



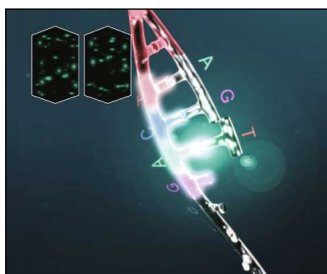
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In 2005, the Genome Sequencer 20 System was launched

- Read length: 100 bases
- 20 million bases in less than 5 hours

In 2007, the Genome Sequencer FLX System was launched

- Read length: 250 to 300 bases
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Available in 2008, the Genome Sequencer FLX with improved chemistries

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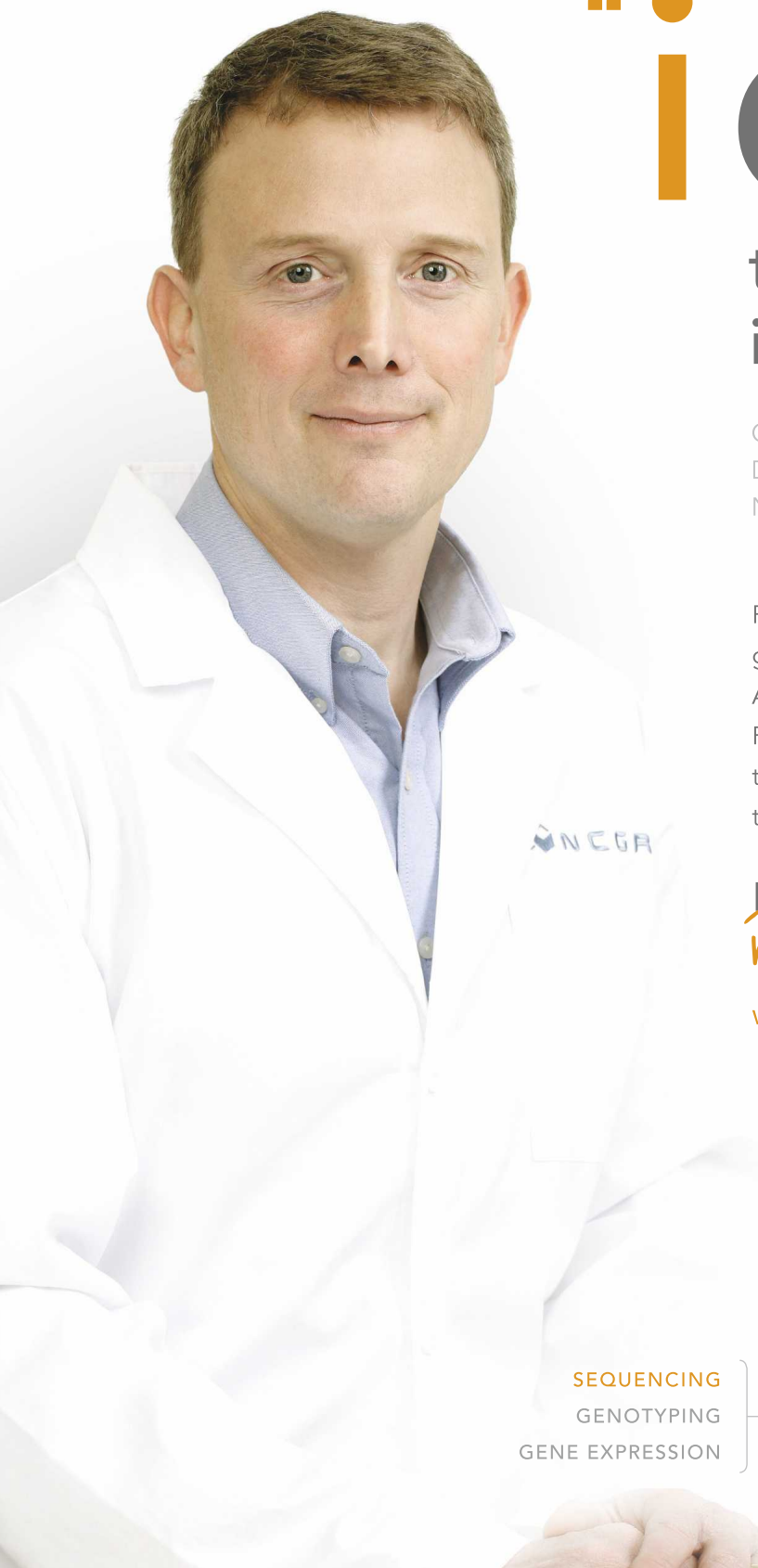
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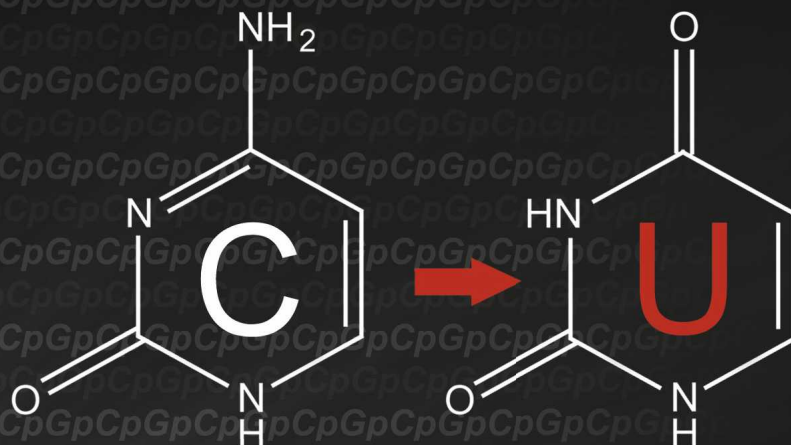
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	Human Genomic DNA	D5011	\$182.00
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Proven... (selected citations)

