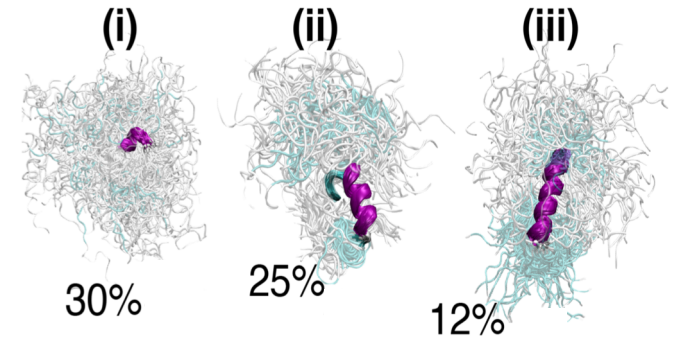
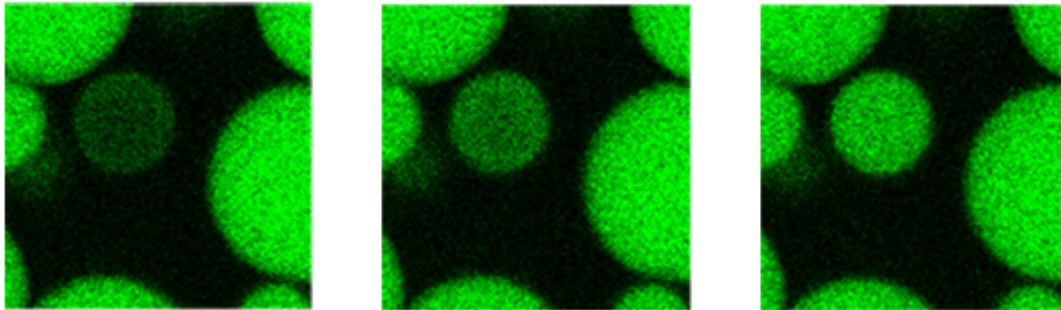


Seeing the disordered structure of liquid-liquid phase separating RNA-binding proteins

Nicolas Lux Fawzi

Department of Molecular Pharmacology, Physiology and Biotechnology
Brown University



Acknowledgements

Fawzi group:

Veronica Ryan
Anastasia Murthy
Kaylee Mathews
Mark Liang
Wai Shing Tang
Myrto Perdikari
Anna Bock
Scott Watters

Looking for Postdoc!



Funding:



BROWN

C·O·B·R·E



SKELETAL
HEALTH
AND
REPAIR

Collaborators:

Jeanne Stachowiak - *UT Austin*

Sapun Parekh - *MPI Polymer/UT Austin*

Jeetain Mittal and Greg Dignon - *Lehigh*

Frank Shewmaker - *USUHS*

Yuh Min Chook and Mike Rosen - *UT Southwestern*

Robert Cole and Robert O'Meally - *Johns Hopkins*

Tanja Mittag and Erik Martin - *St Jude*

Yuna Ayala - *St Louis University*

H Broder Schmidt and Rajat Rohatgi - *Stanford*

Tony Hyman and Richard Wheeler - *MPI Dresden*



HUMAN FRONTIER SCIENCE PROGRAM

FUNDING FRONTIER RESEARCH INTO COMPLEX BIOLOGICAL SYSTEMS



The Judith & Jean Pape Adams
CHARITABLE FOUNDATION

Anonymous Brown Family

DEARS Foundation



RHODE ISLAND
FOUNDATION



National Institute of
General Medical Sciences

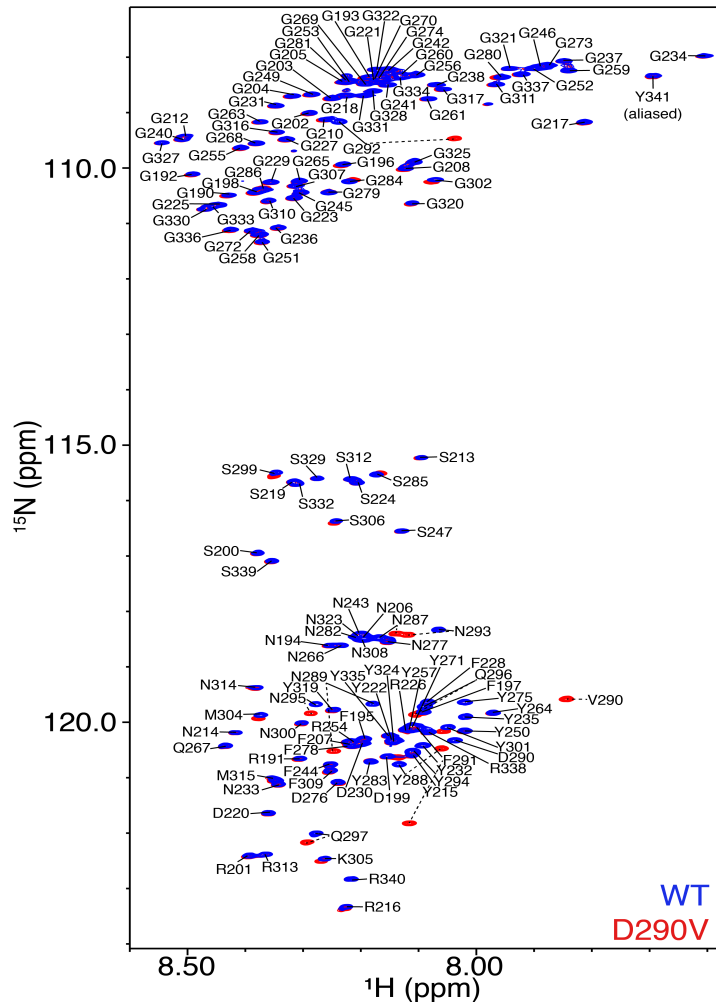
Basic Discoveries for Better Health

R01GM118530

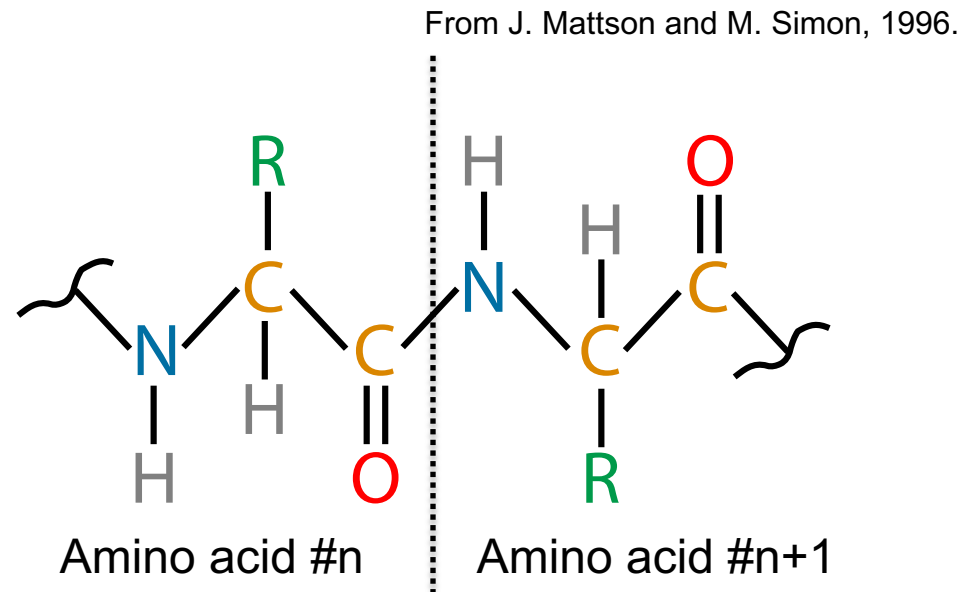


Take aways, tools...

- NMR “sees” disorder domains at atomic scale
 - Atomic details of interactions, structure, effect of mutations and post-translational modifications

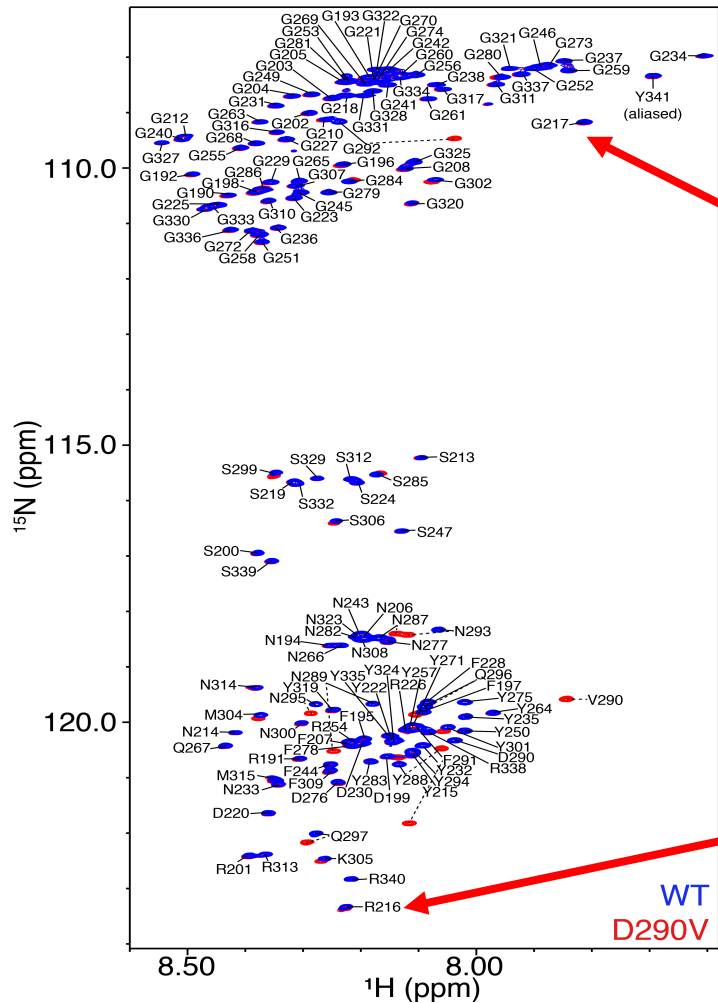


Felix Bloch (Nobel prize winner in NMR) recalling Nobel prize winning physicist Niels Bohr's description of NMR. *You know, what these people do is really very clever. They put little spies in the molecule and send radio signals to them, and they have to radio back what they are seeing.*

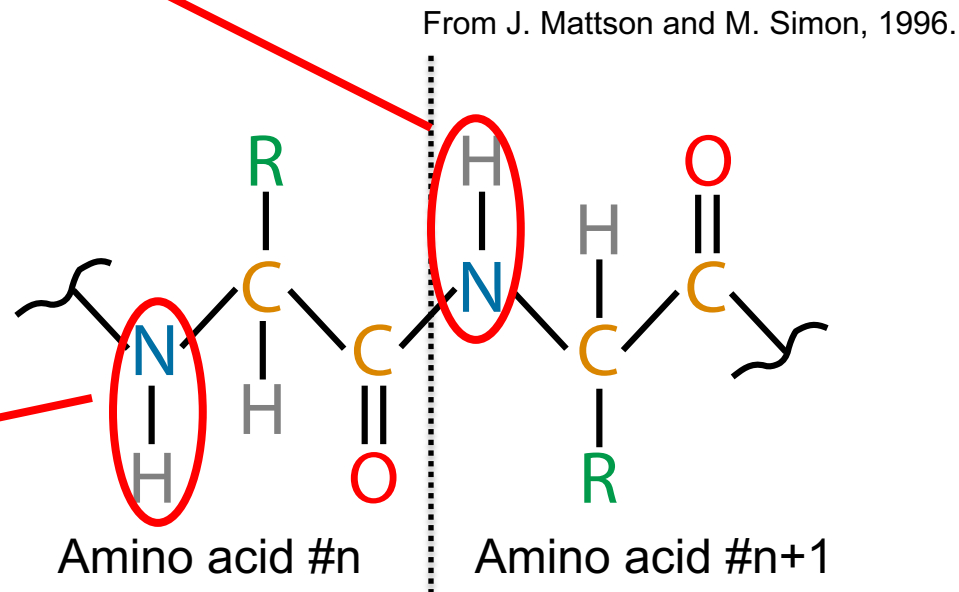


Take aways, tools...

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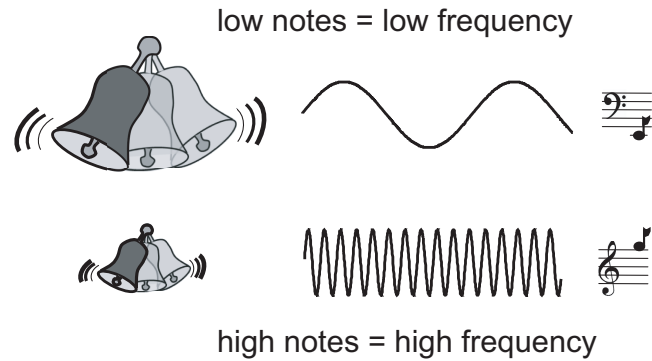
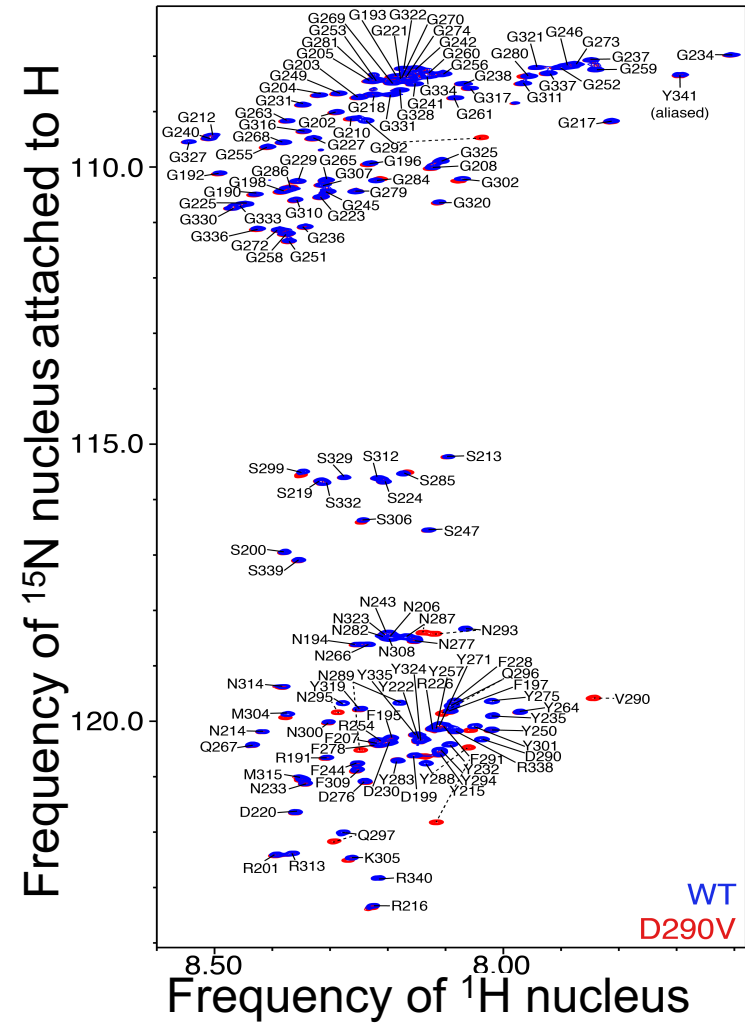


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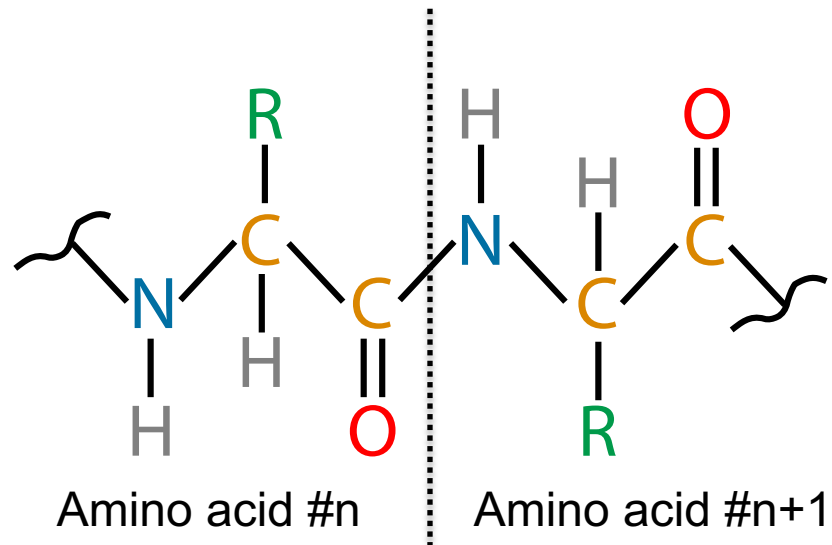
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 - Atomic details of interactions, structure, effect of mutations and post-translational modifications



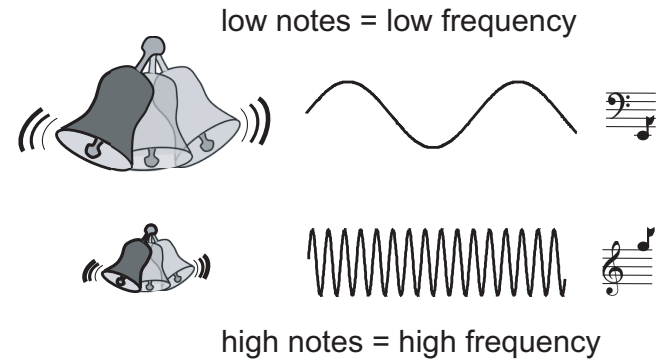
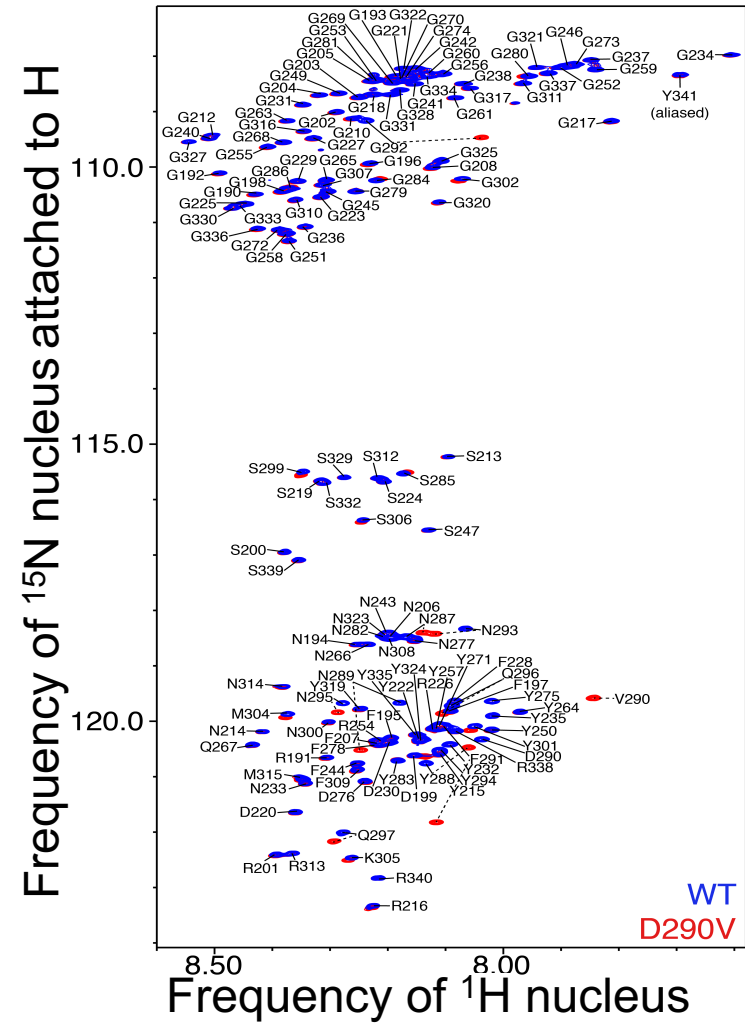
All the nitrogen nuclei are distinct low notes

All the hydrogen nuclei are distinct high notes



Take aways, tools...

