

Molecular mechanisms in human health and disease

- circular RNAs and RNA-binding proteins -

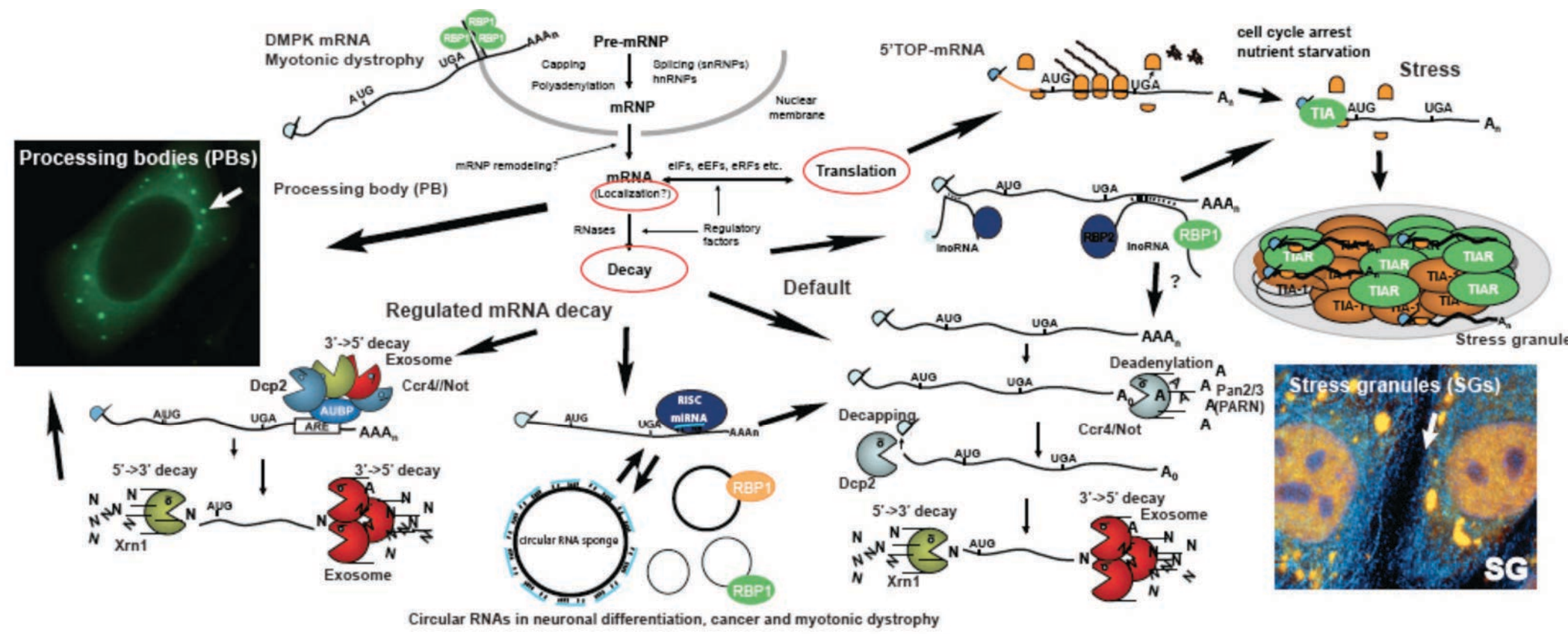
- NEW! RNA therapeutics to target cancer and ALS -

Christian Damgaard, PhD
Associate Professor

1-2 post docs, 1-3 PhD students, 2-3 M.Sc. and 2-3 B.Sc.



