IIeasy

Introducing the Genome Analyzer$_{IIe}$

Easy workflow. Easy data analysis. Easy access to next-gen sequencing. The Illumina® Genome Analyzer$_{IIe}$ delivers proven Illumina technology and industry-leading data quality at an affordable cost.

- Up to 40 Gb of output per run with 2 x 150 bp reads enables an expansive range of applications—including targeted resequencing, RNA-Seq, ChIP-Seq, and small- to medium-sized genome resequencing
- Simplest next-gen sequencing workflow
- Easy-to-us sample prep kits and simplified data analysis
- Flexibility to upgrade to Genome Analyzer$_{IIx}$ performance as your research needs expand

Learn more at www.illumina.com/GAIIe

illumina®

Introducing HiSeq™ 2000

Redefining the trajectory of sequencing.

What if you could:

- Sequence a normal and a cancer human genome at 30x coverage?
- Perform gene expression profiling on 200 samples?
- Sequence a genome on one flow cell and its epigenome and transcriptome on the other flow cell?

Each in a single run?

Now you can with HiSeq 2000. It's a new standard in output, user experience, and cost-effectiveness.

Sequence on a scale never before possible.

Learn more at www.illumina.com/HiSeq2000

illumina®

You know genomics is the future of medicine. Do you have the right partner to take you there?

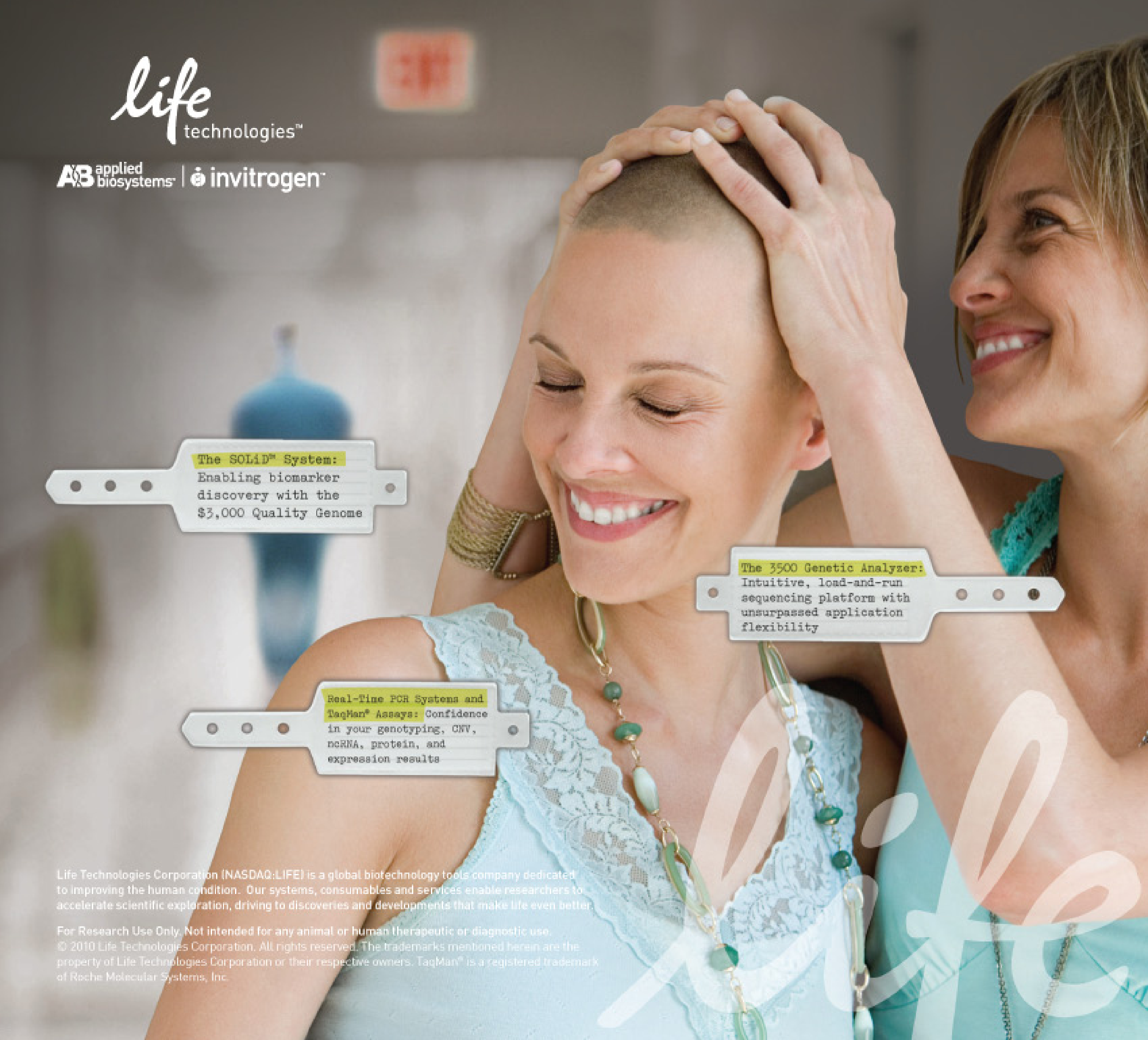
Genomic discoveries are transforming medicine.
But what is the best combination of technologies to help meet your research objectives?

