Big
The Next Thing in Sequencing is small.

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The GS Junior Sequencing System.

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- Benefit from established technology that has enabled hundreds of peer-reviewed publications.
- Rapidly process data using the system’s comprehensive suite of dedicated analysis software.

Figure 1: Example Read Length Distribution of 100,000 reads from *E. coli* K-12 (genome size approximately 4.5 Mb), from a single GS Junior System run.

www.454.com

For life science research only. Not for use in diagnostic procedures.
Choose the 454 Sequencing solution that fits your application needs

<table>
<thead>
<tr>
<th>System</th>
<th>Genome Sequencer FLX System</th>
<th>GS Junior Sequencing System</th>
</tr>
</thead>
<tbody>
<tr>
<td>Throughput</td>
<td>400-600 million high-quality, filter-passed bases per run†</td>
<td>&gt;35 million high-quality, filter-passed bases per run†</td>
</tr>
<tr>
<td>Run Time</td>
<td>10 hours sequencing time, 2 hours data processing†</td>
<td>10 hours sequencing time, 2 hours data processing†</td>
</tr>
<tr>
<td>Read Length</td>
<td>Modal length = 500 bases, Average length = 400 bases†</td>
<td>Modal length = 500 bases, Average length = 400 bases†</td>
</tr>
<tr>
<td></td>
<td><em>Coming later this year: read lengths of up to 1,000 bases</em></td>
<td></td>
</tr>
<tr>
<td>Accuracy</td>
<td>Q20 read length at 400 bases (99% accuracy at 400 bases)</td>
<td>Q20 read length at 400 bases (99% accuracy at 400 bases)</td>
</tr>
<tr>
<td>Reads per Run</td>
<td>&gt;1 million reads</td>
<td>100,000 reads (on average)</td>
</tr>
<tr>
<td>Software Included</td>
<td>GS De Novo Assembler, GS Reference Mapper, GS Amplicon Variant Analyzer</td>
<td>GS De Novo Assembler, GS Reference Mapper, GS Amplicon Variant Analyzer</td>
</tr>
<tr>
<td>Computing Requirements</td>
<td>Cluster recommended (Roche GS FLX Titanium Cluster available)</td>
<td>Linux-based OS on HP desktop computer, included</td>
</tr>
<tr>
<td>Sample Input Requirements</td>
<td>Purified gDNA, amplicons, cDNA, or RNA, depending on the application</td>
<td>Purified gDNA, amplicons, cDNA, or RNA, depending on the application</td>
</tr>
<tr>
<td>Physical Dimensions</td>
<td>Upper assembly: 74.3 cm W x 69.8 cm D x 36.1 cm H including monitor 82.5 cm H Permanently affixed lower assembly: 75.2 cm W x 90.8 cm D x 92.7 cm H Weight: 532 lb.</td>
<td>Benchtop sequencer: 40 cm W x 60 cm D x 40 cm H Weight: 55 lb.</td>
</tr>
</tbody>
</table>

† Typical results using GS FLX Titanium Series chemistry. Average read length and number of reads depend on specific sample and genome characteristics.

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EPICENTRE’s revolutionary Nextera™ technology uses in vitro transposition to prepare sequencer-ready libraries from genomic DNA for multiple sequencing platforms. The technology simultaneously fragments and tags DNA, in a single-tube reaction.

- Use nanogram amounts of starting DNA.
- Prepare sequencer-ready libraries in less than 2 hours.
- Incorporate platform-specific tags and optional barcodes.
- Validated on Roche 454™ GS FLX Titanium™ and Illumina Solexa™ GAI, GAII.

Summary data from Nextera libraries sequenced using GS FLX Titanium chemistry.

<table>
<thead>
<tr>
<th>Sample</th>
<th>Total Reads</th>
<th>% Total Nucleotides Identified</th>
<th>Reference Sequence Length</th>
<th>X Coverage</th>
<th>% Mapped Reads</th>
</tr>
</thead>
<tbody>
<tr>
<td>E. coli</td>
<td>472,007</td>
<td>99.95</td>
<td>4.64 Mb</td>
<td>33.21</td>
<td>88.74</td>
</tr>
<tr>
<td>Plasmid 1</td>
<td>10,657</td>
<td>99.93</td>
<td>19.7 Kb</td>
<td>151.38</td>
<td>93.74</td>
</tr>
<tr>
<td>Plasmid 2</td>
<td>6,291</td>
<td>99.89</td>
<td>6.3 Kb</td>
<td>284.17</td>
<td>86.73</td>
</tr>
<tr>
<td>Soy (W82)</td>
<td>572,162</td>
<td>99.90</td>
<td>973 Mb</td>
<td>0.16</td>
<td>87.64</td>
</tr>
</tbody>
</table>

Visit our blog at: epicentral.blogspot.com/search/label/nextera

For more information visit: www.EpiBio.com/nextera

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Find out how, at www.opengenomics.com/nextgen

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Signaling by diffusible morphogens, such as Hedgehog, Wingless, TGF-β, and various growth factors, is essential during embryogenesis. The establishment of concentration gradients of these morphogens is vital for developmental patterning, ensuring that distinct differentiated cell types appear in the right place and at the right time in forming tissues. Written and edited by experts in the field, this volume explores how morphogen gradients are generated and interpreted during development. The contributors examine the regulation of morphogen synthesis, trafficking, and diffusion, as well as the complex webs of signaling mechanisms and transcriptional responses in recipient cells — whose fates are dictated by these morphogens. Including discussion of the roles of morphogen gradients in various tissues in organisms from yeast to humans, the volume is a vital reference for developmental biologists and cell biologists wishing to know how cell fate is determined during embryogenesis.

