

# Proteomics

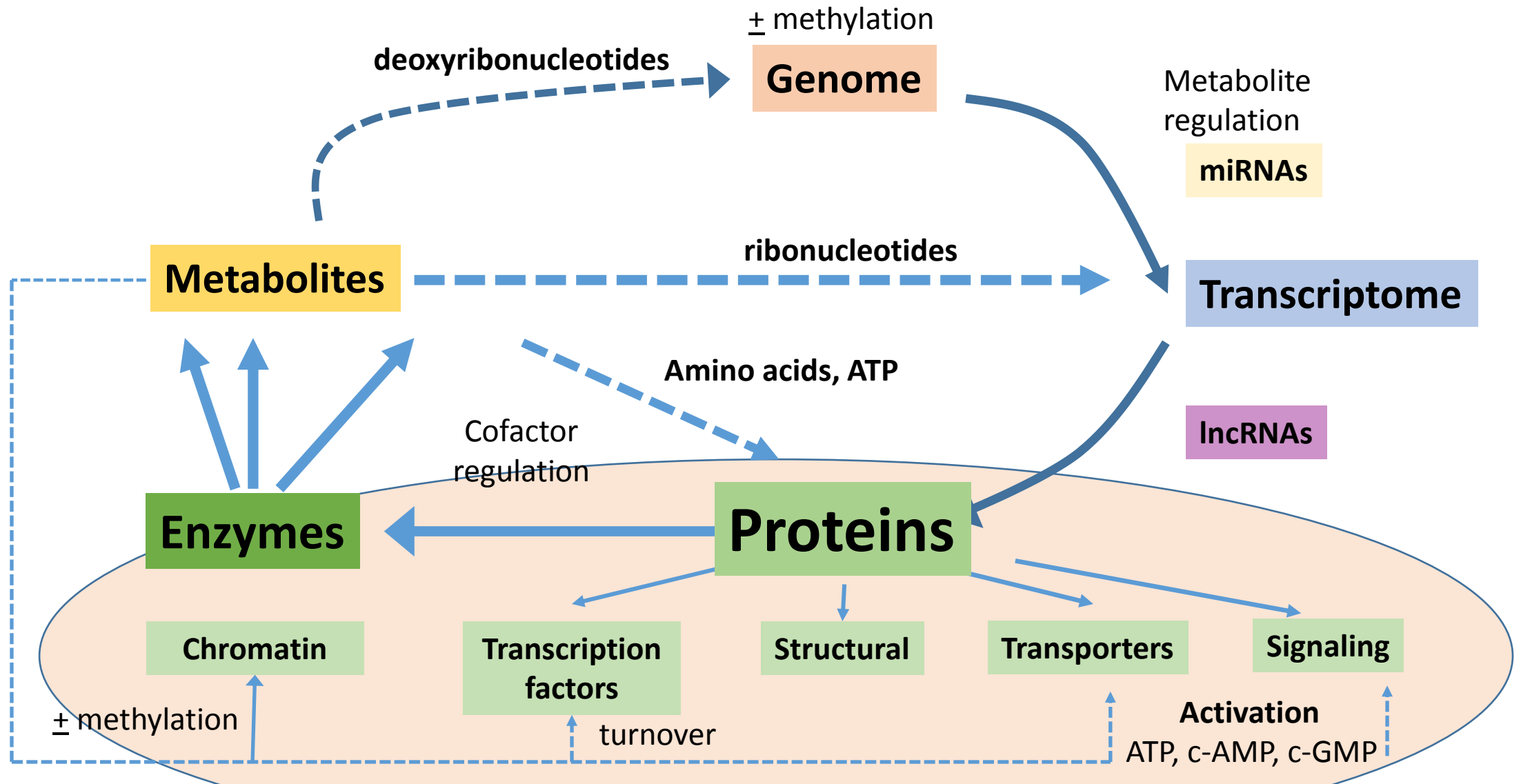
**Helen Kim, Matt Renfrow and Stephen Barnes**

