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Worldwide Innovative Networking in personalized cancer medicine

JULY 6th–8th 2011
Palais des Congrès, Paris [France]

3rd WIN Symposium
in personalized cancer medicine

2011: Gateways to efficacy of cancer diagnostics and therapeutics

> Evidence for efficacy of targeted therapies
> Improving efficacy of biomarker-driven clinical trials
> Discovering new targets and predictive biomarkers
> Combinations of targeted drugs
> Advances in technology, bioinformatics and systems biology

Poster/abstract submission deadline May 15th 2011

Registration online
www.winconsortium.org
I am the neuron of a cancer patient. A geneticist is looking for answers and thinks that I can help. I want to do my part to combat this disease. That's why I'm on the way to expression analysis.

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OligoAnalyzer

Forget the calculations. We supply results.

\[ T_m(\degree C) = \frac{\Delta H^\circ}{\Delta S^\circ + R \ln([\text{alig}])} - 273.15 \]

\[ R = \sqrt{[\text{Mg}^{++}]} \]

\[ K_s = e^{\left(\frac{-(\Delta H^\circ - T\Delta S^\circ)}{RT}\right)} \]

\[ \theta = 1 - \left( \frac{R_s(\text{[strand1]} - \text{[strand2]})}{2K_s(\text{[strand1]} + \text{[strand2]})} \right) \]

\[ \frac{1}{T_m(\text{Mg}^{++})} - \frac{1}{T_m(1\text{M Na}^+)} + \frac{1}{2d(\text{Mg}^{++} - 1)} \ln \left( \frac{[\text{Mg}^{++}]}{[\text{Na}^+]} \right) \times 10^5 \]

\[ a = 3.52 \times \left(0.843 - 3.52\sqrt{\text{[Na}^+]} \ln(\text{[Na}^+]) \right) \]

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

\[ g = 8.31 \times \left(0.486 - 0.239 \ln(\text{[Na}^+]) + 5.25 \times 10^{-3} \ln^2(\text{[Na}^+]) \right) \]

You strive for accurate data in your research, so don’t use out-of-date analysis tools.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

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

Additional Meetings of interest:

Genetics, Immunology and Repair in Multiple Sclerosis
February 15–20, 2011
Taos, New Mexico, USA
www.keystonesymposia.org/1188

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

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- Enable directional sequencing of the library.
- Start with total RNA (1-5 µg) or size-selected RNA (100 pg).
- 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.

<table>
<thead>
<tr>
<th>RNA Sample</th>
<th>Kit Format</th>
<th>Reads Passing Filter</th>
<th>Reads Aligned to hg19</th>
<th>% Aligned</th>
</tr>
</thead>
<tbody>
<tr>
<td>BrRR</td>
<td>Singleplex</td>
<td>17,272,948</td>
<td>16,823,979</td>
<td>97.40</td>
</tr>
<tr>
<td>BrRR</td>
<td>Multiplex</td>
<td>1,384,314</td>
<td>1,380,799</td>
<td>99.75</td>
</tr>
<tr>
<td>HeLa</td>
<td>Multiplex</td>
<td>1,566,105</td>
<td>1,555,406</td>
<td>99.70</td>
</tr>
</tbody>
</table>

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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