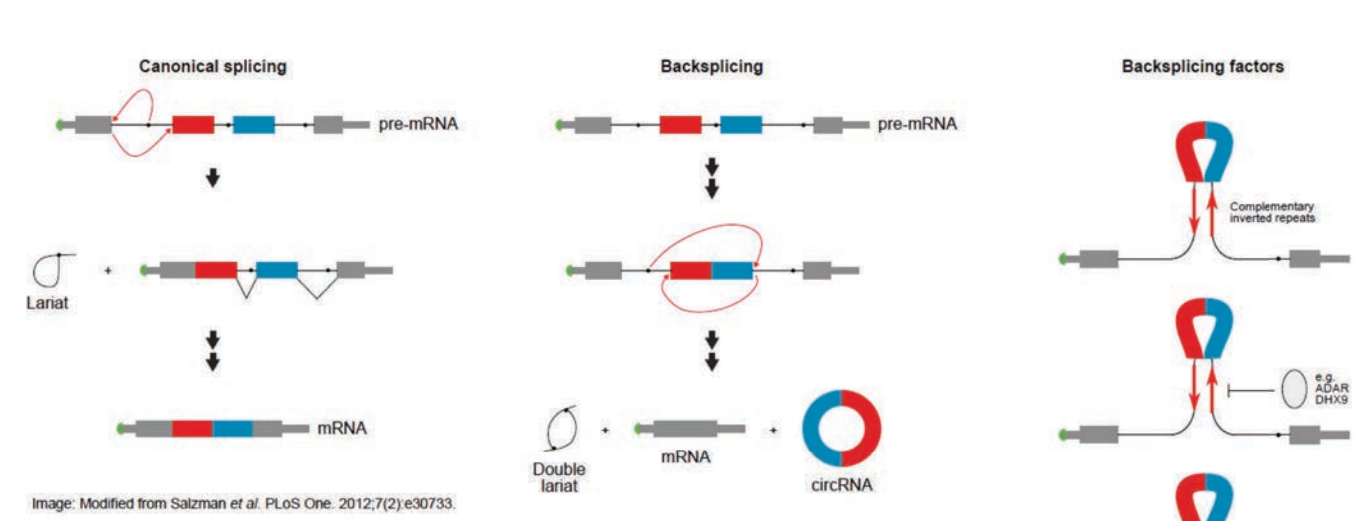
INTRODUCTION



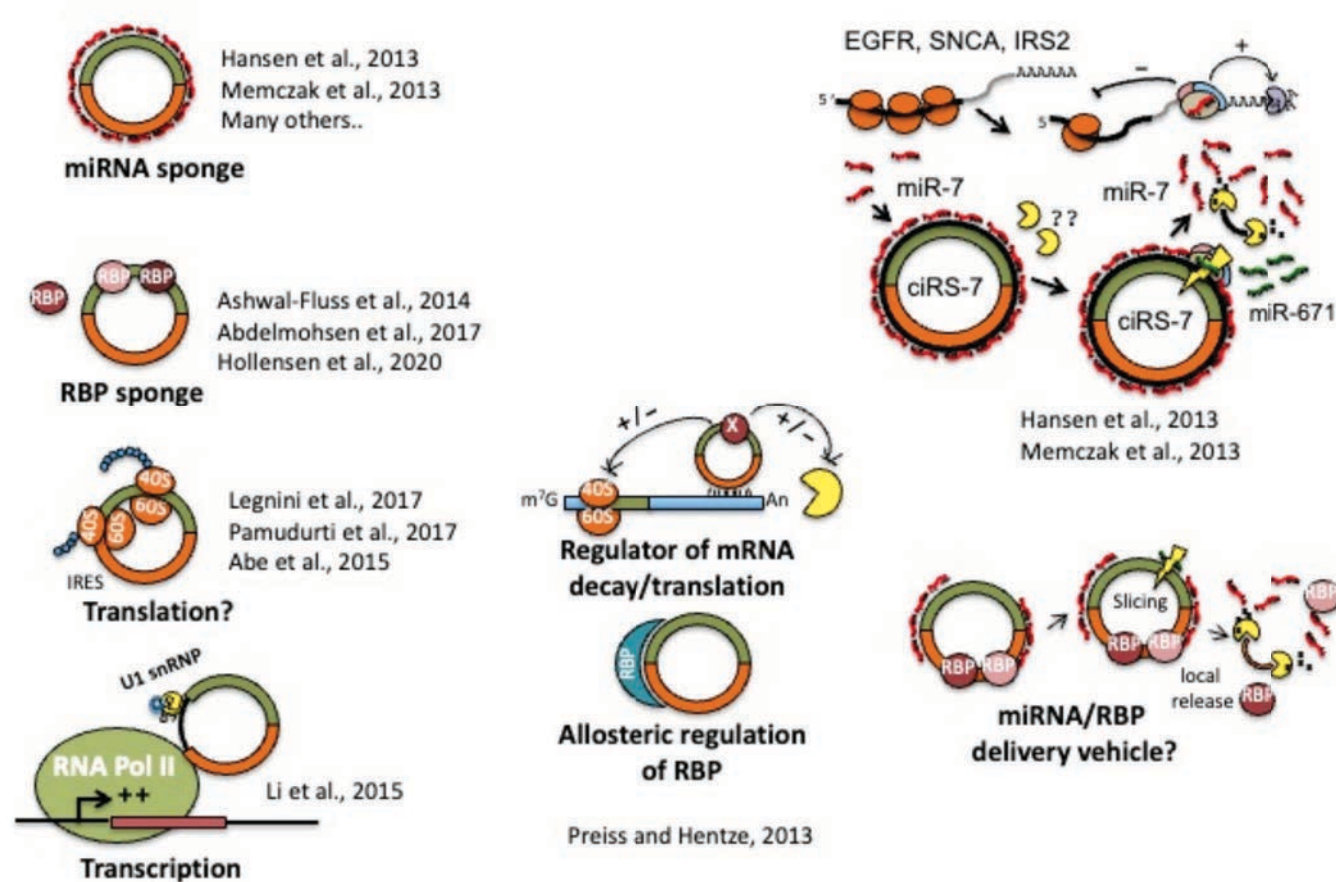
The eukaryotic cell possesses numerous gene-regulatory mechanisms to control cell function according to given conditions and environmental cues. These include rapid changes in gene-expression elicited at almost every thinkable level inside the cell - events often deregulated in disease. Historically, much attention has been given to the regulation of transcription and mRNA processing events, which in turn produce a tremendous diversity from metazoan genes. These important regulated events aside, there is now increasing evidence that cytoplasmic processes, including regulation of both global and local protein translation and mRNA stability are crucial modulatory instruments for the cell during development, cell growth and as primary responses to environmental changes. These processes are governed by, both RNA-binding proteins (RBPs) and large classes of ncRNAs, including circular RNAs (circRNAs), long non-coding RNAs (lncRNAs) and microRNAs (miRNAs). In my laboratory we study the function of all these types of RNA- and protein regulators in tightly controlled translation and mRNA decay and assess how their deregulated function impact diseases like myotonic dystrophy (DM1), Neurodegenerative disease and cancer. Recent efforts include the innovative use of circRNAs as therapeutic agents in amyotrophic lateral sclerosis (ALS) and cancer.

