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- Assesses quality and quantity (size and concentration)
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- Sizes fragments up to 20,000 bp for PacBio sequencers
- Also analyzes gDNA and RNA

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 **ADVANCED
ANALYTICAL**

isothermal detection of RNA

- Rapid detection in minutes
- Single molecule sensitivity
- Little or no hardware requirements
- Easy to use, stable lyophilised reagents



TwistAmp® exo RT

Real-time fluorescent RNA detection

Using TwistDx's RPA technology, the exo RT kit is recommended for detecting RNA targets with a proprietary fluorescent TwistAmp® exo probe in a one-step process.

TwistDx

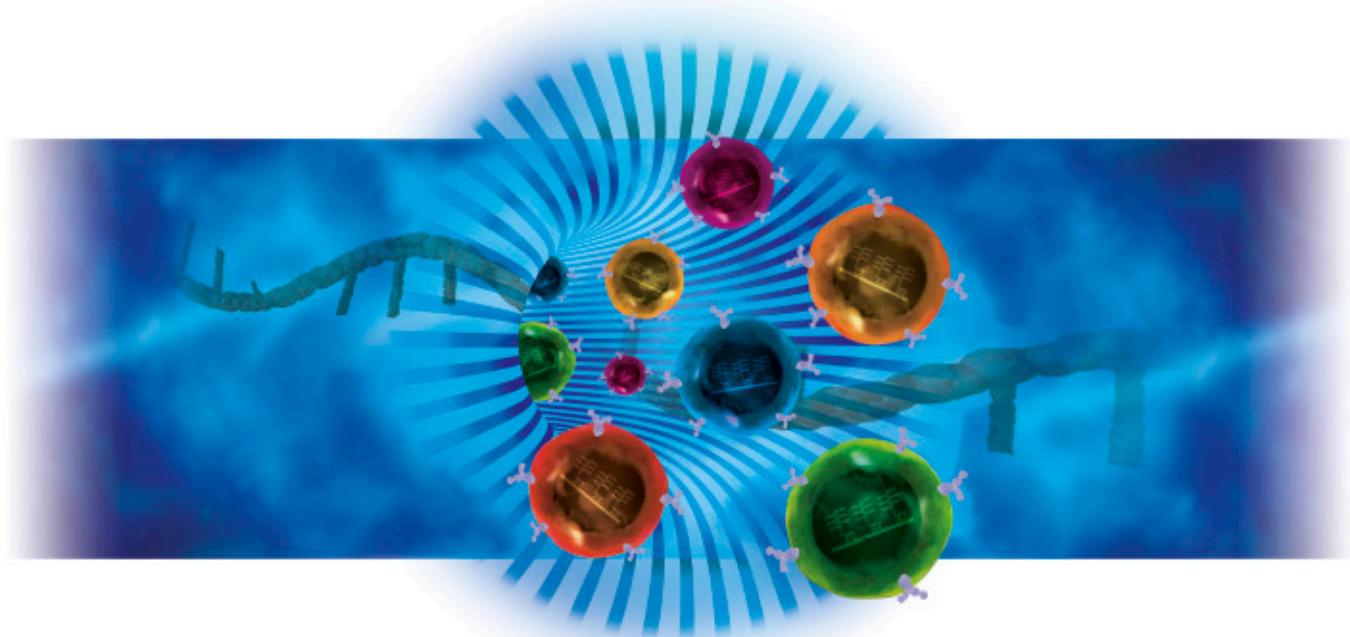
www.twistdx.co.uk





Imagine if you could detect RNA and protein in millions of single cells

Enter a new dimension of single-cell analysis



Detect RNA and protein simultaneously by flow cytometry to:

- See gene expression heterogeneity at the single-cell level
- Compare RNA and protein in the same cell
- Evaluate viral RNA within infected cells
- Detect non-coding RNA in cell subsets
- Analyze mRNA expression levels when antibody selection is limited

**Download
White Paper**

Download your copy of the PrimeFlow™ RNA Assay Validation White Paper at www.ebioscience.com/primeflow-white-paper-genres

Biology for a better world.