2010, 308 pp., illus., index
Hardcover $135

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Write: Cold Spring Harbor Laboratory Press, 500 Sunnyside Blvd., Woodbury, NY 11797-2924
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 1008-base-pair sequencing read from *E. coli* K-12.

Make assembly easier by using the Genome Sequencer FLX System – featuring the longest read length available in next-generation sequencing (up to 1,000 bp) and a powerful suite of analysis tools.

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Abstract & Scholarship Deadline – Sep 14, 2010  
Late-Breaking Abstract Deadline – Oct 11, 2010  
Early Registration Deadline – Nov 8, 2010  
[www.keystonesymposia.org/11A1](http://www.keystonesymposia.org/11A1)

**Genomic Instability and DNA Repair**

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Keystone Resort • Keystone, Colorado • USA  
*Scientific Organizers: Junjie Chen, Karlene A. Cimprich and Michael B. Yaffe*

Abstract & Scholarship Deadline – Sep 30, 2010  
Late-Breaking Abstract Deadline – Nov 2, 2010  
Early Registration Deadline – Nov 30, 2010  
[www.keystonesymposia.org/11B4](http://www.keystonesymposia.org/11B4)

**Changing Landscape of the Cancer Genome**

**June 2011**  
*Scientific Organizers: Lynda Chin, Christoph Lengauer and Michael Stratton*

Deadlines, exact dates and venue to be announced soon. Please visit [keystonesymposia.org/2011meetings](http://www.keystonesymposia.org/2011meetings) for updates on this meeting and others.
University of Maryland, School of Medicine
Postdoctoral Fellow

The newly created Institute for Genome Sciences (IGS) at the University of Maryland, School of Medicine is in a period of rapid expansion. The Institute is led by Claire M. Fraser-Liggett, Ph.D., one of the world’s preeminent genome scientists, and encompasses an inter-disciplinary, multi-departmental team of collaborative investigators with a broad research program related to the genomics of infectious disease agents, human microbial metagenomics, functional genomics and bioinformatics. The impact of the members of IGS on the field of genomics has been substantial, with more than 500 publications during the past 15 years which have been cited more than 30,000 times.

The Institute is currently seeking a postdoctoral fellow with experience in bioinformatics to study human genetic variation. Our main goal is to study “alternative” (non-SNP) forms of genetic variation such as small insertions and deletions (INDELs) and transposon insertions in diverse humans (Mills et al. 2006, Genome Res. 16, 1182-1190; Mills et al. 2007, Trenés Genet. 23, 183-91, 2007; Bennett et al. 2008, Genome Res. 18, 1875-83). A future goal is to develop innovative approaches to study the impact of INDELs and transposon insertions on human traits and diseases, including cancers. The candidate should have advanced informatics skills (ideally, a working knowledge of Java, PERL, Python, MySQL, and web development) and a Ph.D. in a relevant field (Genetics, Biochemistry or Bioinformatics). Experience with data modeling is desirable. Molecular Biology or Biochemistry wet lab skills, a plus. The candidate must be eligible to apply for an NIH postdoctoral fellowship.

Please send your C.V. electronically to:
Scott Devine, Ph.D.
Institute for Genome Sciences
University of Maryland, School of Medicine
Baltimore, MD 21201
sdevine@som.umm.umd.edu

AA/EOE/ADA

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.

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Human Resources
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Mathematical Models for Infectious Disease Dynamics
15–26 February

Virus Discovery in the Clinical Setting
7–12 March

Technologies and Applications for Genome Analysis
13–27 April

Molecular Basis of Bacterial Infection: Basic & Applied Research Approaches
9–15 May

Functional Genomics and Systems Biology
15–25 June

Molecular Neurology and Neuropathology
19–26 June

Practical Aspects of Small Molecule Drug Discovery
4–9 July

Next Generation Sequencing
19–24 July

Human Genome Analysis: Genetic Analysis of Multifactorial Diseases
21–27 July

Design and Analysis of Genetic-based Association Studies
23–27 August

WORKSHOPS

Working with the Human Genome Sequence
10–12 May

Proteomics Bioinformatics
12–18 December

OVERSEAS COURSES

Working with Pathogen Genomes
Ho Chi Minh City, Vietnam
28 February–6 March

Genomic Epidemiology of Malaria
Bangkok, Thailand
23 August–4 September

SCIENTIFIC CONFERENCES 2010

Computational Cell Biology
10–14 February

Therapeutic Applications of Computational Biology and Chemistry: TACBAC
1–3 March

