



**PhasAGE**

EXCELLENCE HUB ON  
PHASE TRANSITIONS IN  
AGING AND AGE-RELATED  
DISORDERS

**TRAINING SCHOOL 1**

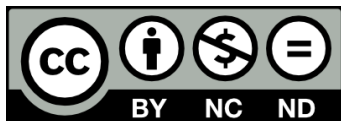
**24 -28 MAY 2021**

## **Computational methods to study Phase Separation**

**Lecture:** Phase separation and emergent functions of intrinsically disordered proteins –

Peter Tompa

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## PhasAGE

EXCELLENCE HUB ON  
PHASE TRANSITIONS IN AGING  
AND AGE-RELATED DISORDERS

TRAINING SCHOOL

### Computational Methods to Study Protein Phase Separation

24-28 May 2021 - Online event

*Monday May 24th, 14:00 - 18:00 CEST | 13:00 - 17:00 GMT+1*

Time (CEST)	Session title	Speaker	Type
14:00 - 15:00	<b>PhasAGE: Excellence Hub on phase transitions in aging and age-related disorders</b>	Sandra Macedo Ribeiro	L
15:00 - 16:45	<b>Phase separation and emergent functions of Intrinsically Disordered Proteins</b>	Peter Tompa	L
16:45 - 17:00	<i>Break</i>		
17:00 - 18:00	<b>Group activity</b>		G

- 1) How it started: three stories
- 2) An outline of LLPS and emergent functions
- 3) LLPS and disease
- 4) Experimental techniques to study LLPS
- 5) Databases and bioinformatics tools

# 1) How it started: three stories



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# Germline P Granules Are Liquid Droplets That Localize by Controlled Dissolution/Condensation

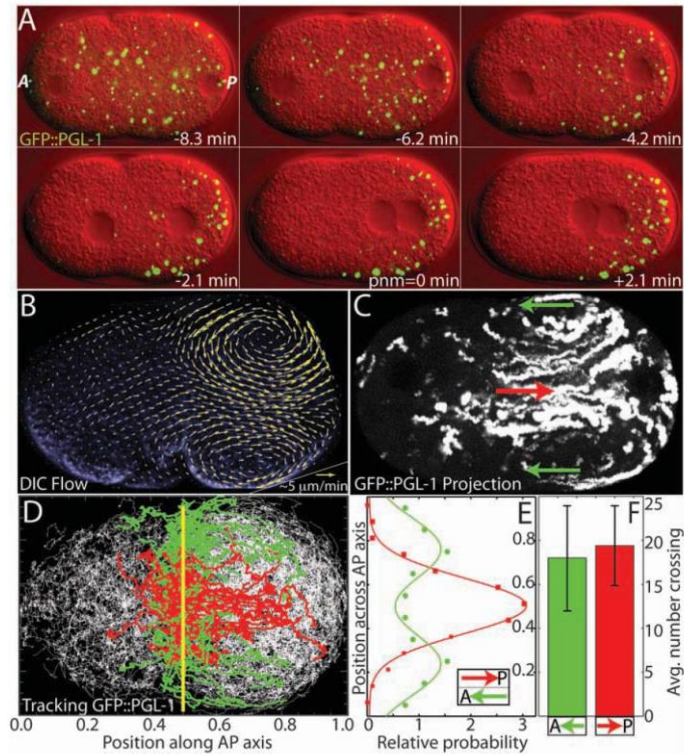
Clifford P. Brangwynne,<sup>1,2,3</sup> Christian R. Eckmann,<sup>1</sup> David S. Courson,<sup>3</sup> Agata Rybarska,<sup>1</sup> Carsten Hoege,<sup>1</sup> Jöbin Gharakhani,<sup>2,3</sup> Frank Jülicher,<sup>2,3</sup> Anthony A. Hyman<sup>1,3\*</sup>

the embryo posterior; however, close to the cortex there was a flux of P granules into the anterior that was of similar magnitude to the posteriorly directed flux (Fig. 1, D to F). This behavior closely matched the overall flow behavior of cytoplasmic material such as yolk granules (6), quantified by particle imaging velocimetry (PIV) (Fig. 1, B and C) (9). P granules cannot preferentially localize to the posterior by convection in the surrounding cytoplasm alone. Thus, flows have little or no role

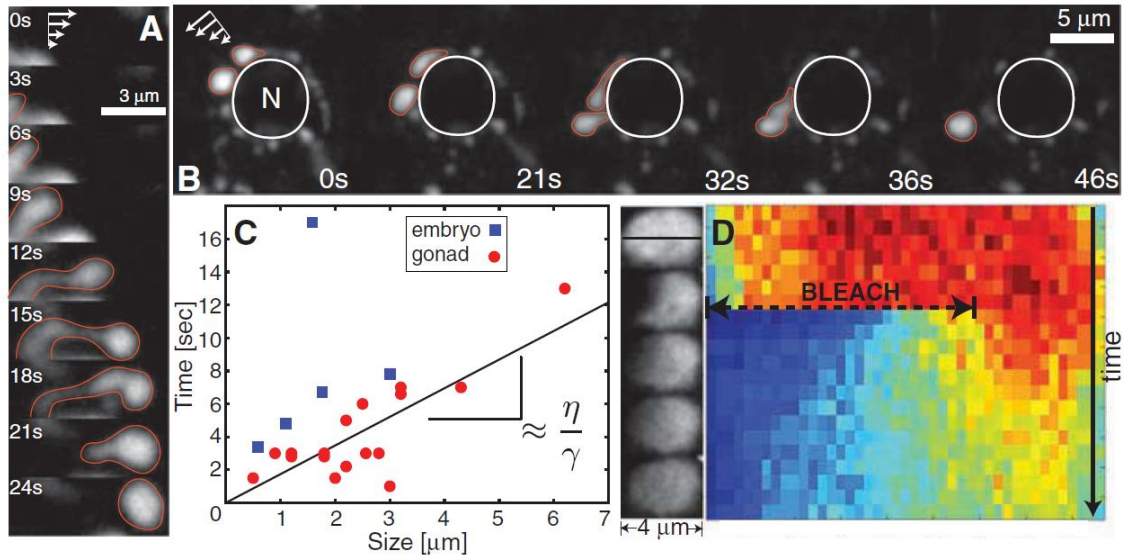
In sexually reproducing organisms, germ cells generate sperm and eggs. In *C. elegans*, the first germ cell is established when RNA and protein-rich P granules localize to the posterior of the one-cell embryo. It was shown that P granules exhibit liquid-like behaviors, including fusion, dripping, and wetting, and arise by condensation (phase separation). Polarity of the embryo is marked by biased localization at the posterior.

# Preferential localization and movement of PGs

- GFP-PGL1, posterior end of embryo -



# Liquid behavior of PGs



(A) jetting from nucleus, (B) dripping and fusion, (C) fusion and viscosity, (D) FRAP

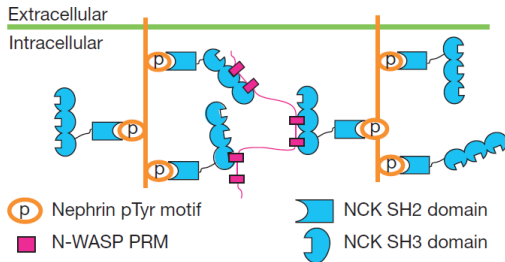
## Phase transitions in the assembly of multivalent signalling proteins

Pilong Li<sup>1\*</sup>, Sudeep Banjade<sup>1\*</sup>, Hui-Chun Cheng<sup>1\*</sup>, Soyeon Kim<sup>1</sup>, Baoyu Chen<sup>1</sup>, Liang Guo<sup>2</sup>, Marc Llaguno<sup>3</sup>, Javoris V. Hollingsworth<sup>4</sup>, David S. King<sup>5</sup>, Salman F. Banani<sup>1</sup>, Paul S. Russo<sup>4</sup>, Qiu-Xing Jiang<sup>3</sup>, B. Tracy Nixon<sup>6</sup> & Michael K. Rosen<sup>1</sup>

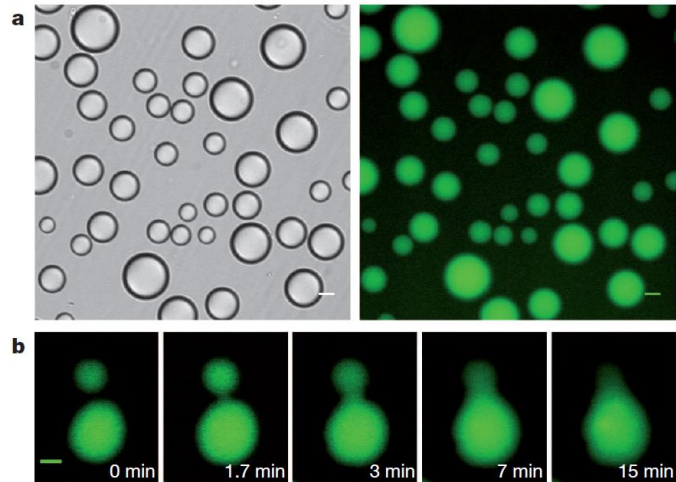
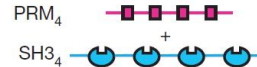
It is shown *in vitro* that mixtures of signaling proteins Wiskott-Aldrich syndrome protein (N-WASP), NCK and phosphorylated nephrin1 (complex for actin cytoskeletal rearrangements) phase separate by liquid-liquid demixing, generating  $\mu\text{m}$ -sized liquid droplets. The concentrations needed are directly related to the valency of the interacting species. The phase transition is regulated by nephrin phosphorylation and corresponds to a sharp increase in activity towards an actin nucleation factor, the Arp2/3 complex.



# Nephrin-NCK-N-WASP system in cytoskeleton remodeling

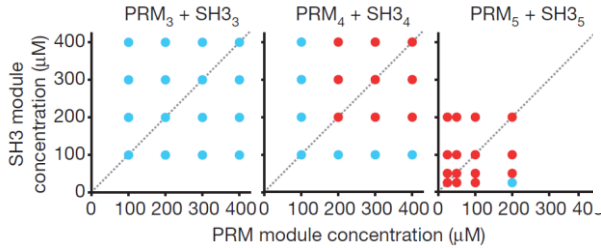


**Multivalency**  
SH2 - pTyr, SH3 - PRM interactions:  
signaling through Arp 2/3 to actin

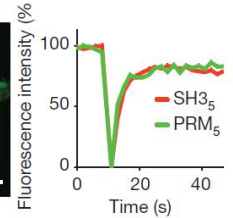
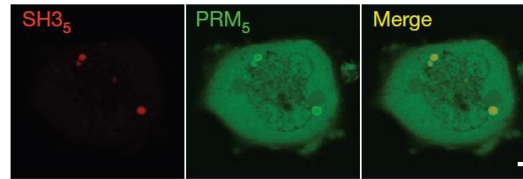


- (A) Differential interference contrast (DIC) microscopy  
(B) Wide-field fluorescence microscopy  
(C) time-lapse imaging of fusion events

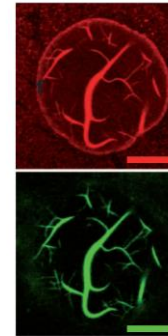
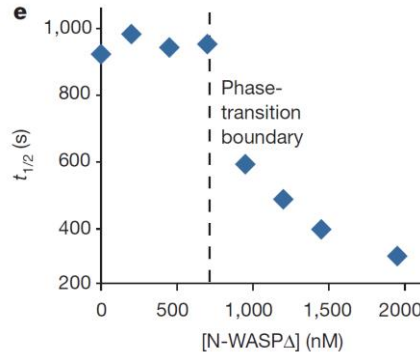
# Nephrin-NCK-N-WASP system in cytoskeleton remodeling



Valency and phase diagram



Colocalization and FRAP



$t_{1/2}$  of actin polymerization (Arp2/3 and rhodamine-actin added)



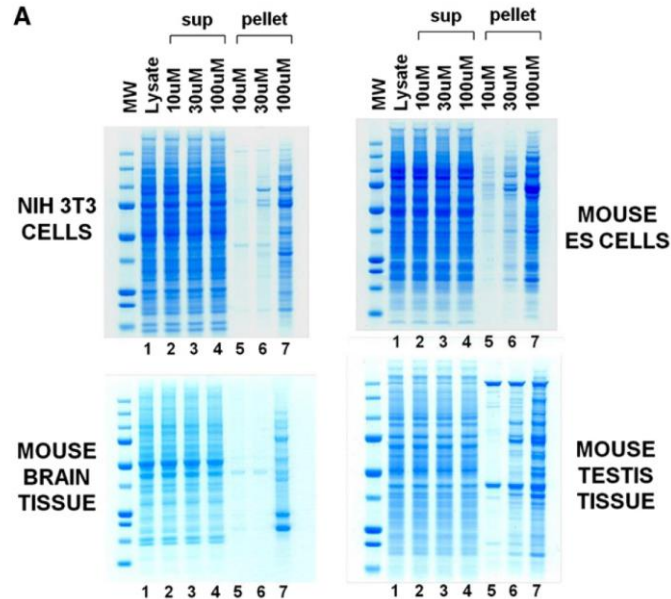
# Cell-free Formation of RNA Granules: Low Complexity Sequence Domains Form Dynamic Fibers within Hydrogels

Masato Kato,<sup>1</sup> Tina W. Han,<sup>1</sup> Shanhai Xie,<sup>1</sup> Kevin Shi,<sup>1</sup> Xinlin Du,<sup>1</sup> Leeju C. Wu,<sup>1</sup> Hamid Mirzaei,<sup>1</sup> Elizabeth J. Goldsmith,<sup>1</sup> Jamie Longgood,<sup>1</sup> Jimin Pei,<sup>1,3</sup> Nick V. Grishin,<sup>1,3</sup> Douglas E. Frantz,<sup>4</sup> Jay W. Schneider,<sup>2</sup> She Chen,<sup>5</sup> Lin Li,<sup>5</sup> Michael R. Sawaya,<sup>6</sup> David Eisenberg,<sup>6</sup> Robert Tycko,<sup>7</sup> and Steven L. McKnight<sup>1,\*</sup>

Eukaryotic cells contain assemblies of RNAs and proteins termed RNA granules. Many proteins within RNA-binding domains and LCDs. Exposure of cell lysates to a biotinylated isoxazole (b-isox) precipitated hundreds of RNA-binding proteins with significant overlap to the constituents of RNA granules. LCDs are both necessary and sufficient for b-isox-mediated aggregation and can undergo a concentration-dependent phase transition to a hydrogel-like state. X-ray diffraction and EM showed that hydrogels are composed amyloid-like (but highly dynamic) fibers.