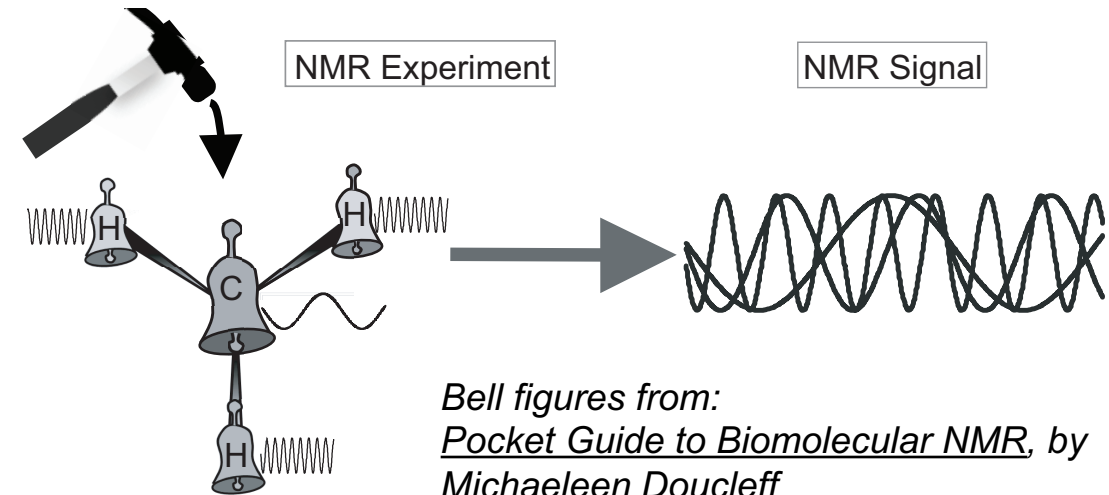
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All the nitrogen nuclei are distinct low notes

All the hydrogen nuclei are distinct high notes

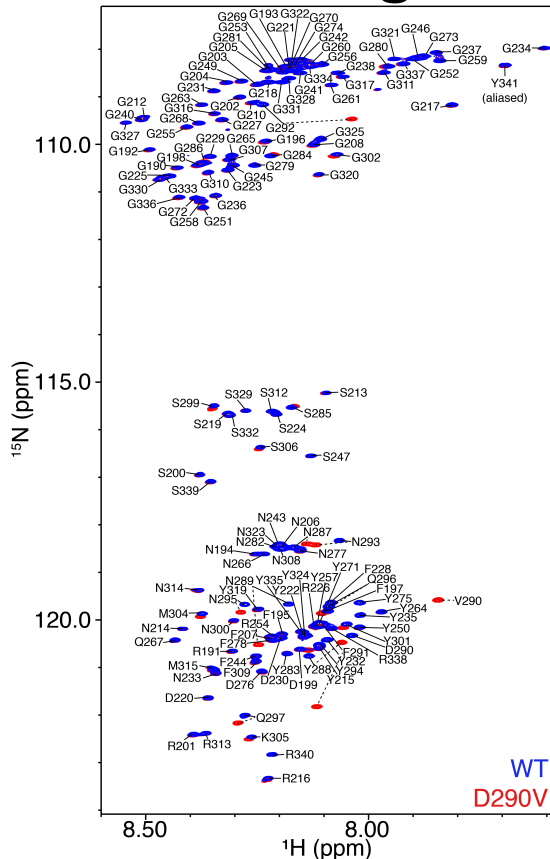
NMR experiment \approx ring all the “bells” and listen for the “notes” that come back.



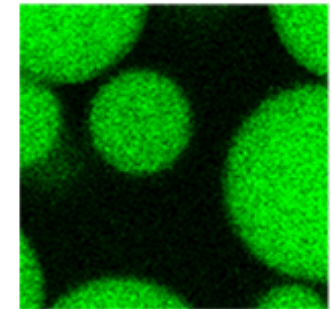
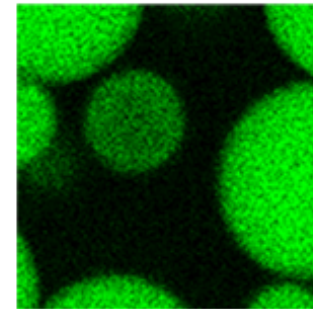
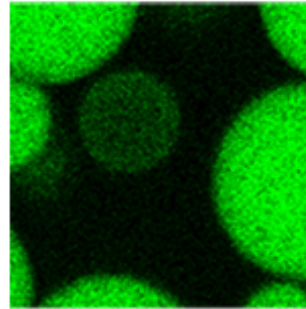
Bell figures from:
Pocket Guide to Biomolecular NMR, by
Michaeleen Doucleff

Take aways, tools...

- NMR “sees” disorder domains at atomic scale
 - Atomic details of interactions, structure, effect of mutations and post-translational modifications
- Combining with microscopy to see micron-scale behavior

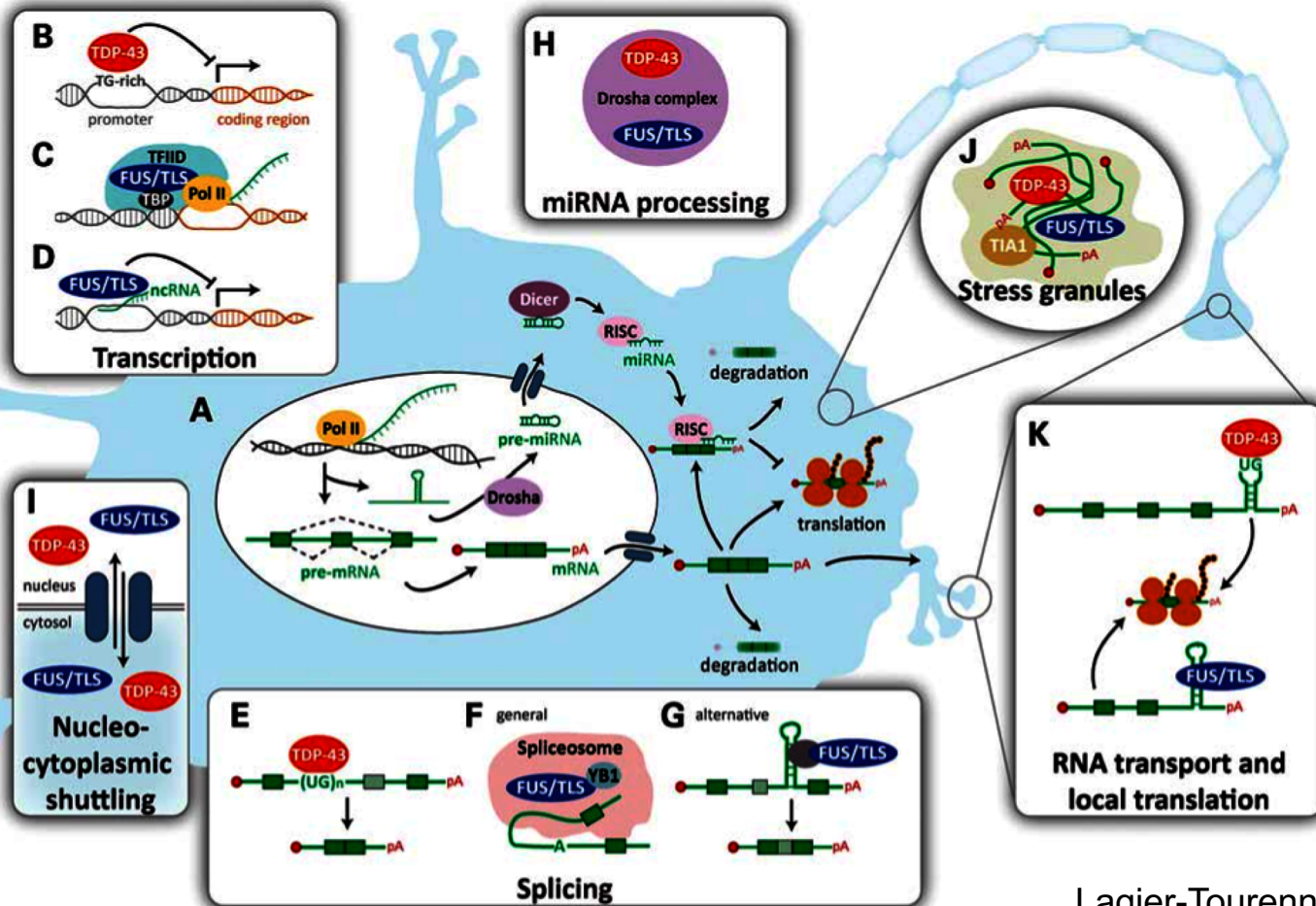
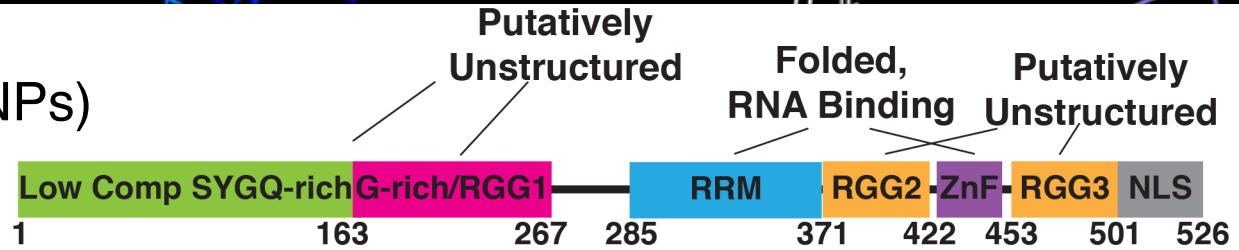


+



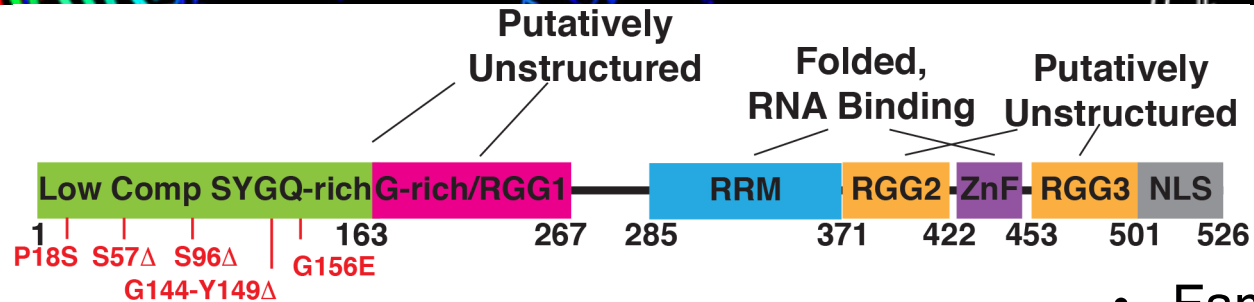
RNA-binding protein - function

Heterogeneous nuclear ribonucleoprotein (hnRNPs)



- Family of RNA-binding proteins
- Folded RNA binding domains
- Regions/domains of “low complexity” = disordered
- Nuclear/cytoplasm shuttling
- Ubiquitously expressed and in high cellular concentration

Fused in Sarcoma (FUS)

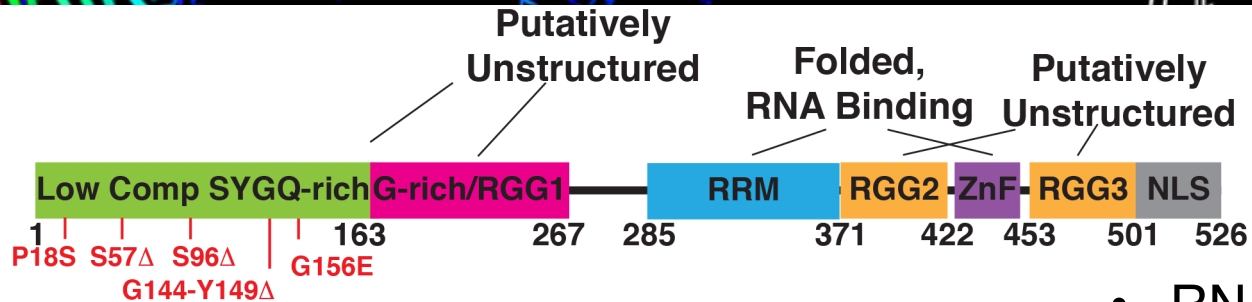


Mutations associated with ALS

- Mutations in NLS and Low complexity (LC aka SYGQ-rich) regions are associated with amyotrophic lateral sclerosis, leading to protein aggregation

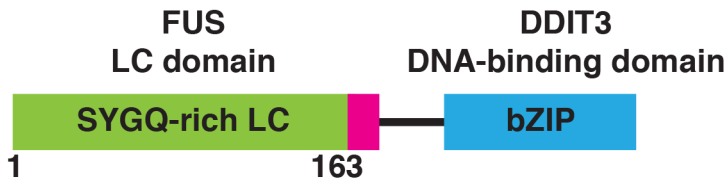
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Fused in Sarcoma (FUS)



Mutations associated with ALS

- Mutations in NLS and Low complexity (LC aka SYGQ-rich) regions are associated with amyotrophic lateral sclerosis, leading to protein aggregation



Fusion associated with sarcoma

- Fusions of FUS LC (and paralogs TAF15 and EWS) with any of a dozen DNA-binding domains \rightarrow sarcoma and leukemia

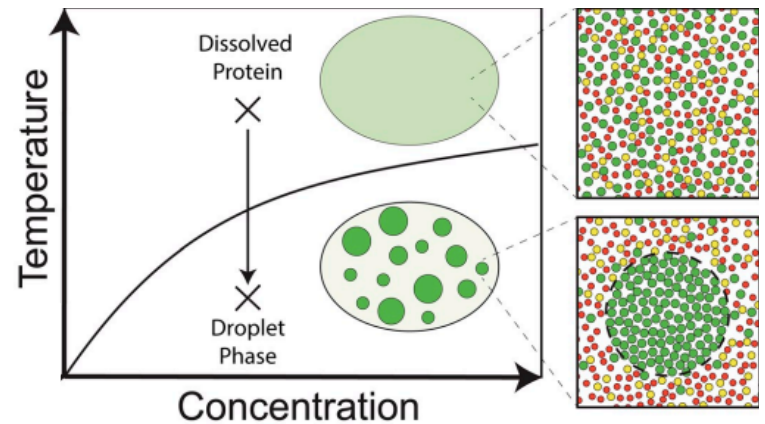
- RNA binding domains
- Low complexity putatively disordered domains
- Nuclear/cytoplasm shuttling
- Cellular [FUS] $> 2 \mu\text{M}$

Protein/RNA phase separation

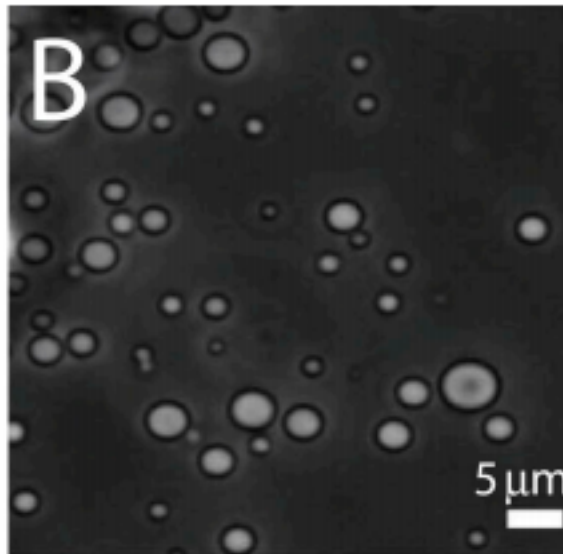
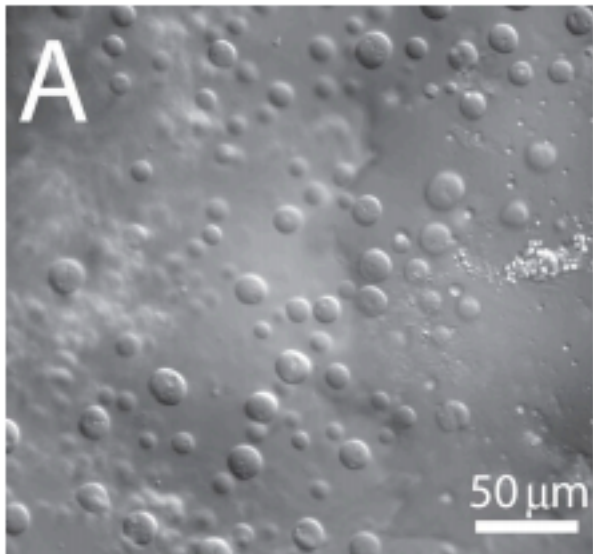
Membraneless organelles

- Non-membrane bound granules or “droplets”
- Nuclear: Nucleoli, Gems, Cajal bodies
- Cytoplasm: Stress granule, processing body
- Flow and fuse and retain spherical shape

JCB Review: Brangwynne JCB (2013)



Molliex et al. Cell (2015)



**Stress Granules
have Liquid
Droplet
Properties**

**Nucleoli (and other RNP granules)
within the nucleus of an *X.
laevis* oocyte**

In vitro myelin basic protein

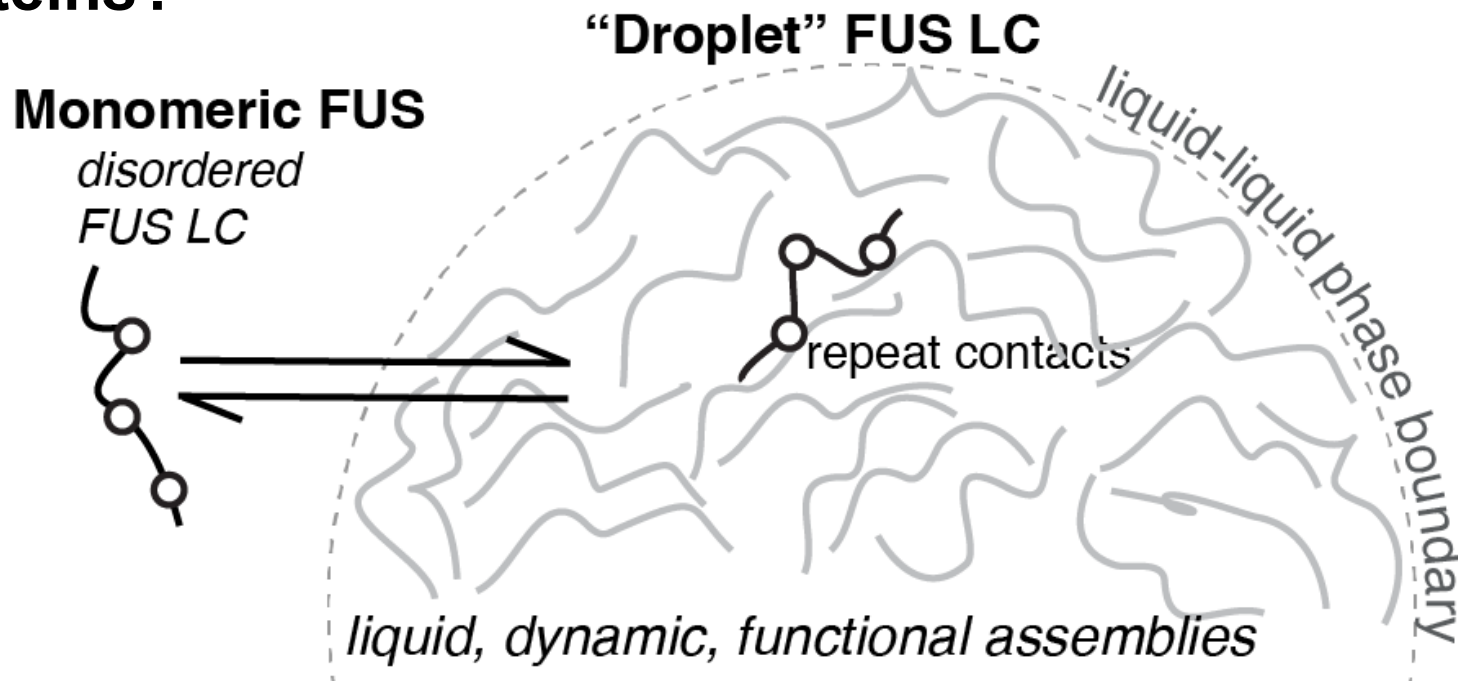
Stress granules in cells

What is the structure of the low complexity domain of FUS?

as a monomer in free solution?

upon liquid-liquid phase separation?