Circular RNAs (circRNAs)

Circular RNA formation is driven by backsplicing



Circular RNAs – a new class of functional non-coding RNAs



circRNAs are generated by the process of backsplicing, where a 5'ss engaged with an upstream 3'ss to create a circular RNA. Placing of splice sites into vicinity of each other can be facilitated by base pairing or by dimerization of RBP's binding in the surrounding introns.

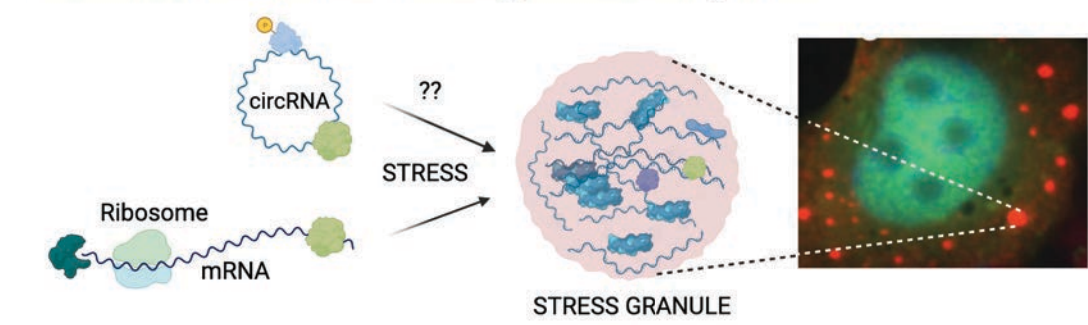
circRNAs have been shown to "sponge" miRNAs and RBPs or to work as scaffolds for protein complex assembly. Many circRNAs are deregulated in disease and may play a direct role in the disease etiology by skewing gene-regulatory mechanisms.