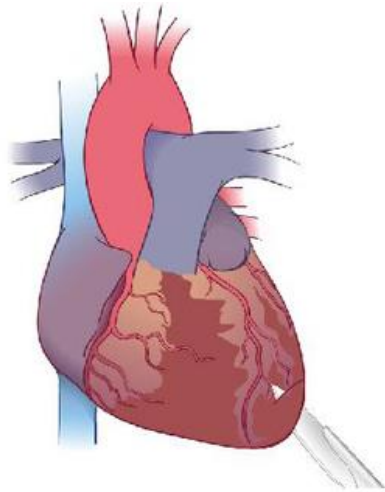
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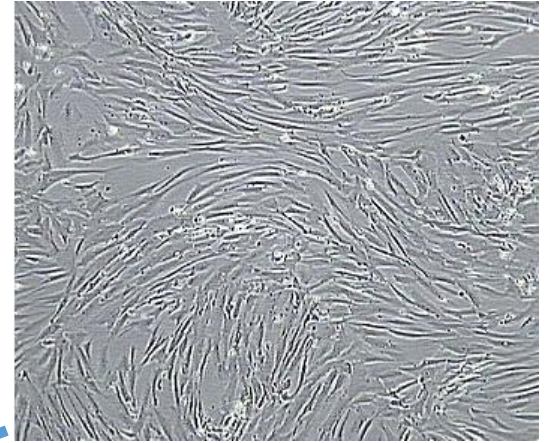
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# NIH and NCI are pushing for integration of -Omics

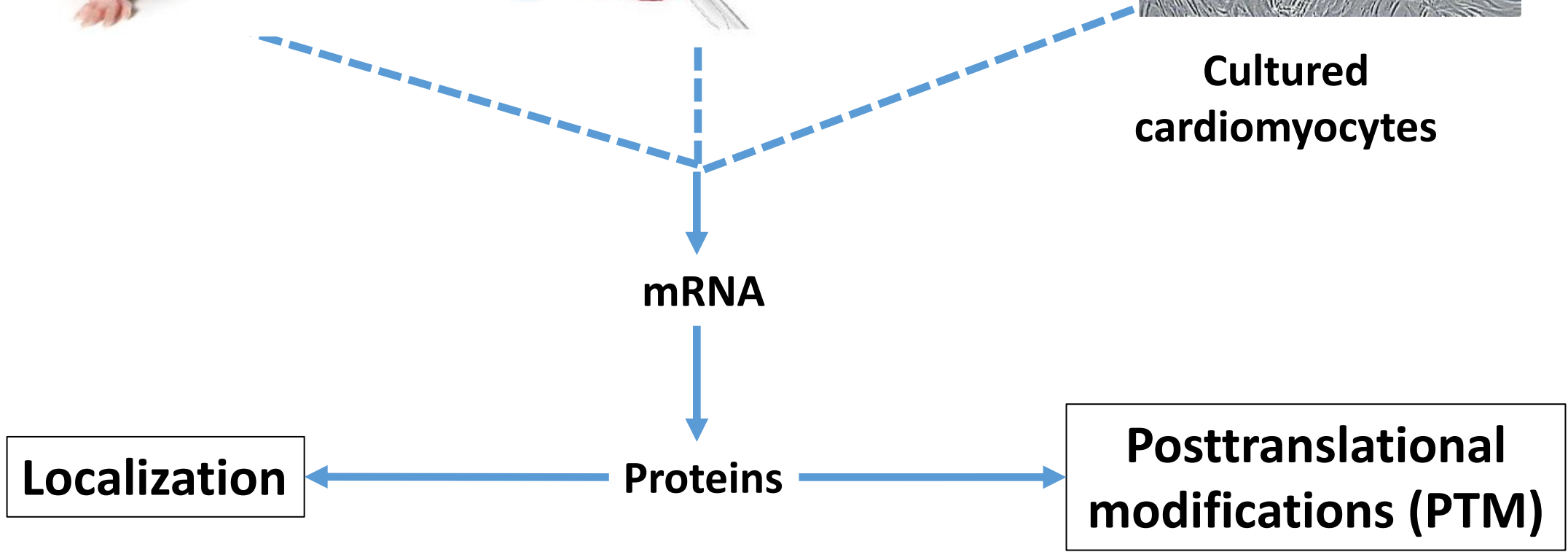




**Mouse heart**



**Cultured  
cardiomyocytes**



**Localization**

**Proteins**

**Posttranslational  
modifications (PTM)**

**Mature and more mature forms**

# Protein networks

- **Interactomes**

- <http://string-db.org>

- Nice visuals

- <http://interactome.dfci.harvard.edu>

## STRING - Known and Predicted Protein-Protein Interactions

search by name    search by protein sequence    multiple names    multiple sequences

protein name: (examples: #1 #2 #3)

