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Dr. Brian Gregory
Postdoctoral Fellow
The Salk Institute for Biological Studies

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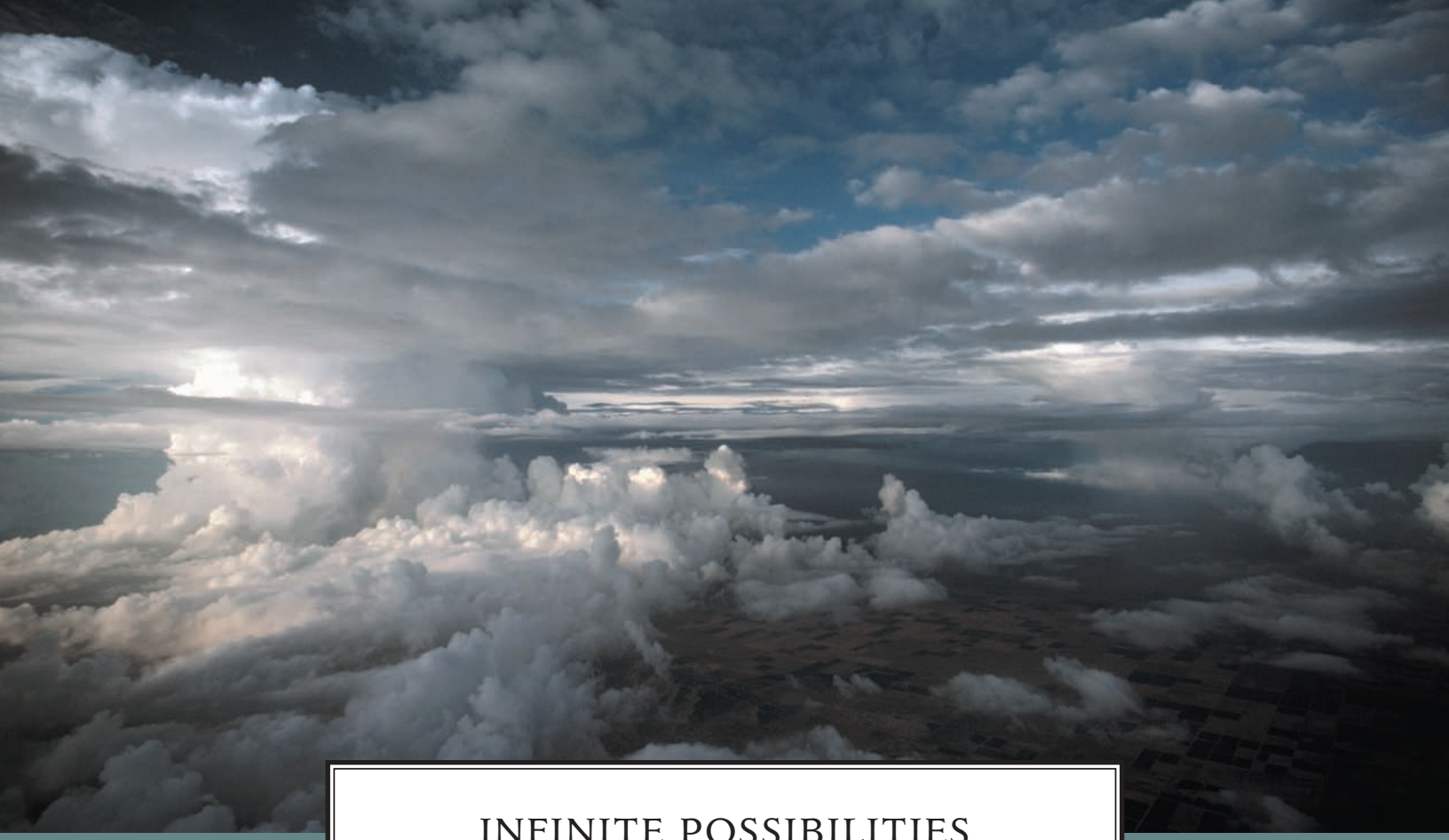
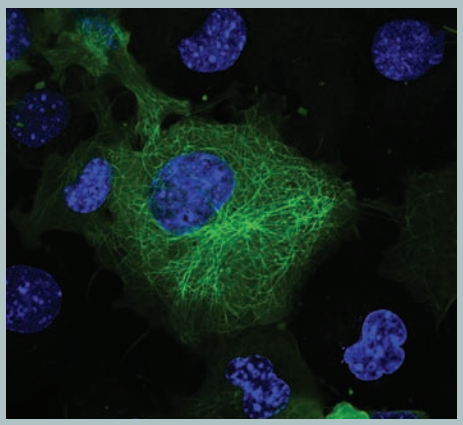