1. Jong-Yeon Shin, *et al.* The EMBO Journal, Jan 2008; 27, 168-178
2. Masayo Kagami, *et al.* Nature Genetics, Jan 2008; Letters
3. Lao H. Saal, *et al.* Nature Genetics, Jan 2008; 40, 102-107
4. F. Shafiei, *et al.* Oncogene, Nov 2007; Original Article
5. Yijun Qi, *et al.* Nature, Sep 2006; 443, 1008-1012
6. Paromita Deb-Rinker, *et al.* J. Biol. Chem., Feb 2005; 280, 6257-6260
7. Yukiko Yamazaki, *et al.* PNAS, Aug 2005; 102, 11361-11366



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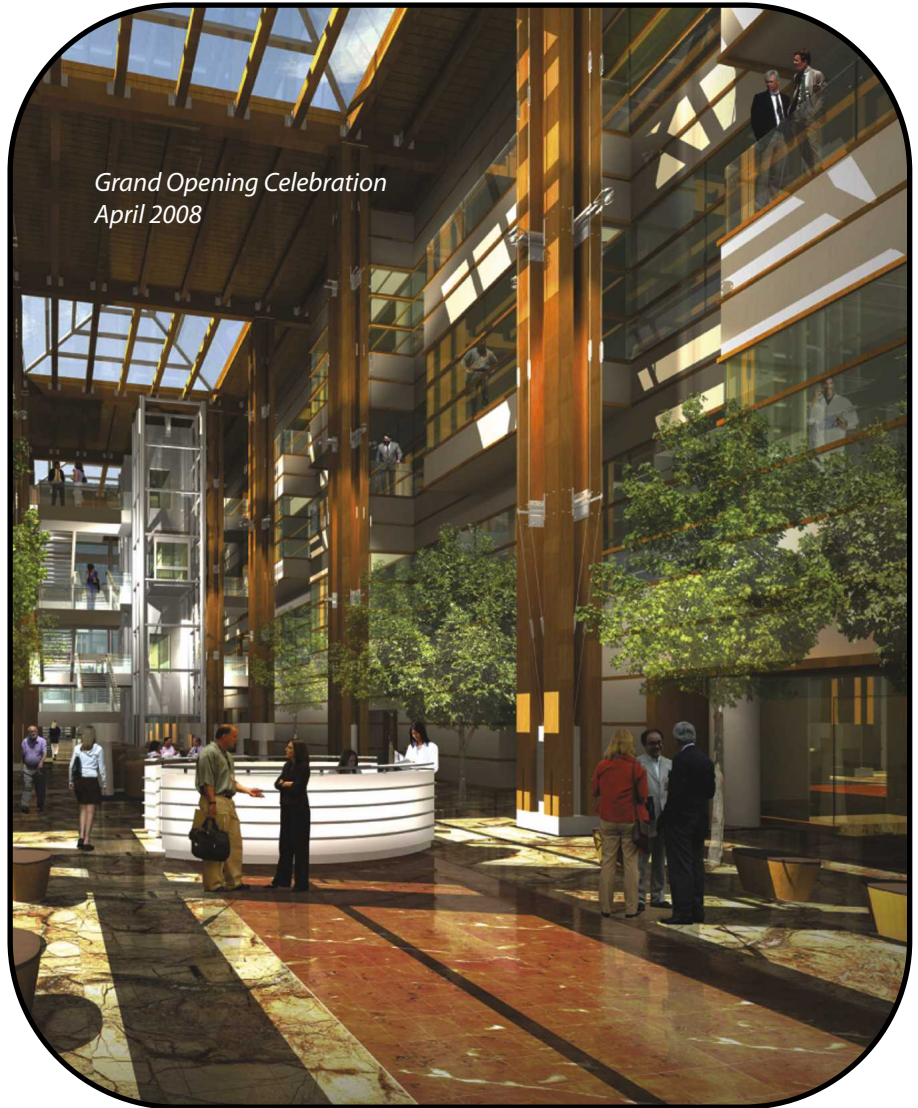
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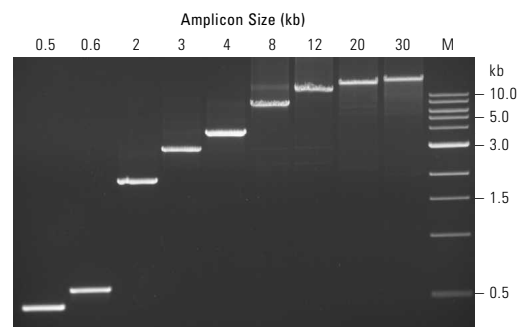
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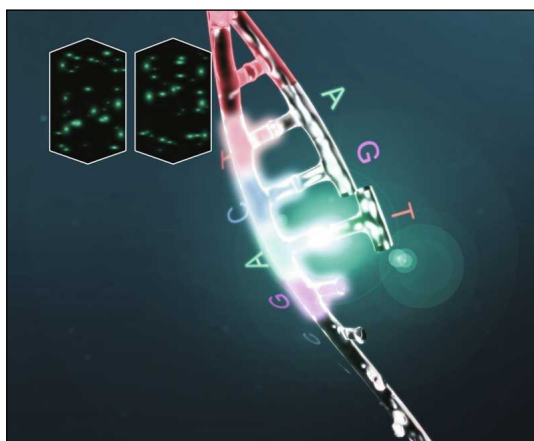


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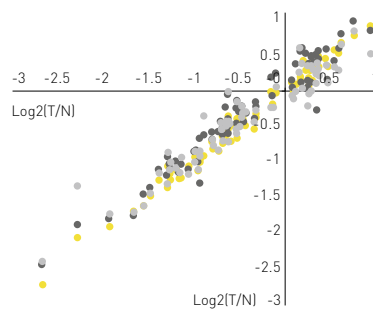


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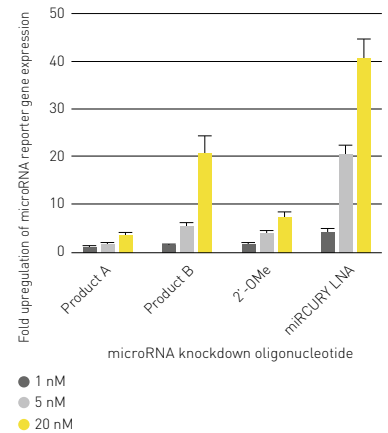