With Life Technologies as your partner, you get more than just a supplier, you get a dedicated guide. For over 25 years, we've developed high-quality, high-accuracy solutions for sequencing, genotyping and expression. Because setting industry standards in genomic research is our mission—and yours.

Visit **LifeTechnologies.com/cancer**

life technologies™

applied biosystems | invitrogen



Life Technologies Corporation (NASDAQ:LIFE) is a global biotechnology tools company dedicated to improving the human condition. Our systems, consumables and services enable researchers to accelerate scientific exploration, driving to discoveries and developments that make life even better.

GS Junior Sequencing System

A *NEW* Scale of Sequencing –

Amplicon Sequencing on Your Benchtop

Amplicon Assay	Samples per Run
HIV drug targets – 5 regions covered by 8 amplicons at 1500x depth (Protease, RT (6), Envelope V3 (2))	6
Gene Sequencing – *e.g.,* **CFTR** 34 amplicons covering 27 Exons at 50X	41
HLA Sequencing – High Resolution Genotyping at 7 loci, 14 amplicons, 500x	10
VDJ Sequencing – *e.g.,* for vaccine response or minimal residue detection of known clonality; 1 locus, 1 amplicon, 12000x	6

Figure 1: Get the right depth and coverage for your amplicon project. You can customize your experimental design to maximize data throughput for optimal sample coverage per sequencing run. Examples of various applications and optimum sample number per run are shown for the GS Junior System.

Bring the power of 454 pyrosequencing to your amplicon projects. Now available, the new small-footprint **GS Junior System** generates 70,000 reads per run, and delivers the performance and long reads (average 400 base pairs) of the GS FLX Titanium chemistry to your benchtop.

- **Detect SNPs, insertions, and deletions.**
- **Discover rare somatic mutations in complex samples based on ultra-deep sequencing of amplicons.**
- **Sequence and analyze collections of human exons for identifications of rare alleles.**
- **Find viral quasispecies present within infected populations.**
- **Identify rare alleles associated with diseases.**

For complete information on the GS Junior System and all of the Roche sequencing solutions, visit ***www.454.com*** or contact your local Roche representative today.

For life science research only.
Not for use in diagnostic procedures.

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SEQUENCING

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Roche Applied Science
Werk Penzberg
82372 Penzberg, Germany

Roche

POSTDOCTORAL POSITIONS

Multiple postdoctoral positions are available in the Human Genetics and Genomics Program at the University of Missouri-Kansas City School of Medicine. This growing program, established and led by Prof. Hong-Wen Deng, encompasses all relevant research fields related to identifying and characterizing genes and their functional contribution to complex human disorders, with a focus on osteoporosis and related health problems. Applicants must have a Ph.D. and/or a M.D. degree. Background and prior experience in human genetics and/or bone biology is desirable. Interested candidates should apply online at our website **www.umkc.edu/hr/jobsearch**. Please make sure to include a research statement, curricula vitae and at least 3 references. This information should be submitted into one PDF or Microsoft Word document.

Position 1 (Molecular/Cellular Bone Biology): The successful candidate will participate in molecular bone biology research projects aimed to identify novel mechanisms of gene regulation for bone formation. Major responsibilities will include performing in vitro and in vivo experiments, such as cell culture, DNA manipulation, Western blot, qPCR, IHC, IF, EMSA. ChIP, genotyping and characterizing knockout and transgenic mice, and analyzing research data. Experience in advanced molecular and cellular biology and genetic mouse models is a plus.

