

TCAG New Technologies Seminar

RNA Amplification for Gene Expression Profiling from Challenging Samples: FFPE, Small and Degraded Samples, LCM, Sorted Cells, and Whole Blood

Date: Tuesday, July 15th, 2008
Time: 11:00 AM
Location: Room 14-203, MaRS TMDT
101 College St.

Speaker: Mark Hurt
Field Application Scientist
NuGen

One of the most formidable tasks for translational researchers is to analyze gene expression from clinical samples. They range from extremely small, homogenous samples isolated by LCM, to more readily available samples such as whole blood and formalin fixed, paraffin embedded (FFPE) tissues. The RNA quantity, quality and integrity from these samples are often limiting. The large proportion of globin message in whole blood reduces the detection sensitivity of endogenous transcripts and the extremely compromised nature of FFPE RNAs makes them challenging, if not nearly impossible to profile, using *in vitro* transcription (IVT) amplification methods. NuGEN Technologies will discuss solutions to profile these difficult and challenging samples.

Hosted by The Centre for Applied Genomics



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