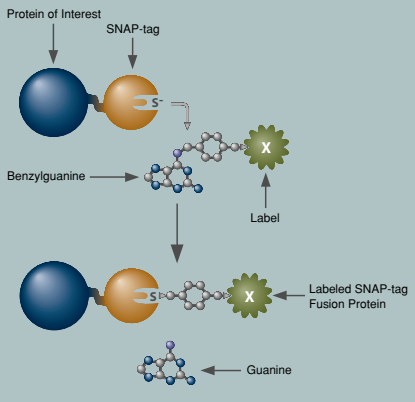
INFINITE POSSIBILITIES

Cellular Imaging & Analysis

NEB introduces SNAP-tag™ and CLIP-tag™ protein labeling systems. These innovative technologies provide simplicity and extraordinary versatility to the imaging of mammalian proteins *in vivo*, and to protein capture experiments *in vitro*. The creation of a single genetic construct generates a fusion protein which, when covalently attached to a variety of fluorophores, biotin, or beads provides a powerful tool for studying the role of proteins in living and fixed cells.



Live COS-7 cells transiently transfected with pSNAPm-Tubulinβ. Cells were labeled with SNAP-Cell TMR-Star (green pseudocolor) for 30 minutes and counterstained with Hoechst 33342 (blue) for nuclei.



SNAP-tag Technology: *SNAP-tag (gold) fused to the protein of interest (blue) self labels releasing guanine.*

Advantages:

Versatile - Compatible systems enable dual labeling

Flexible - Multiple fluorophores allow for choice & flexibility

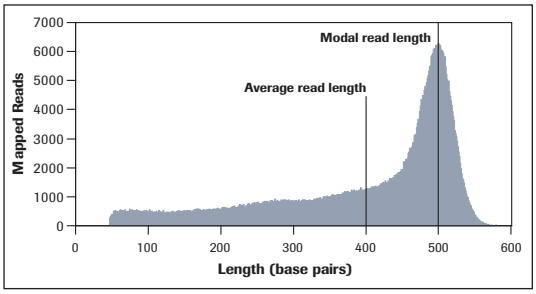
Innovative - A range of applications is possible with a single construct

NEW ENGLAND BioLabs® Inc.

Genome Sequencer FLX System

Really Length Matters

Introducing the GS FLX Titanium Reagents



Example Read Length Distribution of 630,000 reads from *E. coli* K-12 (genome size approximately 4.5 Mb) with a modal read length of 504 bases.

- **Obtain sequencing read lengths of 400 to 500 bases.**
- **Generate more than 1 million sequencing reads per 10-hour instrument run.**
- **Improve performance by using GS FLX Titanium reagents — without instrument upgrades.**
- **Perform more applications with longer sequencing reads.**

Learn more at ***www.454.com***

454 SEQUENCING

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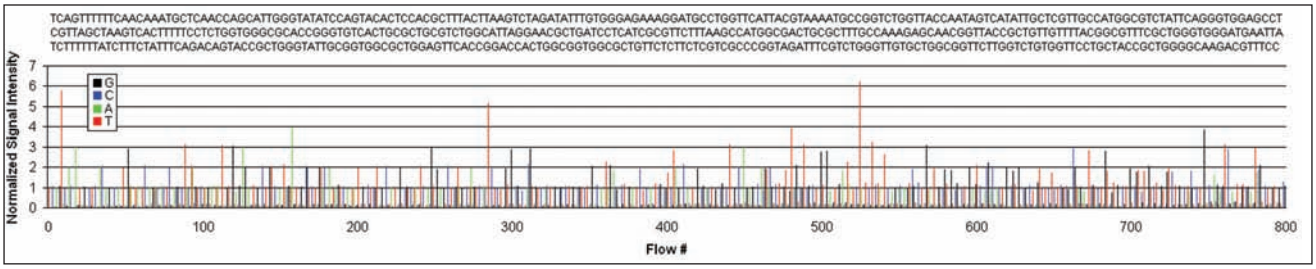
GS FLX Titanium Series Reagents

New Reagents for the Genome Sequencer FLX Instrument



Length Really Matters: Example flowgram showing an 800-flow, 543-base sequencing read that maps perfectly to *E. coli* K-12.

The GS FLX Titanium series reagents enable more than one million sequencing reads per instrument run with a Q20 score at the 400-base-pair position. Requiring no hardware upgrade, the GS FLX Titanium series includes improved consumables and software, increasing the power of the Genome Sequencer FLX System and driving discovery in diverse scientific fields.