METHODS

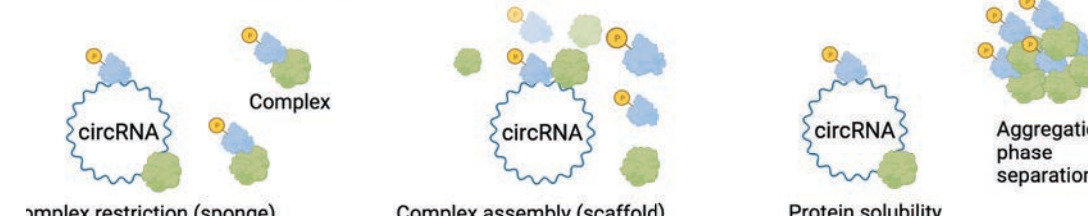
- Human cell culture - primary patient-derived cells, stem cells, and cell lines.
- CRISPR/Cas-manipulation of cells (gene knockout and knockin).
- Transfection and lentiviral transduction. Overexpression/knockdown
- Cell biological assays - Proliferation, migration, invasion, colony-formation, cell-cycle a.o.
- Imaging - Protein/RNA (immunofluorescence/RNA-FISH) and live-cell protein/RNA imaging (e.g. GFP-tagging/GFP-tethering/SUNTAG).
- Gene expression analyses - Western blotting, RT-qPCR, RNA-seq and mass spectrometry.
- Polysome profiling
- Protein and RNA immunoprecipitation (followed by RT-qPCR, RNAseq, Western or mass spectrometry).
- Nanopore sequencing
- Flow cytometry
- In vitro RNA synthesis and design/selection of aptamers
- RNA therapeutics

HYPOTHESES/QUESTIONS

Do circRNAs accumulate in stress granules during stress?



Do circRNAs regulate protein function by enhancing complex assembly or by restricting complexes?



Many circRNAs and RNA binding proteins (RBPs) are dysregulated in disease (e.g. cancer, ALS, Myotonic dystrophy).

Could dysregulated circRNAs be biomarkers in cancer, have driver functions or inhibit cells proliferation?

Do circRNAs impact subcellular localization and/or functions of RNA binding proteins? Are circRNAs primarily RBP sponges (inhibition) or RBP scaffolds that assemble protein complexes (positive regulation)?

Could circRNAs affect phase separated RBPs/RNAs accumulate in large granules (stress granules)? Do cells even localize circRNAs in granules?

circRNAs could work as negative or positive regulators of weak protein-protein interactions. circRNAs could affect the solubility of proteins containing intrinsically disordered regions (IDR).

PROJECTS (EXAMPLES)

Project - Bladder cancer: Study of circRNA impact on bladder cancer cell proliferation, viability and survival.

Some circRNAs affect cell cycle progression in bladder cancer.

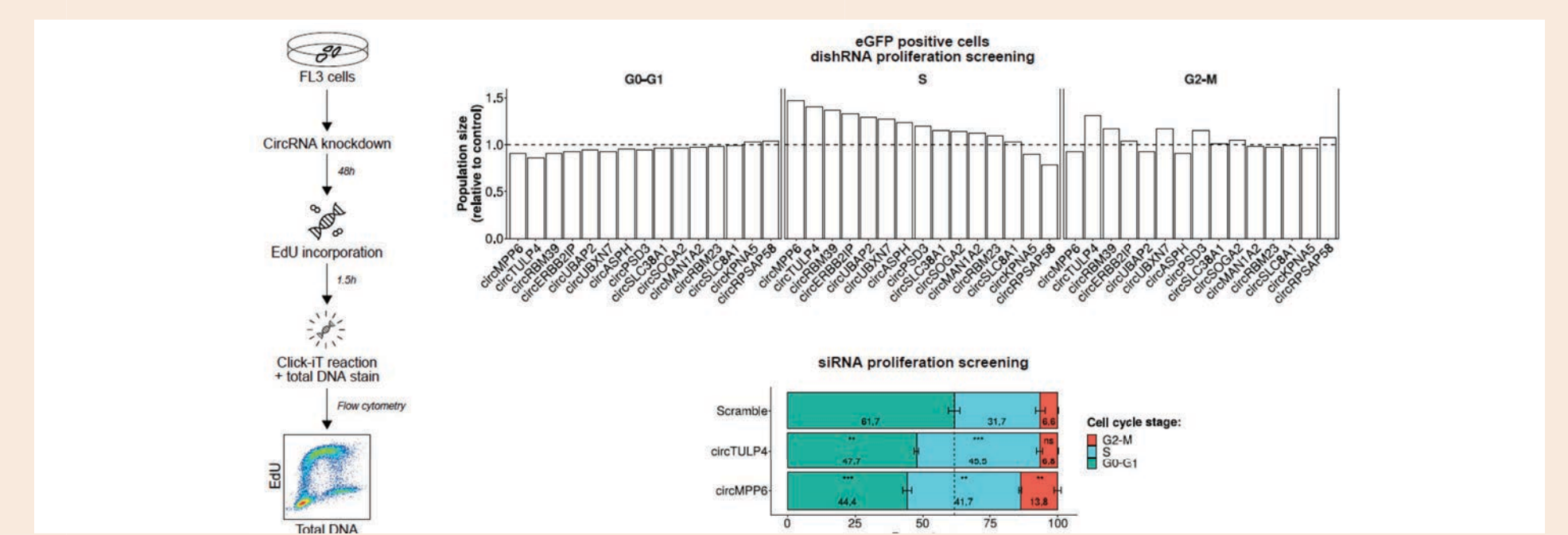
Upper figure shows distribution of cells in G1, S or G2/M phases by EdU incorporation followed by flow cytometry. Note that circTULP4 and circMPP6 knockdown pushes cells beyond G1/S transition and increases DNA replication.

