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Gene functional analysis. Simplified.



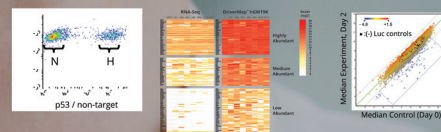
CELLECTA

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- **DriverMap™** Targeted RNA Expression Profiling
- **CloneTracker™** Barcode Libraries

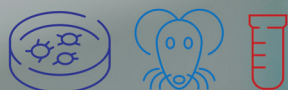
YOUR RESULTS

**Functionally Important Genes
& Biomarkers**



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Cell or Animal Models
Biological Samples



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Who we are

Cellecta is a leading provider of genomic products and services. Our functional genomics portfolio includes gene knockout and knockdown screens, custom and genome-wide CRISPR and RNAi libraries, construct services, cell engineering, NGS kits and targeted expression profiling products and services.

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Bulk M-MLV and RNasin at competitive prices

⊙ M-MLV (H-) Reverse Transcriptase US\$1.5 per KU for more than 1,000 KU

- H minus Moloney Murine Leukemia Virus (M-MLV) Reverse Transcriptase is a recombinant M-MLV reverse transcriptase. RNase H activity has been eliminated by a point mutation in the RNase H domain of M-MLV RTase, ensuring high yields.
- Deficient RNase H activity to reduce RNA template degradation during the first-strand cDNA synthesis.
- cDNA up to 12 kb.

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RNasin is a ribonuclease inhibitor extracted from human placenta with a molecular weight 51 kDa. It inhibits the activity of RNase by specifically binding up to RNase with a non-covalent bond. RNasin, free of RNase or Nickase, can maintain its activity at pH from 5 to 8, and the highest one at pH7.8.

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GLOBAL IMPACT
INDIVIDUALIZED PATIENT CARE



#AACR19



AACR.org/AnnualMeeting



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my NGS Guides[™]

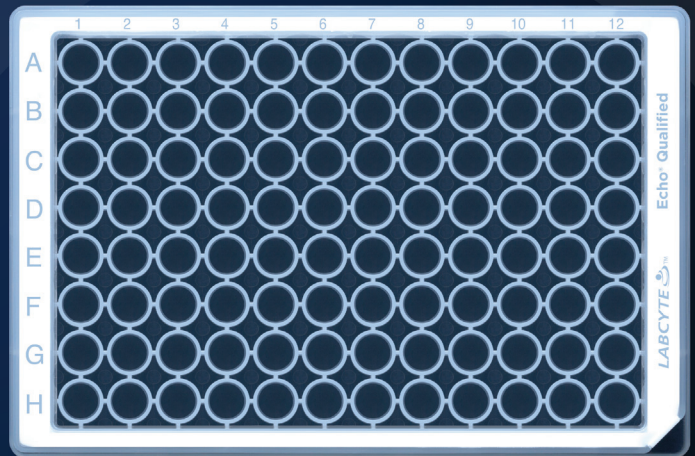
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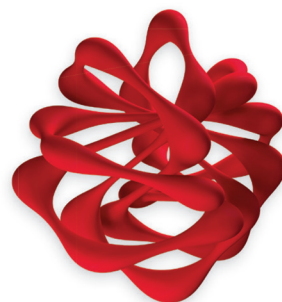
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2019 - 19308 1/2019



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2019 RNA Meetings at CSHL



aerial view of CSHL sandspit and inner harbor during meeting social

RNA Control & Regulation

84th CSHL Symposium May 29 - June 3, 2019 Poster abstracts due March 8

Terri Grodzicker, David Stewart, Bruce Stillman *Cold Spring Harbor Laboratory*

Topics

RNA-Based Structures

RNA Modifications

Nuclear Localization of RNA

Quality Control & Editing

RNA & Gene Regulation

Cotranscriptional Splicing

Intron / Exon Boundaries

Alternative Polyadenylation

Transposon Control

Small Noncoding RNAs

Long Noncoding RNAs

RNA & Development

Membrane-Less Organelles

Phase Separation

RNA-Based Diseases

Novel RNA functions

meetings.cshl.edu/rnasymp

RNA & Oligonucleotide Therapeutics

March 27 - 30, 2019 Abstracts due January 11

Annemieke Aartsma-Rus, *Leiden University Medical Center* Masad Damha, *McGill University*