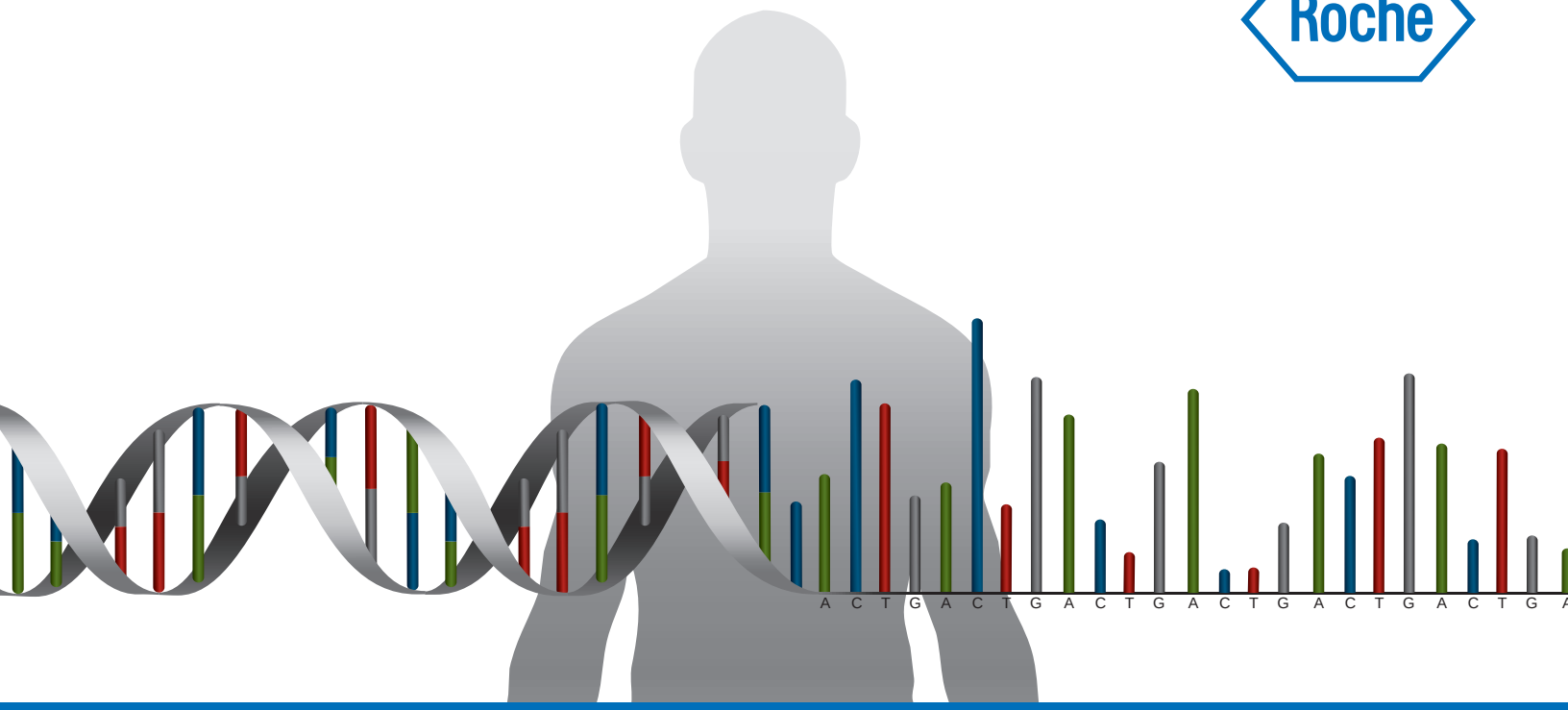
The range of applications supported by the system – including *de novo* sequencing, resequencing of whole genomes and target DNA regions, metagenomics, and RNA analysis – has resulted in more than 275 peer-reviewed publications to date. This latest generation of reagents combined with the Genome Sequencer FLX Instrument delivers:

- **Comprehensive data:** More than one million individual sequencing reads can be generated per run with an average read length of 400 base pairs.
- **Compact data files:** Instrument runs require a minimum of computer memory space (less than 40 gigabytes for all image and metadata files).
- **Accelerated pace of discovery:** Dedicated, easy-to-use analysis tools allow straightforward interpretation of data, leading quickly to biologically meaningful results.

Throughput	400 - 600 million high-quality, filter-passed bases per run*
Read Length	Modal length = 500 bases; Average read length = 400 bases*
Accuracy	Q20 read length of 400 bases (99% at the 400th base, and higher for preceding bases)
Reads per Run	More than 1 million high-quality sequencing reads
Run Time	10 hours
System Robustness	The system does not use complex optics, lasers, or movable parts, ensuring a highly robust instrument; the reagents have a long shelf life

*Typical results: average read length and number of reads depend on specific sample and genome characteristics.