Does FUS phase separation recruit other low complexity proteins?



What regulates biological phase separation?

FUS LC structure?

163 residues, unusual sequence

Rich in amino acids:

serine (S)

tyrosine (Y)

glycine (G)

glutamine (Q)

Lacking other amino acids:

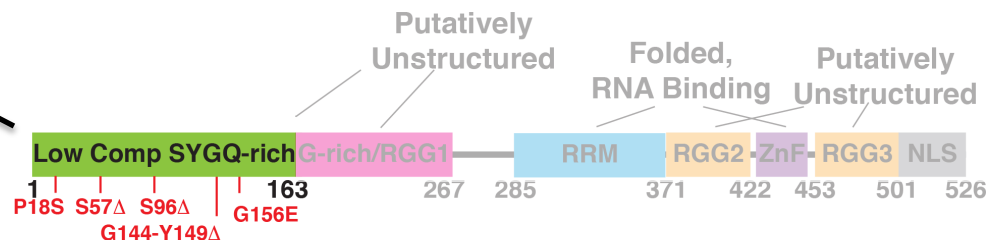
Positively charged (none present)

Negatively charged (only 2)

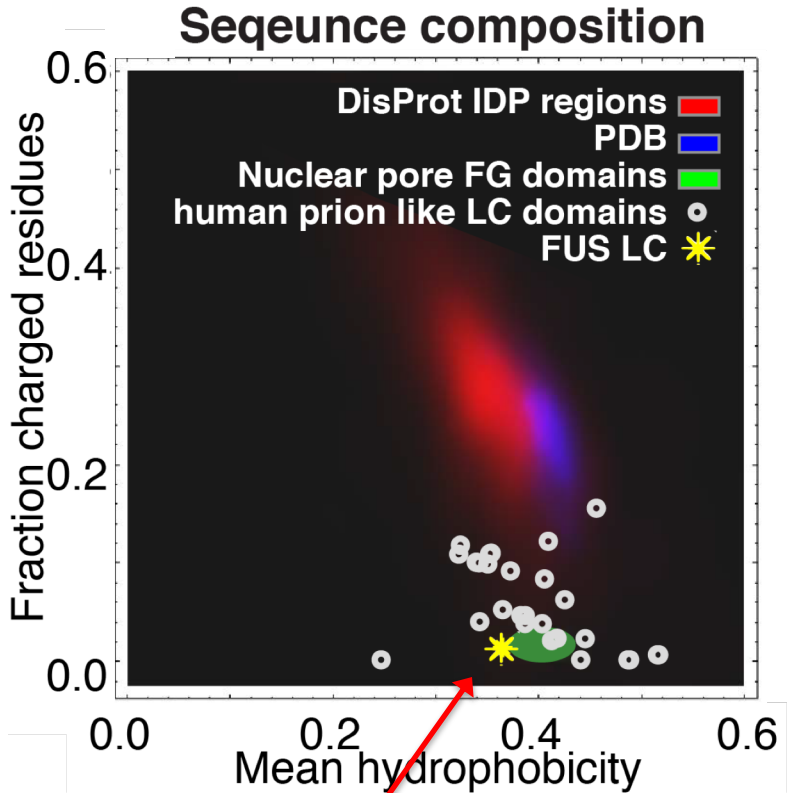
Aliphatic (leucine, isoleucine,
alanine almost entirely absent)

What structure does FUS LC form?

M A S N D Y T Q Q A T Q
 S Y G A Y P T Q P G Q
 G Y S Q Q S S Q P Y G Q Q
 S Y S
 G Y S Q S T D T S
 G Y G Q S
 S Y S
 S Y G Q S Q N T
 G Y G T Q S T P Q
 G Y G S T G
 G Y G S S Q S S Q S
 S Y G Q Q S S Y P
 G Y G Q Q P A P S S T S G
 S Y G S S S Q S S
 S Y G Q P Q S G
 S Y S Q Q P S Y G G Q Q Q
 S Y G Q Q Q S Y N P P Q
 G Y G Q Q N Q Y N S



LC domain structure?



Adapted from: Schmidt and Görlich, *Elife* 2015

“Prion-like” Low complexity (LC) domains: unusual sequences

Rich in amino acids:

serine (S)

tyrosine (Y)

glycine (G)

glutamine (Q)

Lacking other amino acids:

Positively charged (none present)

Negatively charged (only 2)

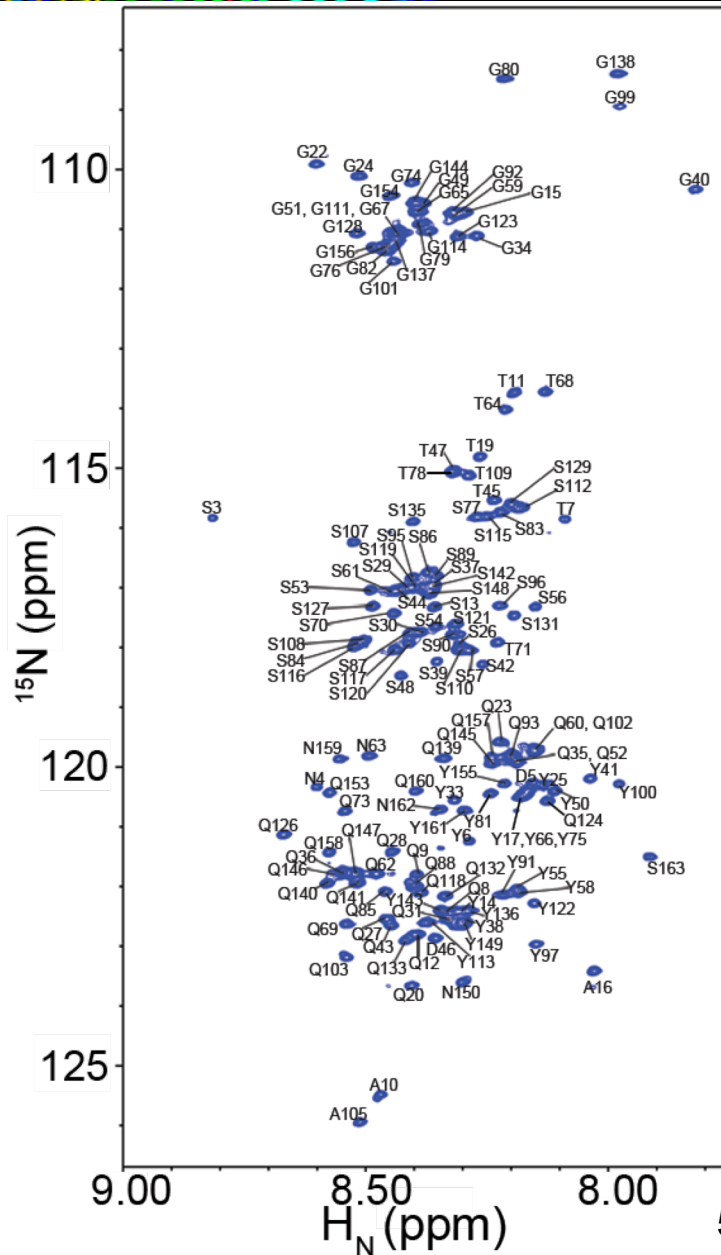
Aliphatic (leucine, isoleucine, alanine almost entirely absent)

What structure does FUS LC form?

Prion-like domains:

- occupy an unusual part of protein sequence universe
- resemble FG Nups in nuclear pore domains? (But no Phe)

FUS LC is unstructured



NMR of dispersed FUS LC

- Atomic resolution NMR
- Narrow range of amide ^1H shifts characteristic of disordered protein

Each dot here is a peak that represents a signal from a single NH backbone position in the FUS LC protein sequence

From the distribution of peak positions this we see that **FUS LC is unstructured**



FUS LC is unstructured

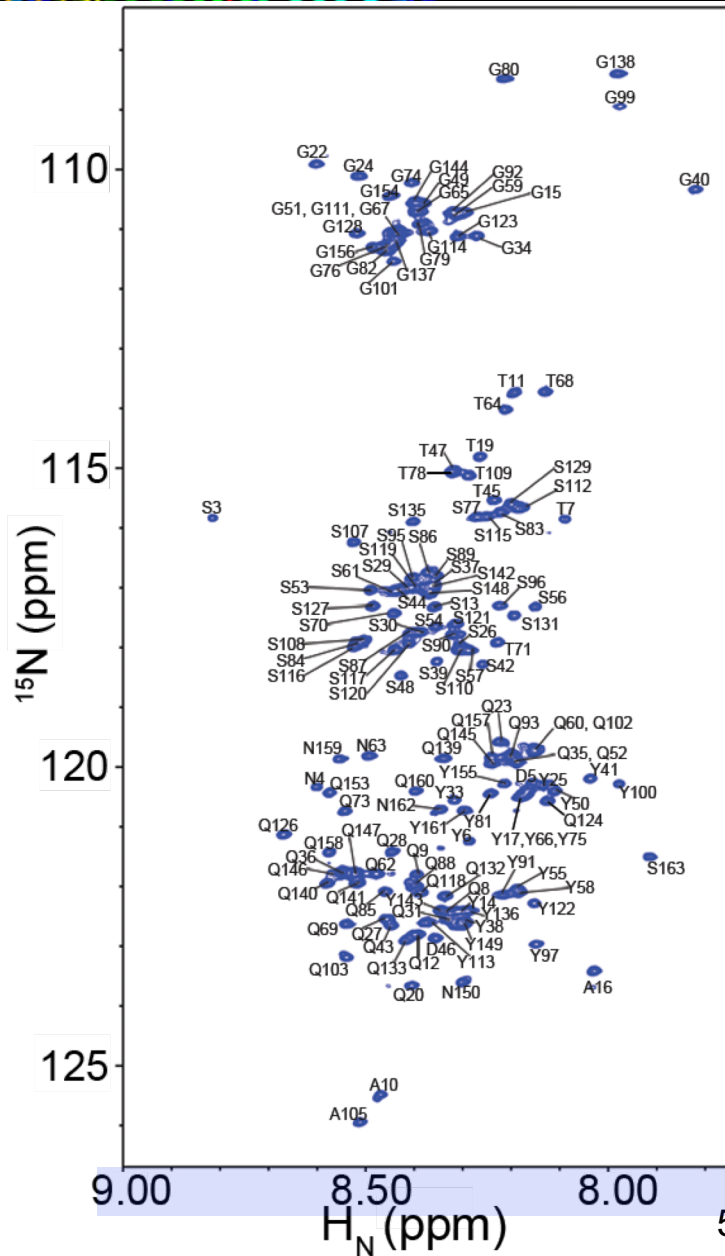
FUS LC structural work by Kathleen Burke

Burke KA et al. *Mol Cell* (2015)



NMR of dispersed FUS LC

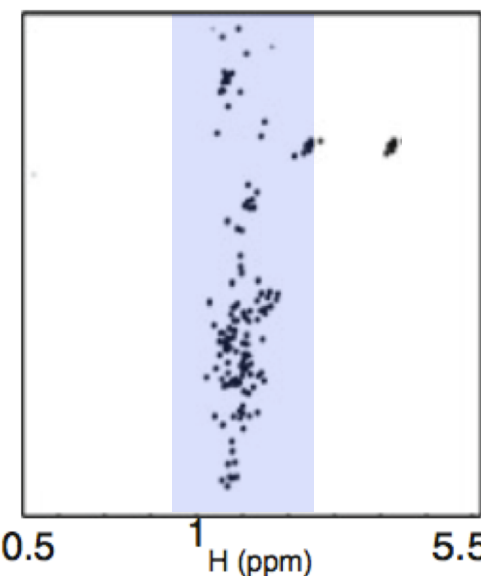
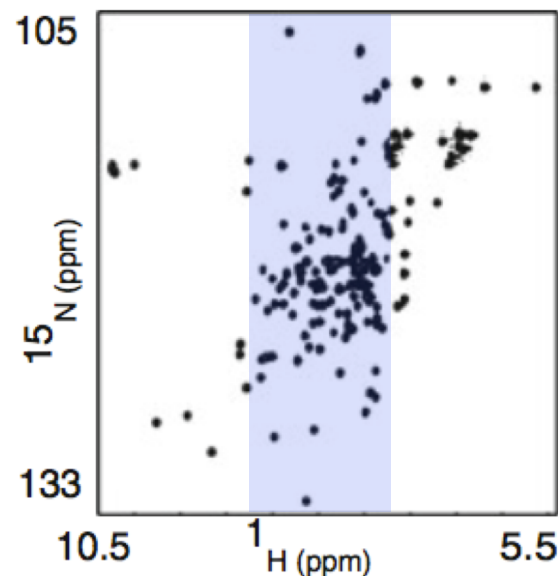
- characteristic of disordered protein



Reference proteins:

Folded

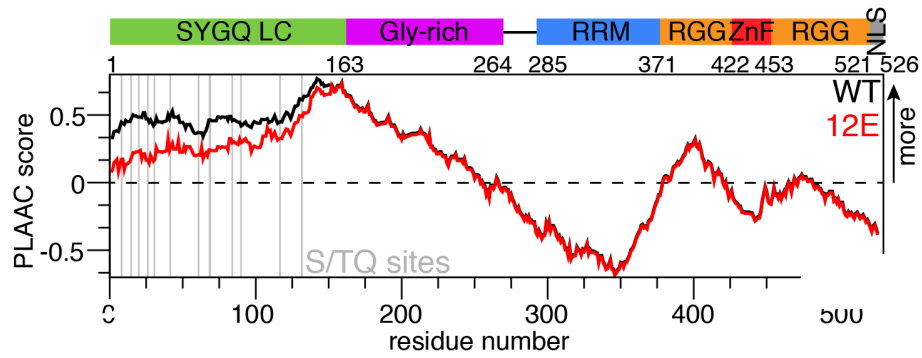
Disordered



Pocket Guide to Biomolecular NMR, by Michael Douclet

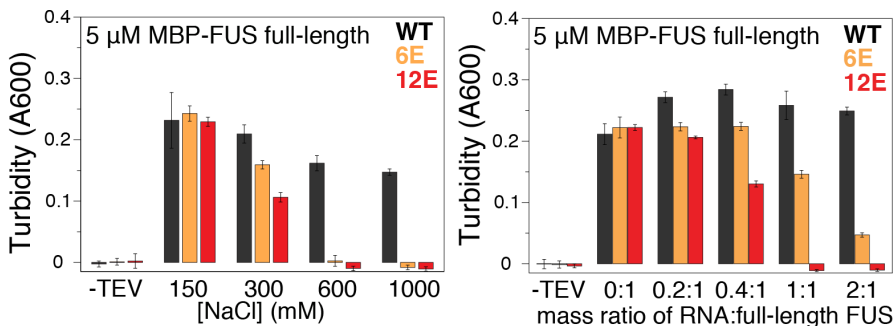
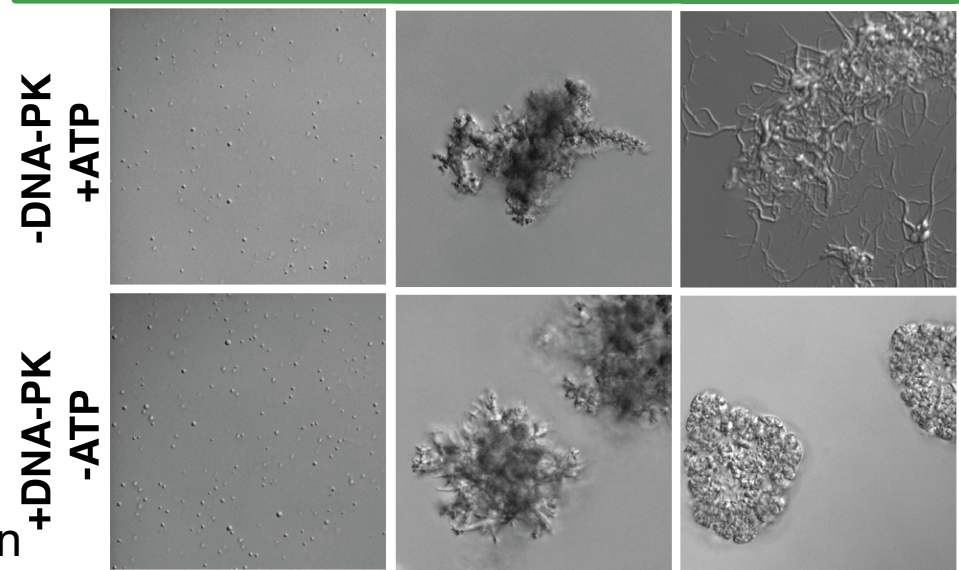
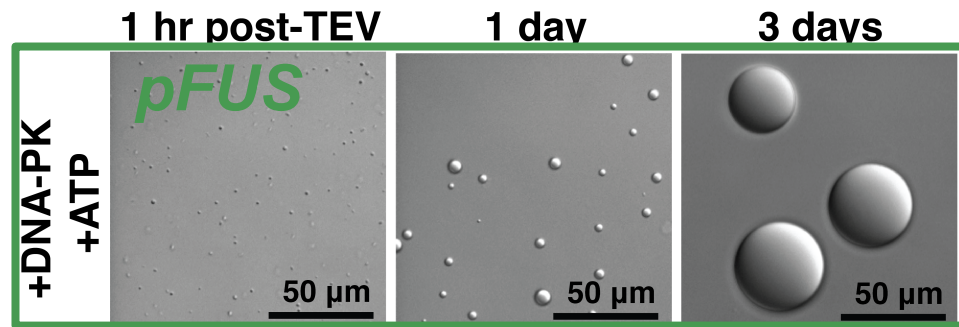
50 μ M FUS LC in 50 mM MES/BisTris 150mM NaCl pH 5.5 @ 25 $^{\circ}$ C

IDR phosphorylation modifies assembly



- Disrupts conversion of phase separated **full-length FUS** into aggregates (following cleavage of MBP solubility tag with TEV protease)

FUS LC phosphorylation/
phosphomimetics reduce
“prion-like” character of FUS
LC domain

