

# Cloning and Sequencing of Transcriptomes

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The recent completion of genome sequences of human and model organisms manifested the beginning of post-genome era in biology. The next immense challenge is to understand the expression of all genes, the transcriptome, and functions of all proteins, the proteome. A fundamental aspect of understanding transcriptome and proteome is to clone, sequence, and analyze all of full-length transcripts including their alternative splicing variants in an organism. A complete identification of all genes will not only shape the global view of a genome, but also provide the substance to fuel the whole range of proteomics research through high throughput expressions of recombinant proteins and gene function studies. At GIS we are developing an array of technologies for transcriptome characterization, including full-length cDNA, 5'LongSAGE, ncRNA cloning, etc. We are in progress to apply our comprehensive technology platform to characterize important transcriptomes of zebrafish, human and mouse stem cells, and human liver cancers.

**Date:** Friday October 25, 2002  
**Venue:** LT 20  
**Time:** 4 - 5 pm  
**Host:** Dr Pan Shen Quan

**All are welcome**

