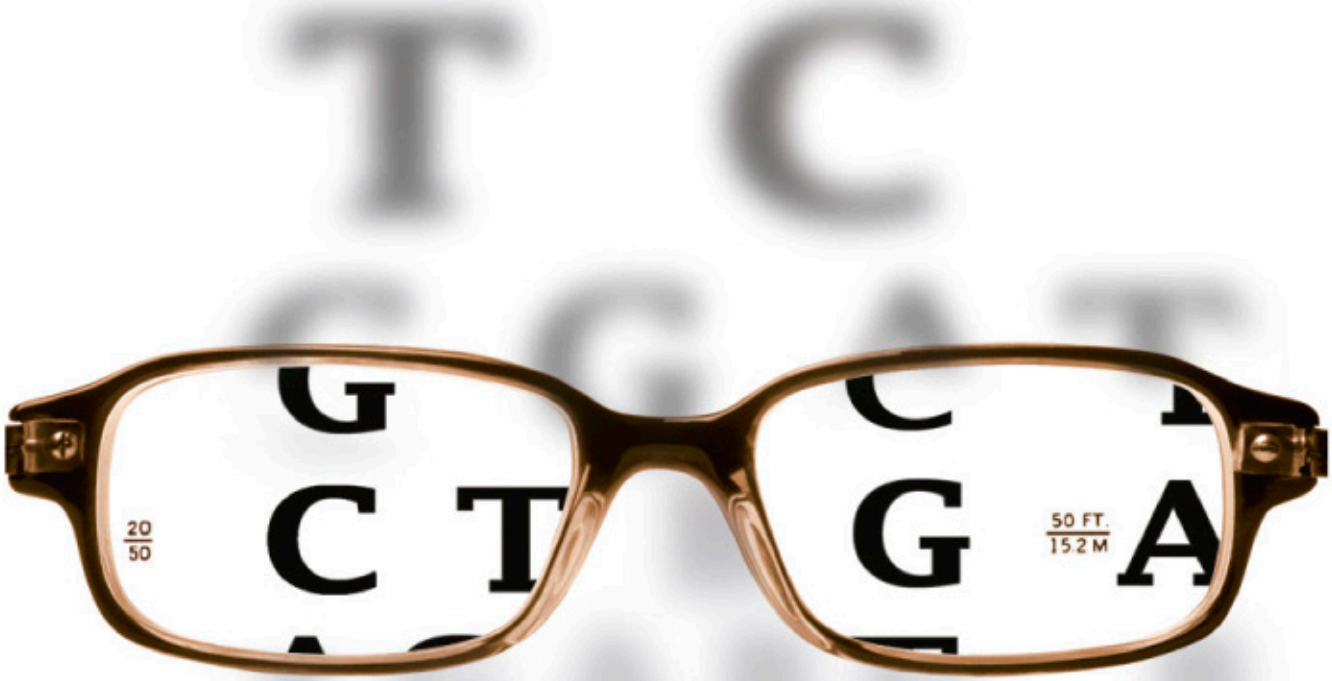


Your DNA lab will move faster if it can see where it's going.

Fragment Analyzer™ replaces lab-on-a-chip for RNA, gDNA, Next Gen Sequencing and SSR Genotyping applications.

- Assess up to 40,000 bp
- 12 or 96 sample format

Fragment Analyzer™ customers since its January, 2012 introduction:

- 20 government institutes and labs in Germany, Austria, Switzerland, Italy, France, the United Kingdom, Japan, China, Brazil, Canada and the U.S.
- 18 leading plant science universities
- 13 medical genetic/genomics testing firms
- 7 U.S. medical schools
- 6 of the 10 biggest seed companies in the world

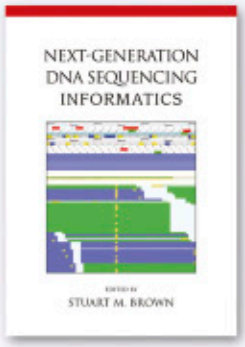
"We found speed, quality, resolution and versatility in the Fragment Analyzer."

— Dr. Sunil Chandran, Senior Scientist, Amyris, Inc.

ADVANCED ANALYTICAL

Phone 515-296-6600 | www.aati-us.com

NEXT-GENERATION DNA SEQUENCING INFORMATICS



Edited by Stuart M. Brown, *New York University School of Medicine*

Next-generation DNA sequencing (NGS) technology has revolutionized biomedical research, making complete genome sequencing an affordable and frequently used tool for a wide variety of research applications. Bioinformatics methods to support DNA sequencing have become a critical bottleneck for many researchers and organizations wishing to make use of NGS technology. This book provides a thorough introduction to the necessary informatics methods and tools for operating NGS instruments and analyzing NGS data. The book also provides extensive reference to best-practice bioinformatic methods for the most commonly used NGS technologies and applications. The book also includes reference to, and guidance on, the setup and use of essential software for NGS data analysis. This is the first book of its kind to address the informatics needs of scientists who wish to take advantage of the explosion of research opportunities offered by new DNA sequencing technologies.