(STRING understands a variety of protein names and accessions; you can also try a [random entry](#))

organism:

interactors wanted:  
 COGs     Proteins       

*please enter your protein of interest...*

### What it does ...

STRING is a database of known and predicted protein interactions. The interactions include direct (physical) and indirect (functional) associations; they are derived from four sources:

Genomic Context



High-throughput Experiments



(Conserved) Coexpression



Previous Knowledge



STRING quantitatively integrates interaction data from these sources for a large number of organisms, and transfers information between these organisms where applicable. The database currently covers 9'643'763 proteins from 2'031 organisms.

### More Info

[Funding / Support](#)

[Acknowledgements](#)

[Use Scenarios](#)

STRING (*Search Tool for the Retrieval of Interacting Genes/Proteins*) is being developed at [CPR](#), [EMBL](#), [SIB](#), [KU](#), [TUD](#) and [UZH](#).

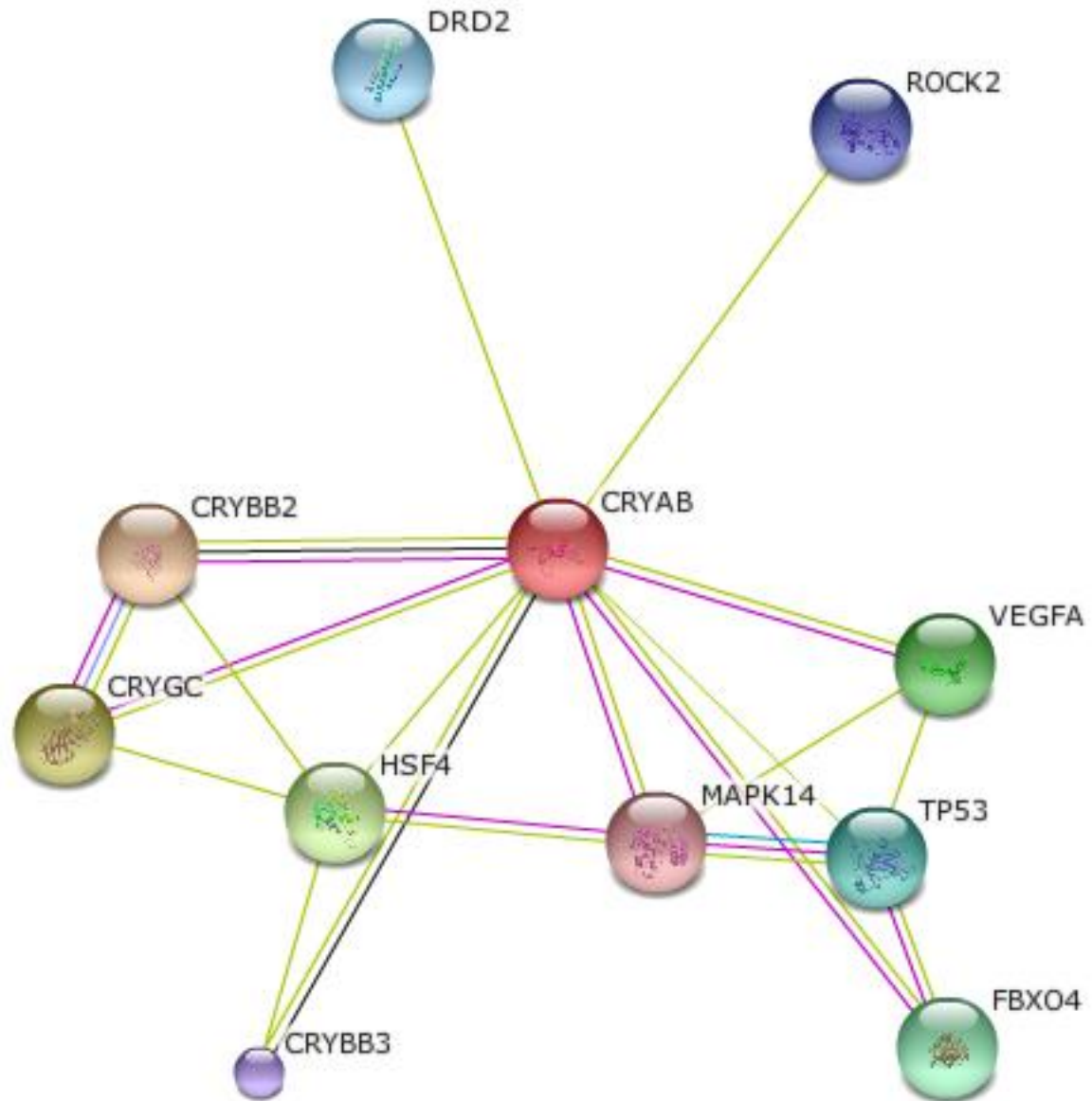
STRING references: [Szklarczyk et al. 2015](#) / [2013](#) / [2011](#) / [2009](#) / [2007](#) / [2005](#) / [2003](#) / [Snel et al. 2000](#).

