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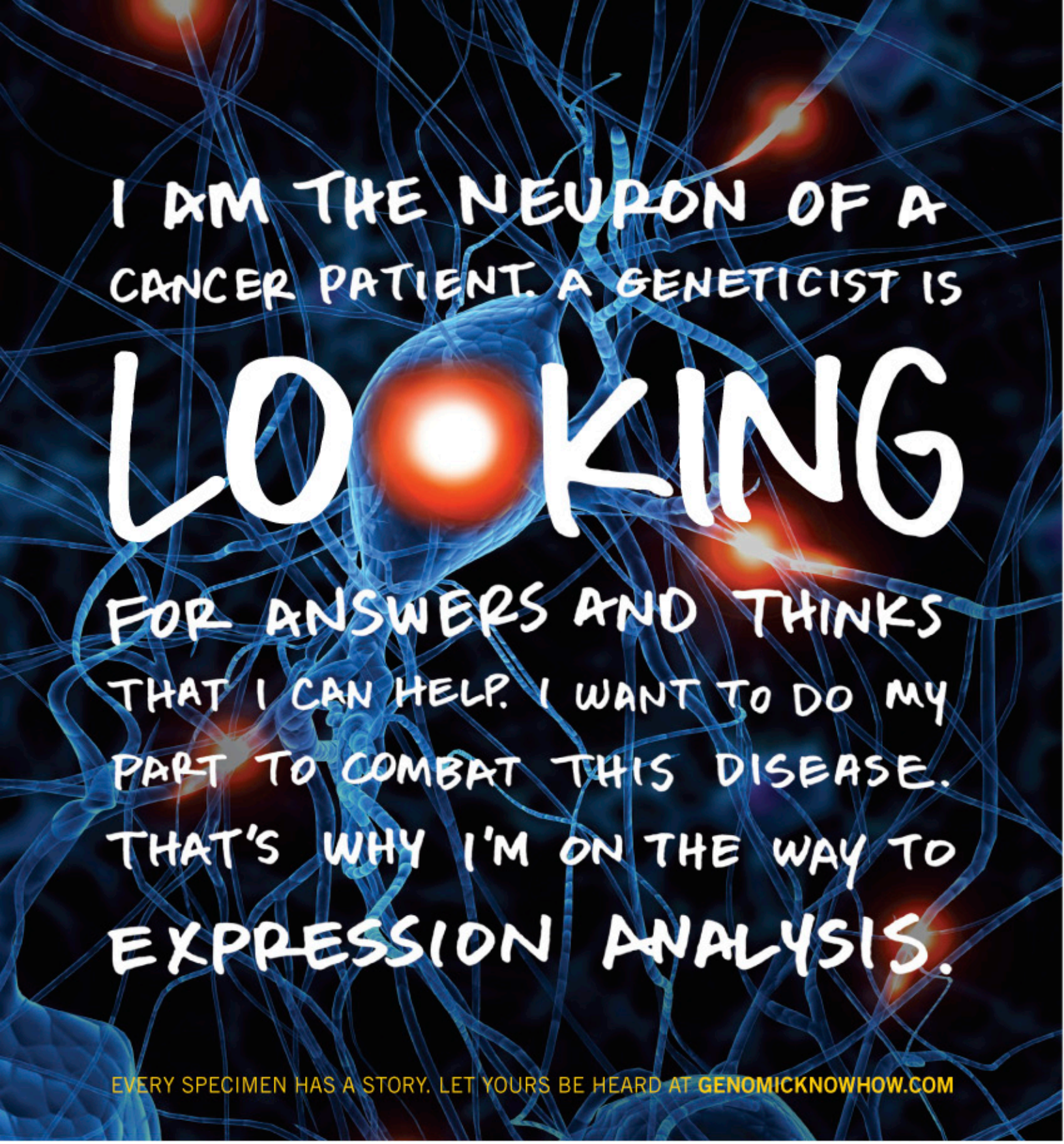