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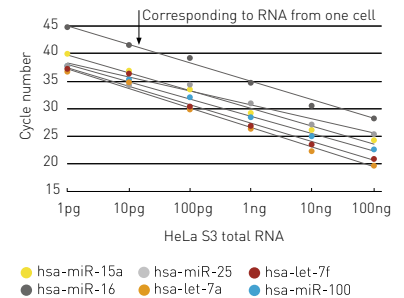
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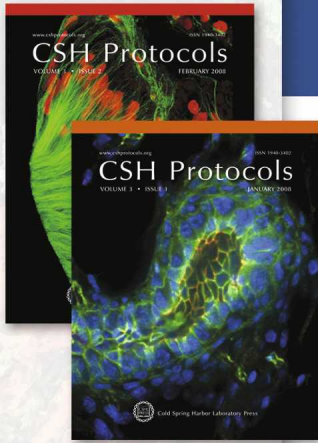
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Our most recent publication is in this issue of *Genome Research*, "A Gene Expression Network Model of Type 2 Diabetes Establishes a Relationship between Cell Cycle Regulation in Islets and Diabetes Susceptibility".

Team members:

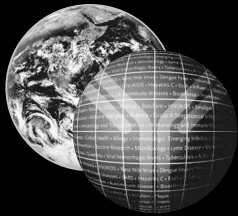
Alan D. Attie, Professor of Biochemistry www.biochem.wisc.edu/attie

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Applicants should send to Alan Attie (adattie@wisc.edu) their CV, a statement describing past research and future goals, and the names and contact information of at least three references.



Help Us Help Millions

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).

Modern technology allows the analysis of immune responses and host-pathogen interactions 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, but also to organize it in a manner that enhances our understanding of how the immune system operates or how pathogens affect their hosts. To do this, it is necessary to develop detailed quantitative models that can be used to predict the behavior of a complex biological system. These models can help explain the mechanisms underlying physiological and pathological responses to infection or vaccination, which can then be employed to design better therapies or vaccines.

Achieving these goals requires an interdisciplinary effort and for this reason the PSIIM is organized as an integrated team of scientists and support staff. Within the PSIIM, there will be groups with expertise in the areas of computational biology, bioinformatics, proteomics, genomics, cell biology, immunology, and infectious diseases. These teams 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 BSL3 facilities for working with infectious agents of high priority for human health and biodefense. Although the 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 the NIH and involving diverse biomedical areas.

Current teams in the PSIIM include Immunology, Computational Biology – Modeling and Simulation, and Molecular / Cell Biology – High-throughput screening. The 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 genomic and proteomic data. The ideal candidate will have a strong background in statistics, mathematics, programming, and modeling biological systems as well as a strong interest in collaboration with biologists for the elucidation of biological mechanisms. The group will include expertise in software development (C++, Java, Perl, SQL etc.), knowledge of bioinformatic tools, databases and algorithms, and experience with heterogeneous computer environments (UNIX, Windows, Mac).

Proteomics: the incumbent will lead a group involved in the development and application of new methods for the determination of protein number, binding affinities, post-translational modification, and other qualitative and

quantitative aspects of protein expression and behavior that are necessary for computer modeling and simulation. Tools such as mass spectrometry and microfluidic-based multiplexed binding assays are expected to be key elements in the efforts of this group. A strong background in protein biochemistry and the relevant instrumentation needed for high-throughput, high-sensitivity analysis is required.

Genomics: the incumbent will be responsible for developing novel approaches to the systems-wide analysis of such issues as transcription factor and epigenetic control of gene expression, the effects of allelic polymorphism on gene expression and function, quantitative measurement of gene expression, and the role of non-coding regions and transcripts such as miRNAs in regulating gene/gene product expression patterns. Knowledge of modern methods in high-throughput analysis of gene transcription, transcription factor binding site identification, analysis of epigenetic modifications, and analysis of gene regulatory circuits is required; bioinformatics experience is desirable.

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 the 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, the NIH has modified its tenure policies to take specific account of contributions made in such a team science setting. Applicants should be seeking a difficult 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 Dr. Ronald Germain, Program Director, PSIIM, DIR, NIAID at (301) 496-1904 or email (rgermain@niaid.nih.gov) for additional information about these positions.