Miscellaneous: [Access Statistics](#), [Robot Access Guide](#), [Supported Browsers](#).

**What's New?** This is version 10 of STRING - now covering more than 2000 organisms, and with improved prediction algorithms!

**Sister Projects:** check out [STITCH](#) and [eggNOG](#) - two sister projects built on STRING data!

**Previous Releases:** Trying to reproduce an earlier finding? Confused? Refer to our [old releases](#).



**Interactome for alphaB crystallin**

# Output of human cryAB by String db

## Your Input:

- CRYAB crystallin, alpha B; May contribute to the transparency and refractive index of the lens. Has chaperone-like activity, preventing aggregation of various proteins under a wide range of stress conditions (175 aa)  
(*Homo sapiens*)

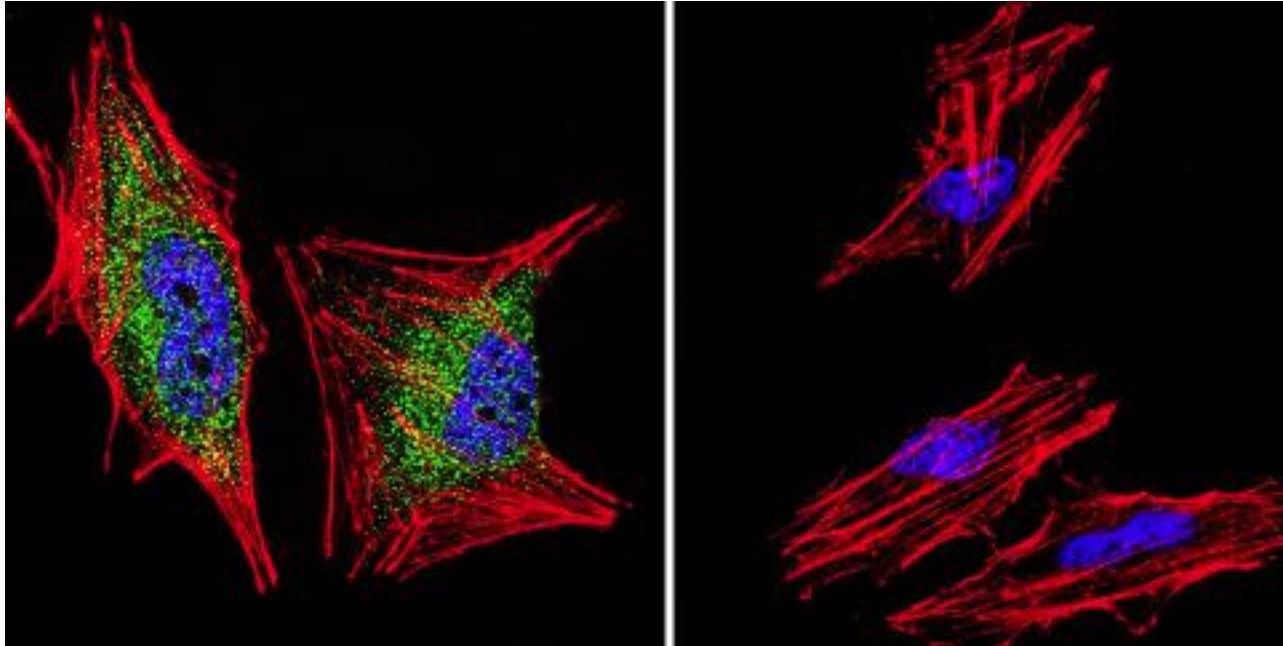
## Predicted Functional Partners:

		Neighborhood	Gene Fusion	Cooccurrence	Coexpression	Experiments	Databases	Textmining	[Homology]	Score
CRYBB2	crystallin, beta B2; Crystallins are the dominant structural components of the vertebrate eye   [...] (205 aa)									0.888
CRYGC	crystallin, gamma C; Crystallins are the dominant structural components of the vertebrate eye   [...] (174 aa)									0.842
HSF4	heat shock transcription factor 4; DNA-binding protein that specifically binds heat shock promo [...] (492 aa)									0.838
VEGFA	vascular endothelial growth factor A (412 aa)									0.833
FBXO4	F-box protein 4; Substrate recognition component of a SCF (SKP1-CUL1-F- box protein) E3 ubiquit [...] (387 aa)									0.822
TP53	tumor protein p53; Acts as a tumor suppressor in many tumor types; induces growth arrest or apo [...] (393 aa)									0.818
DRD2	dopamine receptor D2; Dopamine receptor whose activity is mediated by G proteins which inhibit [...] (443 aa)									0.800
ROCK2	Rho-associated, coiled-coil containing protein kinase 2; Protein kinase which is a key regulato [...] (1388 aa)									0.788
CRYBB3	crystallin, beta B3; Crystallins are the dominant structural components of the vertebrate eye   [...] (211 aa)									0.750
MAPK14	mitogen-activated protein kinase 14; Serine/threonine kinase which acts as an essential compone [...] (360 aa)									0.722

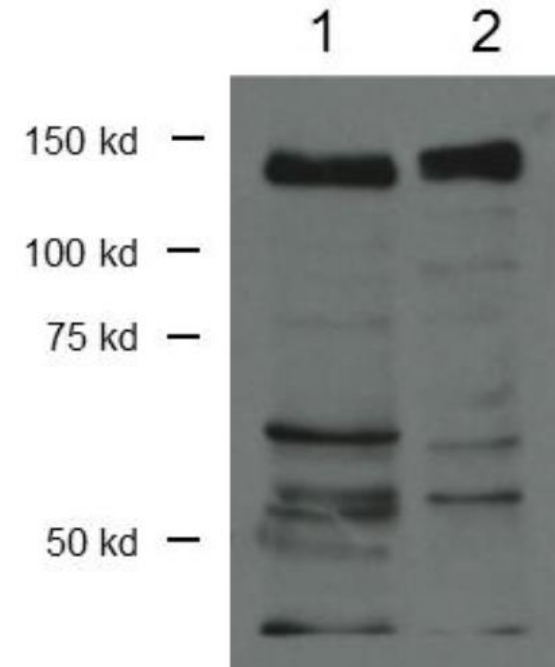
Majority of the connections come from literature textmining