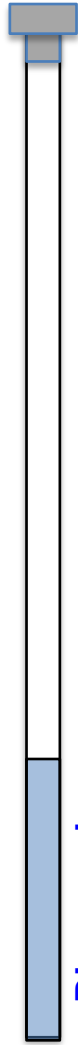
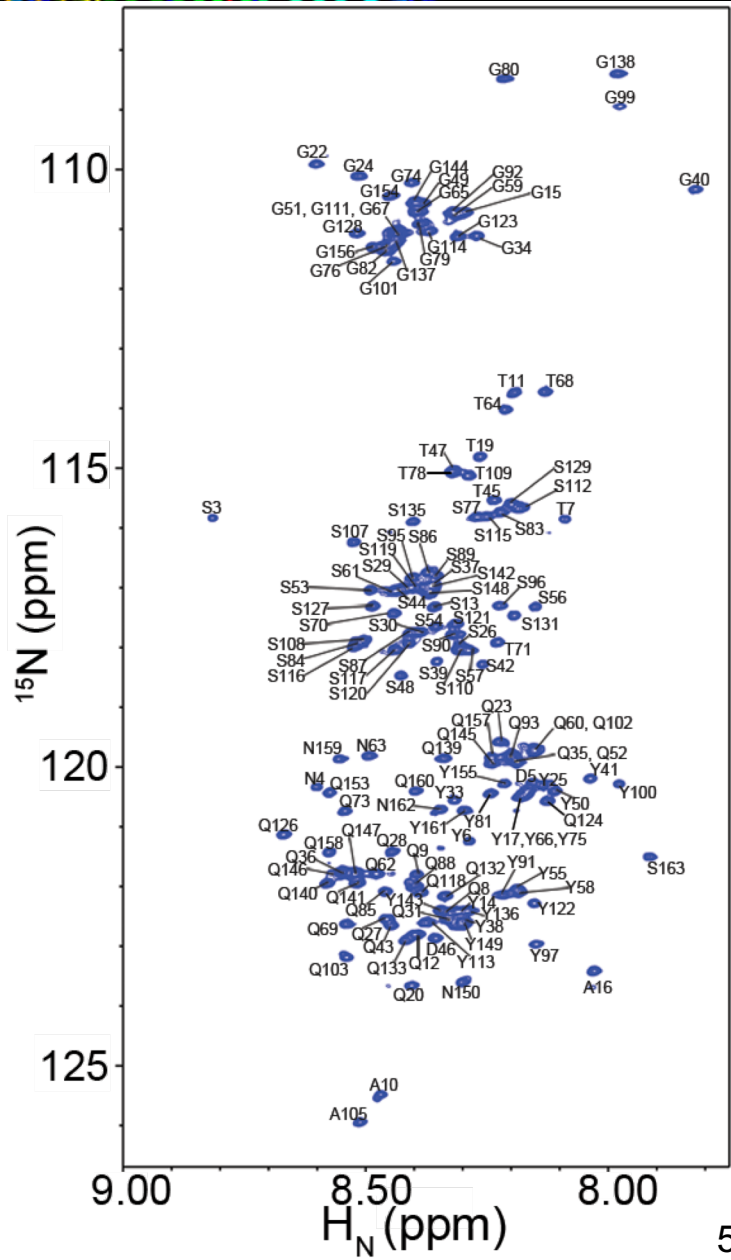


Phosphomimetics disrupt phase separation
when RNA present or with high salt



FUS LC phase separation

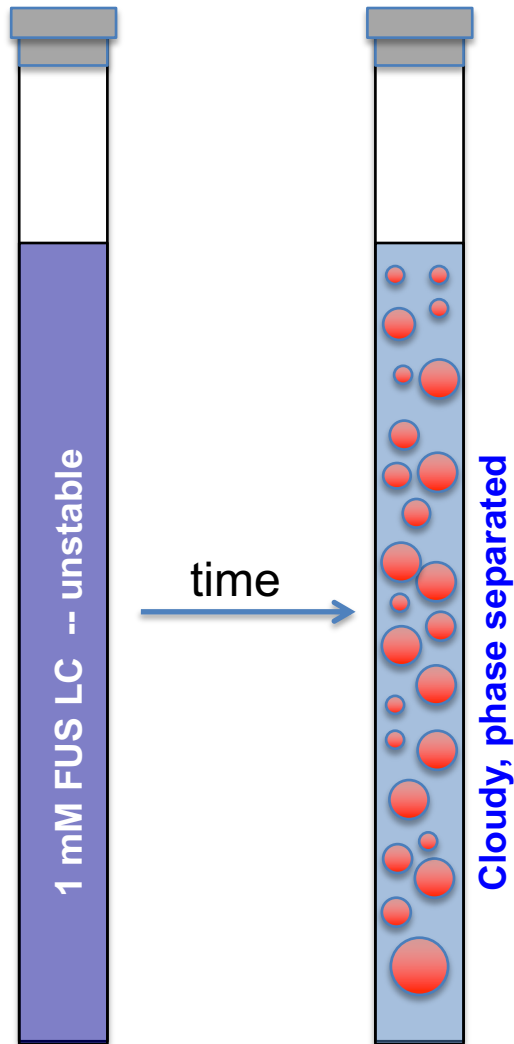
What is the structure of FUS LC inside a “droplet”?



50 μM FUS LC in 50 mM MES/BisTris 150mM NaCl pH 5.5 @ 25 $^\circ\text{C}$

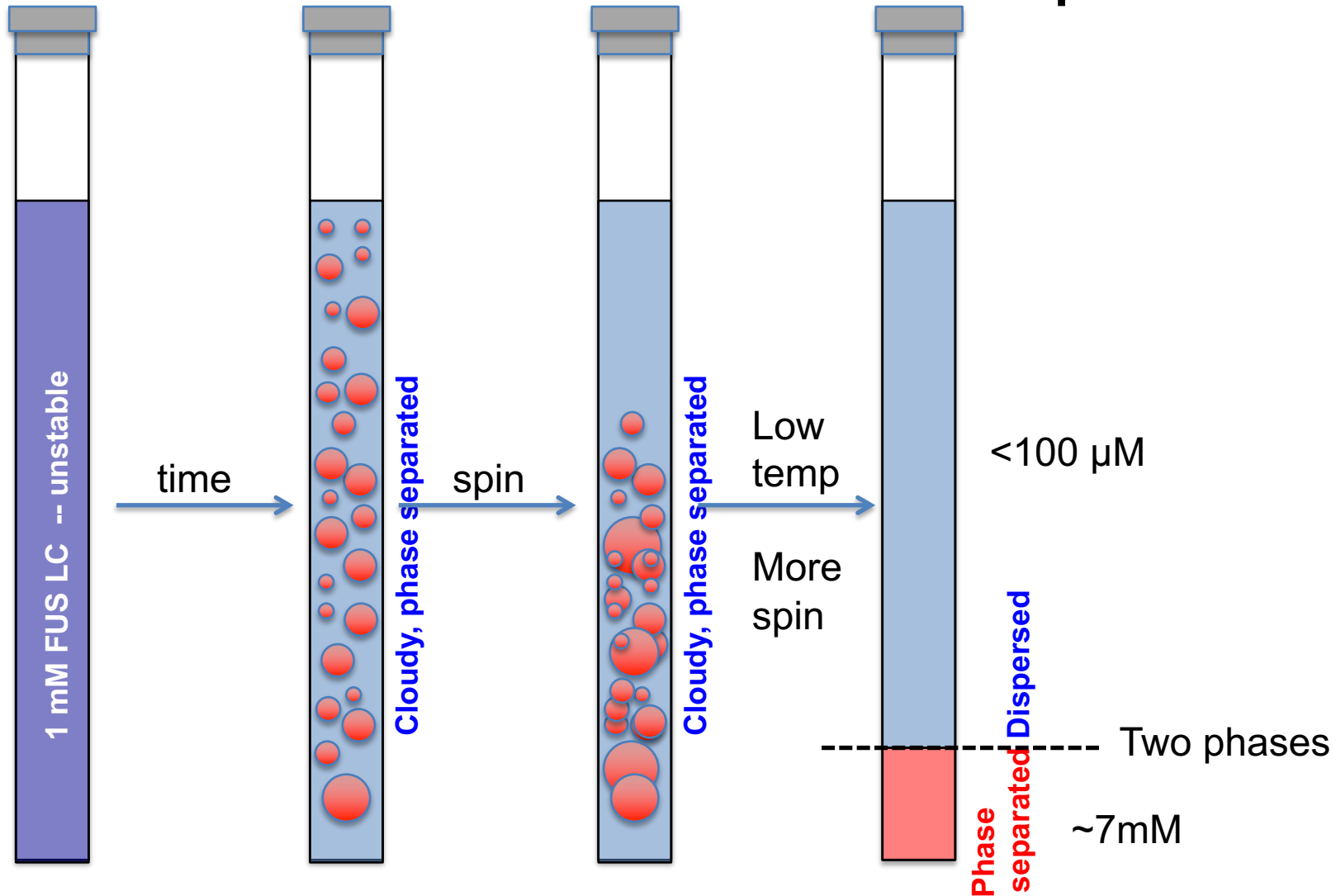
FUS LC phase separation

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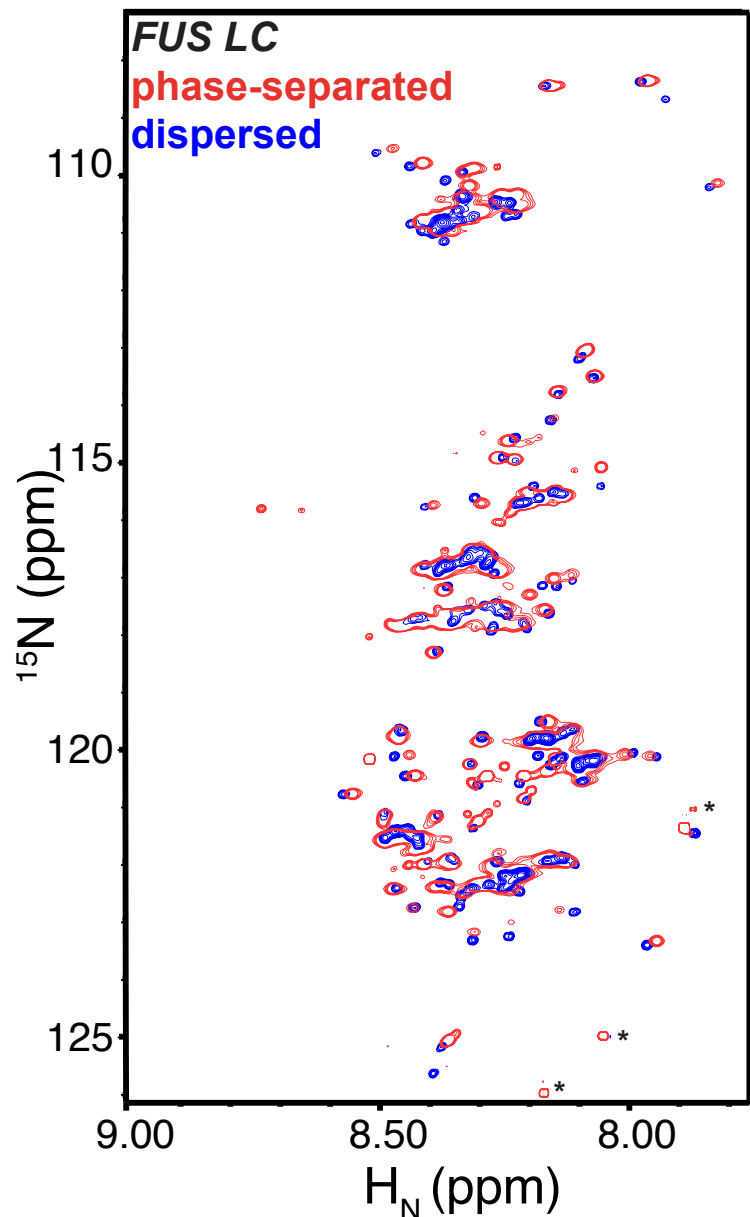


FUS LC phase separation

What is the structure of FUS LC inside a “droplet”?

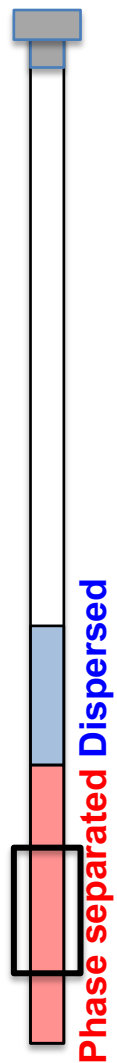


Atomic details of FUS LC droplets



FUS LC primarily disordered in liquid phase separated state

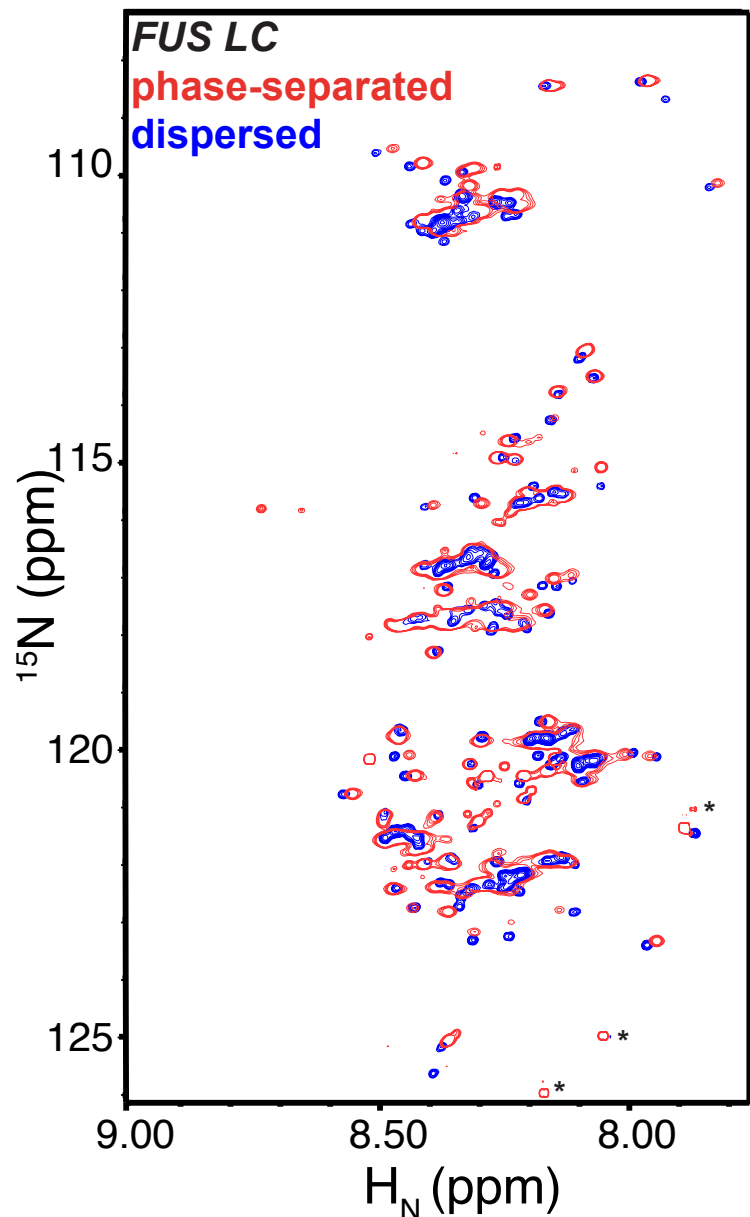
- Phase-separated state overlays with dispersed



NMR Observation volume

~7mM FUS LC at 25 °C derived from a original sample:
1 mM FUS LC in 50 mM MES/BisTris 150mM NaCl pH 5.5

Atomic details of FUS LC droplets



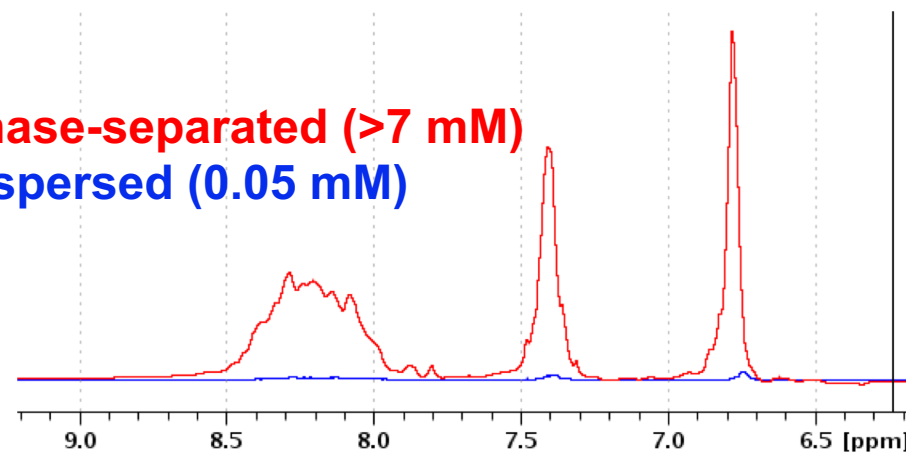
FUS LC primarily disordered in liquid phase separated state

- Phase-separated state overlays with dispersed

Is this a major or minor state?

Raw intensity data

phase-separated (>7 mM)
dispersed (0.05 mM)

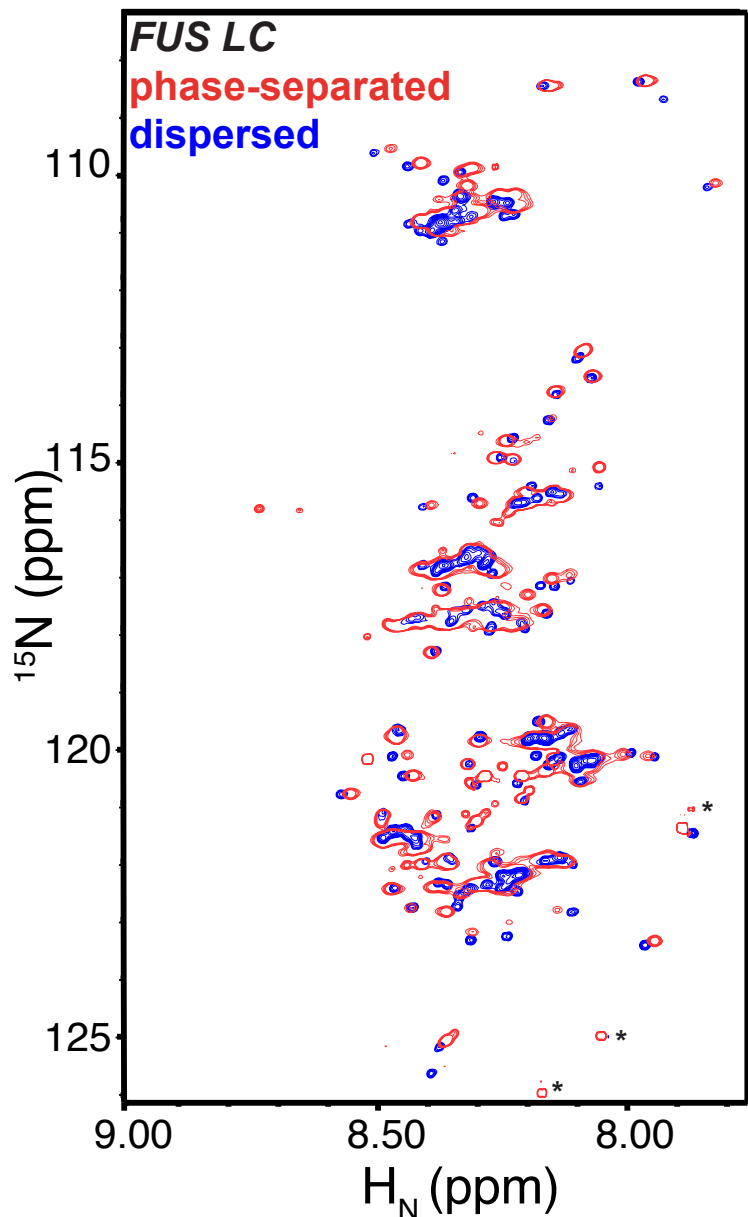


Phase separated
Dispersed

← NMR Observation volume

~7mM FUS LC at 25 °C derived from a original sample:
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Atomic details of FUS LC droplets

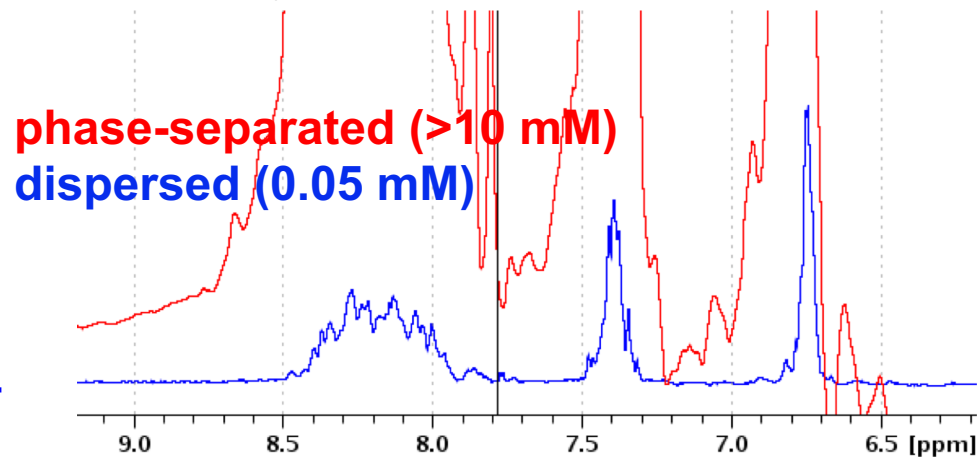


FUS LC primarily disordered in liquid phase separated state

- Phase-separated state overlays with dispersed

Is this a major or minor state?