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$$T_M(^\circ C) = \frac{\Delta H^\circ}{\Delta S^\circ + R\ln[\text{oligo}]} - 273.15 \qquad \frac{1}{T_M(Na^+)} = \frac{1}{T_M(1M\ Na^+)} + \left[(4.29 f_{GC} - 3.95)\ln[Na^+] + 0.940\ln^2[Na^+]\right]\times 10^{-5}$$

$$R = \frac{\sqrt{[Mg^{++}]}}{[Na^+]} \qquad \theta = 1 - \left(\frac{K_a([strand2] - [strand1]) - 1}{2K_a[strand2]} + \frac{\sqrt{K_a^2([strand1] - [strand2])^2 + 2K_a([strand1] + [strand2]) + 1}}{2K_a[strand2]}\right) \qquad K_a = \exp\left(\frac{-(\Delta H^\circ - T\Delta S^\circ)}{RT}\right)$$

$$\frac{1}{T_M(Mg^{++})} = \frac{1}{T_M(1M\ Na^+)} + \left[\begin{array}{l} a - 0.911\ln[Mg^{++}] + f_{GC}\times\left(6.26 + d\ln[Mg^{++}]\right) \\ + \frac{1}{2(N_{bp}-1)}\times\left[-48.2 + 52.5\ln[Mg^{++}] + g\ln^2[Mg^{++}]\right] \end{array}\right]\times 10^{-5}$$

$$a = 3.92\times\left(0.843 - 0.352\sqrt{[Na^+]}\times\ln[Na^+]\right)$$

$$d = 1.42\times\left(1.279 - 4.03\times 10^{-3}\ln[Na^+] - 8.03\times 10^{-3}\ln^2[Na^+]\right)$$

$$g = 8.31\times\left(0.486 - 0.258\ln[Na^+] + 5.25\times 10^{-3}\ln^3[Na^+]\right)$$

$$T_m(^\circ C) = \frac{\Delta H^\circ}{\Delta S^\circ + R\ln\left([strand1] - \frac{[strand2]}{2}\right)} - 273.15$$

You strive for accurate data in your research, so don't use out-of-date analysis tools.

OligoAnalyzer includes the newest algorithms for determining melting temperature and tools for predicting secondary structure. Inaccurate calculation of T_m will increase the probability of failed assay design. Original research in nucleic acid thermodynamics at IDT has shown that T_m depends on specific oligo sequence, base moiety, concentration, and the types and concentrations of cations in the buffer. OligoAnalyzer also provides access to new UNAFold software for accurate secondary structure prediction.

OligoAnalyzer and other SciTools are available free at www.idtdna.com/scitools

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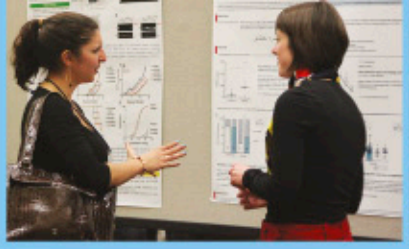

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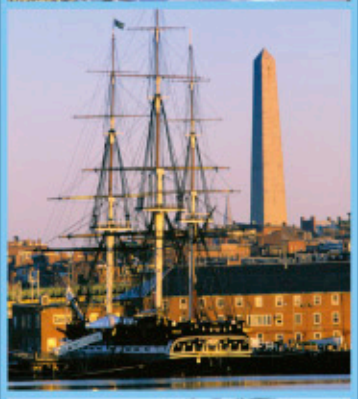


Genomic Instability and DNA Repair

Scientific Organizers: Junjie Chen, Karlene A. Cimprich and Michael B. Yaffe

January 30–February 4, 2011

Keystone Resort • Keystone, Colorado • USA

Keynote Speakers: David M. Livingston, Dana-Farber Cancer Institute, USA
"Genomic Instability and Breast Cancer"
Stephen J. Elledge, Harvard-Partners Center for Genetics and Genomics, USA
"The DNA Damage Response: Making it Safe to Play with Knives"

www.keystonesymposia.org/11B4

Evolutionary Developmental Biology

Scientific Organizers: Sean B. Carroll, Trisha Wittkopp and Nicole King

February 27–March 3, 2011

Granlibakken Resort • Tahoe City, California • USA

Keynote Speaker: Neil Shubin, University of Chicago, USA
"Fossils, Genes and the Evolution of the Vertebrate Limb"

www.keystonesymposia.org/11C1

Environmental Genomics and Disease Susceptibility

Scientific Organizers: Randy L. Jirtle, Moshe Szyf and Frederick L. Tyson

March 27–April 1, 2011

Grove Park Inn Resort & Spa • Asheville, North Carolina • USA

Keynote Speaker: Matt Ridley, Blagdon Seaton Burn, UK
"Nature via Nurture"

www.keystonesymposia.org/11D3

Changing Landscape of the Cancer Genome

Scientific Organizers: Lynda Chin, Christoph Lengauer and Michael Stratton

June 20–25, 2011

Boston Park Plaza Hotel & Towers • Boston, Massachusetts • USA

Keynote Speaker: Tom Hudson, Ontario Institute for Cancer Research, Canada
"Large-Scale Cancer Genomics"

www.keystonesymposia.org/11F3

Additional Meetings of Interest:

Genetics, Immunology and Repair in Multiple Sclerosis
February 15–20, 2011
Taos, New Mexico, USA
www.keystonesymposia.org/11B8

DNA Replication and Recombination
February 27–March 1, 2011
Keystone, Colorado, USA
www.keystonesymposia.org/11C2

Omics Meets Cell Biology
May 8–13, 2011
Alpbach, Austria
www.keystonesymposia.org/11E1

For the most up-to-date information on these and more than 50 other conferences in 2011, please visit ***www.keystonesymposia.org/2011meetings****.*

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- Enable directional sequencing of the library.
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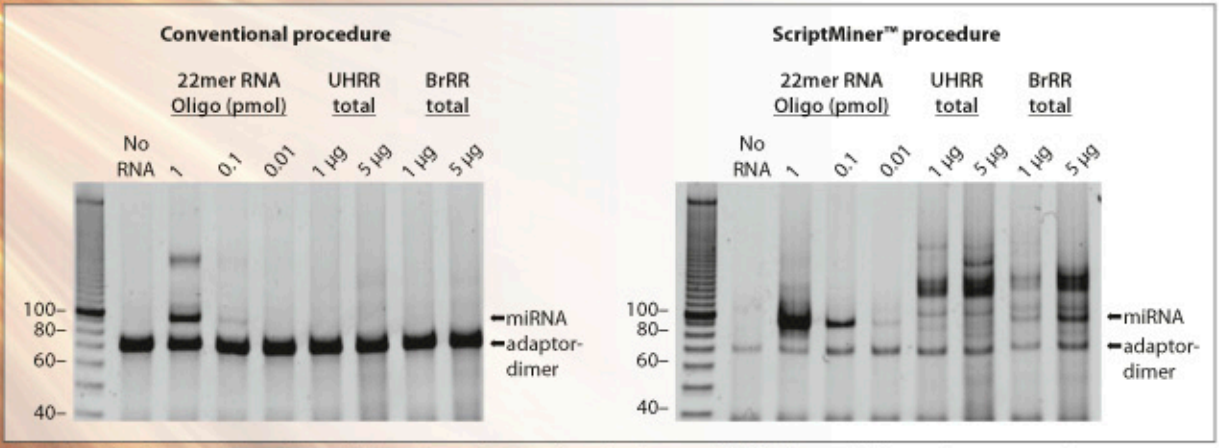
- Obtain more comprehensive capture and sequencing of small RNAs, through an optimized ligation process.

Kits for preparing singleplex (nonbarcoded) or multiplex (barcoded) libraries are available.

**Patent pending*

Summary of sequencing data from ScriptMiner™ libraries.
BrRR, Brain Reference RNA.

RNA Sample	Kit Format	Reads Passing Filter	Reads Aligned to hg19	% Aligned
BrRR	Singleplex	17,272,948	16,823,979	97.40
BrRR	Multiplex	1,384,314	1,380,799	99.75
HeLa	Multiplex	1,560,105	1,555,406	99.70



The ScriptMiner™ procedure substantially reduces adaptor-dimer background. The indicated RNA samples were used to prepare small-RNA libraries, using either a conventional procedure or the ScriptMiner procedure. Samples were examined by denaturing polyacrylamide gel electrophoresis after 12 cycles of PCR. UHRR, Universal Human Reference RNA; BrRR, Brain Reference RNA.

ScriptSeq™ mRNA Library Preparation Kits are also available. For more information, visit:
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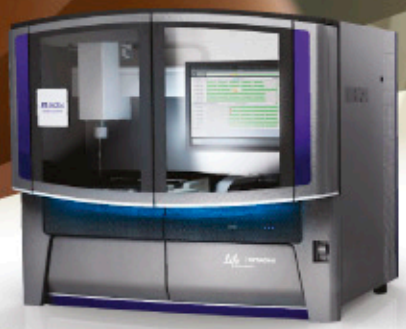

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