GS FLX Titanium Series performance.



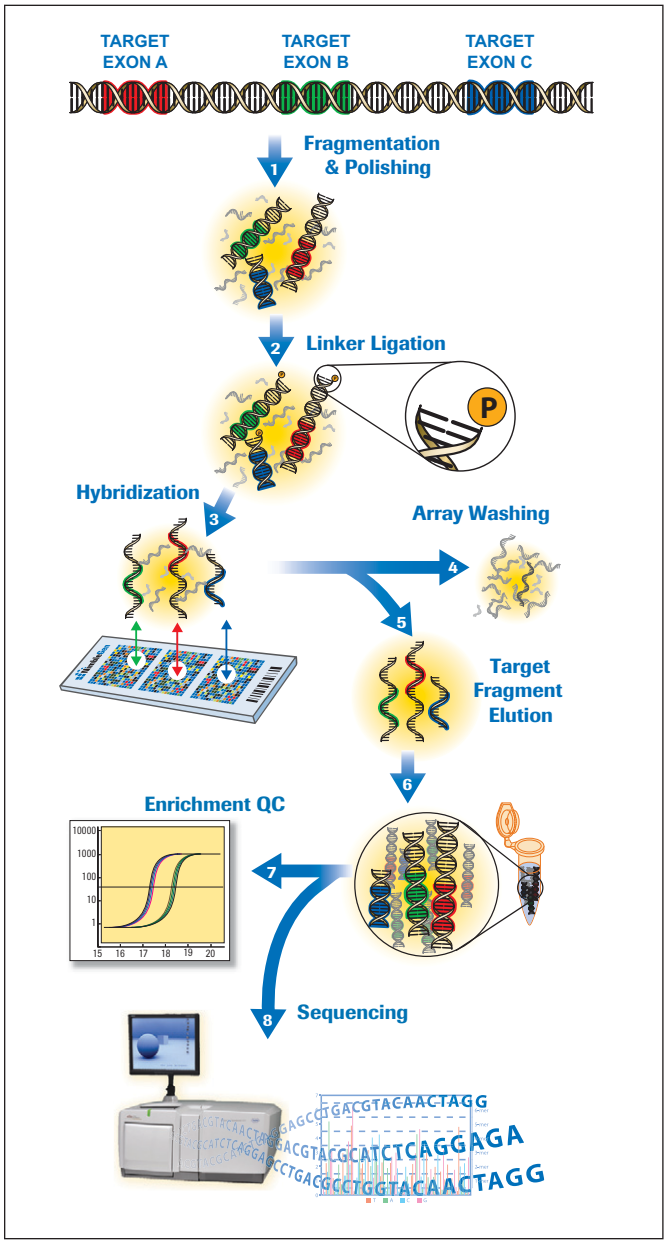
Seize the Exome

NimbleGen Sequence Capture 2.1M Human Exome Arrays

Now Available for 454 Sequencing Systems

Revolutionary sample preparation for targeted next-generation resequencing

Design and perform cost-effective targeted resequencing studies that were effectively impossible with PCR-based methods



▲ **The NimbleGen Sequence Capture Protocol**
1. Genomic DNA sample is fragmented and polished. 2. Linkers are ligated to the fragments. 3. Sample is hybridized to a NimbleGen Sequence Capture 2.1M Human Exome array. 4. Unbound fragments are washed away. 5. Target fragments are eluted. 6. The target-enriched pool is amplified. 7. The enriched, amplified pool is verified by qPCR. 8. Sample is ready for high-throughput sequencing, such as with the Genome Sequencer FLX Instrument from 454 Life Sciences.

2.1 Millon Probes:
Targeted Resequencing Taken to the Next Level

- **Capture the Human Exome:** Use only one 2.1M array to capture ~180,000 exons and ~550 miRNA in your own lab (Table 1).
- **Target Specific Regions of Interest:** Capture up to 30Mb contiguous or non-contiguous human genomic regions with high coverage and specificity, using a 2.1M Custom Delivery array.
- **Reduce Cost:** Save time and cost compared to PCR-based methods.
- **Rely on Design Expertise:** Ensure a high level of specificity and sensitivity for human exome and custom designs with an empirically tested and proven capture design algorithm.