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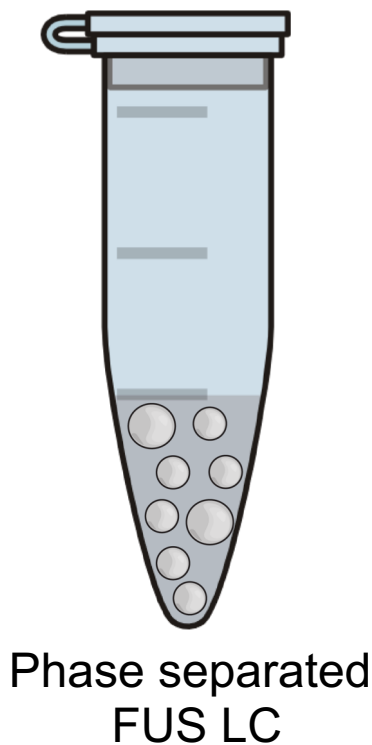


100x signal in phase-separated vs control

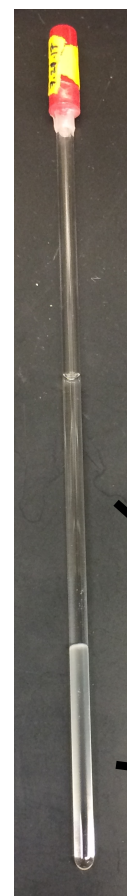
← **NMR Observation volume**

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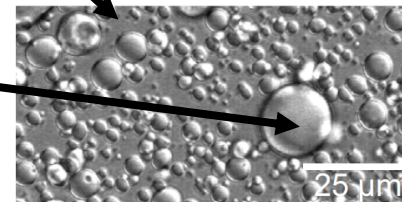
Using NMR spectroscopy to see within the phase separated state



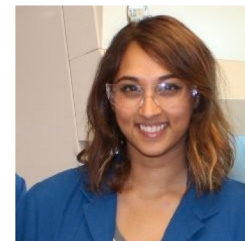
Cool +
Slow centrifugation
in NMR tube



Dilute phase



Concentrated phase

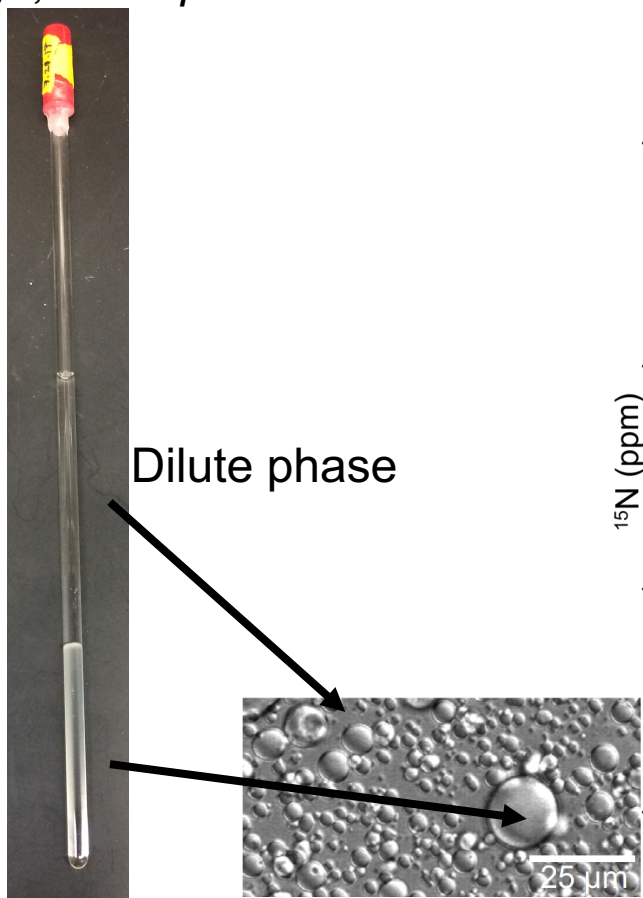


*FUS data from
Anastasia Murthy*

Using NMR spectroscopy to see within the phase separated state

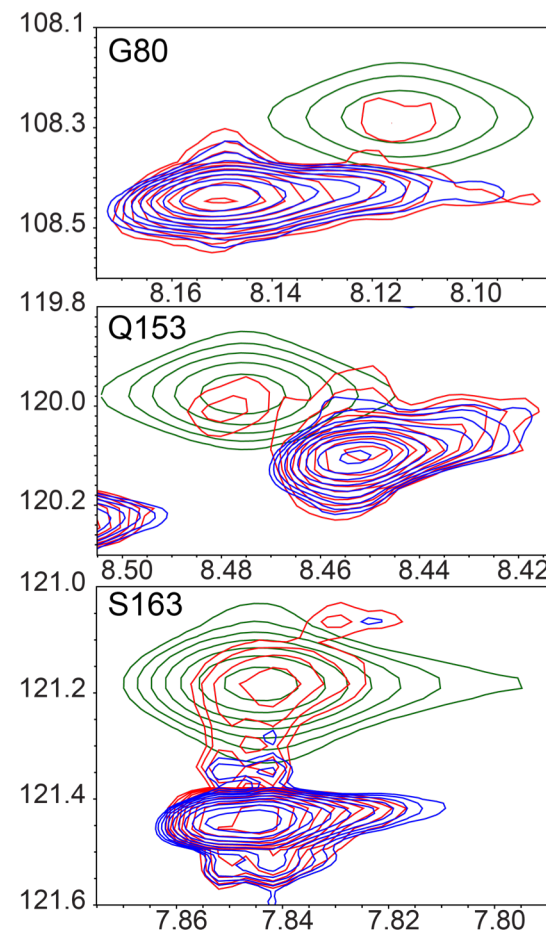
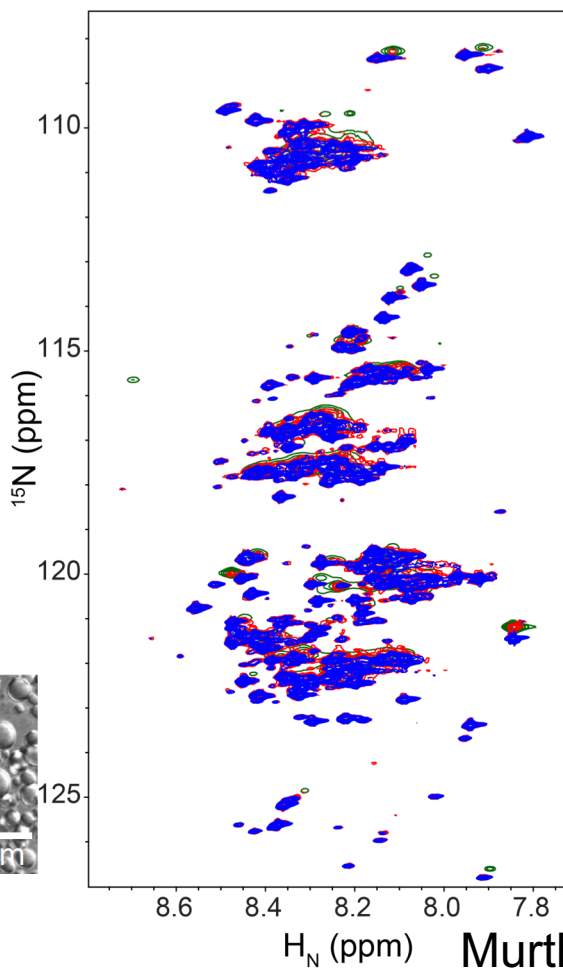
The chemical environment of spontaneous droplets is similar to the large, monophasic condensed droplet.

FUS LC_{Dispersed} + FUS LC_{Condensed}
FUS LC_{Dispersed}
FUS LC_{Condensed}



Dilute phase

Concentrated phase



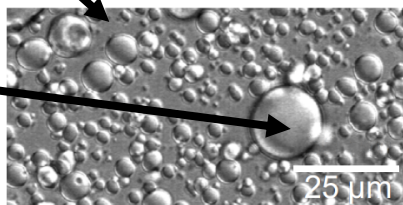
Murthy AM et al. in preparation

Using NMR spectroscopy to see within the phase separated state

FUS LC diffusion in spontaneous droplets is similar to the large, monophasic condensed droplet.



Dilute phase



Concentrated phase

Diffusion coefficient ($\mu\text{m}^2/\text{s}$)

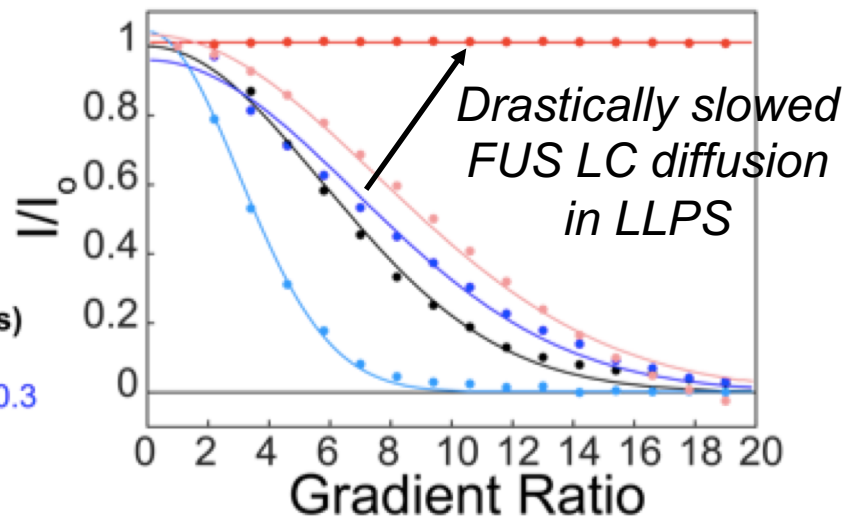
Lysozyme 104 ± 10.1

Dispersed FUS LC 85.1 ± 10.3

Buffer_{Dispersed} 440.0 ± 40.9

Condensed FUS LC n.a.

Buffer_{Condensed} 69.4 ± 7.47

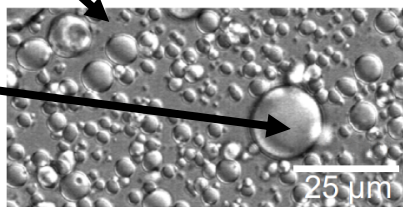


Using NMR spectroscopy to see within the phase separated state

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Dilute phase



Concentrated phase

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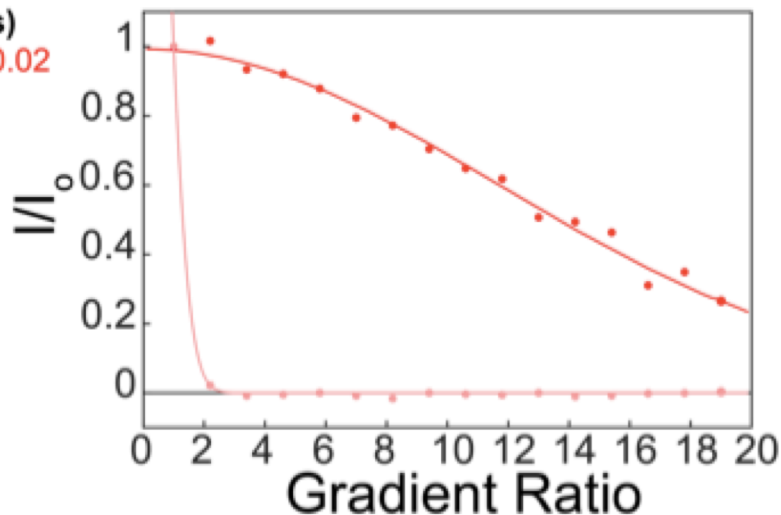
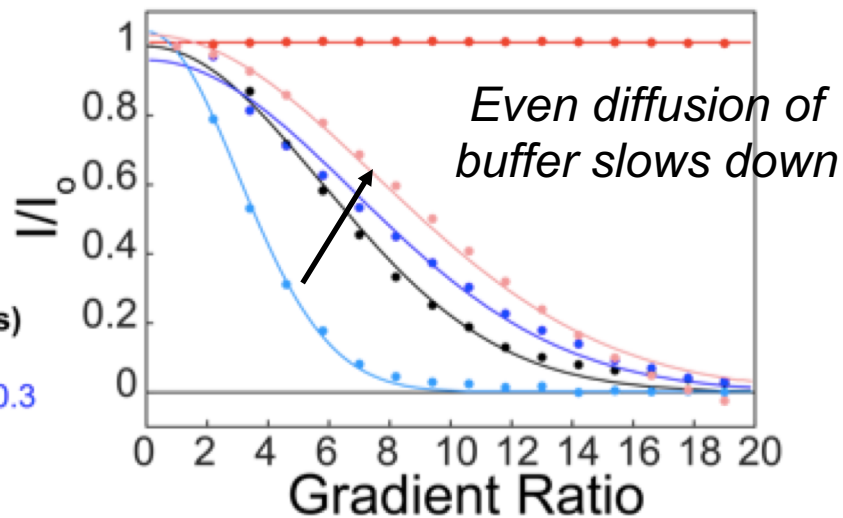
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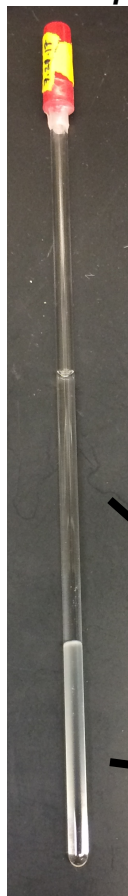
Condensed FUS LC 0.17 ± 0.02

Buffer_{Condensed} 48.0 ± 9.97

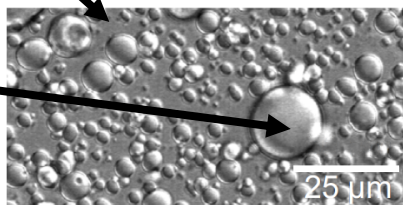


Using NMR spectroscopy to see within the phase separated state

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Dilute phase



Concentrated phase

Diffusion coefficient ($\mu\text{m}^2/\text{s}$)

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Buffer_{Dispersed} 440.0 ± 40.9

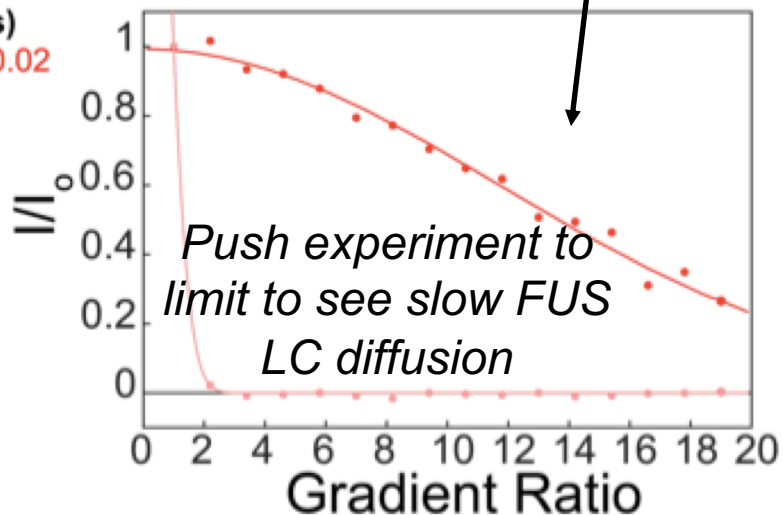
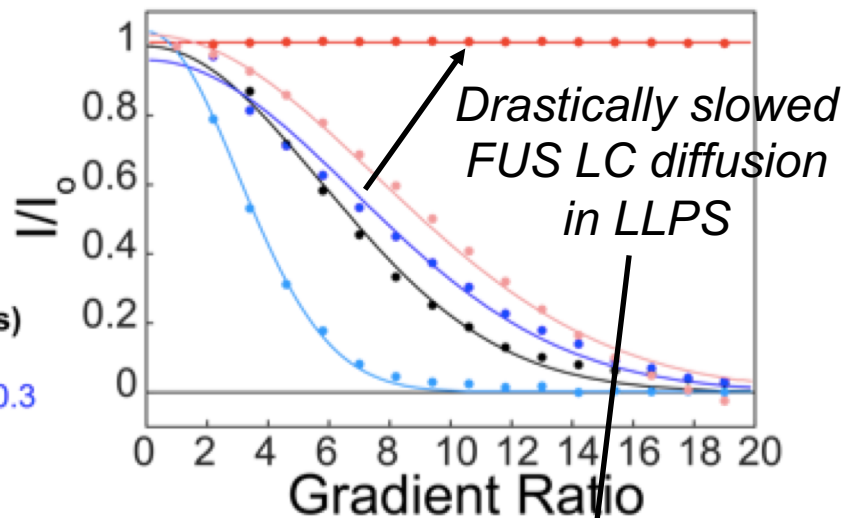
Condensed FUS LC n.a.

