Institute of Molecular Biology

IMB TechTalk

Anina Moritz Ph.D.

Product Manager NGS
Takara Bio Europe

"SMARTer® Solutions for Low Input Transcriptome Sequencing"

15 April 2014, 14:00 h (*s.t.*)

(different time than usually)

Venue: 2nd Floor Seminar Room
Institute of Molecular Biology (IMB)
Johannes Gutenberg University Campus Mainz

All are welcome to attend

Host: Dr. Tina Han, IMB
E-mail: c.han@imb-mainz.de, tel.: +49-(6131)-39-21565

Institute of Molecular Biology

IMB TechTalk

Meet the speaker during a complimentary coffee and cookies after the presentation!

www.clontech.com/stranded-ngs

Abstract:

Next Generation Sequencing (NGS) has increased our understanding of biology by enabling highly sensitive RNA expression analysis throughout the transcriptome, across a wide dynamic range. Two particularly powerful applications, single cell RNA-Seq and stranded RNA-Seq, have been the focus of considerable efforts in protocol innovation. Single cell transcriptome analysis has revealed key properties of individual cells, increasing its importance in fields such as cancer, development, neurobiology, and stem cell research. Strand-specific information is necessary to distinguish closely-related genes and non-coding RNAs (e.g. lincRNA) or to define genes in poorly annotated, coding-rich genomes, such as many bacteria.

By utilizing the template switching activity of reverse transcriptase, Clontech's patented SMART™ technology has enabled researchers to analyze their most challenging samples. The original, dT-primed SMART-based RNA-Seqprotocol, designed to work with high-quality RNA or whole cells, is the gold standard for single cell analysis. SMART's applicability has recently been extended to non-coding RNA and mRNA from degraded samples, such as FFPE. In addition, the use of modified SMART adapters in combination with random priming makes it possible to generate strand-specific sequencing libraries directly from RNA in under four hours. This approach eliminates the laborious enzymatic steps required by other stranded RNA-Seq methods, while maintaining the sensitivity and reproducibility characteristic of SMART.

In this presentation, we will outline these current SMART methods and detail their ability to provide unrivaled mappability, gene body coverage, strand specificity, and sensitivity.

Next Gen Sequencing with SMARTer cDNA Synthesis Kits

RNA-Seq Seminar

SMARTer® Solutions for Low Input Transcriptome Sequencing

that's GOOD science!™

Tuesday, April 15th , 2 PM

Learn how SMARTer® technology facilitates RNA-seq from a limited amount of template:

- Single cell RNA-seq
- Strand specific RNA-seq
- RNA-seq from FFPE or degraded samples
- Non-coding, non-polyA RNA-seq

The SMARTer method provides unrivaled mappability, gene coverage, and gene expression information!

Speaker: Anina Moritz, Ph.D., Product Manager NGS, Takara Bio Europe

Location: Seminarraum, Institut für Molekulare Biologie, Ackermannzeg 4, 55128 Mainz

Meet the speaker during a complimentary coffee and cookies after the presentation!

Info

Dr. Sascha Deppermann, Wissenschaftlicher Aussendienst
sascha.deppermann@takara-clontech.eu
Mobil: 0170 277 2919

Learn more

www.clontech.com/stranded-ngs

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