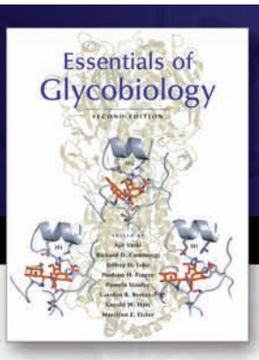
Exome Resequencing of Human Disease Case	
Total size of target region	34Mb
Percentage of 454 unique sequencing reads mapping to exon targets	80%
Percentage of bases with 1x coverage	91%
Median fold coverage	8

▲ **Performance Data.** NimbleGen Sequence Capture 2.1M Human Exome arrays were used to capture approximately 180,000 coding exons and 550 miRNA exons from a research study using a human disease case sample. Two PicoTiterPlate devices were used to generate ~1Gb of raw sequence on the captured sample using GS FLX Titanium kits (400bp reads; 1,000,000 reads per run) and the Genome Sequencer FLX Instrument. Note the high specificity (80%) and percentage of bases with at least one sequencing read (91%) at a median fold coverage of 8-fold.

NimbleGen

To learn more visit **www.nimblegen.com/seqcap**
or call **(877) NimbleGen / (608) 218-7600**

454 SEQUENCING



ESSENTIALS OF GLYCOBIOLOGY

SECOND EDITION

Edited by Ajit Varki, *University of California, San Diego,* Richard D. Cummings, *Emory University School of Medicine, Atlanta,* Jeffrey D. Esko, *University of California, San Diego,* Hudson H. Freeze, *Burnham Institute for Medical Research, La Jolla,* Pamela Stanley, *Albert Einstein College of Medicine of Yeshiva University, New York,* Carolyn R. Bertozzi, *University of California, Berkeley,* Gerald W. Hart, *Johns Hopkins University of School of Medicine, Baltimore,* and Marilynn E. Etzler, *University of California, Davis*

The sugar chains of cells—known collectively as glycans—play a variety of impressive, critical, and often surprising roles in biological systems. Glycobiology is the study of the roles of glycans in the growth and development, function, and survival of an organism. Glyco-related processes, described in vivid detail in the text, have become increasingly significant in many areas of basic research as well as biomedicine and biotechnology.

This new edition of *Essentials of Glycobiology* covers the general principles and describes the structure and biosynthesis, diversity, and function of glycans and their relevance to both normal physiologic processes and human disease. Several new chapters present significant advances that have occurred since the publication of the first edition. Three sections of note describe organismal diversity, advances in our understanding of disease states and related therapeutic applications, and the genomic view of glycobiology. "Glycomics," analogous to genomics and proteomics, is the systematic study of all glycan structures of a given cell type or organism and paves the way for a more thorough understanding of the functions of these ubiquitous molecules.

The first edition of *Essentials of Glycobiology* represented also a notable experiment in publishing, as it became one of the first electronic textbooks. And, now, in recognition of its wide audience and the changing ways in which researchers and students learn and access information, the new edition of *Essentials* will be made available online simultaneously with the print edition. This novel experiment is the result of the collaborative efforts of the Cold Spring Harbor Laboratory Press, the National Center for Biotechnology Information, and the editors of the book. Written and edited by glycobiologists with experience in teaching and in research, this volume will be an invaluable resource, both for students and for established investigators in fields such as developmental biology, cell biology, neuroscience, immunology, and biochemistry who require a complete yet concise introduction to this burgeoning field.

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Hardcover $158 **ISBN 978-087969770-9**

Contents

Advance praise for the Second Edition:

"The basic principles of glycobiology are clearly articulated in this volume, and the roles of complex carbohydrates in disease are an important read for all biomedical scientists." *—Peter Agre, M.D., Nobel Laureate in Chemistry, 2003*

"*Essentials of Glycobiology* is a major resource for understanding these post-translational biochemical reactions that affect the function and fate of proteins produced by the genes that are profoundly changed by their added sugars." *—Baruch S. Blumberg, Nobel Laureate in Medicine, 1976*

"The second edition of *Essentials of Glycobiology,* superbly printed and illustrated, develops in simple and absolutely precise terms the complicated intricacies of glycobiology. I would have killed to get this encyclopedic treatise 40 years ago when I was working my way through this field." *—Edmond H. Fischer, Nobel Laureate in Medicine, 1992*

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From spirit to physical design, the institute's primary facility embodies and nurtures the sharing of ideas and information. Researchers employed by the not-for-profit HudsonAlpha Institute reside in one wing of the 270,000 square-ft. facility, while a separate wing houses 14 for-profit businesses. The wings are physically bridged with walkways spanning a soaring atrium that features inviting common areas. Proximity to the University of Alabama in Huntsville, the University of Alabama at Birmingham, Auburn University and Vanderbilt University adds to a rich intellectual environment for collaboration, discovery and innovation.

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