Perspectives in Clinical Proteomics
Training workshop 17–18 March
Conference 19–19 March

Genomic Disorders
24–27 March

The Evolutionary Biology of Caenorhabditis and Other Nematodes
6–9 June

Genomics of Malaria Epidemiology
9–13 June

EBI-Wellcome Trust Bioinformatics Summer School
14–18 June

Sub Nuclear Structures and Disease
27–30 July

Systems Biology: Networks
11–15 August

Wellcome Trust School of Human Genomics
22–26 August

16th Meeting of the European Society for Pigment Cell Research
4–7 September

Signalling to Chromatin
8–11 September

Infectious Disease Genomics & Global Health
12–15 September

Genome Informatics
15–19 September

RNAP2010 - Structure, function and evolution of RNA polymerases
22–25 September

Bridging the Gap on Biomedical Genetics
27–29 October

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June 12 – 15 • Boston, Massachusetts

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Yeast Genetics and Molecular Biology Meeting
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GENETICS SOCIETY OF AMERICA CONFERENCES

and Coming in 2011...

26th Fungal Genetics Conference
March 15 – 20 • Pacific Grove, California

52nd Annual Drosophila Research Conference
March 30 – April 2 • San Diego, California

18th International C. elegans Meeting
June • Los Angeles, California

MouseGenetics 2011
June 22 – 26 • Washington, D.C.

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EMBO | EMBL Symposium

Human Variation: Cause and Consequence

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SESSION | Mechanisms of Mutation

CHAIR | Andrew Wilkie
Weatherall Institute of Molecular Medicine, UK

Peter Arndt
Max Planck Institute for Molecular Genetics, DE

Laurent Duret
University of Lyon, FR

Evan Eichler
University of Washington, US

Adam Eyre-Walker
University of Sussex, UK

Kateryna Makova
Penn State University, US

Gil McVean
University of Oxford, UK

SESSION | Disease Genetics

CHAIR | Leena Peltonen
Wellcome Trust Sanger Institute, UK

Mark Daly
Harvard Medical School, US

Helen Hobbs
Howard Hughes Medical Institute at UT Southwestern, US

Rick Lifton
Yale School of Medicine, US

Kerstin Lindblad-Toh
Uppsala University, SE

Broad Institute of MIT and Harvard, US

Steven McCarroll
Harvard Medical School, US

Mark McCarthy
Oxford Centre for Diabetes, Endocrinology & Metabolism, UK

Mike Stratton
Wellcome Trust Sanger Institute, UK

John Trowsdale
Cambridge Institute for Medical Research, UK

SESSION | Functional Variation

CHAIR | Ewan Birney
European Bioinformatics Institute, UK

Stephan Beck
University College London, UK

Søren Brunak
University of Copenhagen, DK

Vivian Cheung
University of Pennsylvania, US

Manolis Dermitzakis
University of Geneva Medical School, CH

Jorge Ferrer
Institut d’Investigacions Biomèdiques August Pi i Sunyer, ES

SESSION | Population Genetics

CHAIR | Gonçalo Abecasis
University of Michigan, US

Carlos D. Bustamante
Cornell University, US

Richard Durbin
Wellcome Trust Sanger Institute, UK

Paul Flice
European Bioinformatics Institute, UK

Noah Rosenberg
University of Michigan, US

KEYNOTE SPEAKERS

Svante Pääbo
Max Planck Institute for Evolutionary Anthropology, DE

Kári Stefánsson
deCODE genetics, IS

www.embo-embl-symposia.org
The 11th International Conference on Systems Biology 2010 continues its 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!

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- 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
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- Antigen Processing
- Apoptosis
- Auxin Signaling
- Axonal Guidance
- The Biology of Cardiovascular Disease
- The Biology of Schizophrenia
- Calcium Signaling
- Cell–Cell Junctions
- Cilia and Flagella
- The Cytoskeleton
- DNA Damage and Repair
- The Extracellular Matrix
- The Endoplasmic Reticulum
- The Evolution of Gene Networks
- Generation and Interpretation of Morphogen Gradients
- Germ Cells
- The Golgi Apparatus
- Growth Factor Receptors
- Immune Cell Signaling
- Immune Tolerance
- Lipid Cell Biology
- Lymphocyte Cell Biology
- Mammary Gland Biology
- Mechanotransduction
- Membrane Fusion and Exocytosis
- Mitochondria
- Mitosis
- Molecular Motors
- Muscle Cell Biology
- The NF-κB Family
- Nuclear Hormone Receptors
- The Nucleus
- The Origin of Life
- The p53 Family
- Prions
- Prokaryote Cell Biology
- Protein Homeostasis
- Receptor Tyrosine Kinases
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- Regeneration
- RNA Worlds
- Sex Determination
- Symmetry Breaking in Biology
- Synapses
- Transcriptional Regulation
- Wnt Signaling
- The Y Chromosome

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