Contact: Hien Dang, Ph.D
Email: htdangster@gmail.com

**Liver Cancer Section at Thomas Jefferson University, Department of Surgery**
Philadelphia, PA

There are two positions open: One postdoctoral fellowship and one lab technician. Start date for postdoctoral fellows are flexible. Molecular biology techniques required. Interests in translational science and willing to learn new techniques and bioinformatics is preferred.

For technician position, must be able to start in November at the latest. Looking for well-organized, independent and have experience with molecular techniques person. The position requires basic administrative tasks such as ordering and inventory as well as experiments.

To apply, please send CV to my email: htdangster@gmail.com

**Summary:** Transcriptomic imbalance is pervasive in cancer. An integral group of proteins that regulate the transcriptome is RNA binding proteins (RBPs). We have previously demonstrated that many RBPs are dysregulated in a subset of primary liver cancers (PLCs) with poor prognosis, suggesting that RBPs are selected during tumor evolution. PLC is the 2nd most common cause of cancer-related death worldwide with the fastest rising incidence and mortality in the United States. Despite considerable efforts towards improving diagnosis and developing new treatment modalities, PLC remains among the most difficult-to-treat malignancies, with a 5-year survival rate of less than 15%. Our lab is interested in identifying disease-acquired functions of RBPs, and in parallel, exploit such mechanisms as actionable biomarkers or drug targets to improve diagnosis for PLC patients. Our lab utilizes bioinformatics and bench science spanning from functional genomics, translational science, molecular epidemiology, RNA biology, cancer biology, and animal models to investigate the oncogenic roles of RBPs in PLC (see Figure). Our main focuses are as follows:

**Project 1:** central focus of our research is investigating the dysregulation of mRNA binding proteins (mRBPs) in hepatocellular carcinoma (HCC). Our recent work identified Negative Elongation Factor E as an oncogenic RBP that is associated with poor clinical outcome in more than 1200 clinical specimens. We identified the novel mechanisms in which NELFE enhances the oncogene MYC to promote tumorigenesis. We are currently interested in how NELFE interact and regulate their RNA targets through modular domains such as low complexity sequences (LCS) and RNA recognition motifs (RRMs).

**Project 2:** Tumor heterogeneity represents a significant barrier to improving HCC patient outcome and poses a challenge for the establishment of robust HCC classification, making treatment extremely difficult. Consequently, the ability to discriminate patients with greater homogeneity and clinically relevant therapeutic targets will help guide treatments to improve patient outcome. We have developed a robust 20-NELFE dependent MYC target (NDMT) gene signature, which reflects the biological characteristics of HCC. We are interested in utilizing high-throughput screenings to identify therapeutics for this specific subtype. In collaboration with others, we have developed a MYC-induced NELFE HCC...
Sleeping Beauty mouse model (Trp53\textsuperscript{flox/flox}; Alb-Cre) that can be used to validate drug targets in vivo and patient derived cell lines that can used for screening.

**Project 3:** In addition, we are interested in utilizing several areas of RNA biology, translational, bioinformatics, and molecular biology to identify key oncogenic RBPs involved in transcriptomic alterations associated with disease states. For example, we have recently identified Argonaute 2 (AGO2) as a possible oncogenic RBP that can promote an HCC transcriptome in a RISC-independent manner. By utilizing transcriptomics, we show that activated AGO2 preferentially affects mRNAs by enhancing their stability. This is only evident in HCC with high AGO2 HCCs. We’re now elucidating how AGO2 promotes HCC progression by directly interacting with mRNA targets independent of miRNAs.