Lower figure shows that circTULP4 regulates the expression of many proteins (and RNAs - not shown here).

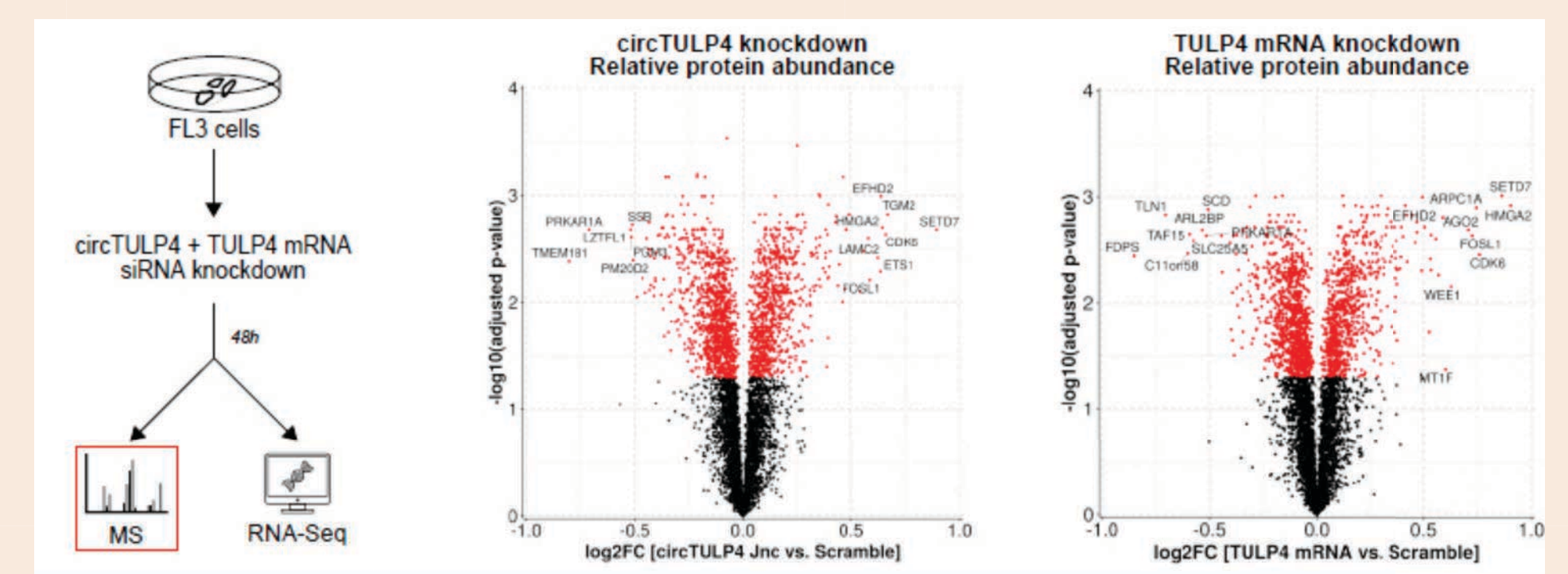
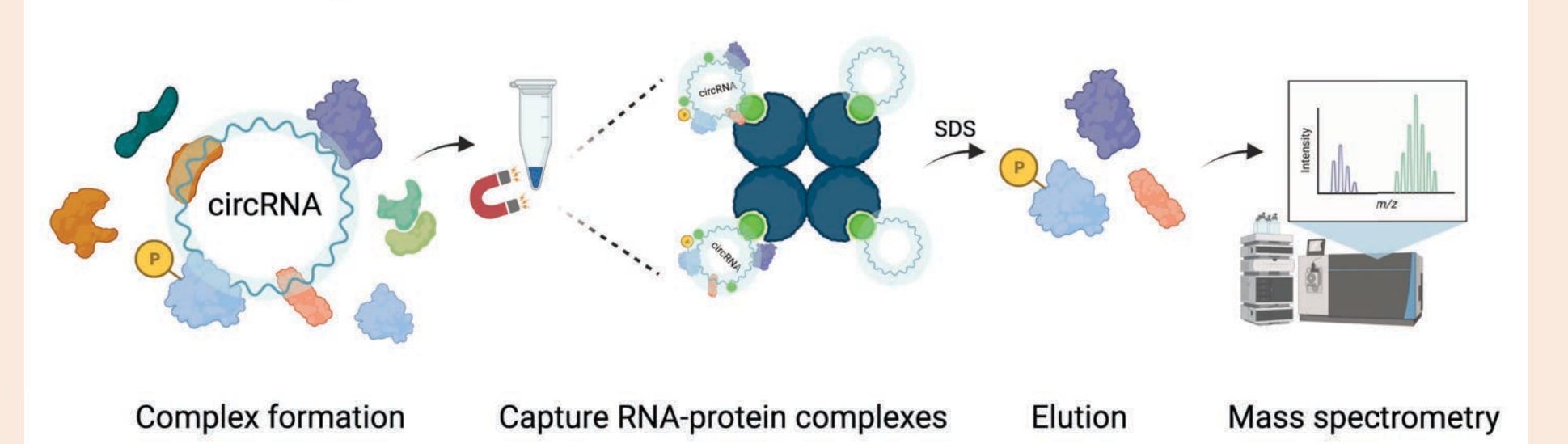
How are these effects achieved? What are the molecular mechanisms?