Buffer_{Condensed} 69.4 ± 7.47

Diffusion coefficient ($\mu\text{m}^2/\text{s}$)

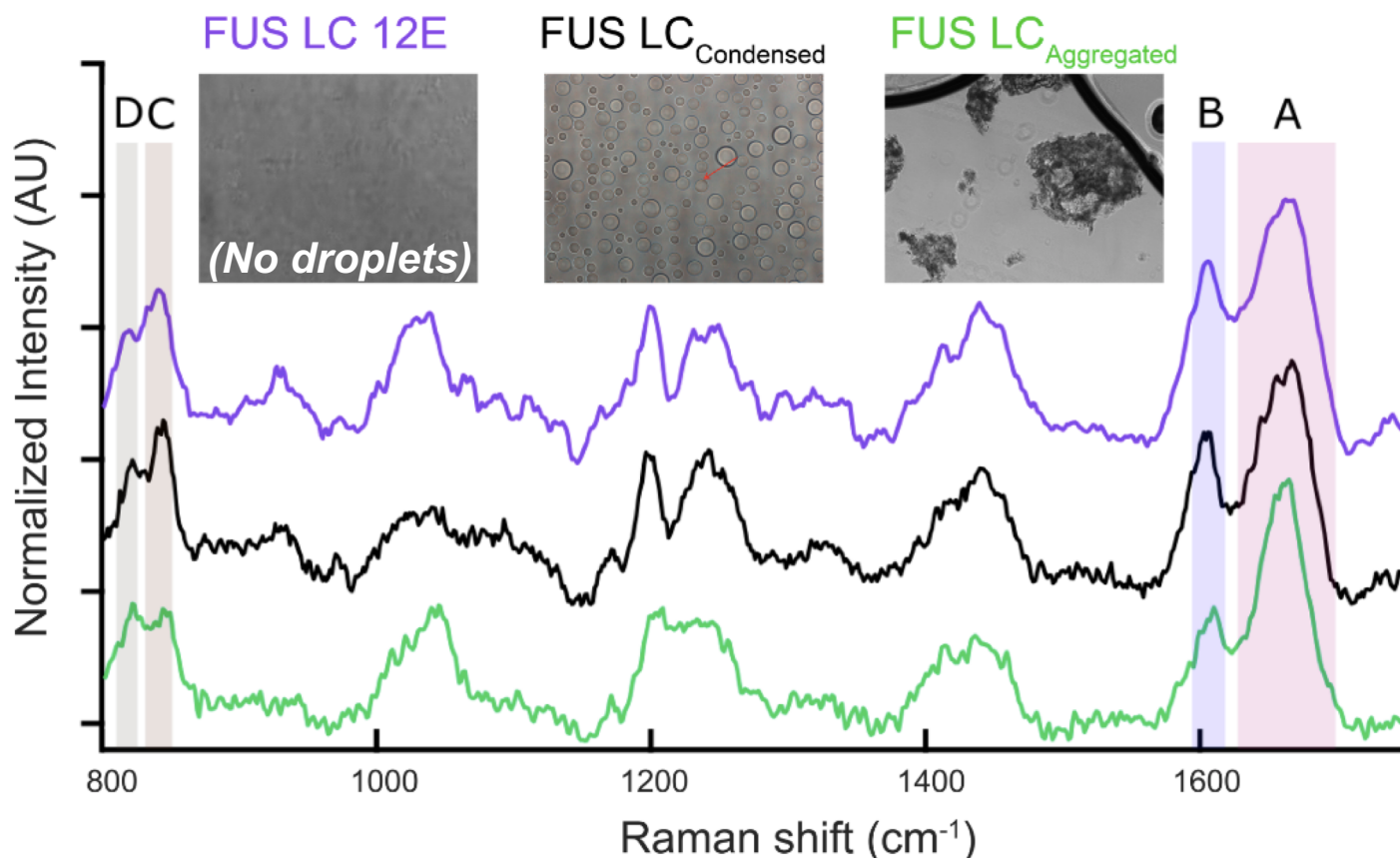
Condensed FUS LC 0.17 ± 0.02

Buffer_{Condensed} 48.0 ± 9.97



Using CARS hyperspectral imaging to see within the phase separated state

*FUS LC vibrational spectrum in droplets resembles a **non-phase separated form** (FUS LC 12E) characterized by NMR in detail, more so than an **aggregated form**.*

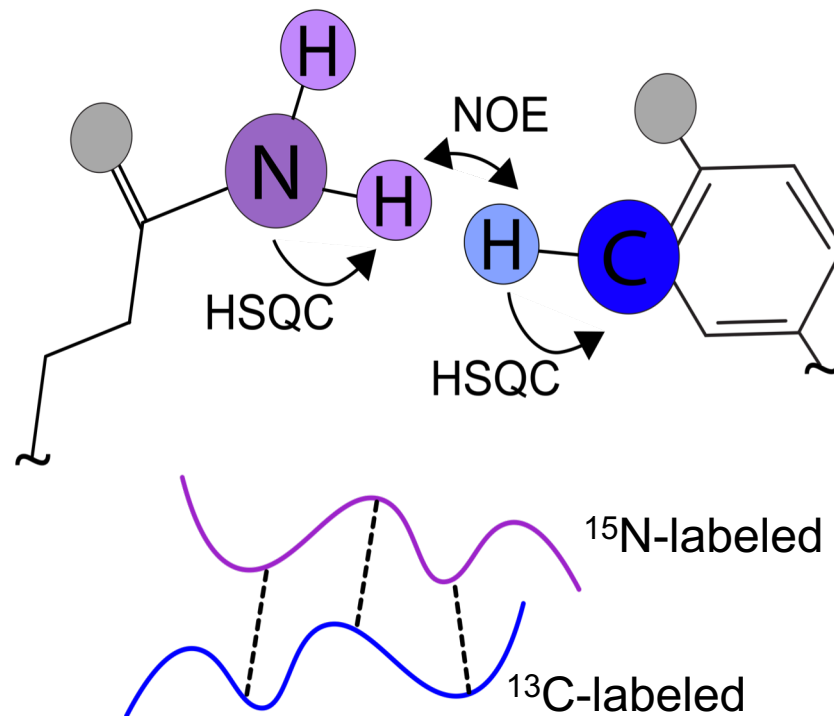
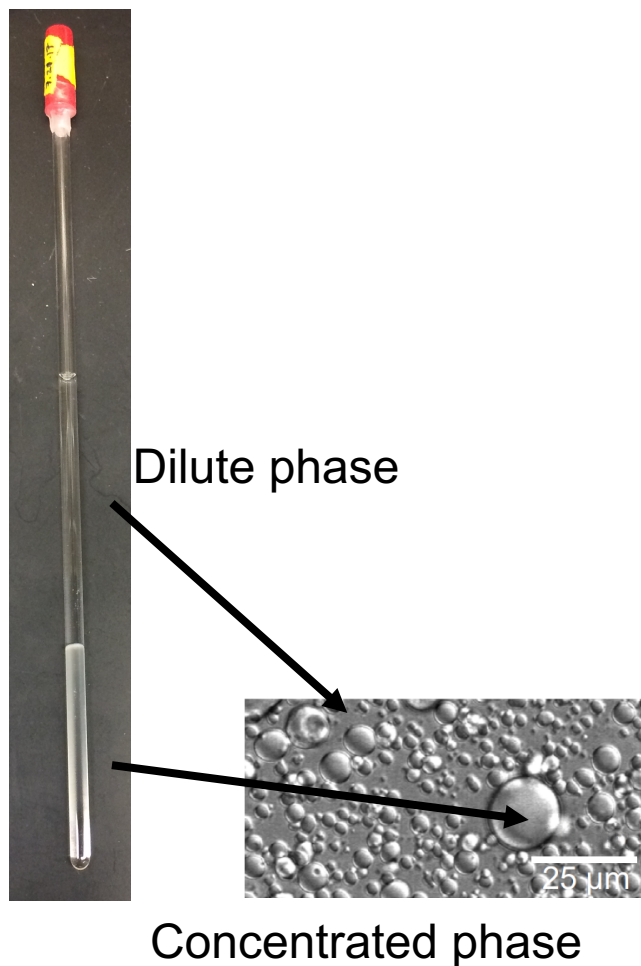


*Yelena Kan
and
Sapun Parekh
(MPI Polymer
and UT Austin)*

Major state of FUS LC residues is structurally disordered

Using NMR spectroscopy to see within the phase separated state

NMR experiments (HSQC-NOESY-HSQC) to observe interactions between **amide hydrogen** and **carbon-attached hydrogen**

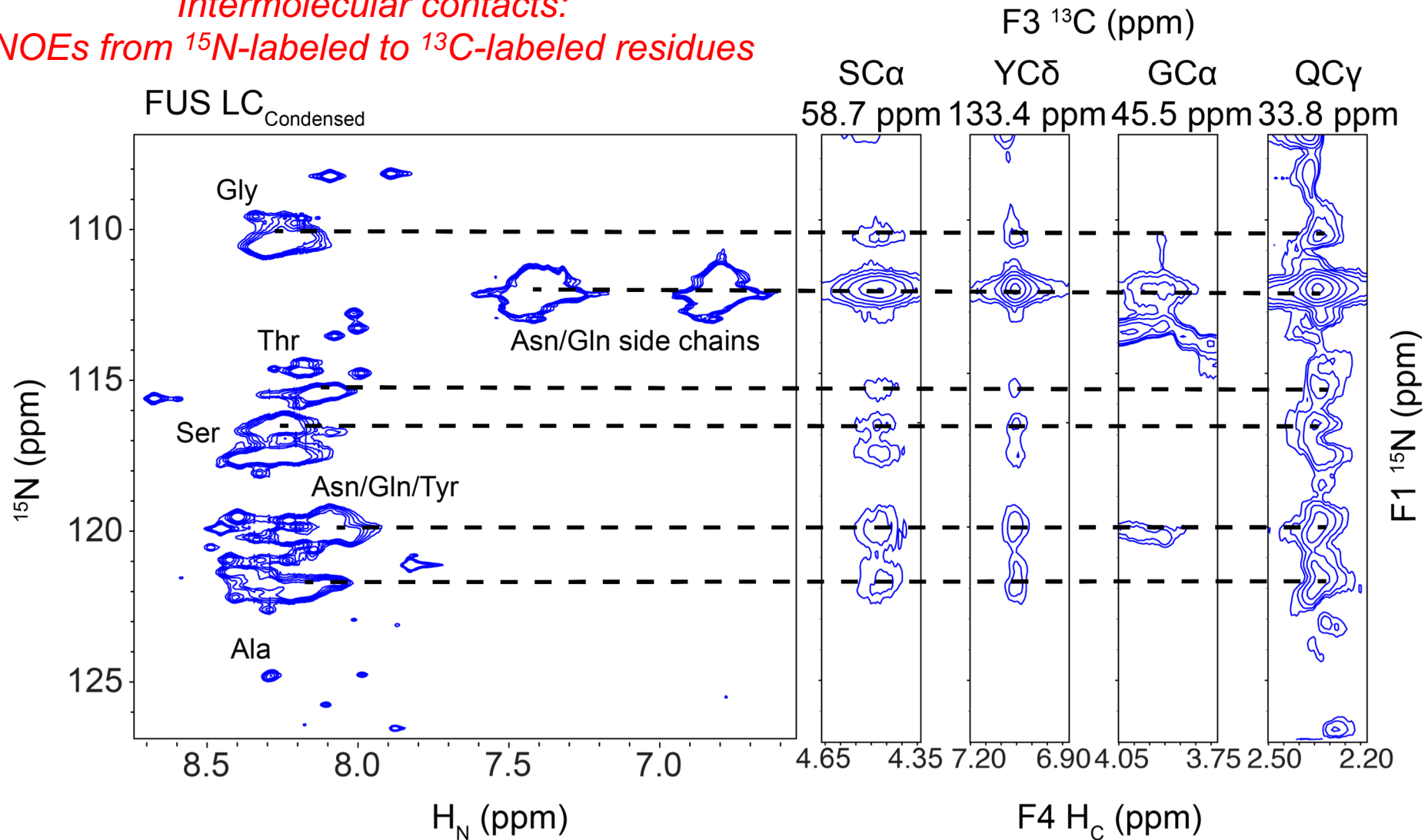


Inter-molecular interactions between FUS LC monomers within phase separated state

Non-specific intermolecular contacts between all residue types underlie FUS LC LLPS

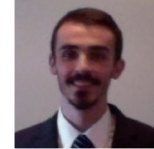
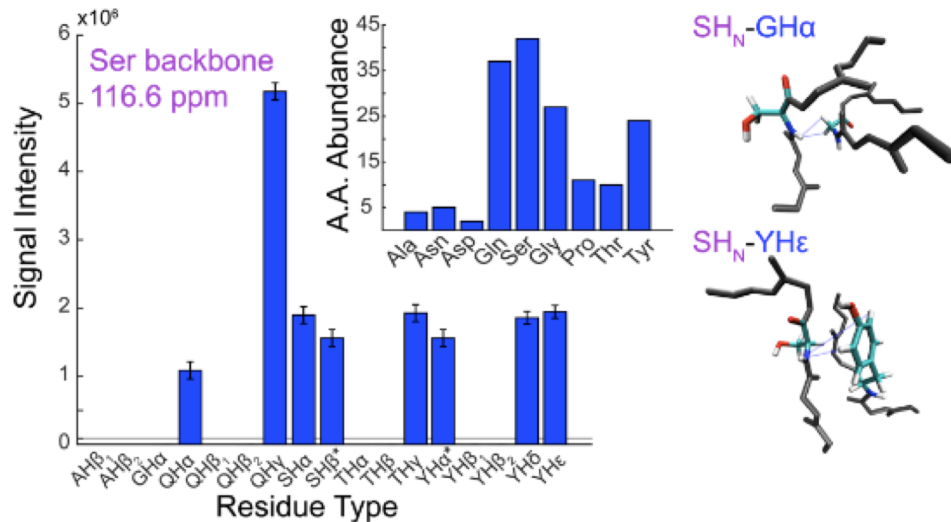
Intermolecular contacts:

NOEs from ^{15}N -labeled to ^{13}C -labeled residues

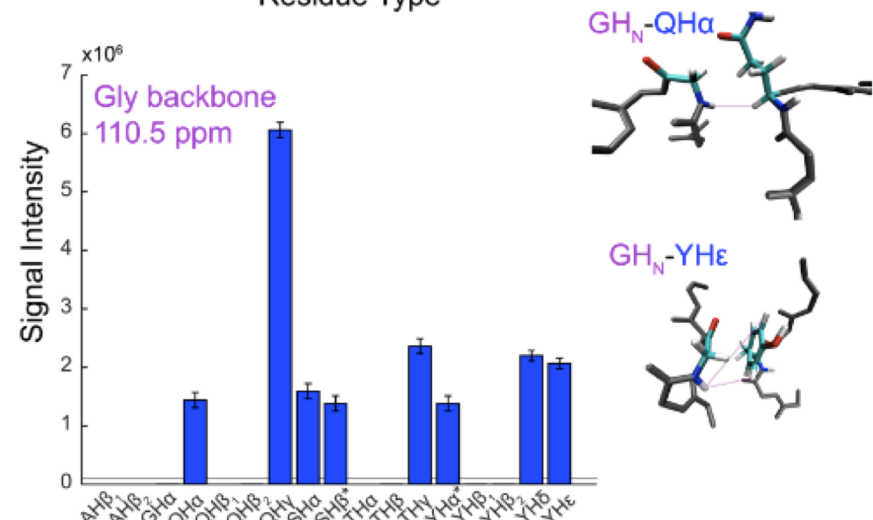
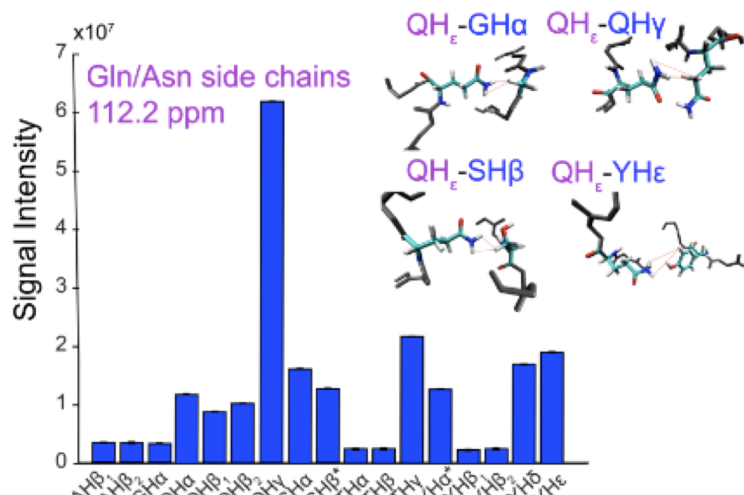
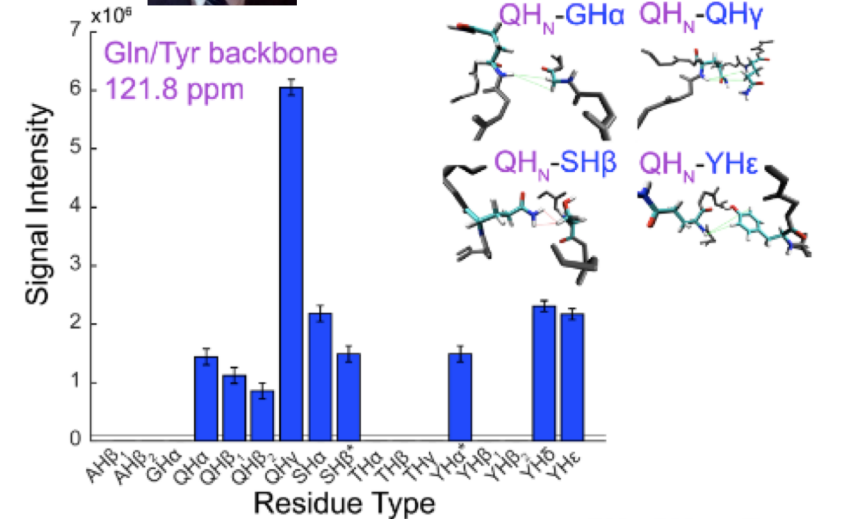


Non-specific intermolecular contacts between all residue types underlie FUS LC LLPS

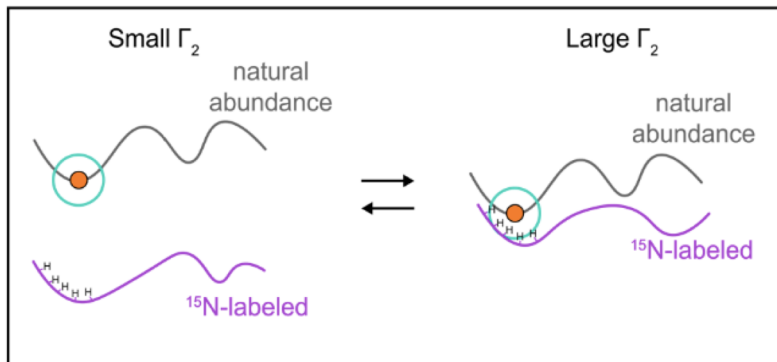
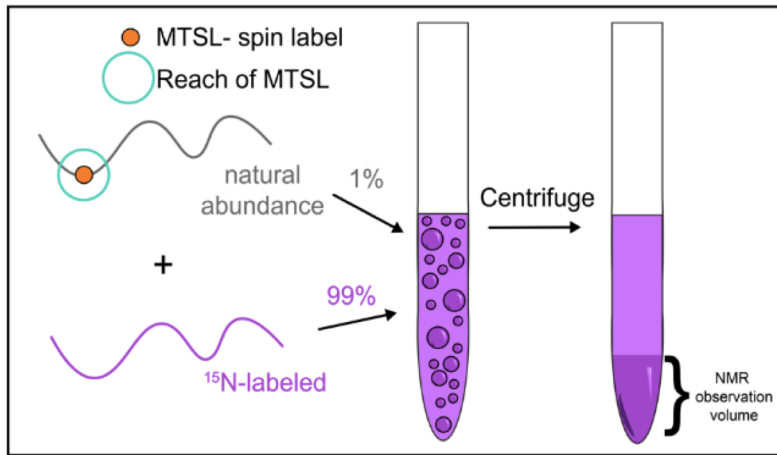
*Intermolecular contacts:
NOEs from ^{15}N -labeled to ^{13}C -labeled residues*



