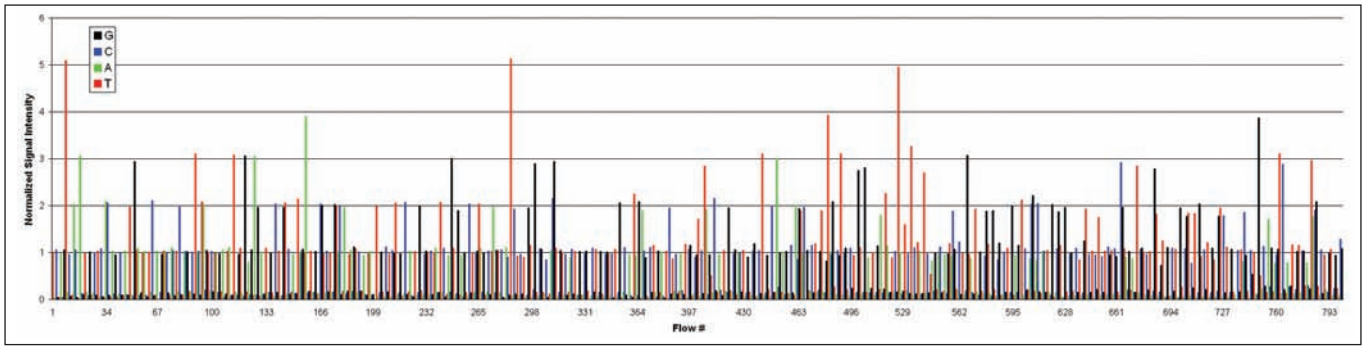

DNA Sequencing Flowgram: Each bar within the flowgram represents a discrete nucleotide (A, T, C, or G) and the height of the bar corresponds to the number of nucleotides detected. The flowgram above represents a 458-base-pair sequencing read from *E. coli* K-12.

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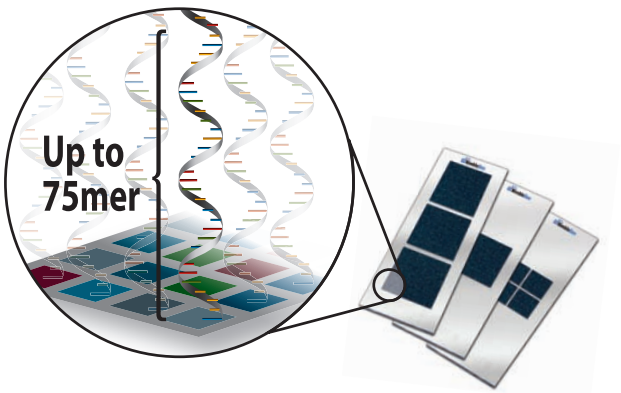

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The Laboratory of Biochemistry and Molecular Biology (LBMB), Center for Cancer Research (CCR), National Cancer Institute (NCI), National Institutes of Health (NIH), Department of Health and Human Services (DHHS), Bethesda, Maryland is seeking a mid-level or senior bioinformatics scientist. The candidate should have a B.S., M.S. or Ph.D. degree in Bioinformatics, Computer Science, or the equivalent. Previous experience with biological research and working knowledge of the statistical tools appropriate to task is preferred.

The successful candidate will have experience analyzing high-throughput genomic datasets derived from ChIP-chip and ChIP-Seq technologies, familiarity with available software tools for analyzing these data, and the ability to develop tools where none are available. Candidate should be proficient in performing basic quality control and analysis such as data set normalization, significance testing, clustering, identification of gene regulatory themes, and mapping of binding events; be able to provide support in custom microarray design and in the visualization and quantification of large datasets; and be able to communicate effectively with and feel comfortable working closely with a group of biochemists and molecular biologists with diverse research interests. Salary will be commensurate with experience and accomplishments, and a full Civil Service package of benefits (including retirement, health, life and long term care insurance, Thrift Savings Plan participation, etc.) Hiring will occur under the Title 42 appointing mechanism, which is a time-limited appointment.

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Cancer Research: Members of the CSHL Cancer Center are involved in studies focused on cancer genomics, signal transduction, mouse models, gene expression, cell proliferation and tumor biology.

Neuroscience: The primary focus of the CSHL Neuroscience program is neural circuits and how disruption of these circuits leads to disorders including autism and schizophrenia. Research is being carried out at the genetic, molecular, developmental, systems, behavioral and computational levels.

Plant Biology: The CSHL Plant Biology program focuses primarily on development, stem cells, morphogenesis, plant genomics and epigenetics.

Genomics and Bioinformatics: The CSHL Genomics program uses state-of-the-art technologies including high-throughput sequencing, copy number variation analysis and transcriptome analysis. Efforts are ongoing to understand genomic variation associated with several human diseases as well as elucidating and characterizing new functional outputs of the genome.

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Tenure Track/Tenure Investigator Positions in Systems Immunology and Infectious Disease Modeling

The National Institute of Allergy and Infectious Diseases (NIAID), Division of Intramural Research (DIR), is seeking several outstanding individuals for its new Program in Systems Immunology and Infectious Disease Modeling (PSIIM — http://www3.niaid.nih.gov/labs/aboutlabs/psiim/).

Modern technology allows the deep analysis of biological systems at multiple levels—from intracellular signaling networks to individual cell behavior to the functioning of a tissue, organ, and even the whole organism. The challenge is not only to collect the large amounts of data these technologies can generate, but also to organize it in a manner that enhances our understanding of how such systems operate. To do this, it is necessary to develop quantitative models that can be used to predict behavior of these complex systems.