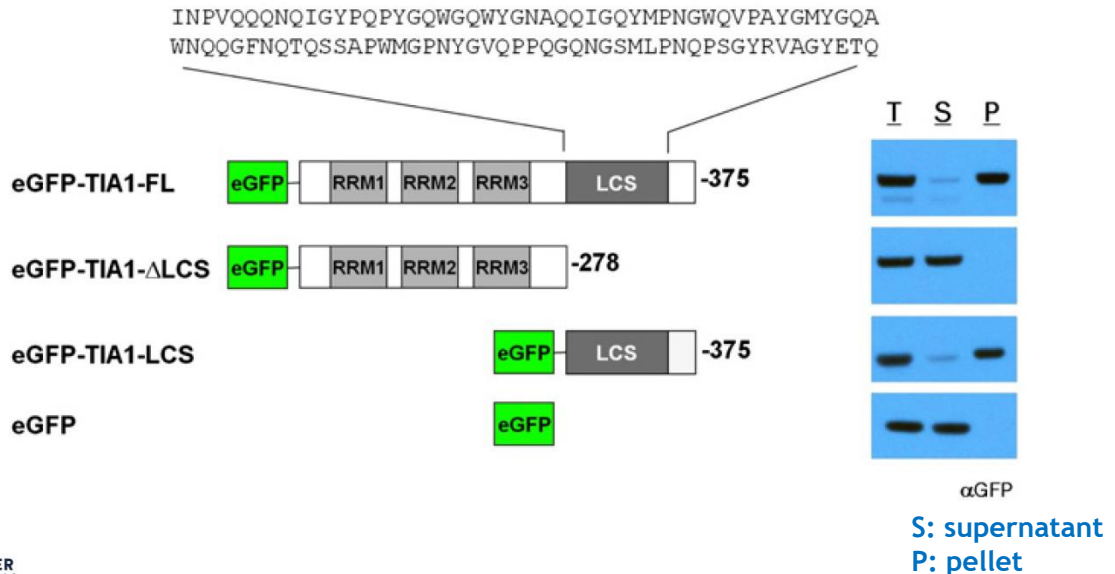
# Cellular extracts treated with b-isox

A high-throughput drug screen for chemicals that promote mouse embryonic stem (ES) cell differentiation toward cardiomyocytes lead to the discovery of 5-aryl-isoxazole-3-carboxamide. Neuronal progenitors further progressed to morphologically mature neurons. The biotinylated derivative (b-isox) was used to find its targets: it selectively precipitated proteins.

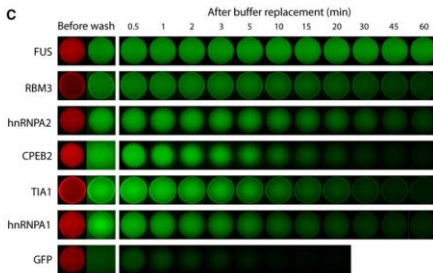
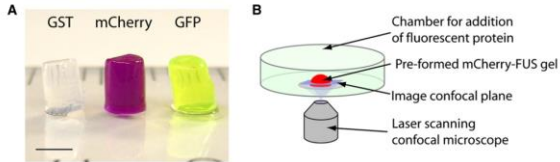


# Enrichment for RNA granule proteins

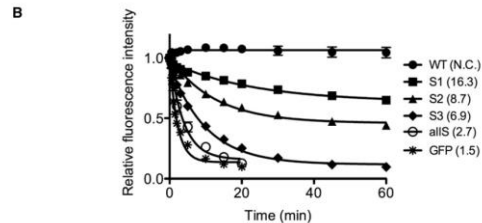
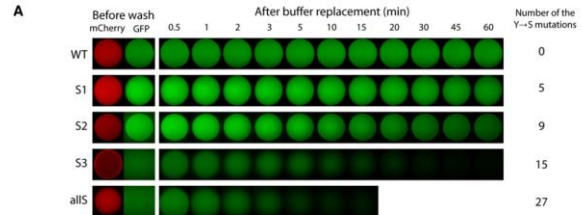
Of 106 proteins found, 53 are among canonical RNA granule proteins (FUS, RBM3, hnRNPA2, CPEB2, TIA1, hnRNPA1, Atxn2, Ddx1, G3BP1, Npm1, Tdp-43, Caprin1). LCD drives b-isox-mediated precipitation.



# LCDs undergo gelation (without b-isox)

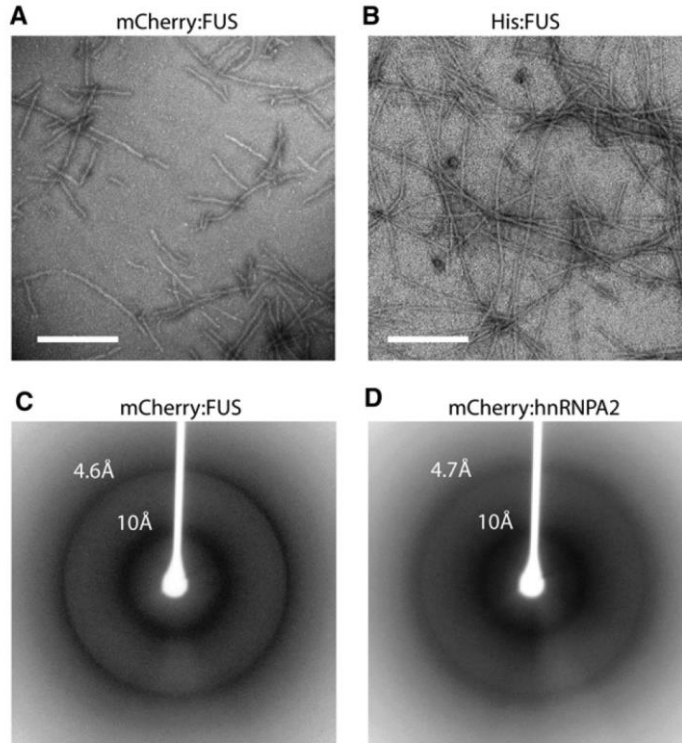


FUS LCD hydrogel  
Retention of other GFP-LCDs



FUS LCD hydrogel, GFP-FUS LCD retention  
Mutation of Tyr residues

# b-isox causes reversible amyloid formation



hydrogel droplets visualized by TEM

Kato... McKnight (2012) *Cell* 149: 753

## 2) An outline of LLPS and emergent functions



REVIEW

CELLULAR BIOPHYSICS

## Liquid phase condensation in cell physiology and disease

Yongdae Shin and Clifford P. Brangwynne\*

Shin, Brangwynne (2017) *Science* 357: eaaf4382

AR ANNUAL  
REVIEWS

*Annual Review of Physical Chemistry*

### Biomolecular Phase Separation: From Molecular Driving Forces to Macroscopic Properties

Gregory L. Dignon,<sup>1,2</sup> Robert B. Best,<sup>3</sup>  
and Jeetain Mittal<sup>1</sup>

Dignon... (2020) *Annu. Rev. Phys. Chem.* 71: 53

# REVIEWS

 Check for updates

Biomolecular condensates at the  
nexus of cellular stress, protein  
aggregation disease and ageing

Simon Alberti<sup>1</sup>  and Anthony A. Hyman<sup>2</sup> 

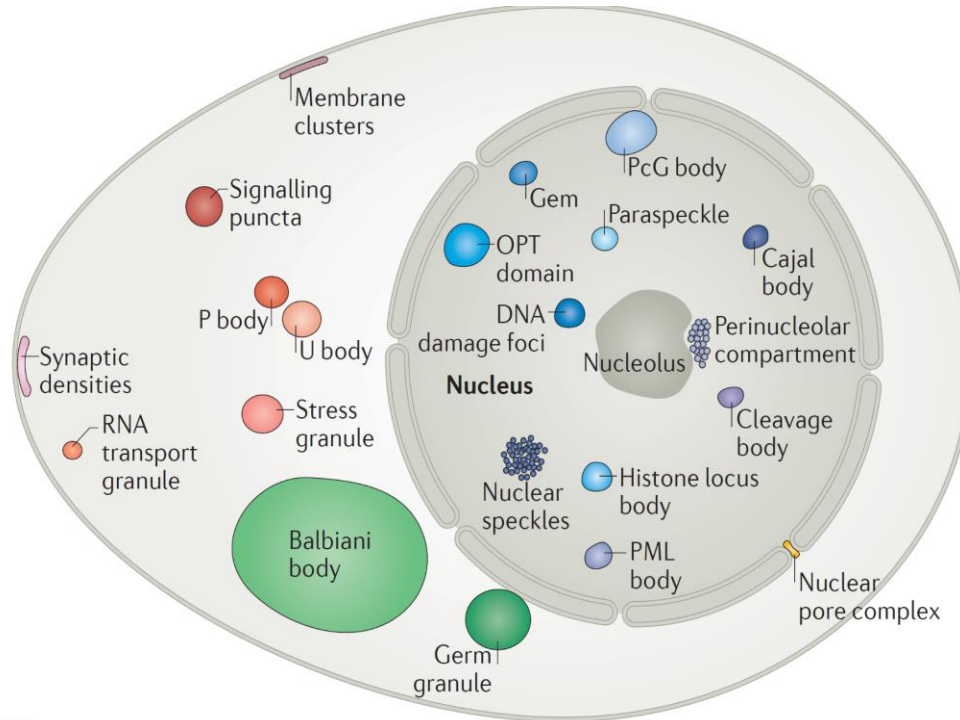
Alberti, Hyman (2021) *Nat. Rev. MCB* 22: 196



PhasAGE

# Membraneless organelles

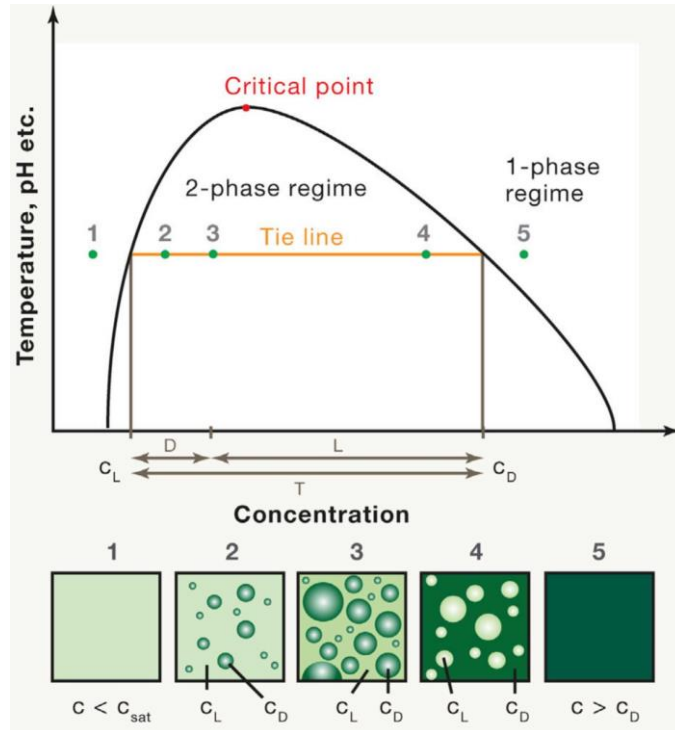
- biomolecular condensates, RNP bodies, LLPS -



# Their mechanism of formation

## - spontaneous demixing, LLPS -

- 1) phase diagram
- 2) binodal/coexistence line
- 3) saturation concentration ( $C_{sat}$ )



# Polymer physics (thermodynamics) of LLPS

## - e.g. Flory-Huggins formalism -

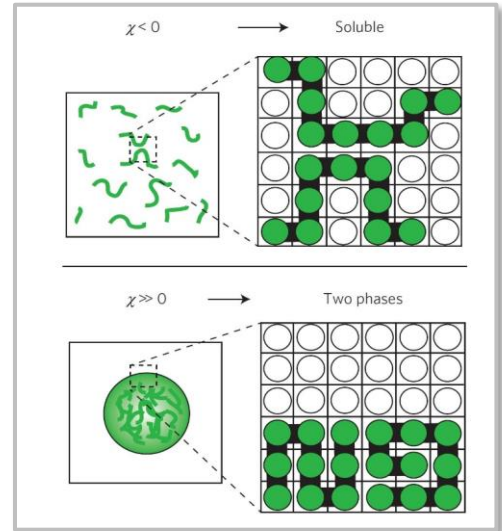
Free energy of mixing per lattice site ( $\Phi$  - volume fraction)

$$\frac{F}{k_B T} = \frac{\phi}{N} \ln \phi + (1 - \phi) \ln(1 - \phi) + \chi \phi(1 - \phi)$$

Entropy
Enthalpy

Chain-chain vs. chain-solvent interaction ( $\chi$  - Flory prmt.)