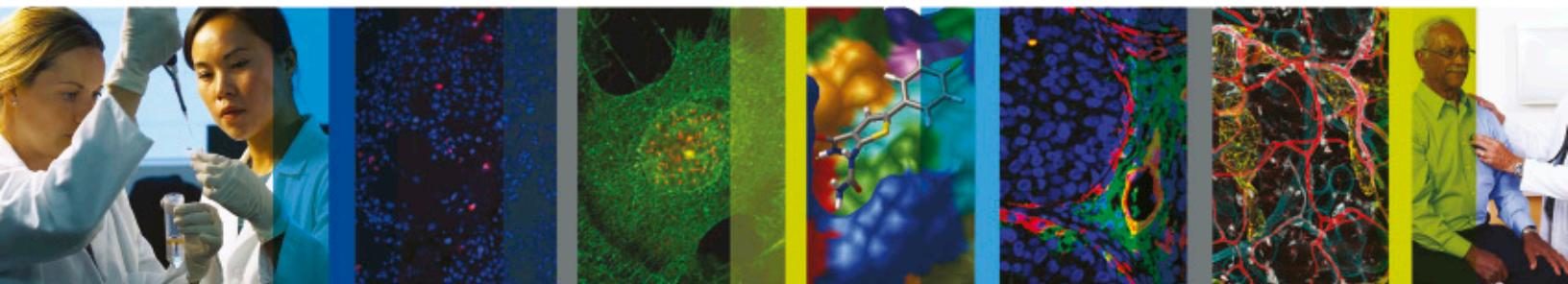
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Join Keystone Symposia'
for the 2015 conference on:

Epigenomics

joint meeting with: *DNA Methylation*

March 29–April 3, 2015
Keystone Resort
Keystone, Colorado, USA

Scientific Organizers: Bing Ren and Daniel Zilberman

Empowered by recent technological advances in DNA sequencing technologies, epigenetic regulatory mechanisms have been investigated in a growing number of organisms at increasingly high resolution and scope. The results are an explosion in new genomic technologies, large-scale datasets and computational resources. Epigenomics is still a young and growing field, and there are many challenges to investigators working on specific model organisms or diseases who want to adopt this approach. This meeting is designed to capture the recent progress in the field while bridging technological gaps, such as dataset availability, method adoption and data interpretation.

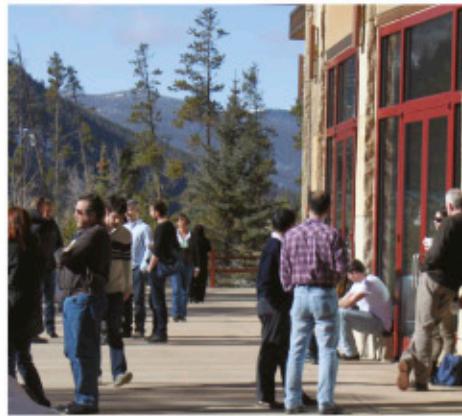
Session Topics:

- Genome-Wide DNA Methylation I & II (Joint)
- Nucleosome Dynamics
- Functional Chromatin Domains
- Chromatin Regulation of Development
- Higher-Order Chromatin
- Small RNA
- Long Noncoding RNA

CONFIRMED SPEAKERS
(as of January 7, 2015):

Adrian P. Bird*
Bradley R. Cairns
Job Dekker
Joseph R. Ecker
Peter Fraser
Mitchell Guttman
Edith Heard
Steven Henikoff
Steven E. Jacobsen
Manolis Kellis
Jason Lieb
Haifan Lin
Alexander Meissner
Barbara J. Meyer
Amy E. Pasquinelli
Craig S. Pikaard
B. Franklin Pugh
Bing Ren
John L. Rinn
Dirk Schübeler
John A. Stamatoyannopoulos
Bas van Steensel
Ting Wang
Iestyn Whitehouse
Joanna Wysocka
Feng Yue
Daniel Zilberman

**Keynote speaker*



To see the full program and for additional details,
visit www.keystonesymposia.org/15Z2.

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Variant (SNP / Indel) calling
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Expression Profiles
DEGs / miRNA
Enrichment Profiles
Gene Annotation

Capillary Sequencing

Microarray

Oligonucleotide Synthesis

Genetically Engineered Mouse

Next Gen Sequencing

Using rapid solutions for high-quality total RNA-seq?



ATTCATTGGAGACCGCAGCCGATCAATCGA
GCAGGCCGCCGTCTTAGCTAATCGGAGACTT
CGATTCATGGAGGCCAGAGGCCGTCTTAGCTATTAGCC
CGTTAGCAGTTGTATGCAGGCCAGAATCGTAGGGCTATTAG
CGATTCAGTGTCCATTGAGACCCGAGCCGATCAATCGA
CGATTCATGGAGGCCGCCGTCTTAGCTAATCGGAGACTT
CGATTCATGGAGGCCAGAGGCCGTCTTAGCTATTAGCC

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For 100 ng–1 µg of RNA, rRNA-removal is integrated directly into the SMARTer Stranded Total RNA Sample Prep Kit - HI Mammalian. Both of these kits deliver the same excellent data found in all SMARTer kits for RNA-seq.

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1,300+
cancer genes
and
200+
miRNA genes

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