Position 2 (Statistical Genetics and Bioinformatics): The successful candidate will involve in data analysis and method development for genome-wide association studies using genomic and sequence data, data modeling and analysis for epigenomic studies, and integrative analysis of genetic variation at multiple biological levels. Applicants must have background in statistical genetics, bioinformatics, or related areas.

Position 3 (Functional Genomics and Proteomics): The successful candidate will participate in functional genomics and/or proteomics research projects for osteoporosis and related diseases (e.g., genome-wide gene expression analyses using microarrays and proteomics analyses using liquid chromatography and mass spectrometry, etc).

Position 4 (Epigenetics and Epigenomics): The successful candidate will involve in developing and executing research projects related to identification and characterization of epigenetic / epigenomic factors associated with osteoporosis and related diseases. Prior experience in chromatin immunoprecipitaion (ChIP) and/or related techniques (e.g., ChIP-chip, ChIP-seq, reporter assay, etc) is necessary.

Position 5 (**Genetic Epidemiology**): The successful candidate will participate in genetic epidemiological research projects for osteoporosis and related diseases (e.g., candidate gene and/or genome-wide association studies, DNA re-sequencing studies, nutrigenetic or nutrigenomic studies, etc).

Multiple-Year Funded Postdoctoral Position at Rice University

Bioinformatic and Statistical Methods to Determine Functionality of Mutations in Cancer-Related Genes and Their Association with Disease

A funded 2-3 years post-doctoral position is available at the Rice University Statistics Department. This is a competitively funded collaboration with Baylor College of Medicine - Texas Children's Cancer Center and Human Genome Center. An active group of researchers conducts a study based on deep sequencing of genomes of children probands with cancer. Applicants should have background in computer science, bioinformatics and/or (bio)statistics. Exposure to genomic studies is a plus.

Qualified candidates should send a CV and two letters of reference to:

Professor Marek Kimmel
Department of Statistics
Rice University
MS 138
6100 Main Street
Houston, TX 77005
Fax (713) 348 5476
Email: kimmel@rice.edu

Rice University is an Equal Opportunity/Affirmative Action/Equal Access Employer

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Postdoctoral position in computational biology to develop algorithms to study transcriptional regulation and epigenetics at Harvard University, MA, USA

Description:
The Mango lab invites applications for a 2-3 year postdoctoral position in the Department of Molecular and Cellular Biology at Harvard University. This position will focus on developing computational statistical algorithms and analyses to study transcriptional/epigenetic regulation in pluripotent and differentiating cells. We combine wet bench approaches with computational biology, in collaboration with the lab of X. Shirley Liu (Biostatistics and Computational Department of Dana Farber Cancer Institute/Harvard School of Public Health), to probe how the gut is made in developing embryos and how environmental cues modify those developmental processes. The fellow will spend half his/her time in the Mango lab and half in the Liu lab.

Mango Lab
http://www2.lsdiv.harvard.edu/mango_lab/

Liu Lab
http://liulab.dfci.harvard.edu/

Interested applicants should submit a letter of interest with a one-page proposal for a possible project, CV, and three references to Susan Mango: smango at mcb.harvard.edu.

Requirements:
Ideally, the applicant should have:
A. a PhD degree in a related field (physical sciences or biology)
B. strong programming skills: ((Python | Perl) & (C | C++ | Java) & R)
C. strong quantitative background (machine learning, Bayesian inference, etc.) or computational genomics experiences (DNA sequence analysis, microarray analysis, etc.)
D. at least two first-author papers in their previous area of research (not necessarily computational biology)

Harvard is an Affirmative Action/Equal Opportunity Employer. Applications from women and minority candidates are strongly encouraged.

Postdoctoral Positions at Cold Spring Harbor Laboratory

Cold Spring Harbor Laboratory is a world-renowned research and educational institution recognized internationally for its excellence in ground-breaking research and educational activities. We invite highly motivated individuals to visit our website at www.cshl.edu to review and apply for current postdoctoral opportunities in the following areas.

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.

Quantitative Biology: The CSHL Center for Quantitative Biology is comprised of scientists in the fields of physics, computer science, engineering, statistics and applied mathematics dedicated to applying quantitative methods to studies in human genetics, genomic, neurobiology, and signal and image processing.