Identify circRNA protein interaction partners and perform manipulations with circRNA/proteins to measure impact on gene-expression, in cell biological assays or on subcellular localization. Are these circRNAs functioning as miRNA, protein sponges or scaffolds for protein complexes? Are circRNAs necessary for the formation of protein complexes?

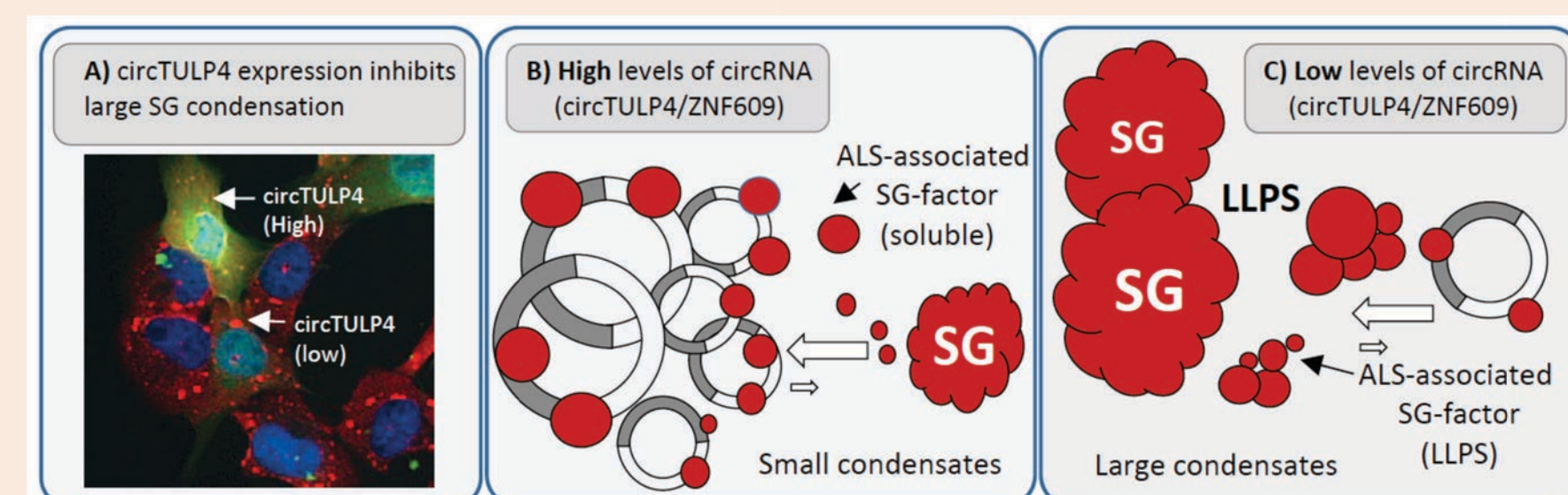
Perform co-immunoprecipitations after knockdown or overexpression of circRNA. Imaging: Combined RNA-FISH and immunofluorescence to test whether proteins/RNAs co-localize.