Matthew Stanton, *Generation Bio* Laura Sepp-Lorenzino, *Vertex Pharmaceuticals Inc.*

Topics

Nucleic Acid Chemistry

Delivery

Emerging Therapeutics

Preclinical Development

Clinical Programs

Safety

meetings.cshl.edu/rnatx19

Eukaryotic mRNA Processing

August 20 - 24, 2019 Abstracts due May 31

Alberto Kornblihtt, *University of Buenos Aires, Argentina*

Jens Lykke-Andersen, *University of California, San Diego*

Karla Neugebauer, *Yale University*

Topics

Alternative splicing

Mechanisms of RNA Splicing

RNA-Protein interactions

RNP complexes

3' end processing

RNA modification

RNA structure

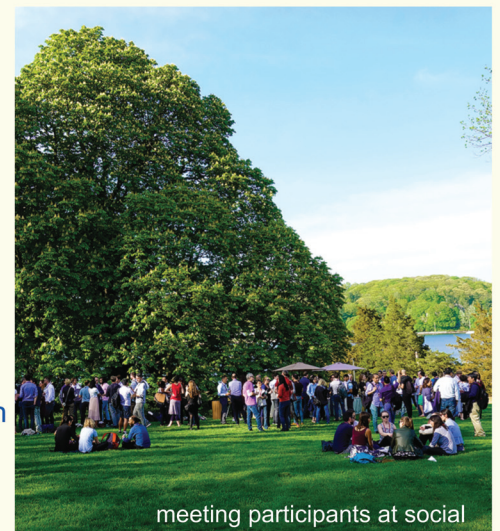
Co-transcriptional RNA processing

RNA turnover & quality control

Small RNA biogenesis and function

Viruses and RNA processing

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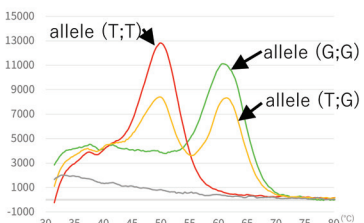
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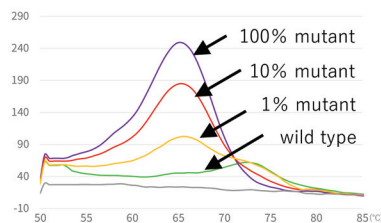
A novel solution for SNP/somatic mutation detection

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- **High resolution SNP detection**—Increased T_m (approx. 10°C) by the thiazole orange enables a shorter probe design and a clearer distinction of SNPs
- **Simple and highly sensitive somatic mutation detection**—sensitive detection of somatic mutations (down to 0.1%) can be achieved by suppression of PCR amplification of wild-type alleles by Eprobe (PCR clamping)
- **Compatible with most real time PCR instruments**—fluorescence emitted by Eprobe can be detected using a filter for SYBR[®] Green I* *SYBR[®] is a registered trademark of Molecular Probes, Inc.
- **Easy to use online design tools**—a design tool for a primer/Eprobe (E-design, www.dnaform.com/edesign2/) and a thermodynamic calculation tool (ECHO, www.dnaform.com/devel/echo/thermodynamics/) are available



SNP genotyping for IL28B (rs8099917 T;G) using an allele G specific Eprobe



Somatic mutation detection of KRAS G12D using an wildtype specific Eprobe.

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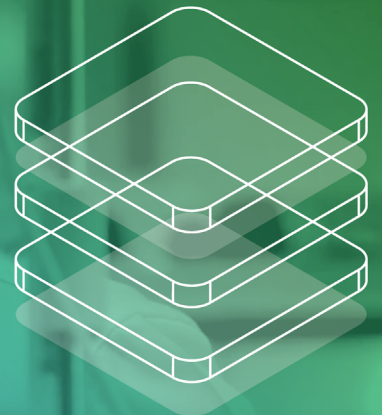
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