$$\chi = \frac{z}{k_B T} \left[ u_{ps} - \frac{1}{2} (u_{pp} + u_{ss}) \right]$$

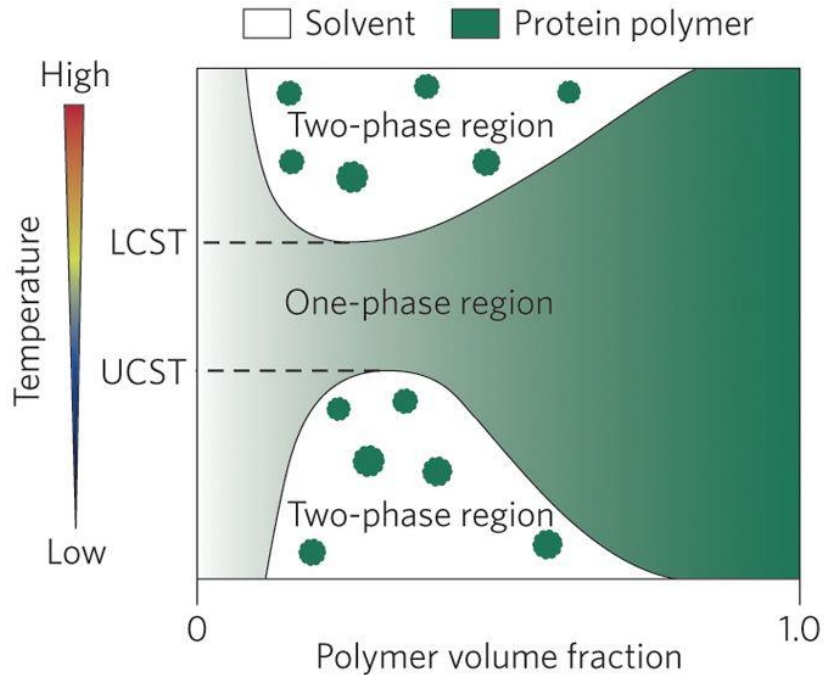


Homotypic, homopolymer

Homogeneous homopolymers

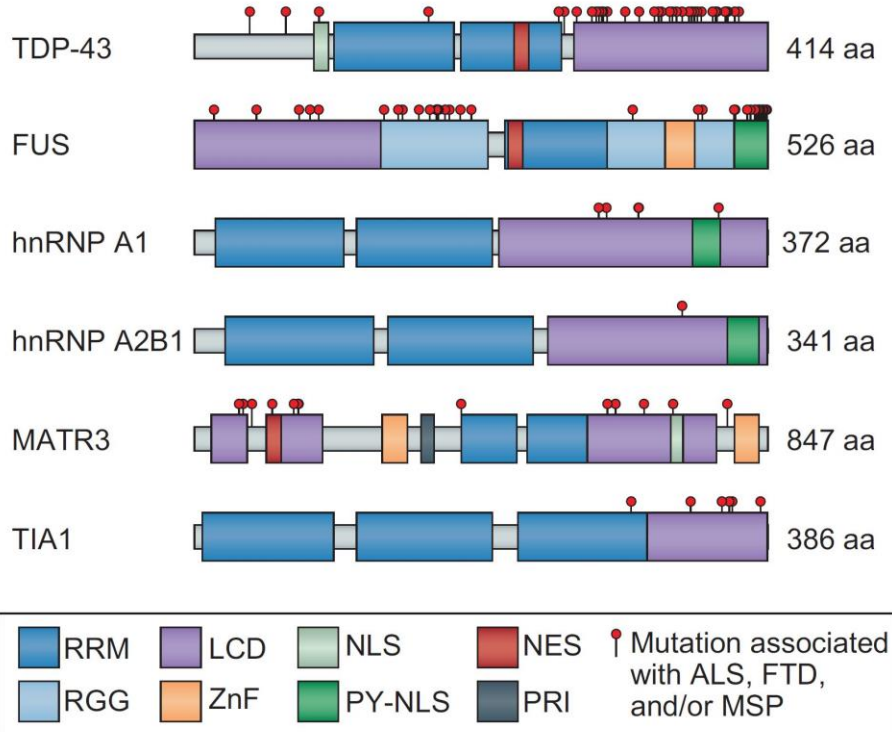
# Sometimes opposite behavior

Temperature dependence of attractive term



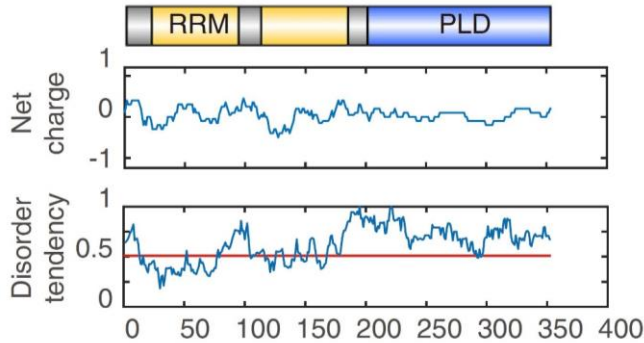
# Structural disorder and RNA binding in LLPS proteins

- LCD: low-complexity IDR -

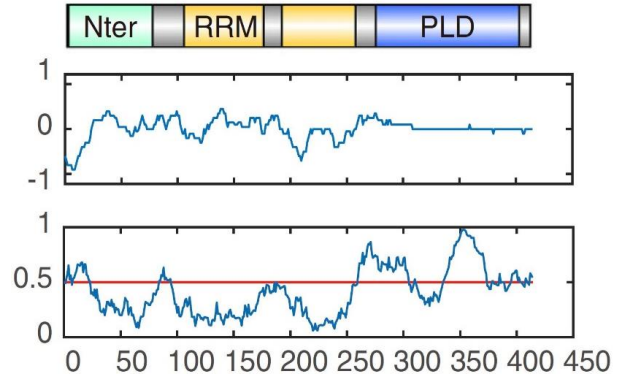


# Structural disorder in LLPS proteins

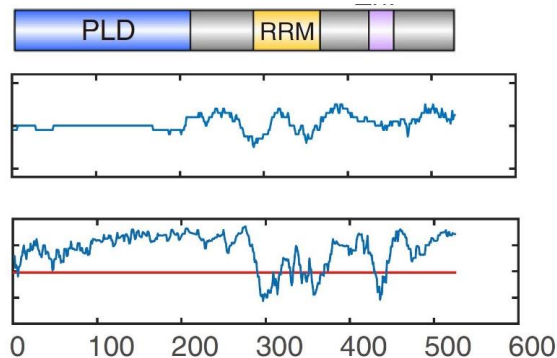
## hnRNP A2B1



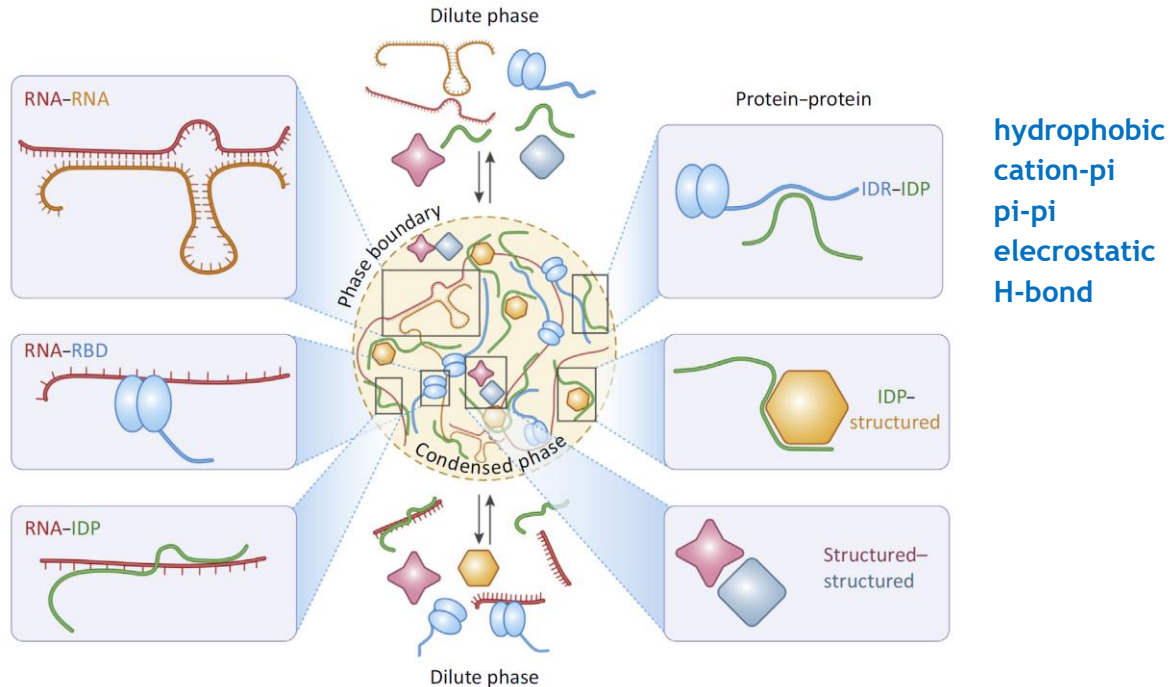
## TDP-43



## FUS



# Different types of interactions driving LLPS

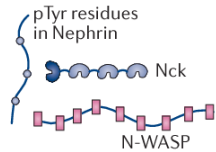


Features: (i) dynamics, (ii) strength, (iii) specificity, (iv) stoichiometry, (v) structure

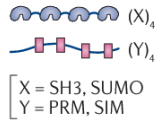


# Multivalency is basic to LLPS

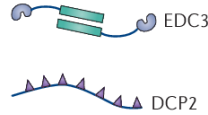
**a** Nephrin-Nck-N-WASP



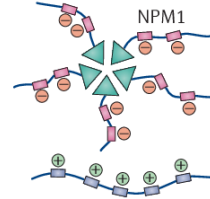
Engineered multidomain polypeptides



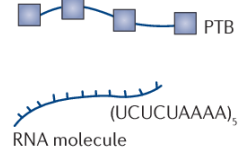
**b** EDC3-DCP2



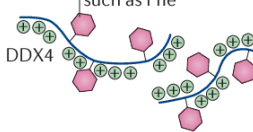
**c** NPM1-R-motifs



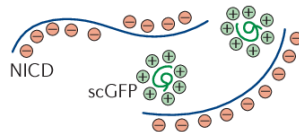
**d** PTB-RNA



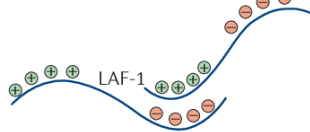
**e** Aromatic amino acid such as Phe



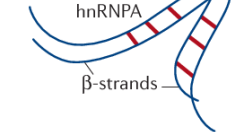
**f**



**g**



**h**



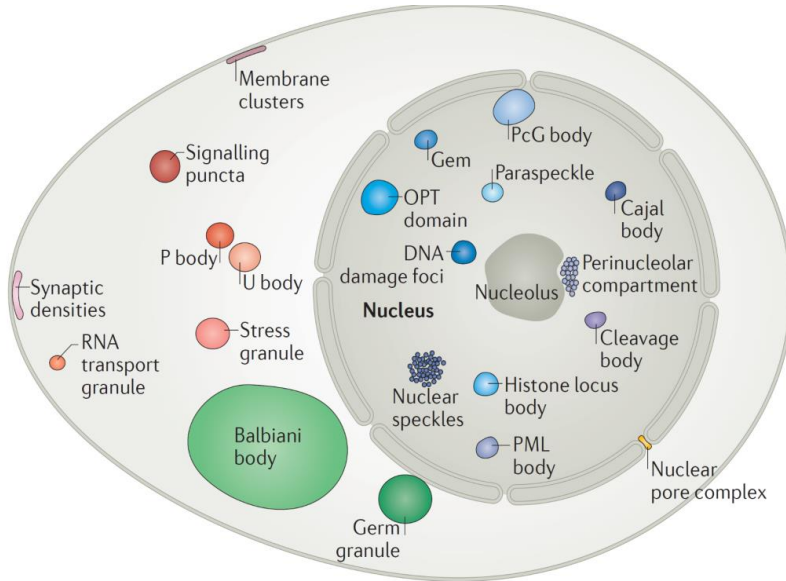
b) Enhancer of mRNA-decapping protein 3 (EDC3) decapping enzyme subunit 2 (DCP2)

d) polypyrimidine tract (RNA) binding protein (PTB)

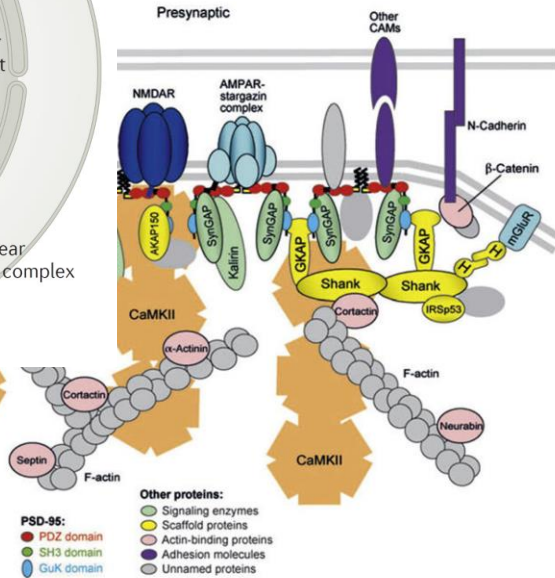
f) nephrin intracellular domain (NICD) and supercharged GFP

g) P-granule LAF-1

# Not every cellular assembly is LLPS though

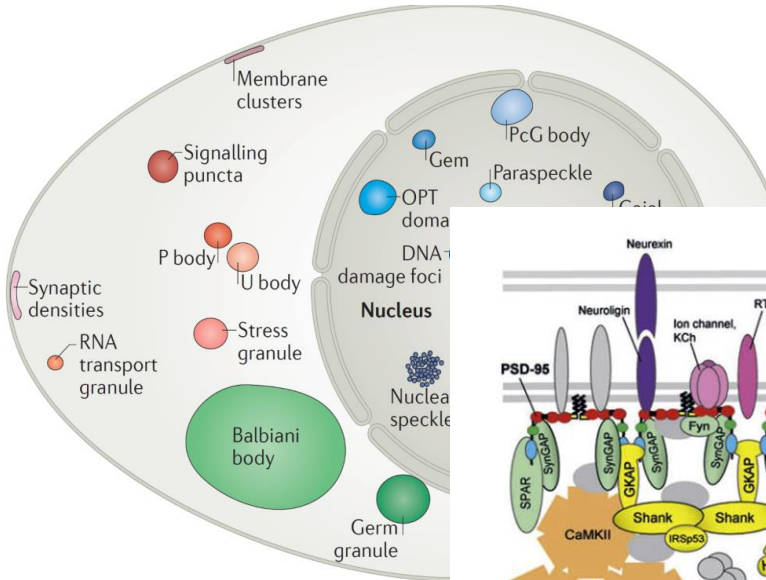


Banani et al. (2017) *NRMCB*

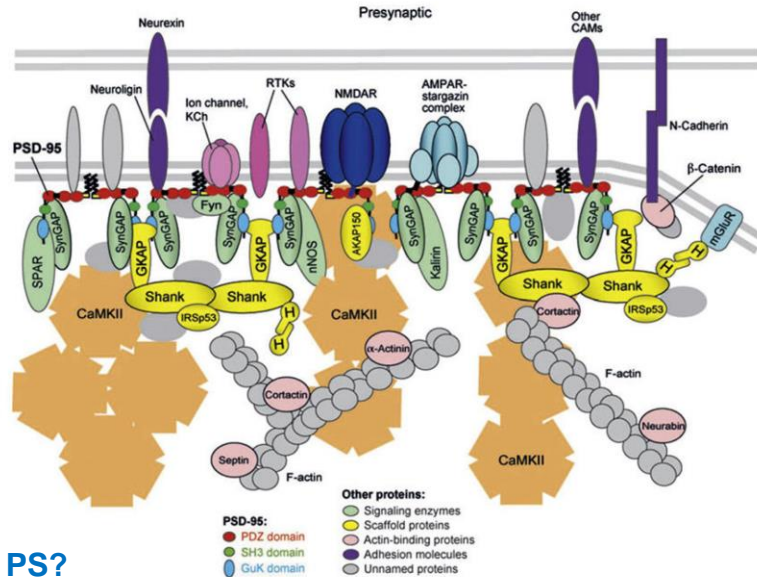


Panca (2019) *BBA*

# Not every cellular assembly is LLPS though



Banani et al. (21)