*MD simulations by
Greg Dignon*

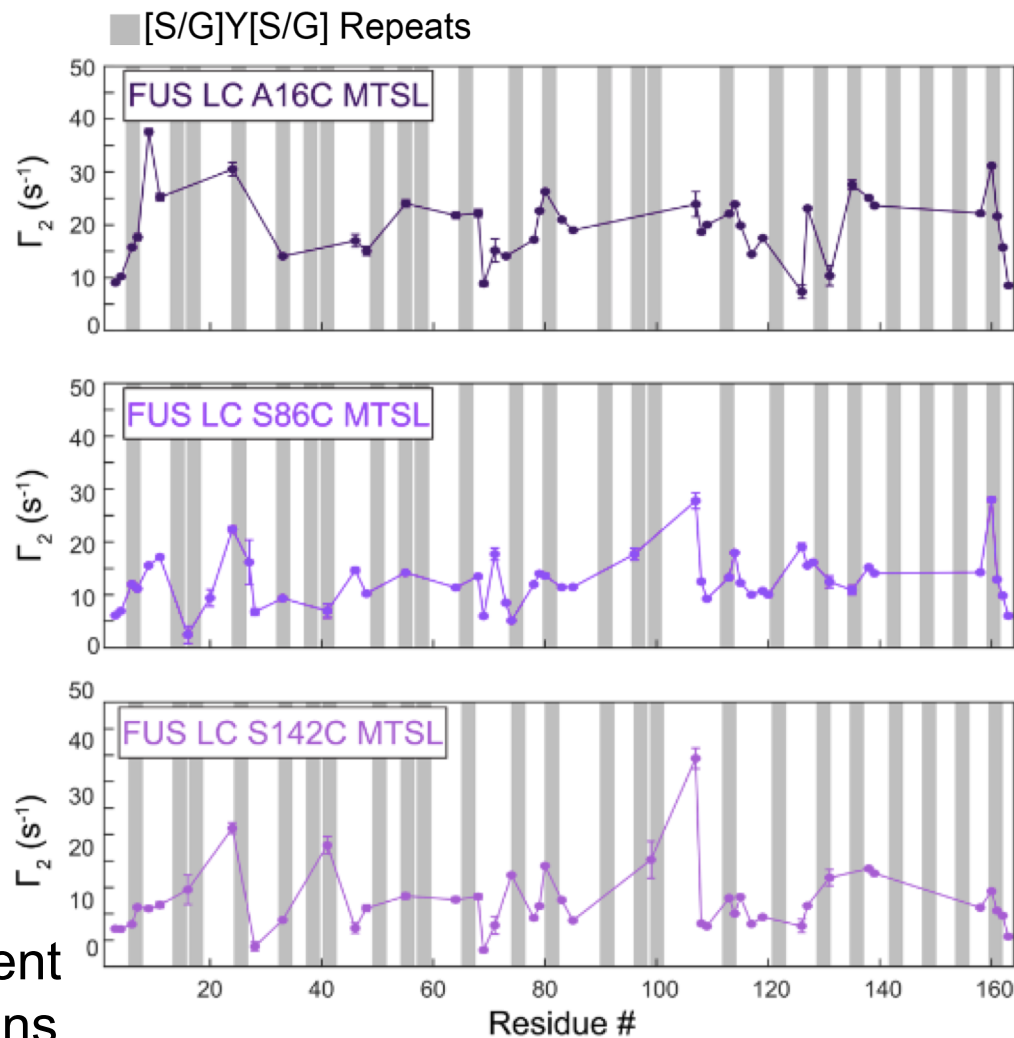
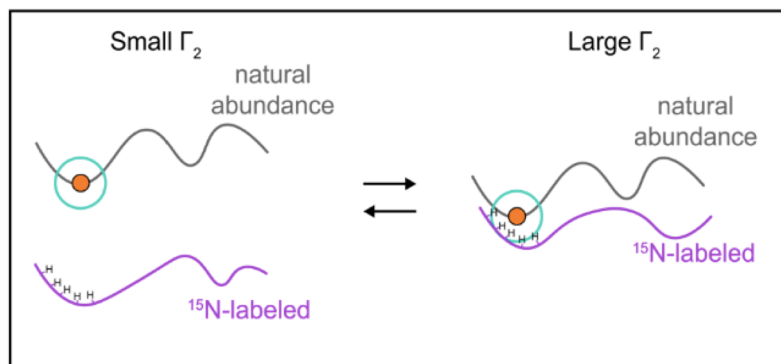
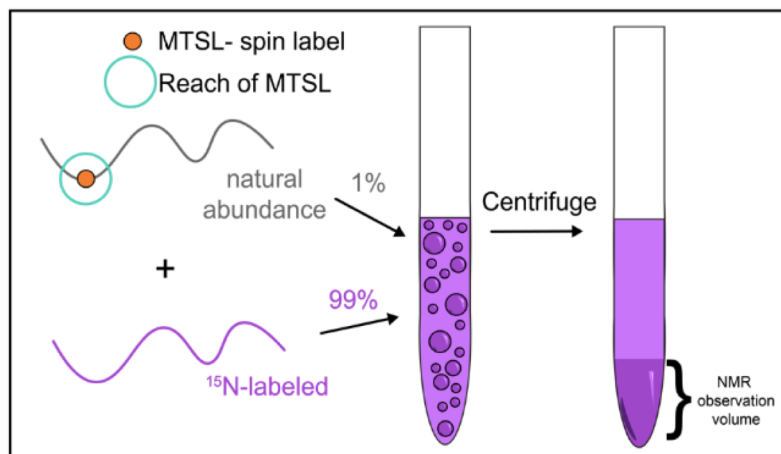


Interactions that stabilize LLPS are not localized to a particular region of FUS LC



Paramagnetic relaxation enhancement
NMR to observe transient, interactions
in the condensed phase

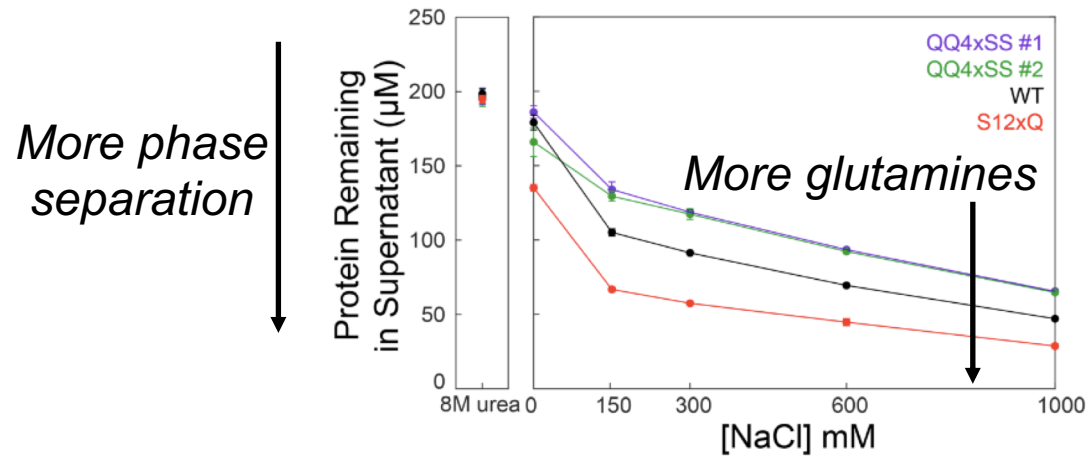
Interactions that stabilize LLPS are not localized to a particular region of FUS LC



Paramagnetic relaxation enhancement
NMR to observe transient, interactions
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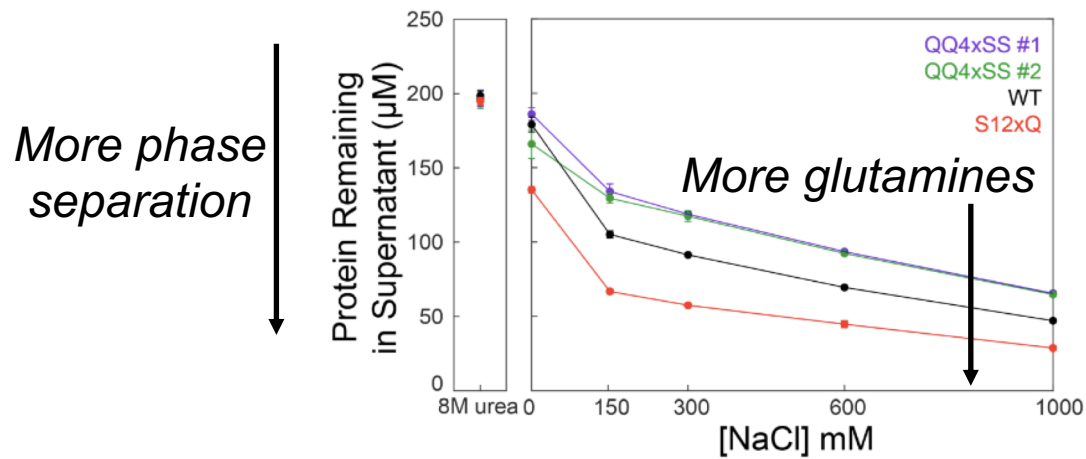
Glutamine residues contribute to FUS LC LLPS

Glutamine substitutions modulate FUS LC LLPS

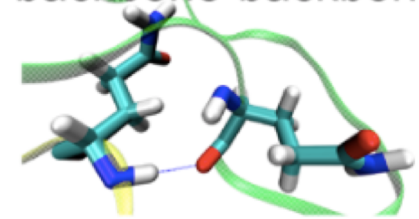


Glutamine residues contribute to FUS LC LLPS

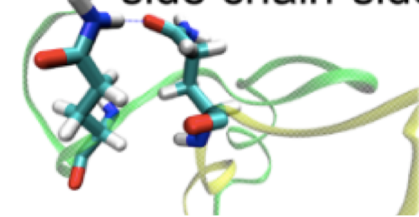
Glutamine substitutions modulate FUS LC LLPS



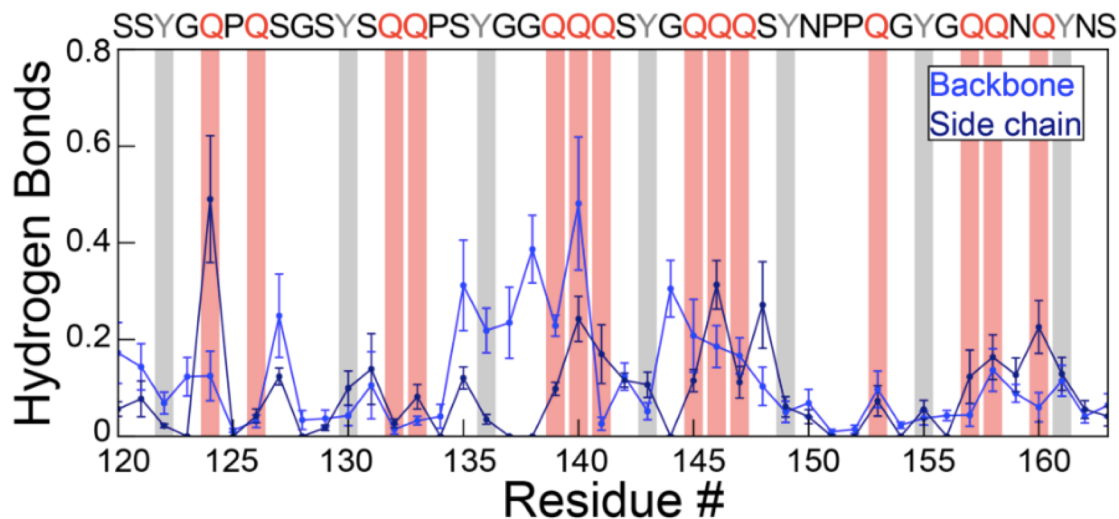
backbone-backbone



side chain-side chain



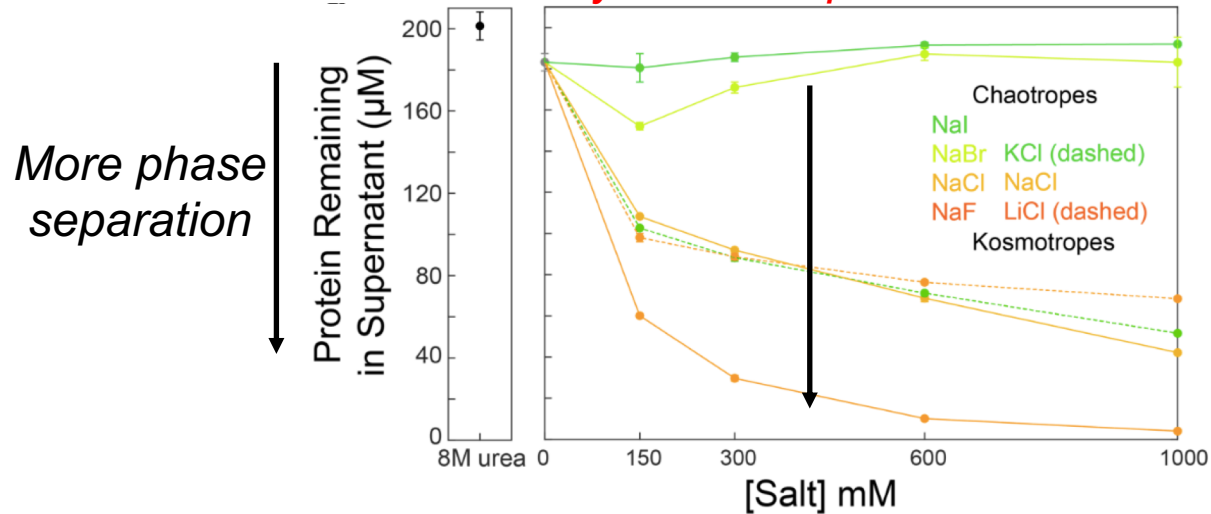
side chain-side chain



Glutamine contacts stabilized by intermolecular hydrogen bonds in FUS LC fragment molecular simulation

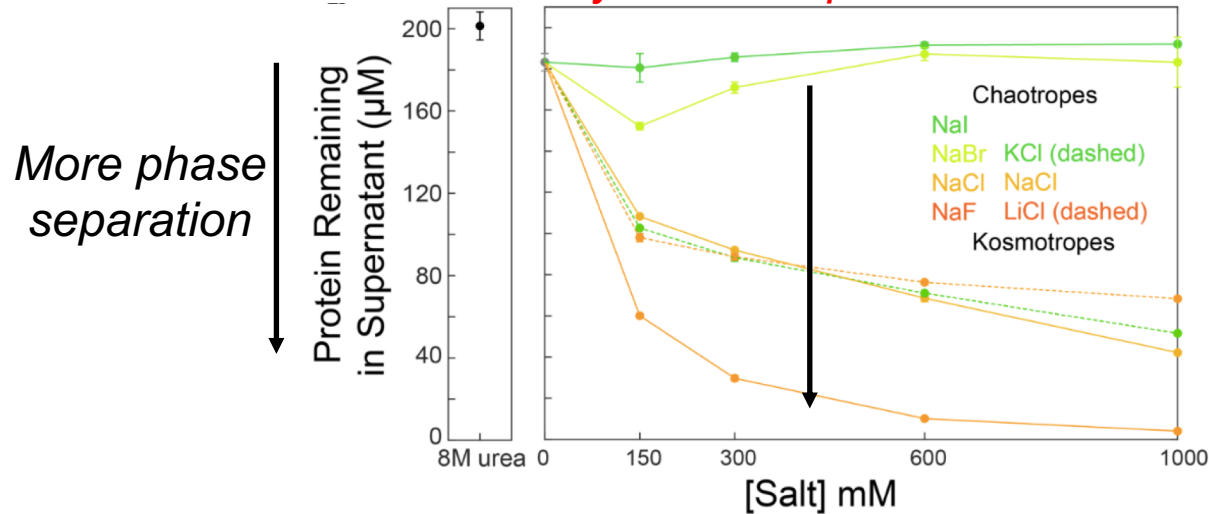
Hydrophobic interactions contribute to FUS LC LLPS

FUS LC LLPS induced by kosmotropic salts

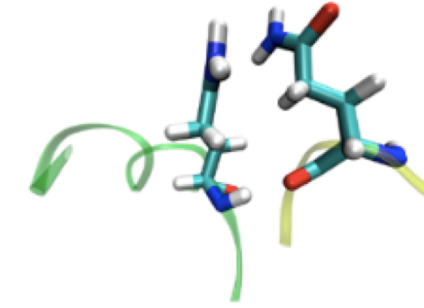


Hydrophobic interactions contribute to FUS LC LLPS

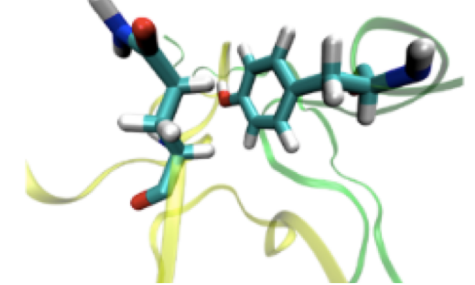
FUS LC LLPS induced by kosmotropic salts



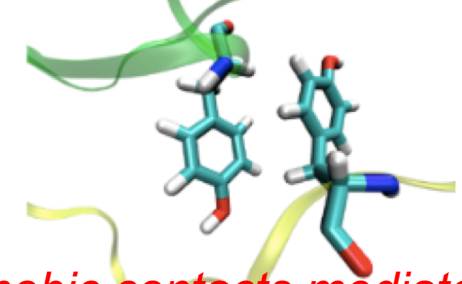
Q153-Q160



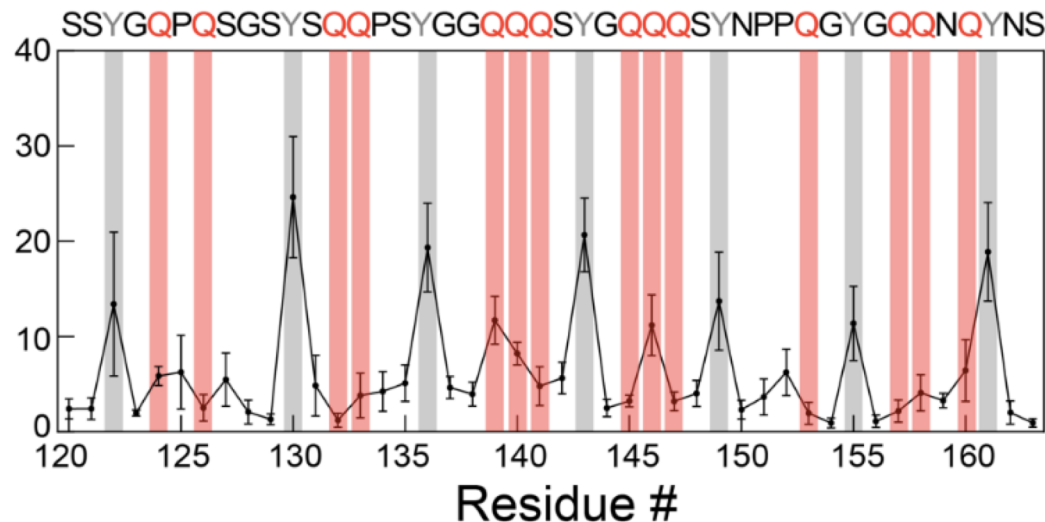
Y130-Q139



Y130-Y122

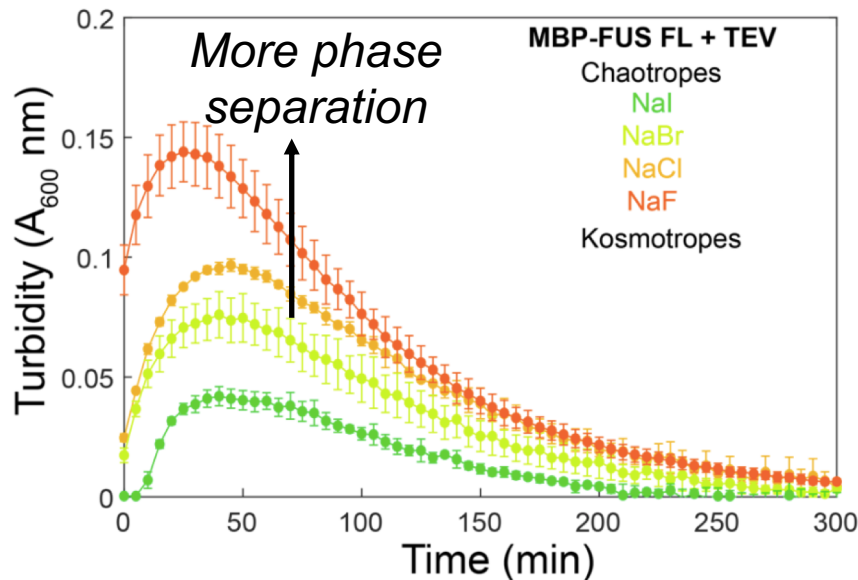
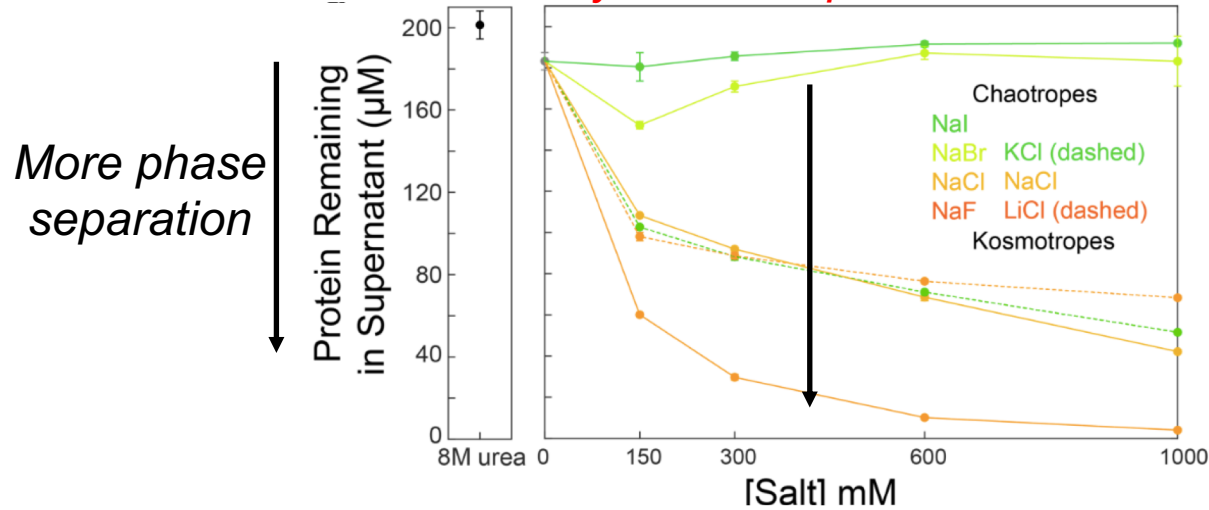