Determining the circRNA-interactome



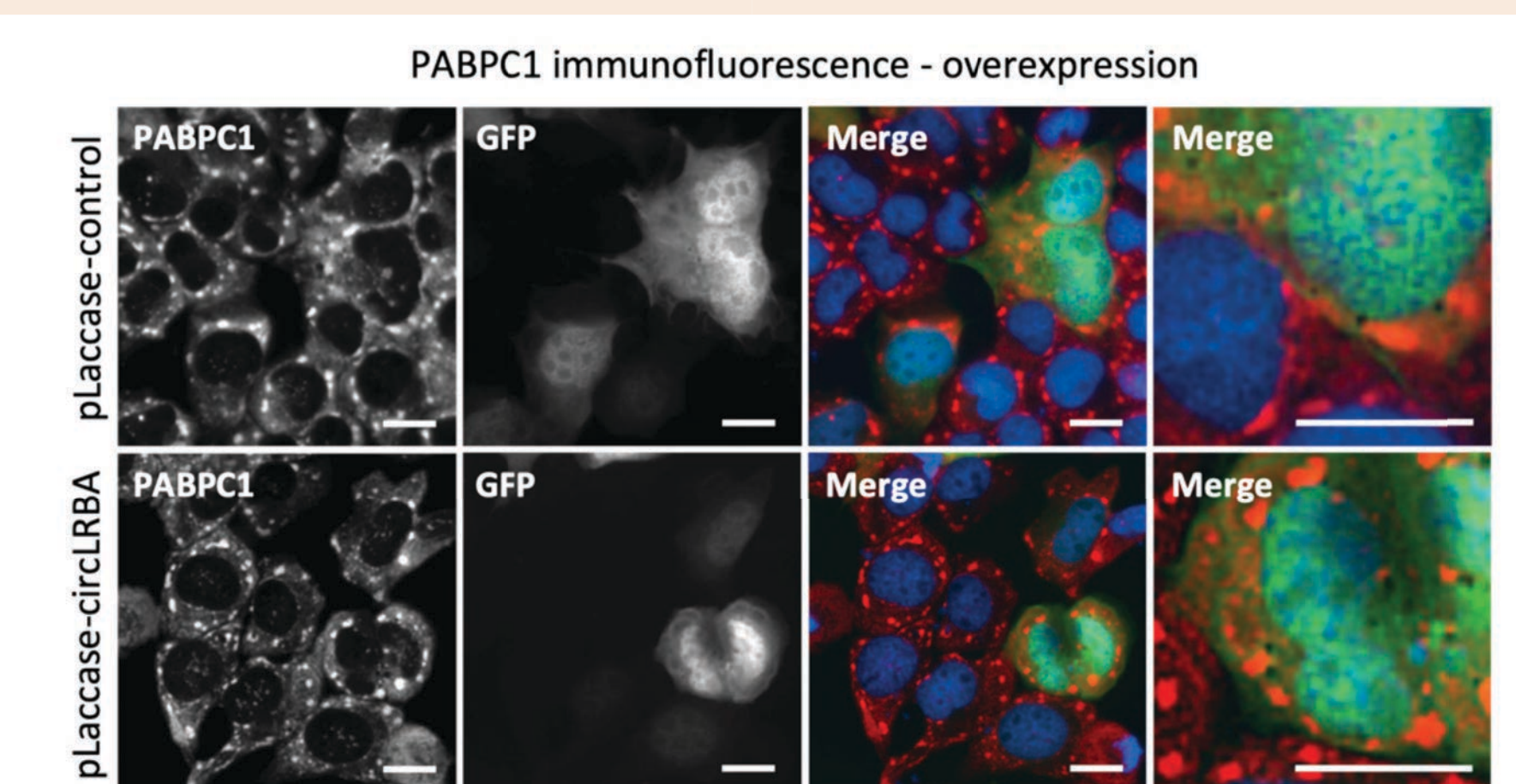
Upper: EdU incorporation assay followed by flow cytometry to screen impact of circRNA knockdown. Middle: Identification of circRNA binding proteins. circRNA pulldown- mass spec assay. Lower: Knockdown of circRNA or mRNA followed by mass spectrometry.