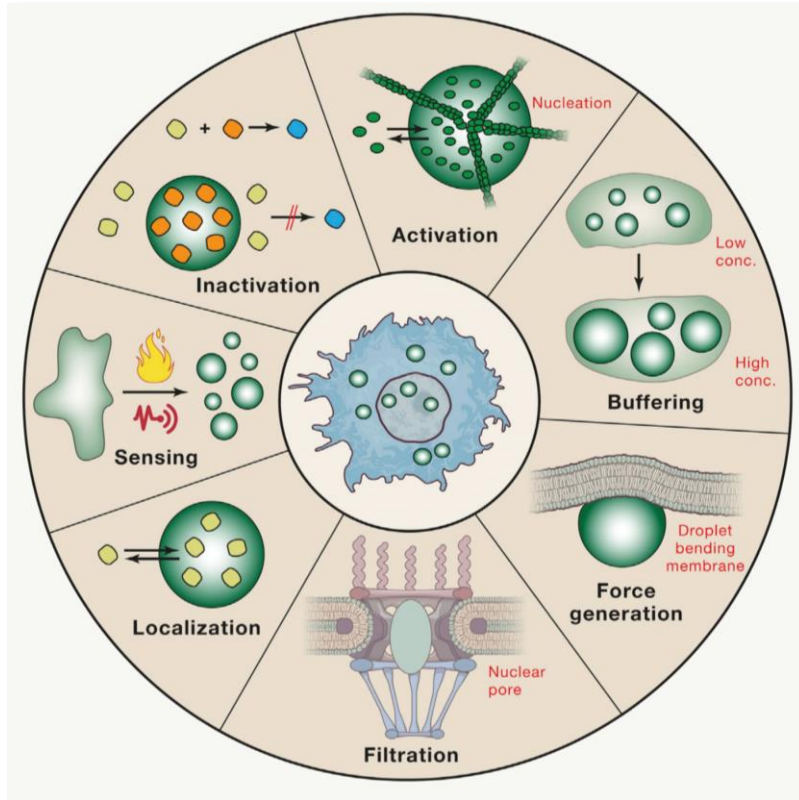
Panca (2019) BBA

- 1) Assembly by PS?
- 2) Cooperativity
- 3) Structure (beyond 1<sup>st</sup> neighbor)

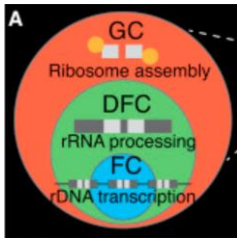
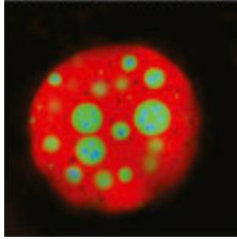
# Functional consequences of LLPS

- 1) an emergent property, might not manifest at the level of individual proteins
- 2) means two different things (remember Gene Ontology MF, BP and CC)
  - the way an LLPS droplet functions (MF)
  - what it does in the cell (BP)

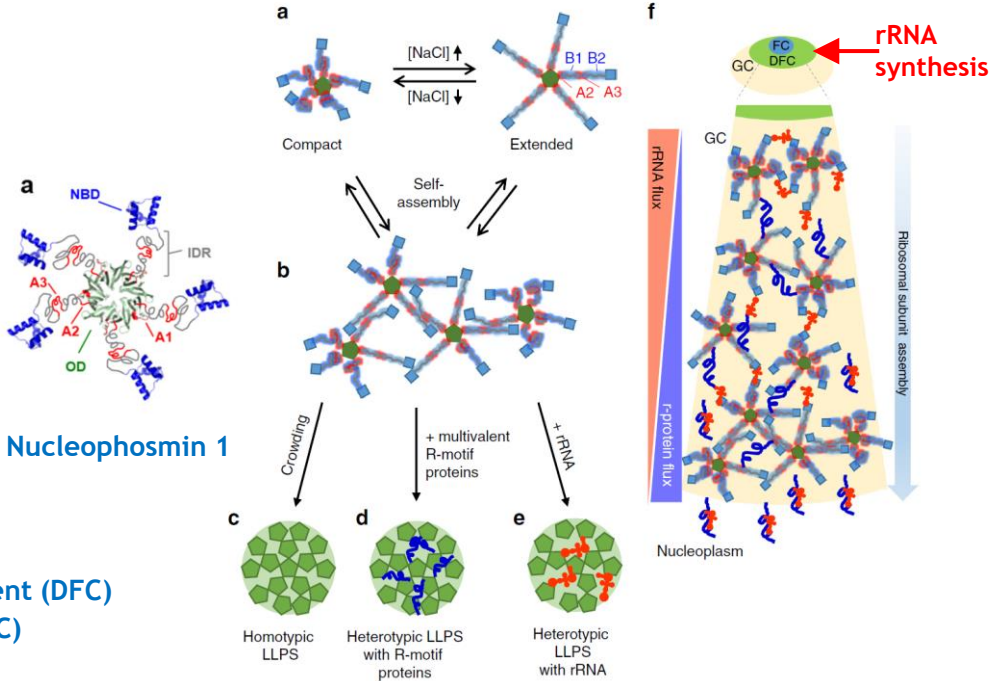
# Functional consequences of LLPS (Molecular Function ontology)



# Function of nucleolus - ribosome biogenesis -

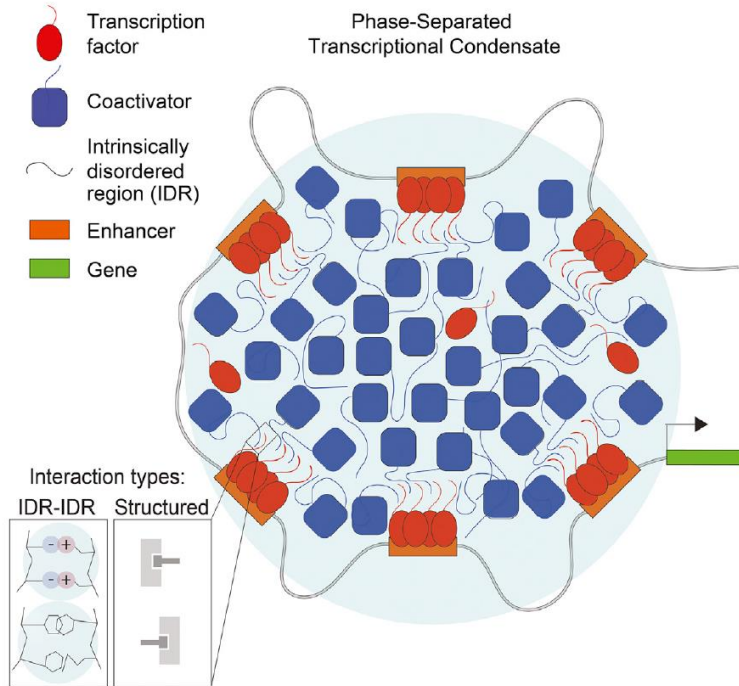


fibrillar center (FC)  
dense fibrillar component (DFC)  
granular component (GC)



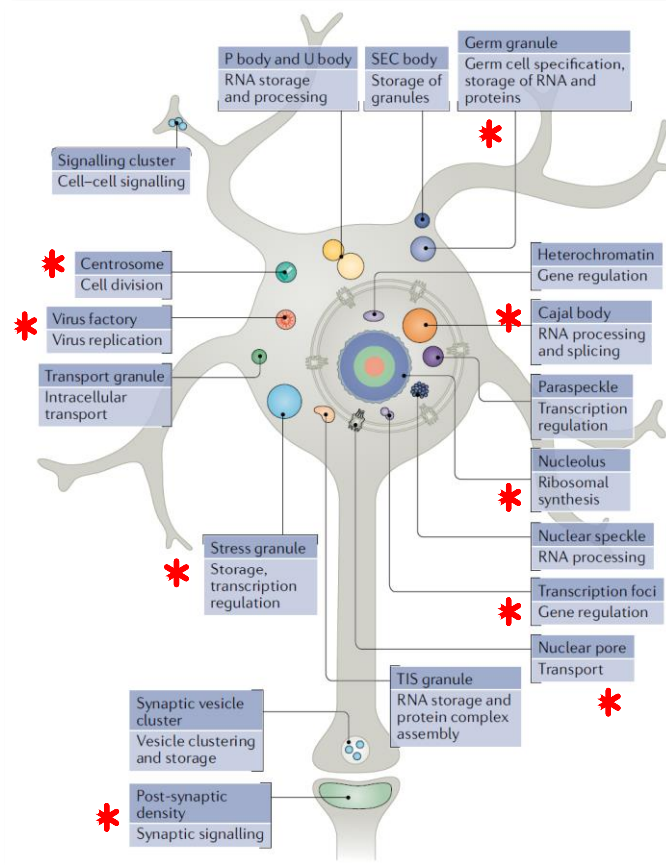
Nucleophosmin 1

# Function of super-enhancers (SEs) in transcription regulation



# Functional consequences of LLPS

## (Biological Process ontology)



Alberti, Hyman (2019) *Nat. Rev. MCB* 22:196



### 3) LLPS and disease

# LLPS may lead to disease

- ALS/FTD, Lou Gehrig's disease



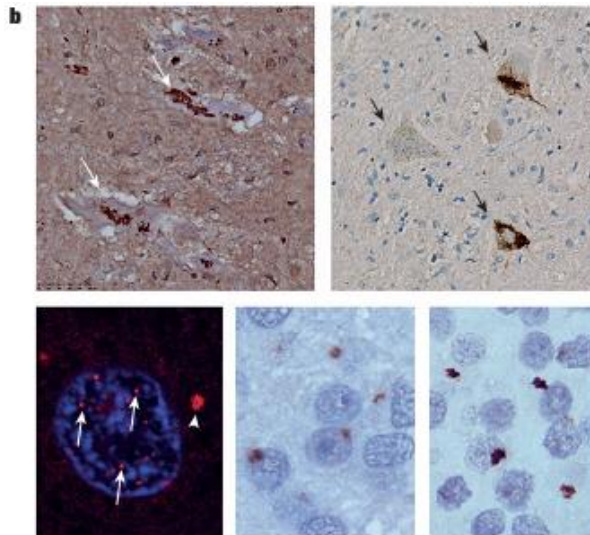
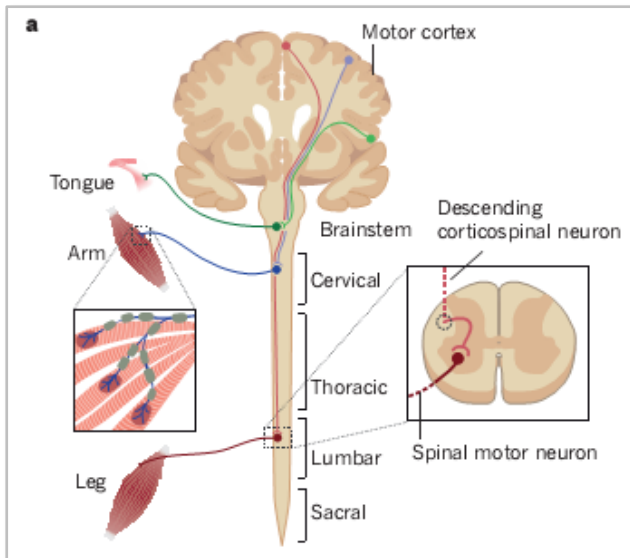
Lou Gehrig



Stephen Hawking

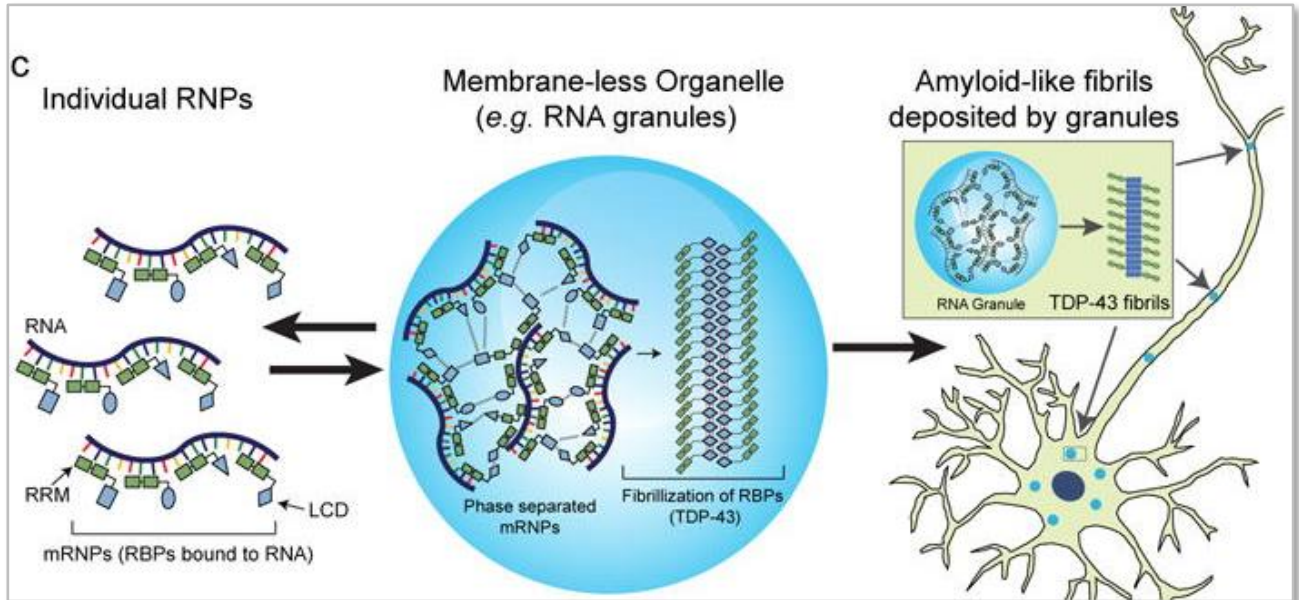
- Progressive loss (atrophy) of muscles
- Survival after first symptoms: 2 - 5y
- No cure

