

# Spectroscopic Imaging of Interactions in the Cell

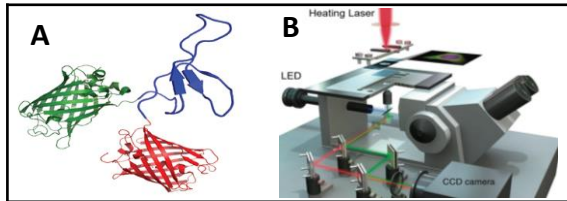
Eddie Knab, Eitan Acks, Brahmami Patel, Caitlin Davis

Department of Chemistry, Yale University, 255 Prospect Street, New Haven, CT 06511, USA

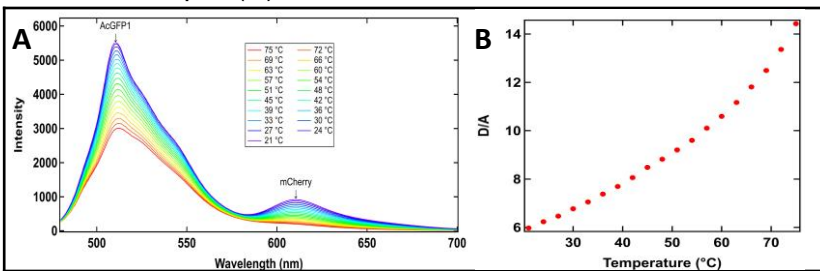
Yale

## FRET Labeling for WW Domain

Computational studies of small peptide kinetics and stabilities *in cellulo* need to be corroborated with experimental results. Therefore, a method of visualizing conformational changes of a protein in a cell without perturbing the stability is required. **Using WW Domain proteins as a model, we will test two different FRET labeling methods, fluorescent proteins and dyes, to determine which provides the smallest perturbation to the protein's stability.** We predict that while both methods will be able to detect unfolding, the dyes will provide the smallest perturbation due to their size.



**Figure 1.** hPin1 WW domain labeled with AcGFP1 and mCherry (A) and an example of a T-Jump microscope<sup>1</sup> (B)

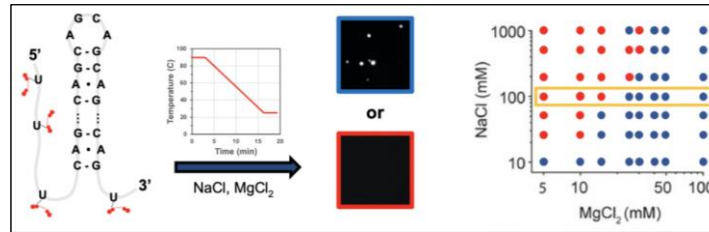


**Figure 2.** FRET fluorescence spectrum (A) is used to determine the temperature dependent D/A (B), which can be fitted to determine protein stability

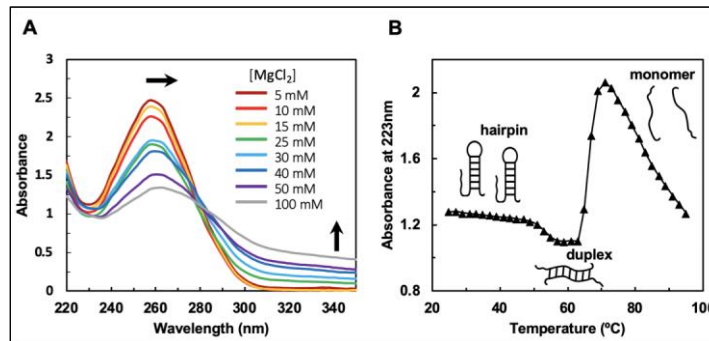
1).Ebbinghaus et al. *Nature Methods* 7, 319-323 (2010).

## RNA Phase Separation

Formation of RNA Foci in the cell nucleus is a hallmark of repeat expansion disorders (e.g. Huntington's Disease and ALS). Above a critical number of repeats, RNAs consisting of disease-associated nucleotide repeats readily form phase separated droplets *in vitro* in a base-pairing dependent process. **We use UV-Vis spectroscopy to identify structural transitions in CAG RNA foci.**



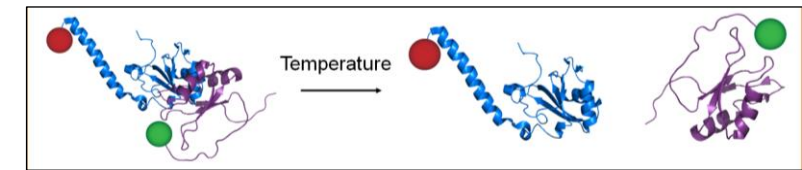
**Figure 1.** Huntington's CAG RNA Foci form in a temperature and salt dependent process.



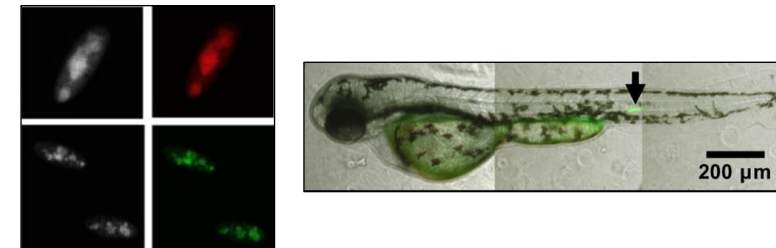
**Figure 2.** Phase Separation dependent changes in RNA UV-Vis spectra (A) can be used to identify structural transitions (B).

## Kinetic Regulation of Splice Sites

Failure to properly recognize 5' splice sites during pre-mRNA splicing may affect assembly of spliceosome components – resulting in disease-prone outcomes. Due to this, it is important to fully characterize interactions that dictate splice site recognition. SRSF1 and U1-70K, two RNA-binding proteins involved in splicing, are thought to interact with each other via their RNA-recognition motifs (RRMs). **How do the proteins, U1-70K and SRSF1, interact with each other and with RNA to catalyze the splicing mechanism?**



**Figure 1.** U1-70K and SRSF1 are fluorescently tagged with mCherry and EGFP, respectively. Binding kinetics and thermodynamics will be measured with FRET using FRel.



**Figure 2.** Left: Transfection of plasmid DNA with successful expression of fluorescently-tagged proteins in U2-OS cells Right: Microinjection of plasmid DNA into living zebrafish embryos with transient expression of FRET-labeled protein.