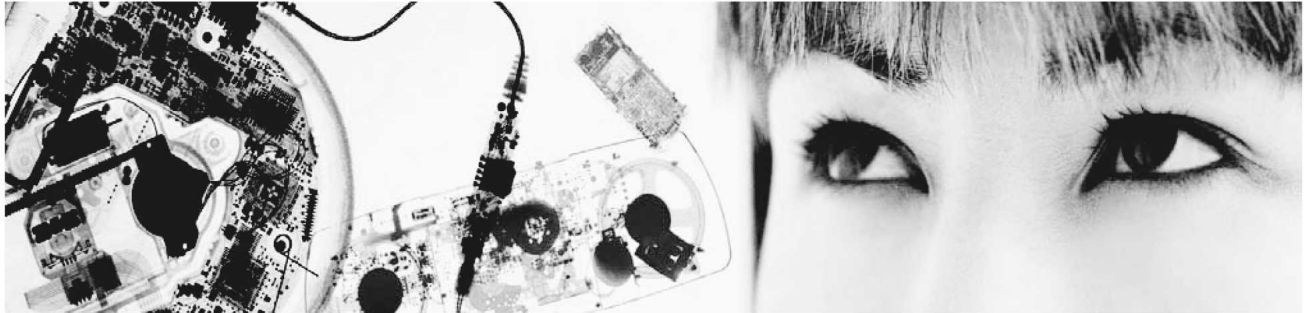
To apply, submit your curriculum vitae, bibliography, and a detailed statement of how your expertise can contribute to the success of the PSIIM program, to Wanda Jackson at NIAID.DIR.Search@niaid.nih.gov. In addition, three letters of reference must be sent directly from your three referees to Dr. Robert Hohman, 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, Maryland 20892-1356. Email is preferred. Completed applications MUST be received by Friday, May 23rd. Please refer to ad #019 for bioinformatics/biostatistics, #020 for proteomics, and #021 for genomics on all correspondence. 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 website at: <http://healthresearch.niaid.nih.gov>

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We are looking for PhD holders to join us in our Data Mining Department and Assistive ICM for Health Monitoring & Rehabilitation (AIM) Programme. The positions are for up to three years and may lead to a long-term position. Successful applicants will receive a competitive salary and a comprehensive benefits package. They may also be provided with assistance for relocation.

The Data Mining Department in I²R, focuses on the effective mining of complex patterns from both structured and unstructured data, as well as the innovative uses of such techniques to discover new knowledge for a wide range of application domains. With a unique history of starting out as a bioinformatics group more than a decade ago, the Department excels in cross-disciplinary data mining research, and it is expanding its success in bioinformatics to other challenging domains such as financial data analysis, business analytics, and social network mining.

The Assistive ICM for Health Monitoring & Rehabilitation (AIM) Programme aims to develop Infocomm & media technologies for healthcare applications. The programme focuses on health monitoring & rehabilitation, especially for chronic disease patients (for example, CVD, stroke) and elderly. The programme explores systems and solutions for physiological and physical monitoring, as well as for sensorimotor and cognition rehabilitation. The programme will also develop technologies to enhance safety and independent living.

Interested applicants, please fill up the online application form in the career section of our website. Look for the position with this reference number: GENOME 2008/01



Institute for
Infocomm Research

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XX INTERNATIONAL CONGRESS OF GENETICS, BERLIN, 2008

BERLIN, GERMANY, JULY 12 – 17, 2008

Genetics reveals the structure, function and evolution of living systems.

Genomics revolutionized genetic research. Now, complete annotated genome sequences are available for the human, our closest relative, the chimpanzee, and for many other model organisms. Multiple genomes have been compared and scrutinized for past and ongoing processes of variation, adaptation and speciation. Traces of the foregoing RNA world show it to be far more influential than previously suspected. Comprehensive maps of genome variation and polymorphism paint a rich picture of our population and evolutionary history and illustrate new strategies that will explain genetic, epigenetic and environmental contributions to disease risk. Transcriptomes comprehensively documenting gene expression and proteomic data sets are being built into functional networks and systems. Bioinformatics and modeling of genomic data attempt to predict and explain the functional architecture of genomes across the diversity of organisms.

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(selection)

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- › Biodiversity
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- › Computational genetics and systems biology
- › Development of multicellular organisms
- › Epigenetics and chromatin
- › Evolutionary genomics, adaptation, speciation
- › Human evolution
- › Human genetics and human disease
- › Metagenomics
- › Neurogenetics
- › RNA world
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