# ALS is motor neuron disease



# LLPS may lead to disease

- stress granules in ALS (?) -

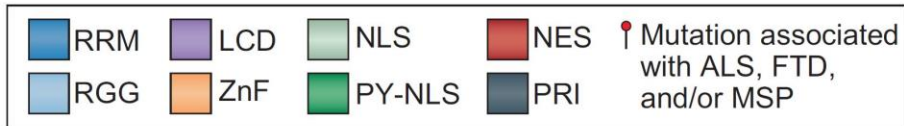
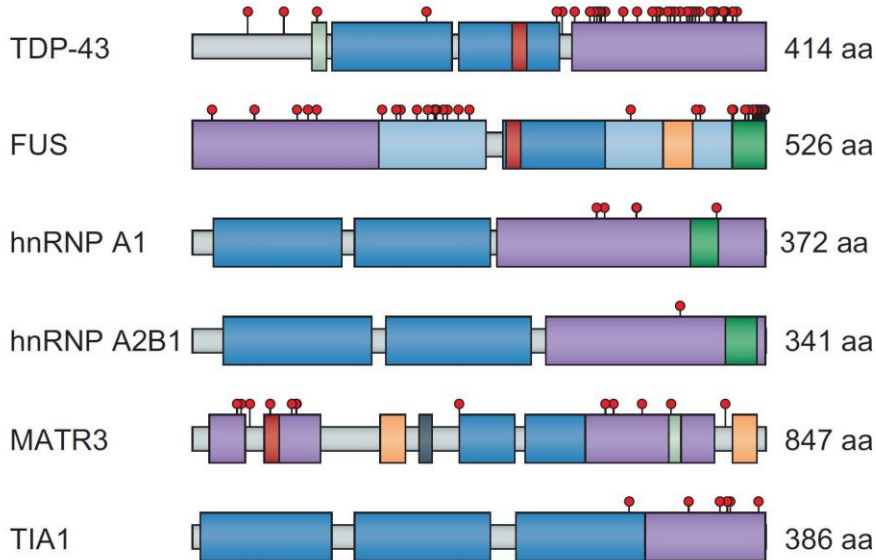


# Many neurodegenerative proteins phase separate

Table 1. Summary of Neurodegenerative Diseases and LLPS/MLOs

Protein	Associated diseases	Evidence for disease association	Granule types	Evidence for <i>in vitro</i> LLPS	Evidence for <i>in vivo</i> LLPS or granules
FUS	ALS/FTD	Point mutations (NLS and others)	Stress	[18,44,89]	[44,89]
TDP-43	ALS/FTD, AD	Point mutations, truncations	Stress, transport	[19,90]	[47,48,90,105]
hnRNPA1	ALS/FTD/multisystem proteinopathy (MSP), MS	Point mutations in ALS/FTD/MSP, mislocalized in MS [64]	Stress, transport	[6]	[6]
hnRNPA2	ALS/FTD/MSP	Point mutations in ALS/FTD/MSP	Stress, transport	[17]	[106]
C9ORF72	ALS/FTD, SCA	G4C2 expansion in ALS/FTD, SCA [72]	Stress	[45,46,52]	[45,46,51,52]
UBQLN2	ALS/FTD	Point mutations in ALS/FTD	Stress	[54,107]	[54]
TIA1	ALS/FTD, AD, MS, SMA	Point mutations in ALS/FTD; mislocalized in AD [61], MS [64], and SMA [77]	Stress	[55,56]	[55,56]
Profilin	ALS/FTD, HD	Point mutations in ALS/FTD; modifies HD aggregation <i>in vitro</i> [66]	Stress		[57]
Ataxin-2	ALS/FTD, SCA	PolyQ expansion, 32 or more in SCA, 29–32 is a risk factor for ALS [73]	Stress, transport	[38]	[38]
Tau	AD	Mutated in AD	Stress	[29,60,108]	[29]
DJ-1	PD	Mutated in PD	Stress (P bodies)		[67]
Huntingtin	HD	PolyQ expansion in HD	Stress	[65,66]	[65]
Staufen-1	SCA	Modifies SCA; recruited to aggregates and increased expression [74]	Transport		[74]
SMN	SMA	Mutated/reduced levels in SMA	Stress, transport		[77,78]
FMRP	Fragile X, FXTAS	5'-UTR repeat expansion in fragile X, FXTAS	Stress, transport	[22,80]	[8,13]

# And carry disease-specific mutations

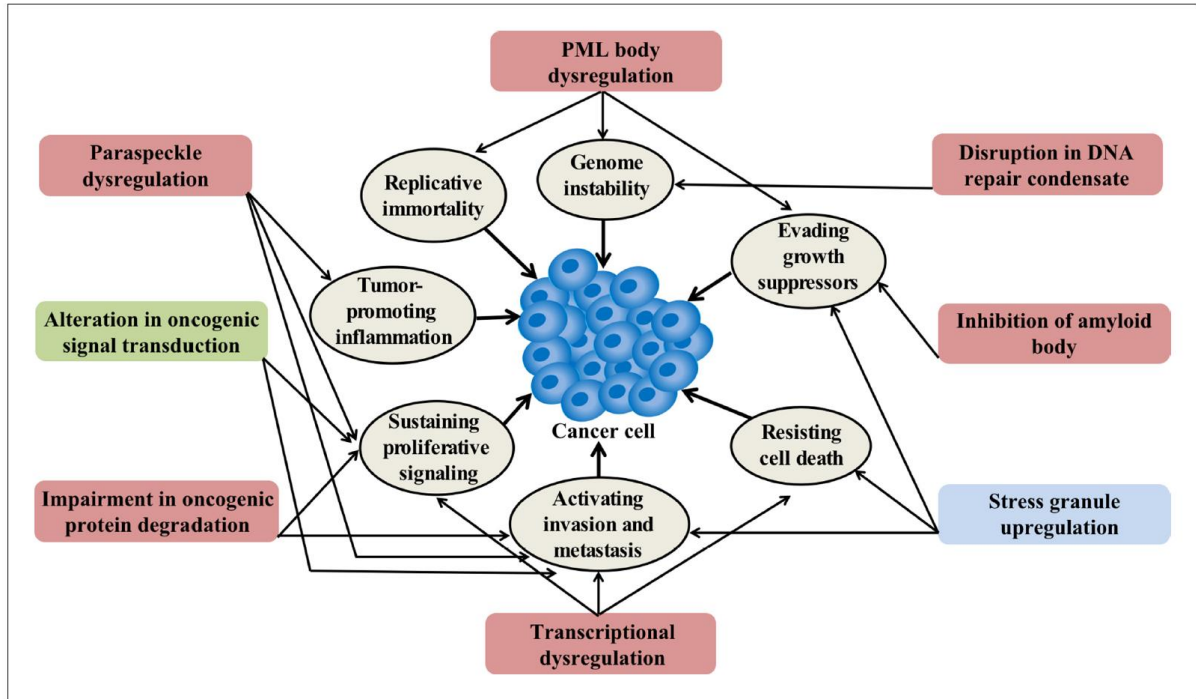


Break (?)



# LLPS might also be involved in cancer

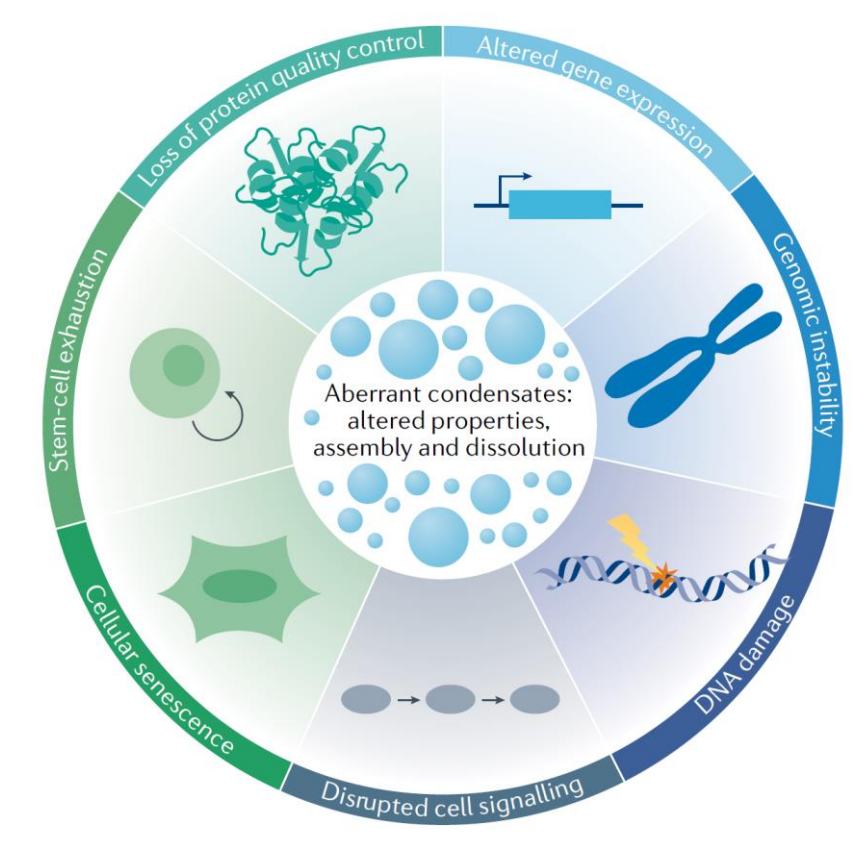
- "hallmarks of cancer" -





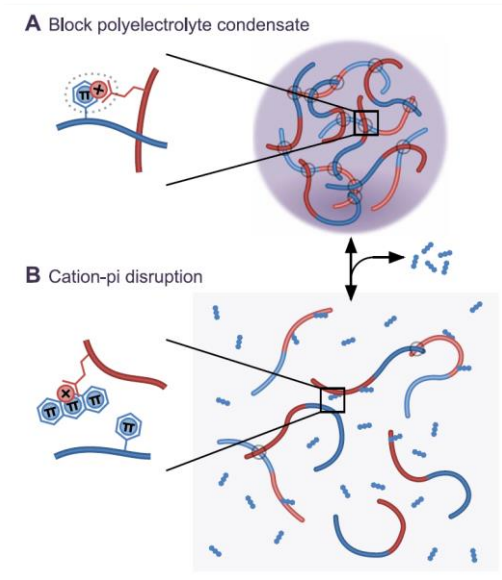
# LLPS might also be involved in ageing (!)

- “hallmarks of ageing” associated with ageing -

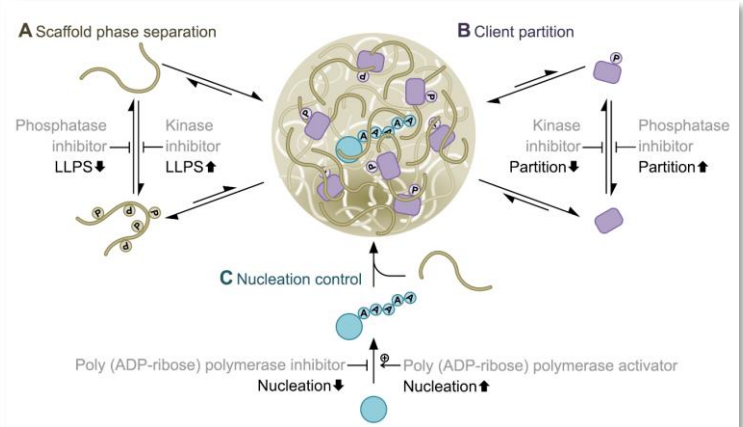


# Targeting LLPS?

## Targeting LLPS and aggregation



## Targeting LLPS via regulation



# “Competitive landscape”

dewpoint<sub>x</sub>

Tony Hyman, Rick Young  
\$ 60M Series A, \$ 77M Series B  
Merck: \$ 305M (HIV)  
Bayer: \$ 77M (cardiovascular, gynecology)  
Pfizer: \$ 239M (myotonic dystrophy type 1)  
oncology, neuro, metabolic, immunology

nerēid

Cliff Brangwynne  
\$50M Series A  
neurodegeneration, cancer

FAZE  
MEDICINES™

Michael Rosen  
\$81M Series A  
ALS

 TRANSITION  
BIO

David Weitz, Tuomas Knowles, Peter St George-Hyslop  
\$9M Seed

  
PhasAGE

## 4) Experimental techniques to study LLPS



## A User's Guide for Phase Separation Assays with Purified Proteins

[Alberti... \(2018\) \*J. Mol. Biol.\* 430: 4806](#)

Simon Alberti<sup>†</sup>, Shambaditya Saha<sup>†</sup>, Jeffrey B. Woodruff, Titus M. Franzmann, Jie Wang and Anthony A. Hyman



## Methods for Physical Characterization of Phase-Separated Bodies and Membraneless Organelles

[Mitre... \(2018\) \*J. Mol. Biol.\* 430: 4773](#)

Diana M. Mitrea<sup>1</sup>, Bappaditya Chandra<sup>1,†</sup>, Mylene C. Ferrolino<sup>1,†</sup>, Eric B. Gibbs<sup>1,†</sup>, Michele Tolbert<sup>1,†</sup>, Michael R. White<sup>1,†</sup> and Richard W. Kriwacki<sup>1,2</sup>

Leading Edge  
**Primer**

Cell

## Considerations and Challenges in Studying Liquid-Liquid Phase Separation and Biomolecular Condensates

Simon Alberti,<sup>1,2,\*</sup> Amy Gladfelter,<sup>3,4,\*</sup> and Tanja Mittag<sup>5,\*</sup>

[Alberti... \(2019\) \*Cell\* 176: 419](#)



PhasAGE

# Protein purification

LLPS proteins are often aggregation prone, frequently found in inclusions in neurodegenerative diseases

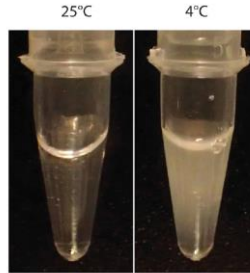
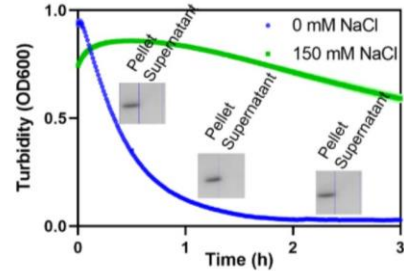
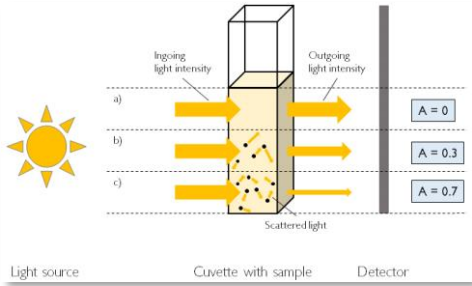
1) Often require a trick to keep them in solution: (i) solubility tag (MBP, GST, GFP), (ii) non-native/denaturing conditions (e.g. urea, pH away from pI), (iii) additives disfavoring LLPS (high salt, high Arg)

2) Purification not only from *E. coli* (insect cell, mammalian cells)

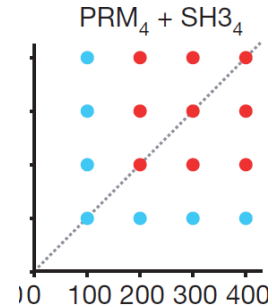
3) Advised to be aliquoted, only used once (no repeated freeze-thaw cycles)

# Turbidity

-  $OD_{340}$ ,  $OD_{400}$ ,  $OD_{600}$  -



## hnRNP2 LCD LLPS



Neph. - Nck - WASP (Rosen 2012)

