Institute of
Molecular Biology

# IMB TechTalk

## Harry Boeltz

Regional Sales Manager DACH
NanoString Technologies Europe

## “Gene Expression Analysis down to the single Cell Level by Digital Quantification of Nucleic Acids Utilizing a Color-Coded Barcode Technology”

18 December 2012, 11:00 (*s.t.*)

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

All are welcome to attend

Host: Dr. Bernhard Korn, Director CF & Technology, IMB
For further information, please contact: Bianca Steinbach, E-mail: b.steinbach@imb-mainz.de, tel.: +49-(6131)-39-21510

# Gene Expression Analysis Down to the single Cell level by Digital Quantification of Nucleic Acids Utilizing a Color-Coded Barcode Technology

The nCounter System from NanoString Technologies uses direct single molecule imaging with molecular barcodes to detect up to 800 targets in a single reaction direct from total RNA or DNA. The assay technology captures nucleic acid targets through hybridization, eliminating the need for reverse transcription or amplificaton by PCR.
The multiplex probe assay or CodeSet, reduces pipetting and the need for multiple reactions. The input is 100ng total RNA, there is no loss of sample from aliquoting, no gaps in data from gene dropouts, five-log dynamic range, reproducible less than integer fold change. Publications show high correlations between sample types, including FFPE samples or data from other platforms such a NGS and peer-to-peer studies.

The introduction of the nCounter® Single Cell Gene Expression Assay, allows researchers to study entire biological pathways for single cells without the necessity to match the gene number to the format of a microfluidic PCR consumable. In contrast to the standard protocol a linear amplification step will be performed prior to the final detection. The Multiplexed Target Enrichment (MTE) step uses primers that flank the region targeted by the nCounter Capture and Reporter probes, and allows transcripts within individual cells to be linearly amplified after a reverse transcription step. MTE can linearly amplify up to 800 targets from a single cell in a single tube without bias.
The resulting amplified material is then directly hybridized with an nCounter CodeSet targeting the genes of interest - no sample clean-up or sample splitting is required.

The system supports applications for copy number Analysis, ChIP-String-epigenetic analysis, miRNA profiling and gene expression analysis down to the single cell level.