Achieving this goal requires an interdisciplinary effort, and for this reason PSIIM is organized as an integrated team of scientists and support staff. Within PSIIM, there will be groups with expertise in the areas of computational biology, bioinformatics, proteomics, genomics, cell biology, immunology, and infectious diseases. These groups will have access to the latest technology for gene expression profiling, high content screening of RNAi libraries for the discovery of pathway components, imaging tools, genomic and proteomic analysis, cores for the genetic manipulation of animals, and a substantial computer infrastructure. They will also have access to BSL-3 facilities for working with infectious agents of high priority for human health and biodefense.

Although PSIIM has been established within NIAID and has an immune/infectious disease focus, it is also expected to play a major role in fostering the growth of systems biology efforts throughout NIH and involving diverse biomedical areas. PSIIM staff will interact extensively with investigators in other components of the NIH intramural research program, including but not limited to the National Center for Biotechnology Information, NIH Chemical Genomics Center, Center for Information Technology, and Center for Human Immunology, all of which have activities emphasizing systems and informatic approaches to biomedicine.

Current groups in the PSIIM include Computational Biology—Modeling and Simulation, Molecular/ Cell Biology—High-throughput Screening, Proteomics, and Immunology. PSIIM is now recruiting for tenure-track or tenure level team leader appointments in the following areas:

Bioinformatics/Biostatistics: The incumbent will lead a group focused on developing and implementing computational tools and statistical methods for the analysis of large-scale genomic, proteomic, and cell biological datasets. The ideal candidate will have a strong background in statistics, mathematics, programming, and modeling biological systems, as well as a strong interest in collaborating with experimentalists to elucidate biological mechanisms through application of informatic methods, including construction of networks suitable for predictive analysis. The group will include expertise in statistics, software development (C++, Java, Perl, SQL, etc.), knowledge of existing and emerging bioinformatic tools, databases and algorithms, and experience with heterogeneous computer environments.

Genomics: The incumbent will be responsible for applying and, when necessary, developing novel methods for the systems-wide analysis of such issues as transcription factor and epigenetic control of gene expression, quantitative measurement of gene expression, and the role of non-coding regions and small RNAs in regulating gene/gene product expression patterns. PSIIM is especially interested in recruiting an individual with a strong interest in the application of these methods to the study of gene regulatory circuits and to the integration of information on cell signaling events, developmental state, and such gene regulatory circuits into comprehensive models of the control of cellular differentiation, for example, of effector CD4+ T cells or iPS.

These positions and the research activities they conduct are fully funded by the intramural research program of NIAID. Each team leader is expected to build a working group consisting of postdoctoral fellows, students, technicians, and staff scientists. The team leaders will work with the program director to help set the goals for PSIIM and to determine how best to reach these goals as an integrated group. To ensure appropriate career trajectories for those joining the PSIIM team effort, NIH has modified its tenure policies to take specific account of contributions made in such a team science setting. Members of PSIIM will be expected to play a major role in development of an integrated computational systems approach to biology, the application of these methods to questions of substantial biomedical importance, and the dissemination of the tools and techniques developed in PSIIM across the NIH intramural program and in the extramural academic and industrial spheres. Applicants should be seeking a challenge in which creativity, technical expertise, and a strong desire to achieve in a team setting will be critical for success

Interested candidates may contact:

Ronald Germain, M.D., Ph.D., Program Director, PSIIM, DIR, NIAID, at 301-496-1904 or **rgermain@niaid.nih.gov** for additional information about these positions.

Applicants must have a Ph.D., M.D., or equivalent degree in a relevant field with extensive post-doctoral experience, as well as a strong publication record demonstrating potential for creative research.

To apply, submit your curriculum vitae, bibliography, and a detailed statement of how your expertise can contribute to the success of the PSIIM program to Wanda Jackson at **NIAID.DIR.Search@niaid.nih.gov**. In addition, three letters of reference must be sent directly from the referee to Robert Hohman, Ph.D., Chair, NIAID Search Committee, c/o Wanda Jackson at **NIAID.DIR.Search@niaid.nih.gov** or 10 Center Drive, MSC 1356, Building 10, Room 4A22, Bethesda, MD 20892-1356. Email is preferred. **Completed applications MUST be received by May 1, 2009.**

Further information regarding the DIR laboratories is available at **http://www3.niaid.nih.gov/about/organization/dir/default.htm**, and information on working at NIAID is available on our Web site at **http://www.niaid.nih.gov/careers/dps**.

For more information about the NIAID systems biology program, please visit **http://www.nih.gov/catalyst/2006/06.09.01/page1.html**

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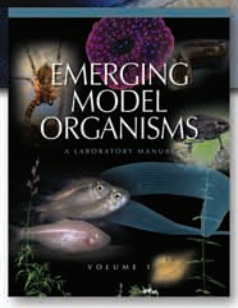
EMERGING MODEL ORGANISMS

A Laboratory Manual, Volume 1



Until recently, a small number of model organisms has been the focus of most research in molecular, cellular, and developmental biology. But in the last few years, due in part to increased interest in questions of evolution, technical advances in selectively altering gene expression patterns, and the reduced costs of genome sequencing, the range of organisms used for research is greatly expanding. *Emerging Model Organisms, Volume 1,* introduces the reader to this new generation of model organisms, providing a diverse catalog of potential species useful for extending research in new directions. In this volume leading experts provide chapters on 23 emerging model systems, ranging from bat and butterfly to cave fish and choanoflagellates; cricket and finch to quail, snail, and tomato. Subsequent releases of the *Emerging Model Organisms* series, already in preparation, will focus on additional species.

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