How to verify the connections

# Detecting proteins with antibodies



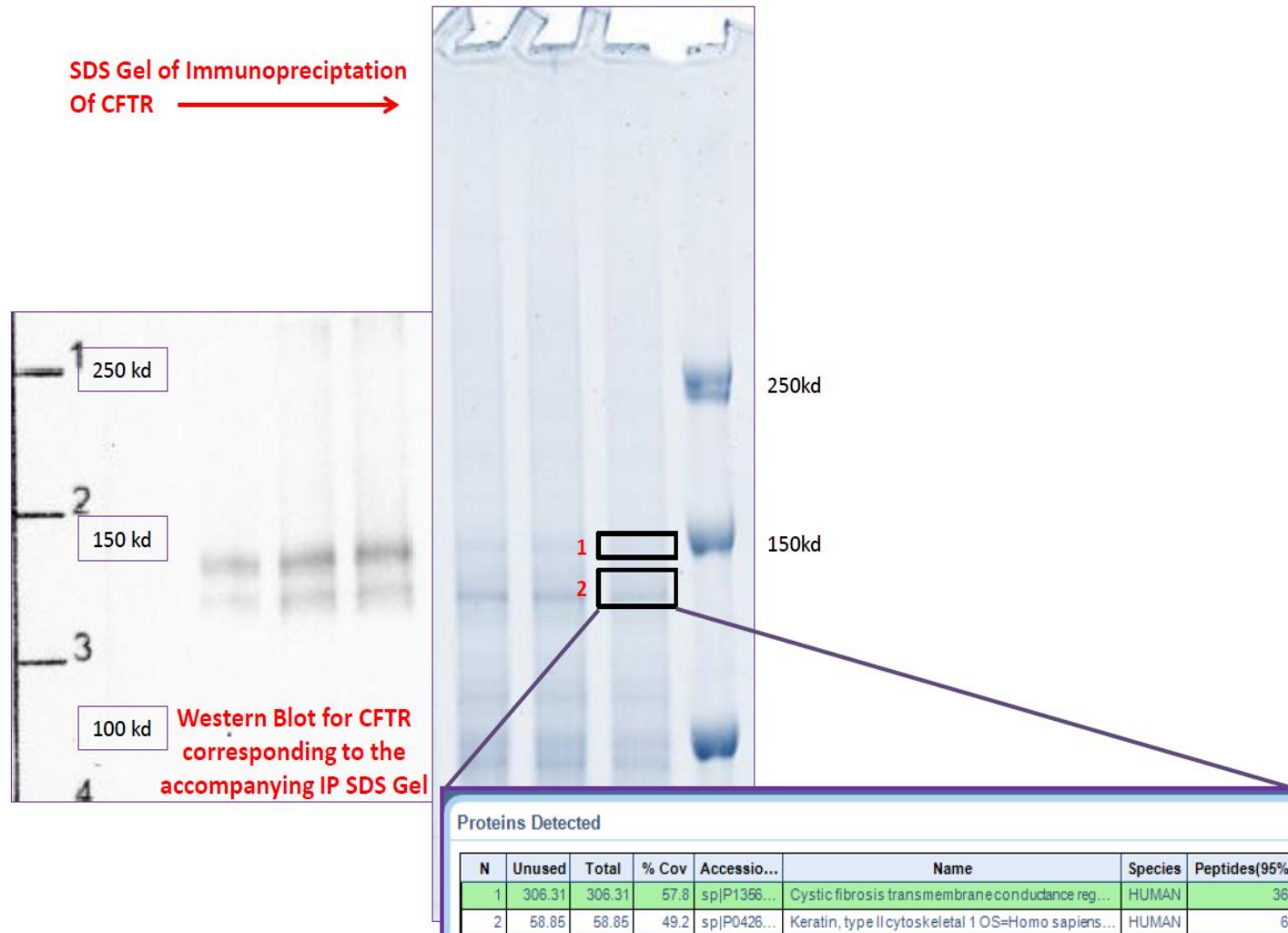
Immunohistochemistry provides beautiful vistas on protein distribution in cells.  
Is it seduction?



Antibodies can bind to more than one protein band. In this case for CTCF to splice variants. The protein is nominally 82 kDa.



# An example of antibody validation



# Overview of what we'll present

- **Extraction and fractionation of proteins**
  - Purification methods (basic and protein tags)
  - 1D- and 2D-analysis
  - Cy-dye methods for quantitative intact proteomics (Top-down)
  - Detection of PTMs
- **Analytical mass spectrometry and proteomics**
  - Analytical Strategies for getting an answer by MS
  - Importance of mass accuracy
  - Verification and quantification of PTMs
- **Mass spectrometry imaging and quantitative analysis**
  - Localizing where and in what form?
  - How much of each protein form – targeted or untargeted?