

**Docket #:** S11-281

# ChiRP - RNA interactome analysis

ChiRP (“Chromatin Isolation through RNA Purification”) is a patented RNA “interactomics” technique developed in Prof. Howard Chang's laboratory to capture and identify DNA, RNA or protein molecules that interact with any RNA of interest in a cell. This method includes a single, unbiased, high throughput protocol for isolating all macromolecules associated with an RNA molecule. This is followed by downstream assays for identification and quantitation. The technology also includes a computational pipeline to both design oligonucleotide probes and analyze results (click thumbnail image below to view illustration of work flow).

Thousands of non-coding RNA molecules are now known to have a variety of functional roles - such as regulating chromatin remodeling, gene expression, cancer, aging and many other important biological processes. Just as ChIP-seq has opened the door for genome-wide DNA-protein interactions, ChIRP-seq studies of the “RNA interactome” may reveal many new kinds of biology.

## Stage of Research

The inventors have demonstrated the sensitivity and specificity of ChIRP on known interactions with roX2 (FDR = 0). They have also used the technique to reveal new principles of noncoding RNA biology with two human long noncoding RNAs (lncRNAs TERC and HOTAIR).

## Applications

- **RNA Research** to characterize the entire space of molecules that interact with any given RNA:
  - DNA (ChIRP-seq)
  - RNA (ChIRP-RNAseq)
  - proteins (ChIRP-protein-mass spectrometry)

# Advantages

- **High throughput** - designed for genome wide assays (compared to prior techniques that analyze one locus at a time)
- **Comprehensive and unbiased:**
  - general protocol allows concurrent identification of proteins, DNA, and RNA, saving time from optimization of separate purification processes
  - applicable to any RNA of interest without prior knowledge of the structure or functional domain of the RNA
- **Specific:**
  - for ChIRP-DNA-sequencing, extensive controls are in place to ensure specificity (FDR = 0 in positive control experiments)
  - for ChIRP-protein-mass spectrometry, stringent protocol measures the RNA capture profile in a quantitative manner and demonstrate a typical 1:1000 fold enrichment of target RNA, yielding highly specific proteome data
- **RNA capture** - this is the first method developed that can identify RNA interactions with other RNA molecules

# Publications

- Ci Chu, Kun Qu, Franklin L. Zhong, Steven E. Artandi, Howard Y. Chang, [Genomic Maps of Long Noncoding RNA Occupancy Reveal Principles of RNA-Chromatin Interactions](#), *Molecular Cell* Nov. 18, 2011, published online Sept. 29, 2011 (doi:10.1016/j.molcel.2011.08.027)
- Mary Muers, [RNA: Genome-wide views of long non-coding RNAs](#) *Nature Review Genetics* 12, 742-743 (November 2011).

# Patents

- Published Application: [20130123123](#)
- Issued: [8,748,354 \(USA\)](#)

# Innovators

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