Due December 2012, 241 pp., illus. (48 4C and 15 B&W), index
Hardcover $59
ISBN 978-1-936113-87-3

CONTENTS

Preface

Acknowledgments

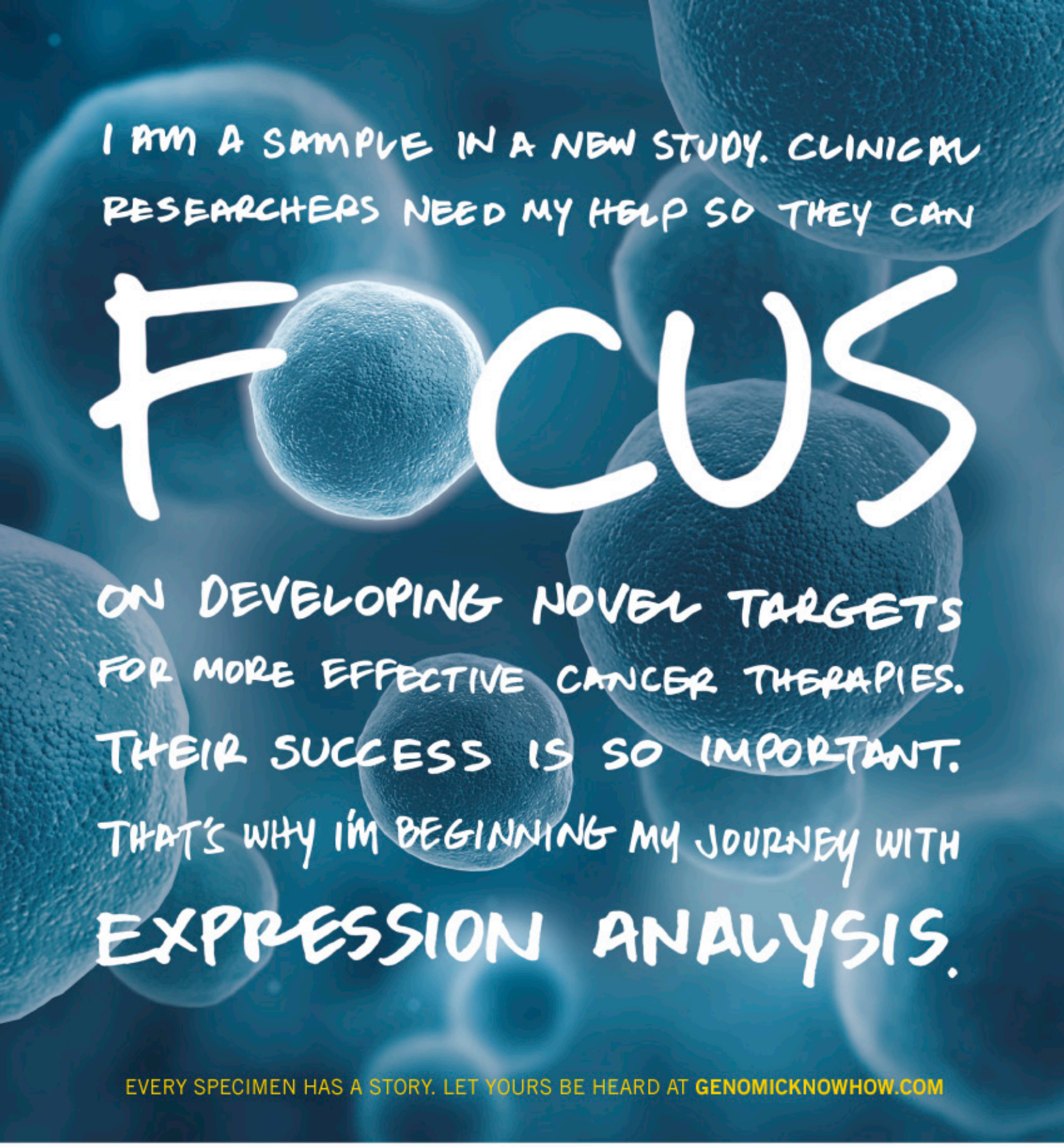
About the Authors

1. Introduction to DNA Sequencing
   Stuart M. Brown
2. History of Sequencing Informatics
   Stuart M. Brown
3. Visualization of Next-Generation Sequencing Data
   Phillip Ross Smith, Kranti Konganti, and Stuart M. Brown
4. DNA Sequence Alignment
   Efstratios Efstathiadis
5. Genome Assembly Using Generalized de Bruijn Digraphs
   D. Frank Hsu
6. De Novo Assembly of Bacterial Genomes from Short Sequence Reads
   Silvia Argimón and Stuart M. Brown
7. Genome Annotation
   Steven Shen
8. Using NGS to Detect Sequence Variants
   Jinhua Wang, Zuojian Tang, and Stuart M. Brown
9. ChIP-seq
   Zuojian Tang, Christina Schweikert, D. Frank Hsu, and Stuart M. Brown
10. RNA Sequencing with NGS
    Stuart M. Brown, Jeremy Goecks, and James Taylor
11. Metagenomics
    Alexander Alekseyenko and Stuart M. Brown
12. High-Performance Computing in DNA Sequencing Informatics
    Efstratios Efstathiadis and Eric R. Peskin

Glossary

Index

www.cshlpress.org



ea

A Quintiles Company

Ribosome FootPrinting

Evolution of NGS Applications

ARTSeq™ (**A**ctive m**R**NA **T**ranslation) provides a 'snapshot' of the ribosomes active in a cell at a specific time point by deep sequencing the ribosome-protected mRNA fragments. This powerful method can be used to:

- Investigate translational control
- Measure gene expression
- Determine rate of protein synthesis, and
- Predict protein abundance

Follow the steps

www.epicentre.com/artseq

epicentre®
an Illumina® company