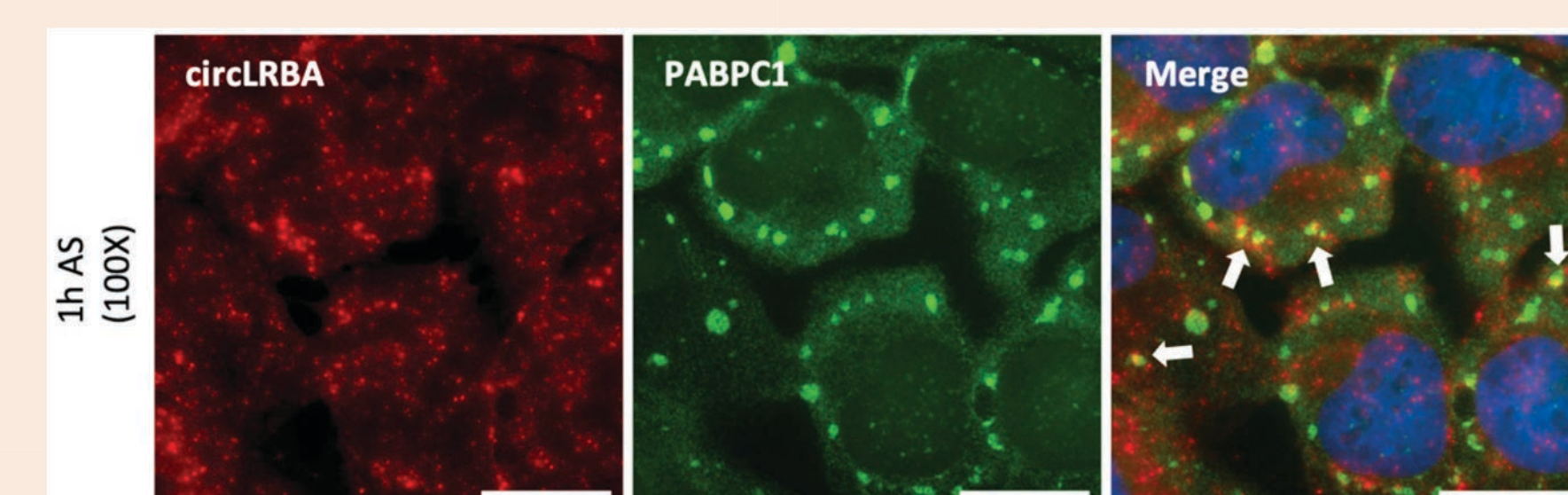
Overexpression of certain circRNAs inhibit RNA granule formation, potentially by inhibition of weak IDR interactions and phase separation.

Project: Study of ALS-associated granules and stress granule (SG) homing circRNAs.

Why are some circRNAs overrepresented in RNA granules? Do they play structural role here? High levels of certain circRNAs can inhibit SG-formation. What is the basis for this and are pathological inclusions found in ALS regulated by circRNAs?



RNA granule visualization by immunofluorescence.



circRNA localization by tyramide amplification of DIG-probe signal in RNA-FISH

Project: Can small circRNAs be used to target and harness disease-causing protein and RNA-binding proteins?

- circRNAs are incredibly stable in cells.
- circRNAs can be engineered to express proteins or short peptides.
- circRNAs can function as scaffolds or sponges for RNA binding proteins.

We have developed strategies for targeting specific oncogenes in specific cancers and neurodegenerative disease. These include Amyotrophic Lateral Sclerosis (ALS) and Myeloproliferative Neoplasms (MPNs). However, our strategies also allow us to target general cancer related genes including p53 and EGFR, that are defective or dysregulated in many cancers.