Cold Spring Harbor Laboratory
Human Resources
One Bungtown Road
Cold Spring Harbor, NY 11724
Website: www.cshl.edu

Cold Spring Harbor Laboratory is an Equal Opportunity Employer.

ICSB
edinburgh
2010

EICC Edinburgh

10 - 16 October 2010

The 11th International Conference on Systems Biology 2010
continues it's annual series in the famous historic city of Edinburgh, Scotland

The ICSB serves as the main meeting for The International Society for Systems Biology (ISSB) who aim to help coordinate researchers to form alliances for meeting the unique needs of multidisciplinary and international systems biology research.

- Join us for the latest advances in systems biology
- Find out the new discoveries in pathways, informatics and computing
- Don't miss out on the cutting edge science!

Important Information for ICSB 2010

Session Topics:

- Applications in Medicine
- Functional Genomics and Biological Networks
- Computational Theory in Systems Biology
- The Spatial Dimension of Intracellular Dynamics
- Biomedical Simulations
- Understanding the Brain Function
- Computational Methods and Tools
- Cell Signalling Dynamics
- Systems Biology in Health and Disease
- Parameterising Proteomics
- Biological Rhythms
- Combinational Multi-scale Systems Responses in Biology and Medicine
- Engineering Aspects in Systems Biology
- Systems Biology and Metabolism
- Systems Science Behind Medical Application in Industry
- Biological Noise and Cellular Decision-Making

Keynote Speakers will include:

- Sydney Brenner *(Nobel Laureate)*
- David Rand
- Denis Noble
- Steve Kay
- Luis Serrano
- Thomas Pollard

Important Dates:

5 January 2010	Delegate Registration Open
5 January 2010	Call for Papers Open
15 January 2010	Call for Tutorials Deadline
15 January 2010	Call for Workshops Deadline
3 May 2010	Call for Papers Deadline
2 June 2010	Early Registration Deadline
4 June 2010	Notification of Acceptance
1 October 2010	Pre-Registration Deadline
10 October 2010	ICSB 2010 Tutorials
11 - 14 October 2010	ICSB 2010 Conference
15 October 2010	ICSB 2010 Workshops

www.icsb2010.org.uk

Plant & Animal Genome XIX

The International Conference on the Status of Plant & Animal Genome Research

January 15–19, 2011
Town & Country Hotel, San Diego, California

Speakers

Roger Beachy, USDA/Washington
Joe Ecker, Salk Institute
Ed Green, UC Santa Cruz
Dave Lipman, NCBI, NLM, NIH
Sharon Long, Stanford University
Michael Lynch, Indiana University
Pam Ronald, UC Davis

Workshops

- Abiotic Stress
- Allele Mining
- Animal Epigenetics
- Apomixis
- Aquaculture
- Arthropod Genomics
- Banana Genomics
- Barley
- Bioinformatics
- Brachypodium Genomics
- Brassicas
- Cacao Genome Sequencing
- Cassava Genomics
- Cattle/Sheep/Swine
- Citrus Genome
- Coffee
- Comparative Genomics
- Cool Season Legumes
- Cotton Genome Initiative
- Cucurbit
- Ecological Genomics
- Equine
- Evolution of Genome Size
- Forage & Turf Plants
- Forest Tree
- Fruit/Nuts
- Functional Genomics
- Fungal Genomics
- Gene Expression Analysis
- Genomics Assisted Breeding
- Genomics for Disease Resistance
- Grape Genome Initiative
- Grass Genome Initiative
- Host-Microbe Interactions
- Large Insert DNA Library
- Lolium Genome Initiative
- Maize
- Molecular Markers
- Mutation Screening
- Oats
- Ornamentals
- Phylogenomics
- Plant Cytogeneics
- Plant Interactions/Pests
- Plant Introgression
- Plant Reproductive Genomics
- Polyploidy
- Population & Conservation
- Poultry
- Proteomics
- QTL Cloning
- Rice Blast
- Rice Functiional Genomics
- Root Genomics
- Sex Chromosomes
- Solanaceae
- Somatic Genome
- Soybean Genomics
- Statistical Genomics
- Sugar Beet
- Sugar Cane
- Swine Genome Sequencing
- Transposable Element
- Weedy & Invasive Plant Genomics
- Wheat Genome Sequencing

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