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“Technologies for Efficient Generation of Transcriptome Data by Next Generation Sequencing”

20 May 2014, 11:00 h (s.t.)

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

All are welcome to attend

Abstract:

Technologies for Efficient Generation of Transcriptome Data by Next Generation Sequencing

We have developed a set of novel tools to better support efficient production of expression NGS data from a variety of different sample types ranging from single cells to FFPE extracted RNA and microbial to plant samples. In this talk I'll describe our technologies and share some RNA-Seq data generated with our Single Cell RNA-Seq system obtained from HEK 293 cells, our Whole Blood and Human FFPE RNA-Seq systems which employ an enzymatic transcript depletion method (InDA-C) applied to rRNA and globin transcripts, and our Target Enrichment system (SPET) applied to cDNA libraries for the detection of splicing events and gene fusion products. Both the InDA-C and Target Enrichment methods can be customized by researchers to different organism (e.g. drosophila, frog, zebrafish) to target transcript regions of interest. These systems all feature directional cloning of the cDNA during synthesis resulting in NGS libraries with greater than 95% strand retention, illustrating utility in the detection of antisense expressed transcripts.