- 1) fast
- 2) easy control (of conditions, T)
- 3) appropriate for determining  $C_{sat}$
- 4) can be made highly parallel (phase diagram)
- 5) but: convolution of number and size of scattering particles

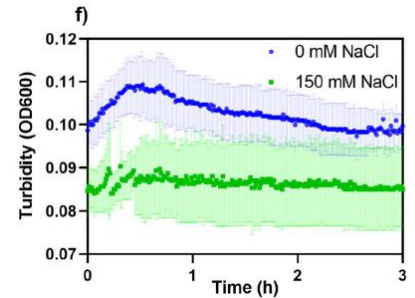
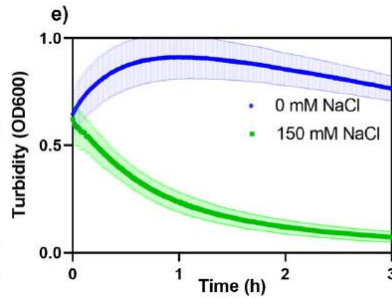
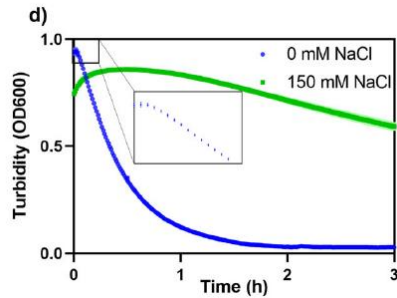
# Turbidity

- hnRNPA2 LCD LLPS initiated by: -

pH jump: 11.0  $\rightarrow$  7.5

Urea: 8M  $\rightarrow$  80mM

Cleavage of MBP tag

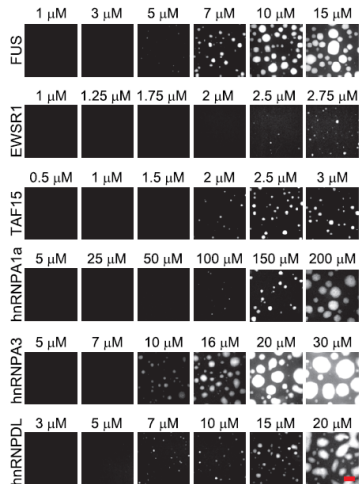




# Microscopy

## A Molecular Grammar Governing the Driving Forces for Phase Separation of Prion-like RNA Binding Proteins

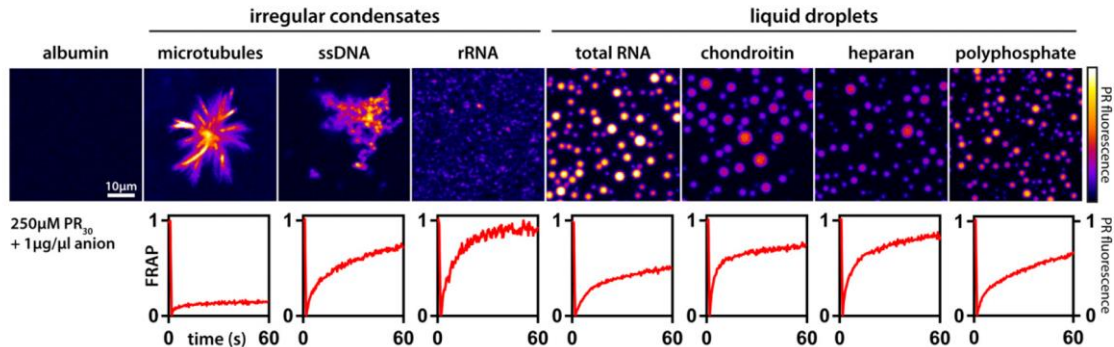
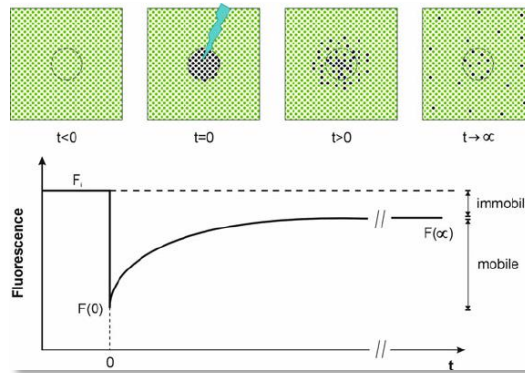
Jie Wang,<sup>1</sup> Jeong-Mo Choi,<sup>2</sup> Alex S. Holehouse,<sup>2</sup> Hyun O. Lee,<sup>1</sup> Xiaojie Zhang,<sup>1</sup> Marcus Jahnel,<sup>1</sup> Shovamayee Maharana,<sup>1</sup> Régis Lemaître,<sup>1</sup> Andrei Pozniakovsky,<sup>1</sup> David Drechsel,<sup>3</sup> Ina Poser,<sup>1</sup> Rohit V. Pappu,<sup>2</sup> Simon Alberti,<sup>1,\*</sup> and Anthony A. Hyman<sup>1,4,\*</sup>



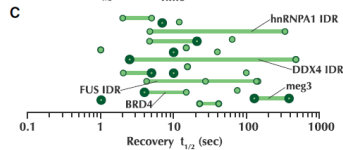
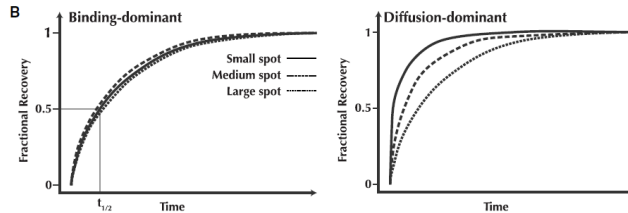
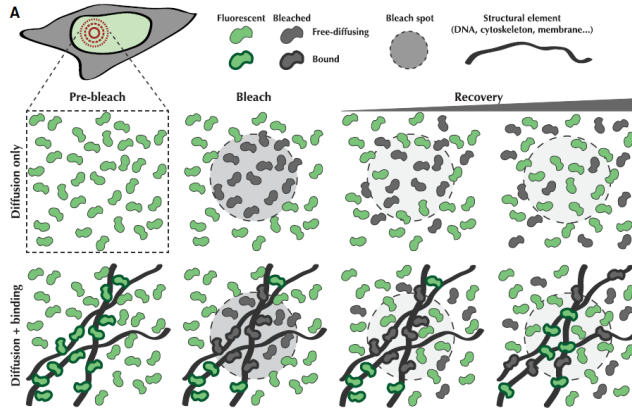
Here: FUS family of proteins

- 1) direct visualization
- 2) confirmation of spherical shape
- 3) shape change, fusion, colocalization
- 4) targeted FRAP
- 5) cellular applications

# Fluorescence recovery after photobleaching (FRAP)

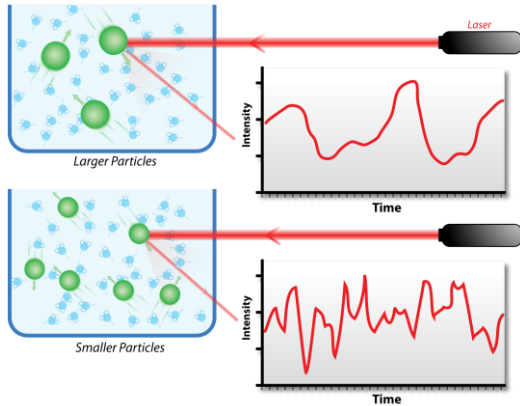


# Interpretation of FRAP: model dependent

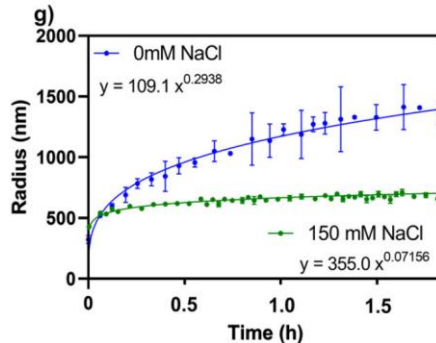
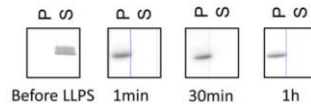
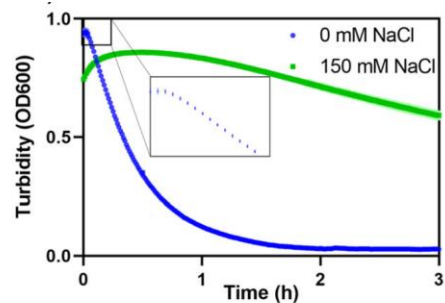


# Dynamic light scattering (DLS)

- measuring size distribution profile of droplets -



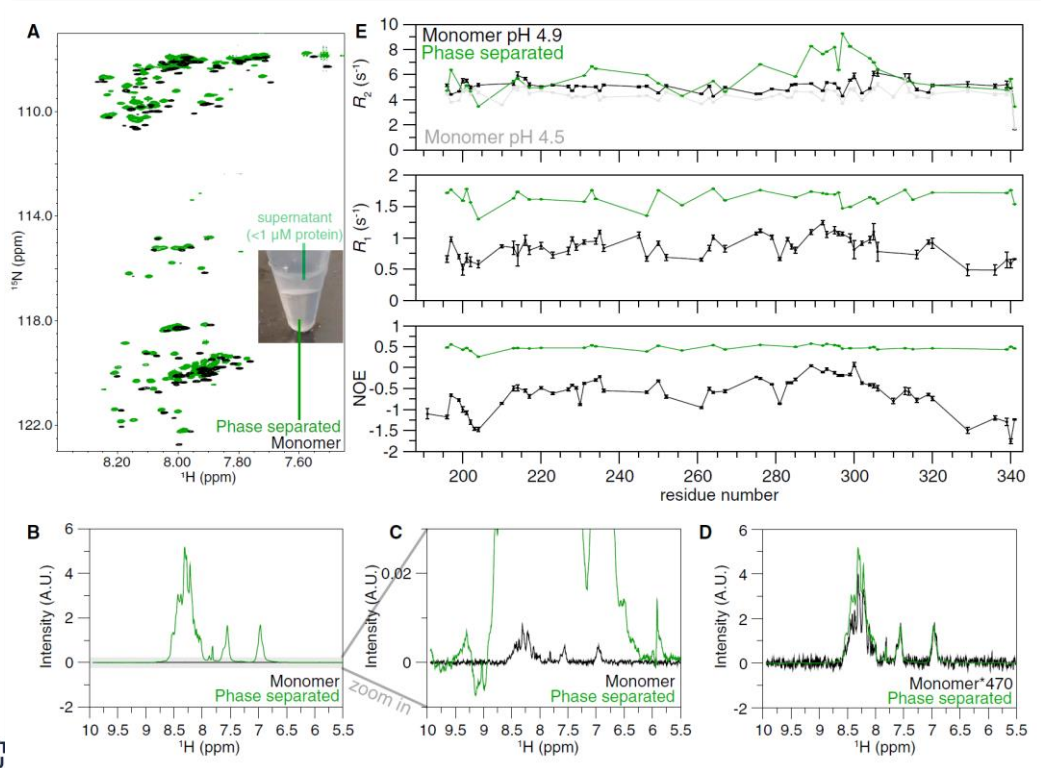
Analyzing temporal fluctuations (autocorrelation) of light intensity



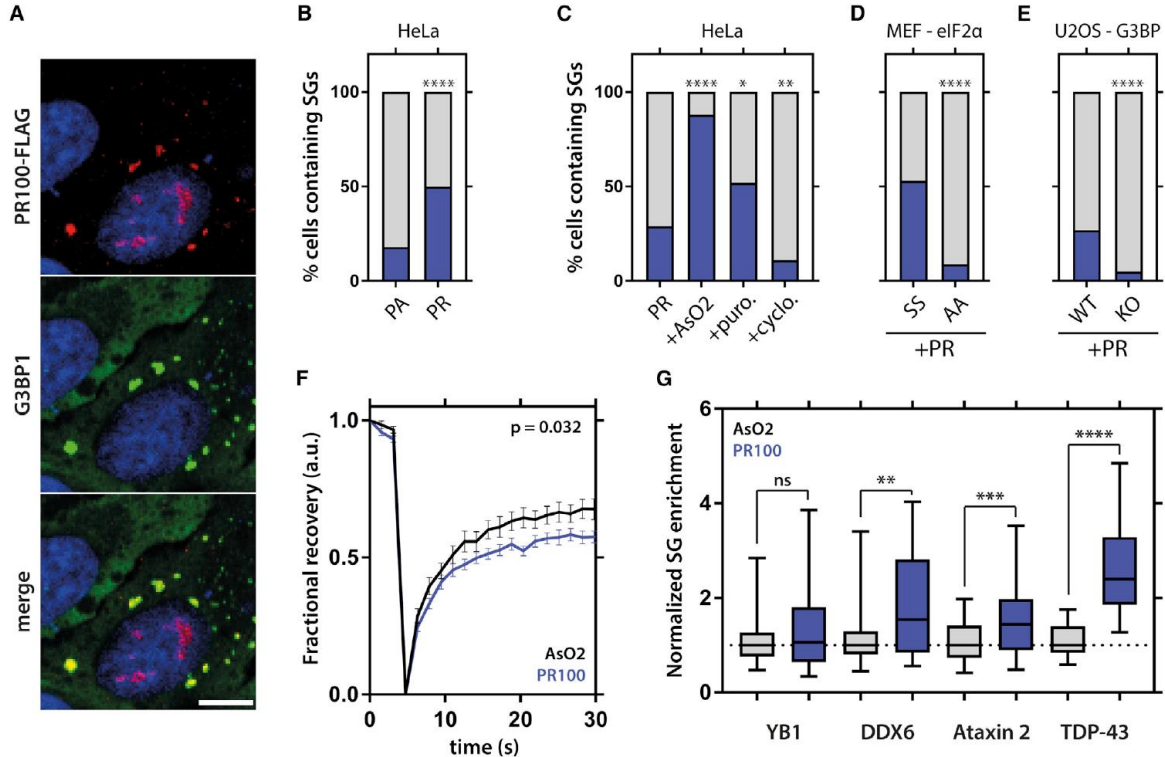
hnRNP2 LCD LLPS

# Nuclear magnetic resonance (NMR)

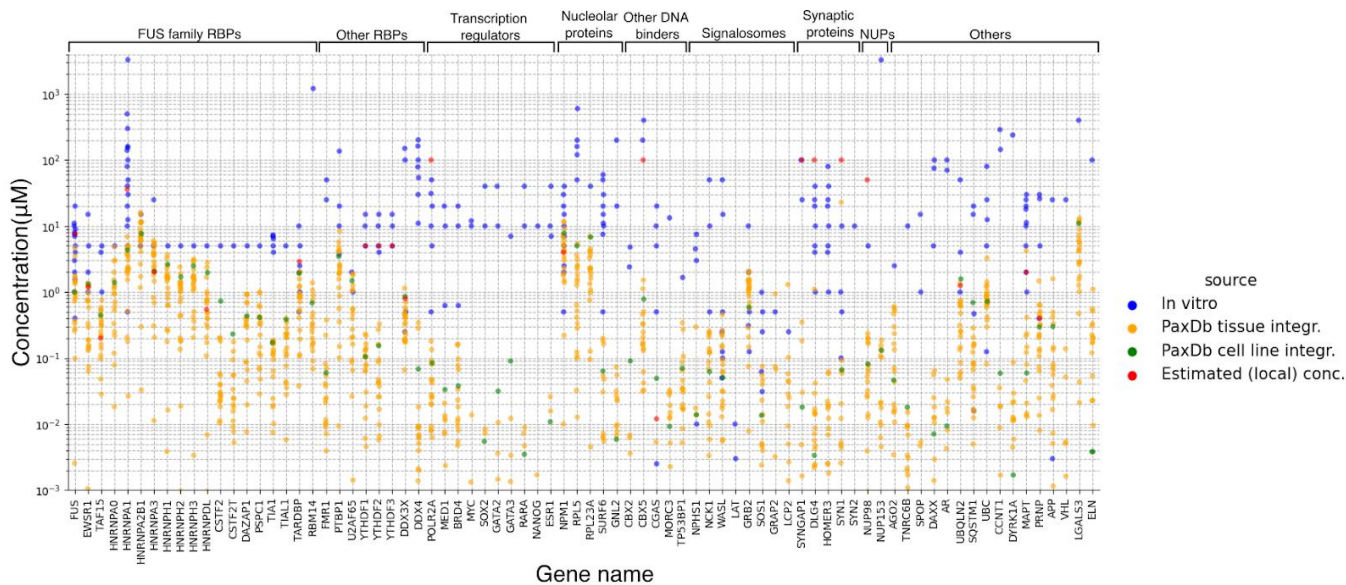
## - hnRNPA2 LCD remains disordered in the droplet -



# Cellular: overexpression - better: driver/modifier -



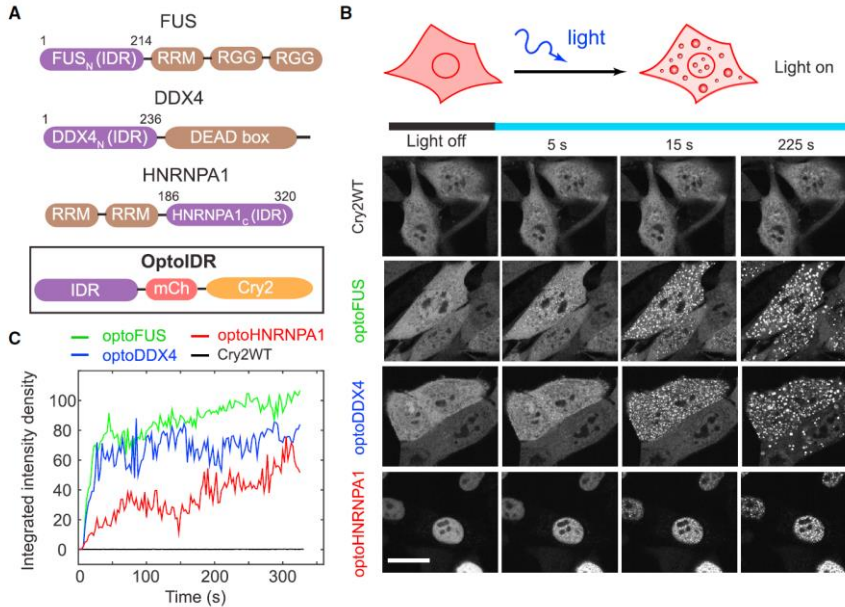
# Issue with concentrations



# Cellular: optogenetics

## - Cry2 (cryptochrome) based -

Photolyase homology region (PHR) of *A. thaliana* Cry2, a light-sensitive protein that dimerizes upon blue light exposure

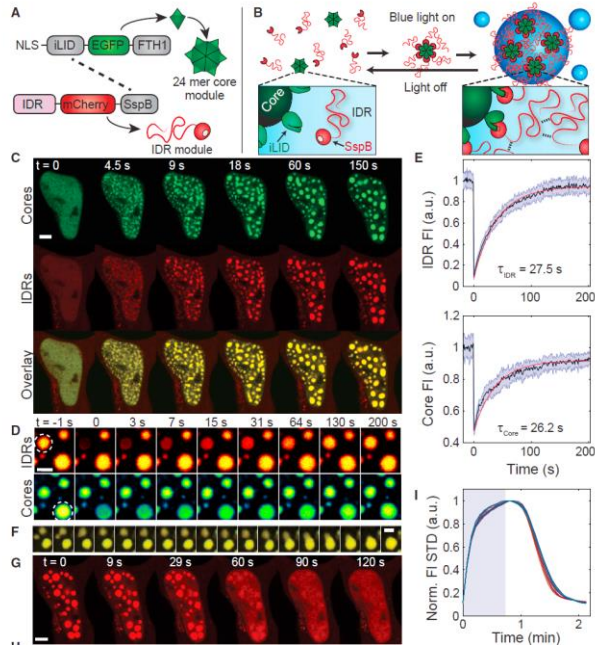




# Cellular: optogenetics

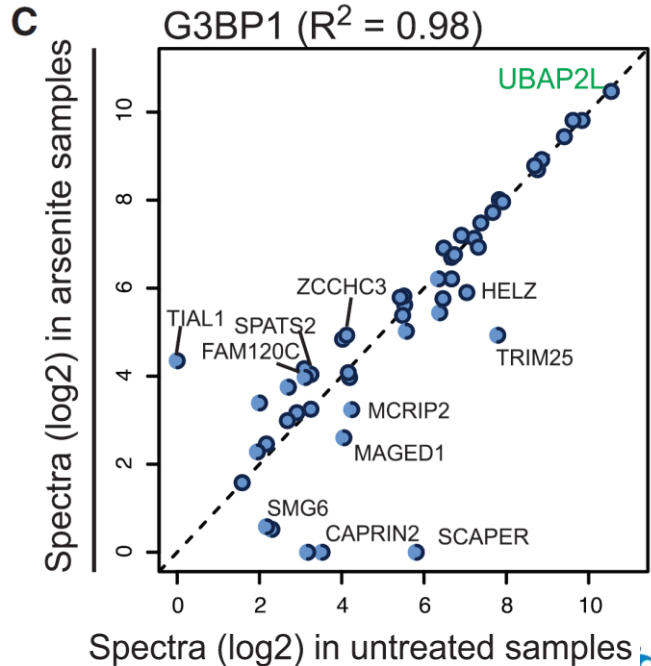
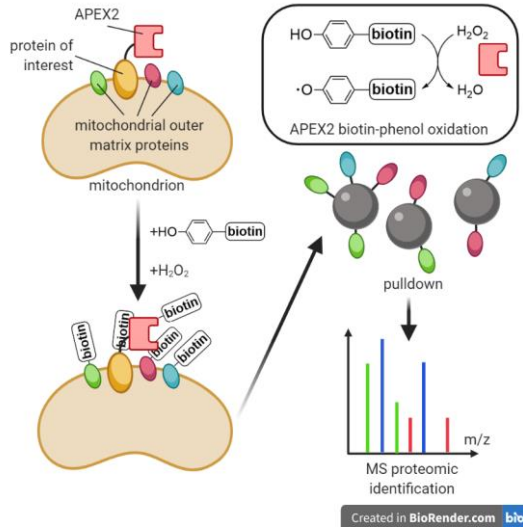
## - Corelets -

24-mer ferritin (FTH1) derivatized by photoactivatable iLID domain, plus its cognate partner, SspB



# Cellular: proximity tagging

Protein of interest carries an enzyme fused (biotin ligase, BirA\* or ascorbate peroxidase, APEX) that can biotinylate nearby proteins in the cell.



## 5) Databases and bioinformatics tools



ELSEVIER

Available online at [www.sciencedirect.com](http://www.sciencedirect.com)

**ScienceDirect**

Current Opinion in

**Structural Biology**


## **First-generation predictors of biological protein phase separation**

Robert M Vernon<sup>1</sup> and Julie D Forman-Kay<sup>1,2</sup>



Vernon, Forman-Kay (2019) *COSStBi* 58: 88

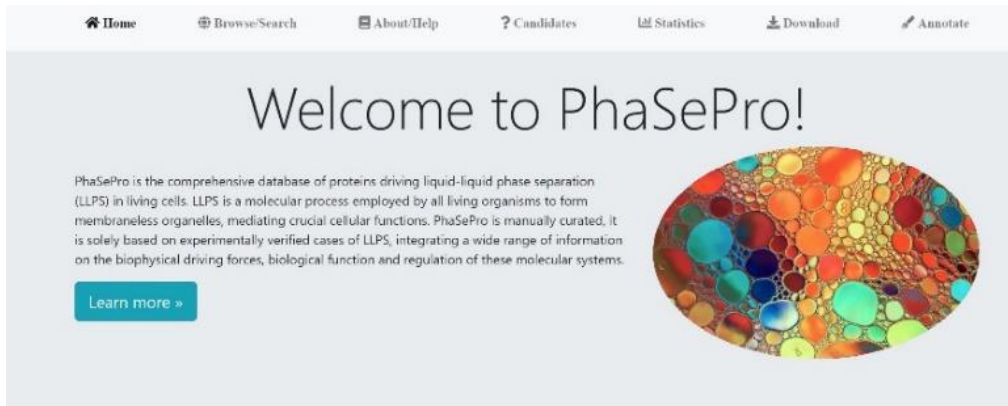
## **Computational resources for identifying and describing proteins driving liquid–liquid phase separation**

Rita Pancsa, Wim Vranken and Bálint Mészáros 

Pancsa... (2021) *Brif. Bioinfo.* 1-20

# LLPS databases

- <https://phasepro.elte.hu> -



Home Browse/Search About/Help Candidates Statistics Download Annotate

## Welcome to PhaSePro!

PhaSePro is the comprehensive database of proteins driving liquid-liquid phase separation (LLPS) in living cells. LLPS is a molecular process employed by all living organisms to form membraneless organelles, mediating crucial cellular functions. PhaSePro is manually curated. It is solely based on experimentally verified cases of LLPS, integrating a wide range of information on the biophysical driving forces, biological function and regulation of these molecular systems.

[Learn more »](#)

Search for gene names, full or partial common/UniProt protein names, or UniProt accessions. [Example 1](#) [Example 2](#)

### Getting started

To get an introduction to the structure and use of PhaSePro, you can visit the selected examples (FUS and TDP-43) by clicking the buttons above, or read the About/Help pages by clicking below.

[View details »](#)

### Explore

You can start searching the database by entering keywords in the above field, or by browsing the available entries by clicking below.

[Browse/Search entries »](#)

### Annotate

Help us expand the knowledge about proteins involved in liquid-liquid phase separation by submitting new entries into PhaSePro.

[View details »](#)

By using PhaSePro in compliance with Protection Requirati

R. Pancsa et al.



Manually curated for LLPS drivers that has both *in vitro* and *in vivo* relevance

Farahi et al. (2021) *Int J Mol Sci.* 22: 3017



# LLPS databases

- <http://bio-comp.org.cn/llpsdb/home.aspx> -

**Welcome to LLPSDB !**

Liquid-liquid phase separation (LLPS) of proteins has been discovered to underlie the compartmentalization of cells, through the formation of liquid biological condensates including membraneless organelles (MLOs), signaling puncta and so on. LLPS is associated with numerous biological processes such as RNA metabolism, gene regulation and signal transduction. However, the fundamental mechanism of protein LLPS still remains to be elucidated. It is important to systematically analyze all the available experimental data for a better understanding of LLPS. To this end, through extensive literature curation, we summarized the proteins and corresponding experimental conditions under which their phase separation tendencies have been detected *in vitro*, and deposited them in this database.

LLPSDB contains LLPS related proteins together with the corresponding phase separation conditions validated by experiments. For each protein, the database provides various information, including the protein sequence, modifications on specific amino acids, its ability of coalescing with nucleic acids, biological function etc., as well as specific experimental conditions such as temperature, salt concentration, pH, crowding agent, detected techniques, phase behavior and so on. In addition, several related databases are linked from LLPSDB including UniProt, MobiDB, DisProt, OMMIM, IDEAL, AmyPro, FunzDB and PubMed. All the data summarized in LLPSDB are available for users.

**News**

- Correction of several entries was made, and PMID option was added in search module on Sep 19, 2019.
- LLPSDB currently holds 1175 entries. Last updated: July 1, 2019.

**Database Linked**

[UniProt](#) [PubMed](#) [MobiDB](#)  
[DisProt](#) [OMMIM](#) [IDEAL](#)  
[FunzDB](#) [AmyPro](#)

**Contact Us**

Email: [biocomp\\_llpsdb@ucas.ac.cn](mailto:biocomp_llpsdb@ucas.ac.cn)  
Computational Biology Research Group,  
College of Life Sciences,  
University of Chinese Academy of Sciences,  
Beijing, P.R.China, 100049

Component Count	Count	Percentage
One component	536	48%
Two components	501	43%
More components	128	11%

*In vitro* LLPS experiments as entries, containing both natural designed proteins (the role of protein is not defined).

# LLPS databases

- <http://db.phasep.pro/> -



## What is PhaSepDB?

PhaSepDB is a novel database that provides a collection of phase separation related proteins manually curated from publications and public database.

As of October 2015, this database includes 2957 eligible proteins, 1303 (77.9%) of the proteins were localized in different organelles.

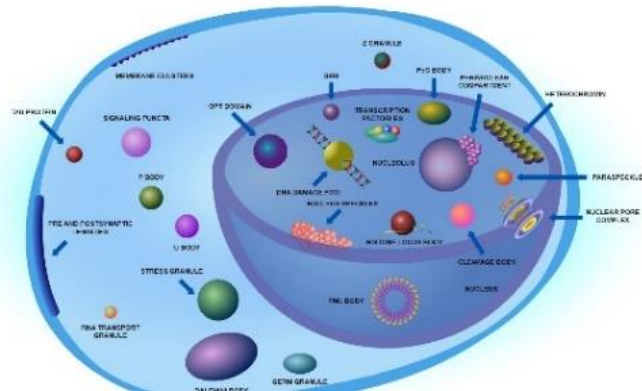
[Click a body to browse by organelles.](#)

While 661 (22.1%) of them were not associated with known organelles.

[Click here to browse those proteins.](#)

In addition to curated proteins, PhaSepDB also provides the researchers with molecular signatures that may facilitate phase separation related proteins identification for all human proteins.

[Click here to browse human proteins.](#)



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VRIJE  
UNIVERSITEIT  
BRUSSEL

Annotations based on MLO localization (literature evidence, UniProt annotations, and HTS localization experiment).

Farahi et al. (2021) *Int J Mol Sci.* 22: 3017



PhasAGE

# LLPS databases

- <http://llps.biocuckoo.cn> -

**DrLLPS**. Data resource of liquid-liquid phase separation

Version 1.0

THE CUCKOO WORKGROUP

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PRODUCTS OF CUCKOO

× Overview

Phase separation, or liquid-liquid phase separation (LLPS), is a ubiquitous and important mechanism for the formation of membraneless condensates in cells. Living cells contain various types of membraneless condensates enriched with proteins and RNA molecules. These condensates, including stress granule (Mollnes *et al.*, 2007), P granule (Brangwynne *et al.*, 2009), spindle apparatus (Jiang *et al.*, 2015) and nucleolus (Hult *et al.*, 2017), play critical roles in regulating a variety of biological response (Rbeck *et al.*, 2017), RNA metabolism (Taylor *et al.*, 2016), DNA damage response (Paldi *et al.*, 2015) and signal transduction (Frisman *et al.*, 2018).

Here, we presented a data resource of LLPS (DrLLPS), a comprehensive data resource that contained **437,887** known and computationally detected LLPS associated species. For LLPS-associated proteins in nine model organisms, we provided rich annotations by compiling and integrating the knowledge from additional **110** widely cover **16** aspects, including (i) Intrinsically disordered region; (ii) Domain annotation; (iii) Post-translational modification; (iv) Genetic variation; (v) Cancer mutation; (vi) Disease-associated information; (vii) Drug-target relation; (viii) Physicochemical property; (ix) Protein functional annotation; (x) Protein expression/proteomics; (xi) Subcellular localization; (xii) mRNA expression; (xiii) DNA & RNA element; (xiv) DNA methylation. The online service of DrLLPS was implemented in PHP + MySQL + and annotations are freely accessed for all users. We anticipate DrLLPS can serve as a helpful resource for further analysis of LLPS, and confirm that the database will be updated.

9,285 Curated Proteins

40 Condensates

164 Species

110 Pathways

Simple Search

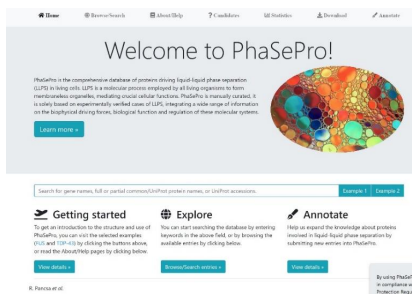
Please search the DrLLPS to find the information you need. Please input one keyword to find the related information:

MLO-associated proteins classified as scaffolds, regulators, and clients as assessed by automated text mining, followed by curator assessment. *In vitro*, *in vivo* and computational evidence is accepted (HTS, LTS), such as KO, silencing, overexpression.



# What does “LLPS protein” mean?

## PhaSePro: 120 proteins



Welcome to PhaSePro!

PhaSePro is the comprehensive database of proteins driving liquid-liquid phase separation (LLPS) in living cells. LLPS is a widespread process employed by all living organisms to form macromolecular condensates, mediating crucial cellular functions. PhaSePro is manually curated, it is widely based on experimentally verified cases of LLPS, integrating a wide range of information on the biophysical driving forces, biological function and regulation of these molecular systems.

Search for gene names, full or partial accession/UniProt protein names, or UniProt accessions.

Getting started | Explore | Annotate

## LLPSDB: 1200



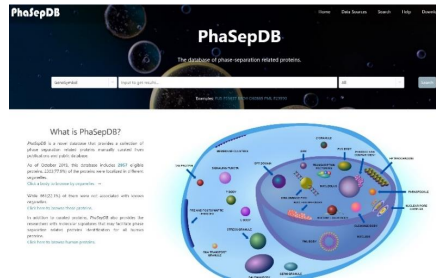
Welcome to LLPSDB!

LLPSDB is a database of proteins undergoing liquid-liquid phase separation in cells. LLPS is a widespread process employed by all living organisms to form macromolecular condensates, mediating crucial cellular functions. LLPSDB is manually curated, it is widely based on experimentally verified cases of LLPS, integrating a wide range of information on the biophysical driving forces, biological function and regulation of these molecular systems.

Search for gene names, full or partial accession/UniProt protein names, or UniProt accessions.

Getting started | Explore | Annotate

## PhaSepDB: 3000



PhaSepDB

PhaSepDB is a database of phase separation related proteins. LLPS is a widespread process employed by all living organisms to form macromolecular condensates, mediating crucial cellular functions. PhaSepDB is manually curated, it is widely based on experimentally verified cases of LLPS, integrating a wide range of information on the biophysical driving forces, biological function and regulation of these molecular systems.

Search for gene names, full or partial accession/UniProt protein names, or UniProt accessions.

Getting started | Explore | Annotate

## DrLLPS: 9300



DrLLPS

DrLLPS is a data resource of liquid-liquid phase separation. LLPS is a widespread process employed by all living organisms to form macromolecular condensates, mediating crucial cellular functions. DrLLPS is manually curated, it is widely based on experimentally verified cases of LLPS, integrating a wide range of information on the biophysical driving forces, biological function and regulation of these molecular systems.

Search for gene names, full or partial accession/UniProt protein names, or UniProt accessions.

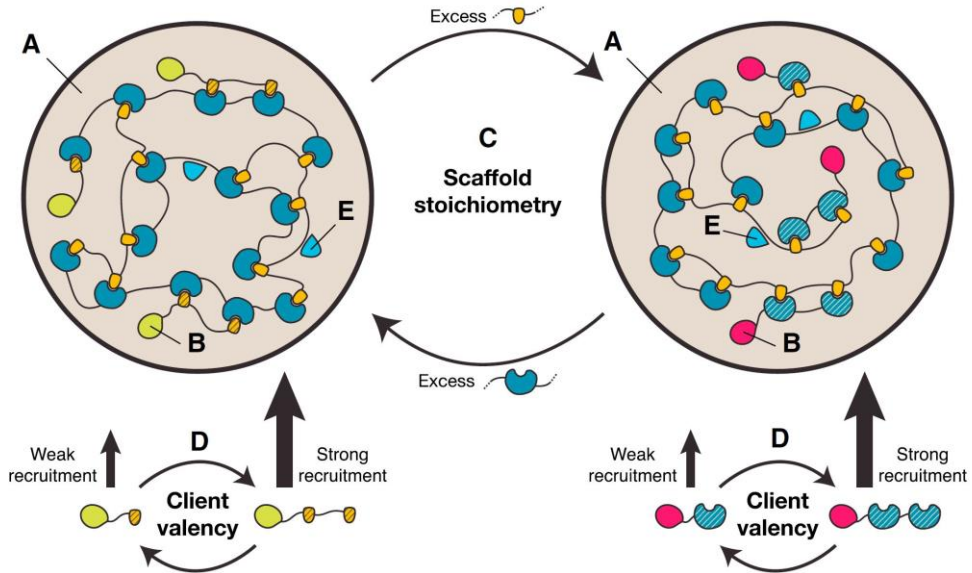
Getting started | Explore | Annotate



# Why is not straightforward to call an LLPS protein?

- 1) the capacity to phase separate is **not a binary classifier** (not intrinsic but contextual property of the protein and its environment)
- 2) phase separation depends on the **concentration** of the protein (physiological?)
- 3) proteins have **distinct roles** in phase separation
- 4) LLPS is not equivalent to **biomolecular condensation** (which includes gelation, crystallization, clustering, pleiomorphic assembly, polymerization and amorphous or amyloid aggregation) or **templated assembly**.

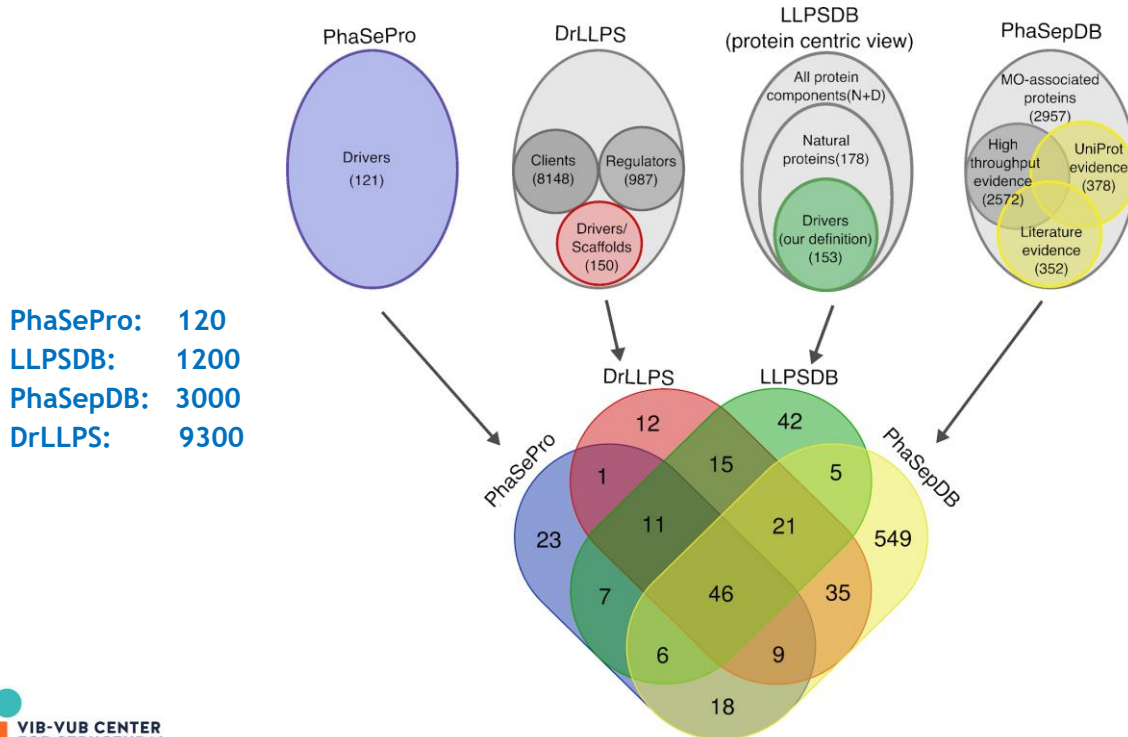
# Scaffolds and clients



# Different roles of proteins in LLPS.

- 1) **Driver (scaffold)**: can phase separate on their own. If RNA is mandatory, we consider it as a “co-driver”. Small molecules (and crowder) are “condition”.
- 2) **Co-driver**: a macromolecule (protein, RNA or DNA) that strictly requires another macromolecule for phase separation (then both are “co-drivers”)
- 3) **Regulator**: its presence/activity is required for LLPS, but no part of condensate (modifying enzyme, transport protein, transcription factor, etc...)
- 4) **Client**: not required for and has no effect on LLPS, but localizes to the condensate formed (through interactions with driver/co-driver.

# Different databases contain different type (and amount) of data



# A primary goal: develop LLPS predictors

**Table 1**

**Phase-separation prediction methods**

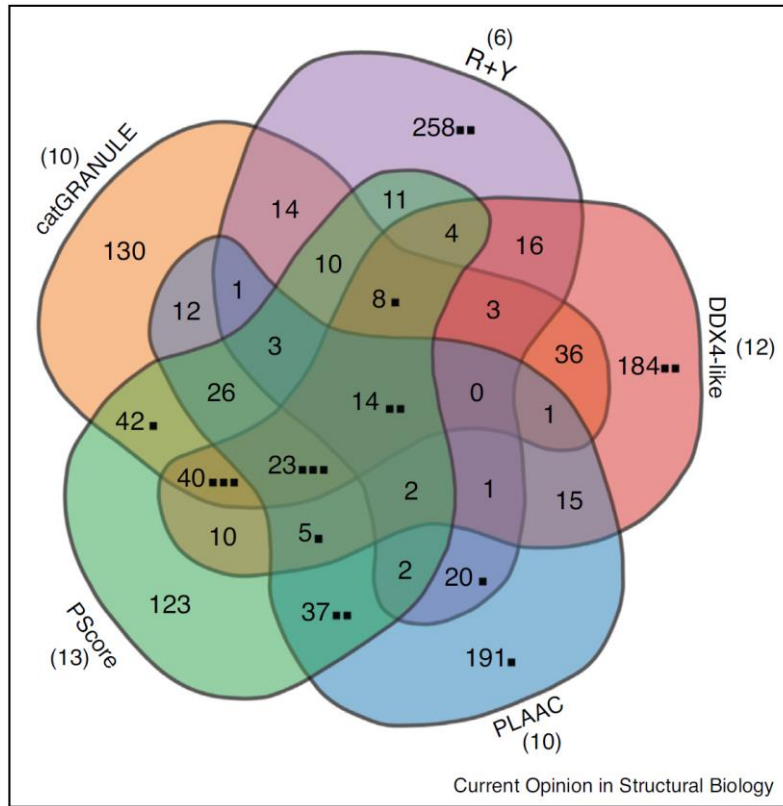
Method name	Description	Residue # information	Availability	Ref.
PLAAC	Prion-like domain prediction by hidden Markov model	Yes	<a href="http://plaac.wi.mit.edu">plaac.wi.mit.edu</a>	[43,46]
LARK	Energetic compatibility with aromatic-rich kinked amyloid structures, by threading sequences and modeling with Rosetta	Specific regions	In supplement of original paper	[23**]
R + Y	Critical concentration prediction based on number of arginine and tyrosine residues, extrapolated from FET family proteins	No	In supplement of original paper	[50**]
DDX4-like	Sequence composition and residue spacing similarity to DDX4	Specific regions	From authors	[51]
CatGranule	Composition weighted by sequence length, R/G/F content, and amino acid propensity for nucleic acid binding and disorder	Yes	<a href="http://tartaglialab.com">tartaglialab.com</a>	[52]
PScore	Prediction based on expected numbers of long-range planar sp2 pi-pi contacts	Yes	<a href="http://abragam.med.utoronto.ca/~JFKlab/">abragam.med.utoronto.ca/~JFKlab/</a>	[42**]
CRAPome	Empirical measurement related to non-specific interactions and <i>in vivo</i> concentration, taken from the frequency at which each human protein is identified by affinity purification mass spectrometry negative controls	No	<a href="http://crapome.org">crapome.org</a>	[54]

PSPredictor machine learning based on LLPSDB database

<http://www.pkumdl.cn:8000/PSPredictor/>



# Prediction of LLPS proteins in human proteome



**Thank you**