Hydrophobic contacts mediated by glutamine and tyrosine

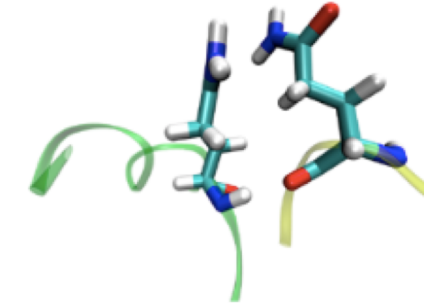


Hydrophobic interactions contribute to FUS LC LLPS

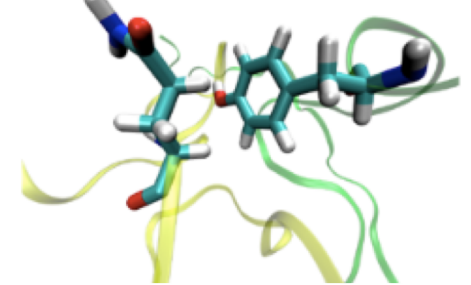
FUS LC LLPS induced by kosmotropic salts



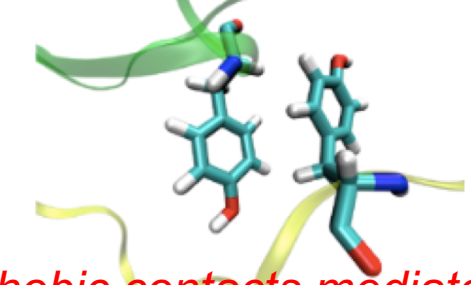
Q153-Q160



Y130-Q139



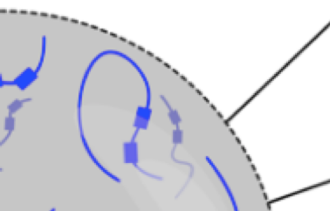
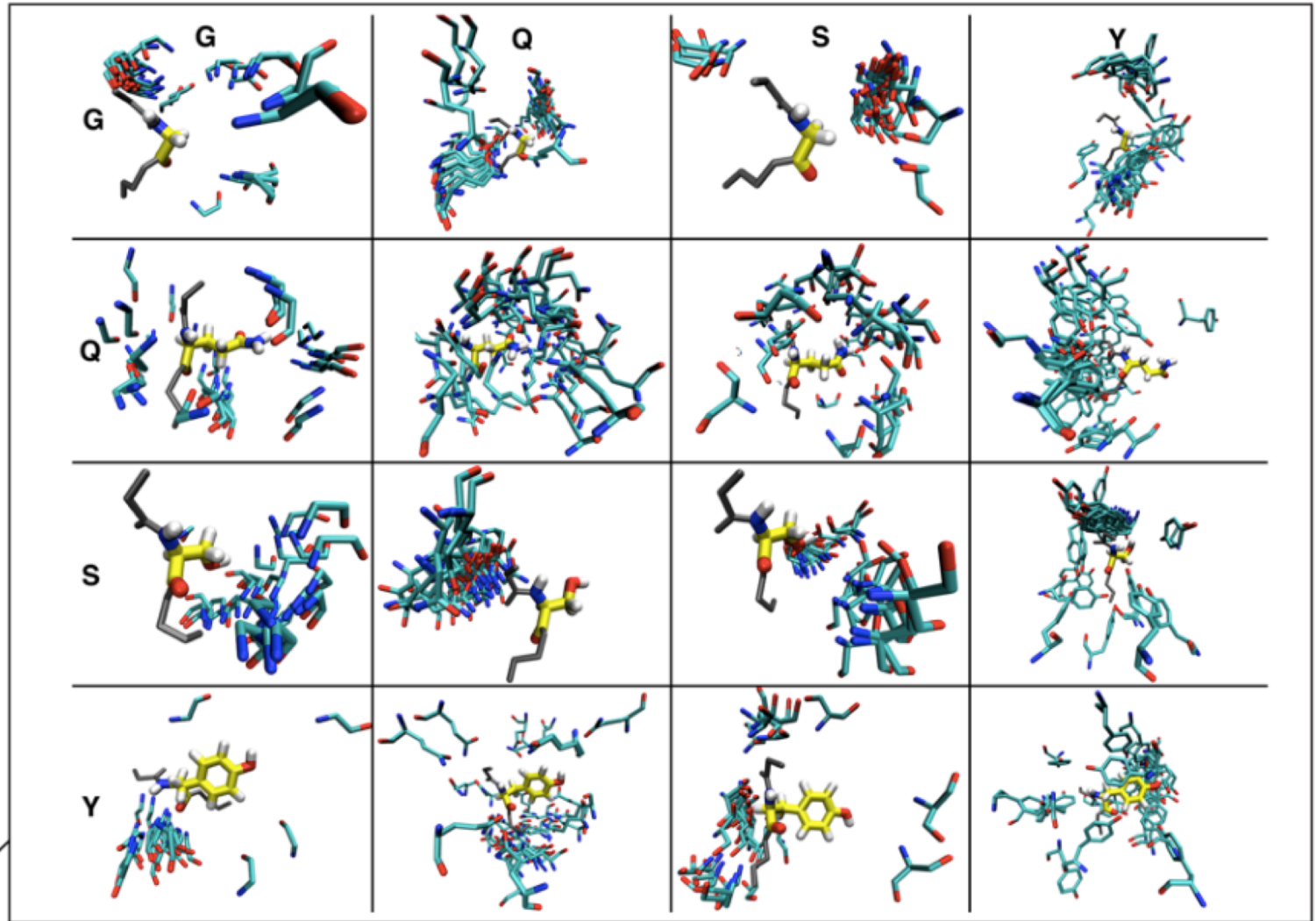
Y130-Y122



Full length FUS LLPS also induced by kosmotropic salts

Hydrophobic contacts mediated by glutamine and tyrosine

Dynamic contacts mediating FUS LC LLPS

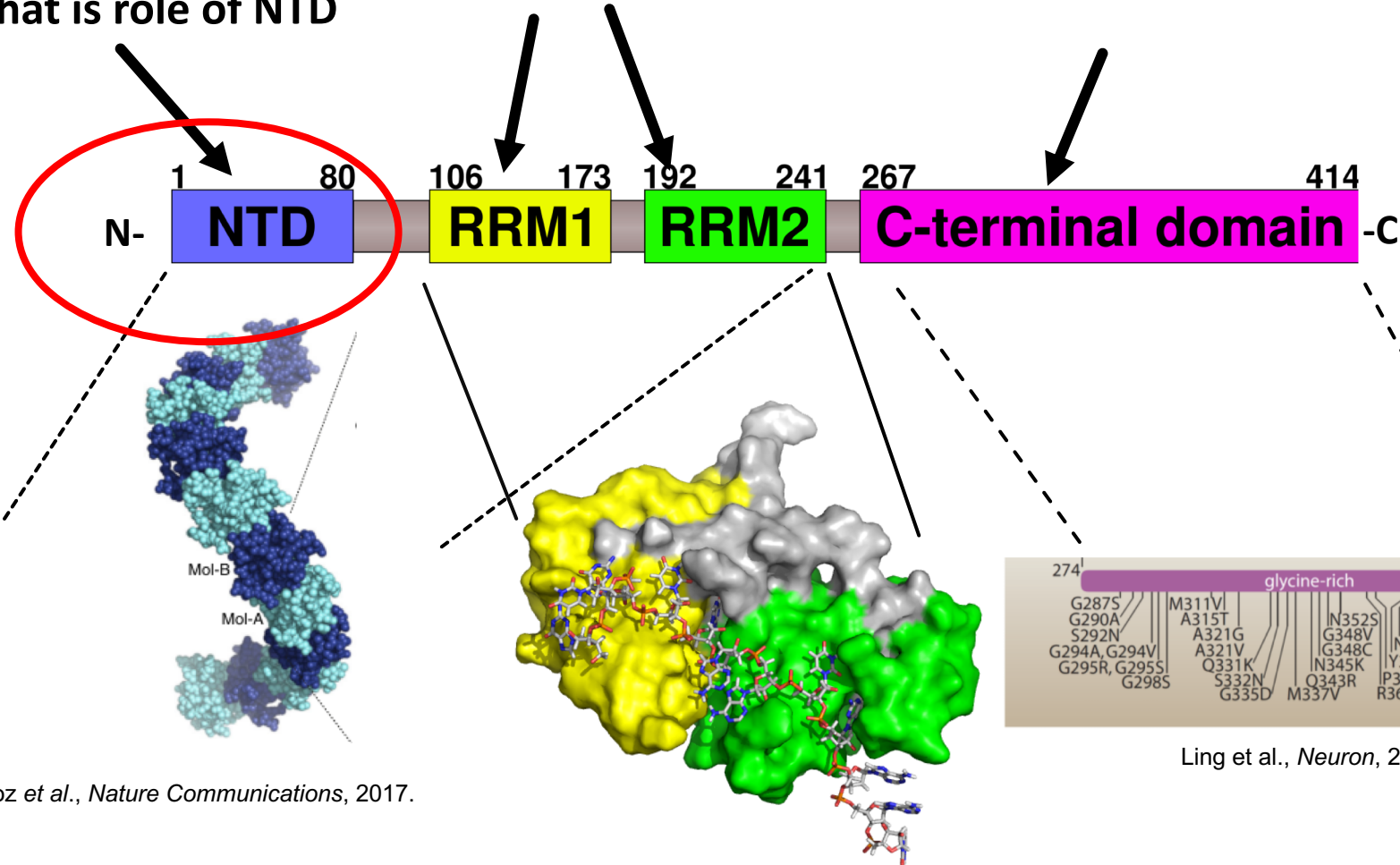


TDP-43 structure

Mediates aggregation in ~90% of ALS
Site of 50 out of 52 known ALS mutations

Multimerization
What is role of NTD

RNA-binding



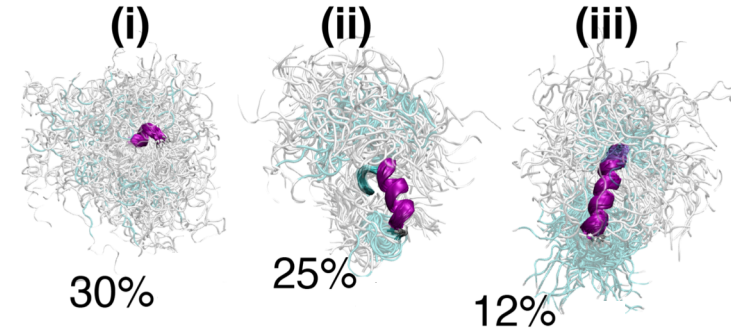
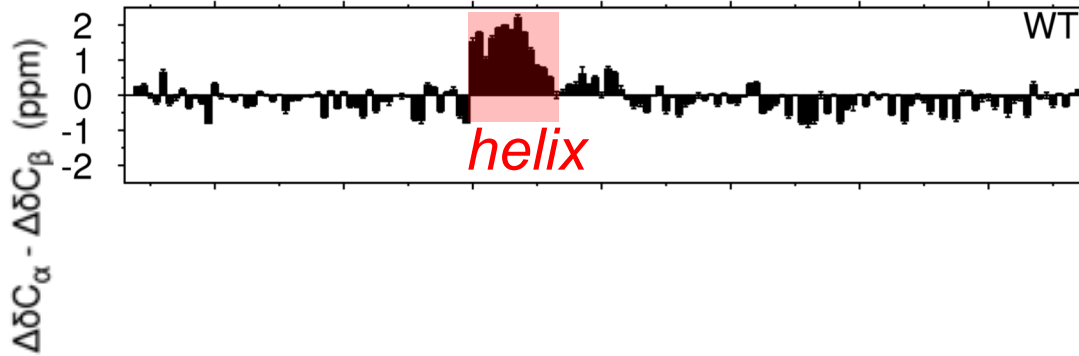
Afroz et al., *Nature Communications*, 2017.

Lukavsky et al., *Nat. Struc. Mol. Bio.*, 2014.

Ling et al., *Neuron*, 2013.

TDP-43 structure

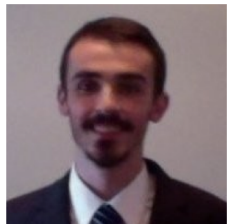
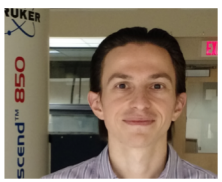
TDP-43 CTD contains **helical** region



Human TDP-43 268 RQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSTINPAMMAAAQAALQSSWGMGMLASQONQSGP SGNNQNGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGS-GFNGGFGSSMDSKSSGWGM 414

Zebrafish TAR 275 QMMERAGRFG---NGFGGQ-GFAGSRSNMGGGGSSSLG---NFGNFNLINPAMMAAAQAALQSSWGMGMLA-CQNQSGTSGTSTSGTSSSRDQAQTYSSANSNY-GSSS-AALGWGTGSNSGAASAGFNSSFSSMESKSSGWGM 412

DNA binding protein

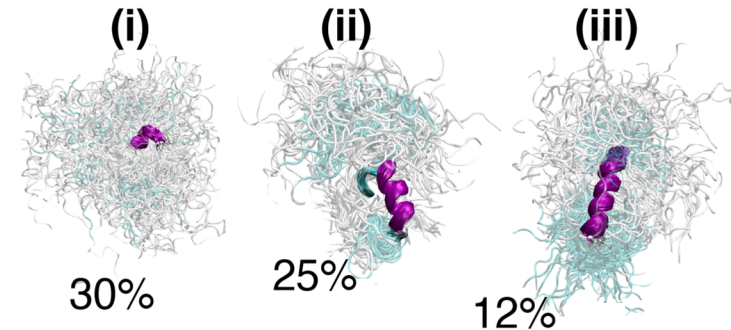
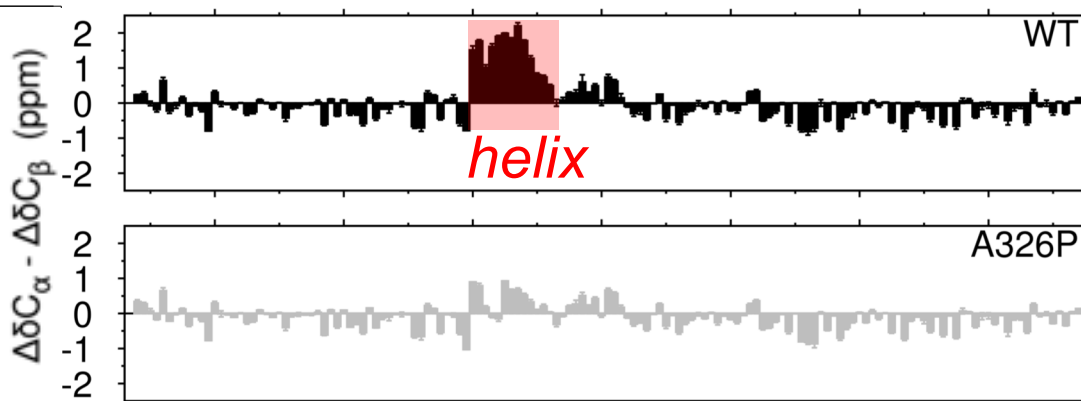


TDP-43 CTD work by
Alex Conicella, Gul Zerze, Greg Dignon

Conicella et al., *Structure*. (2016)

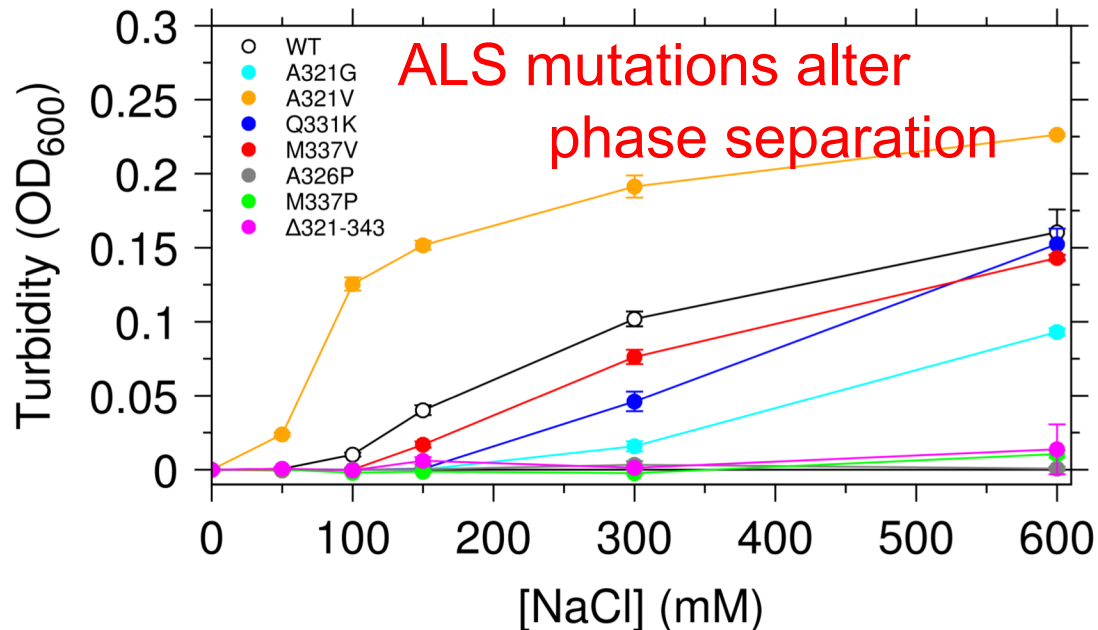
TDP-43 Phase Separation

TDP-43 CTD contains **helical** region



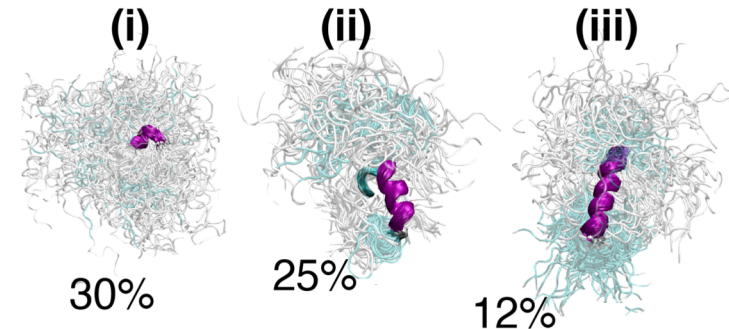
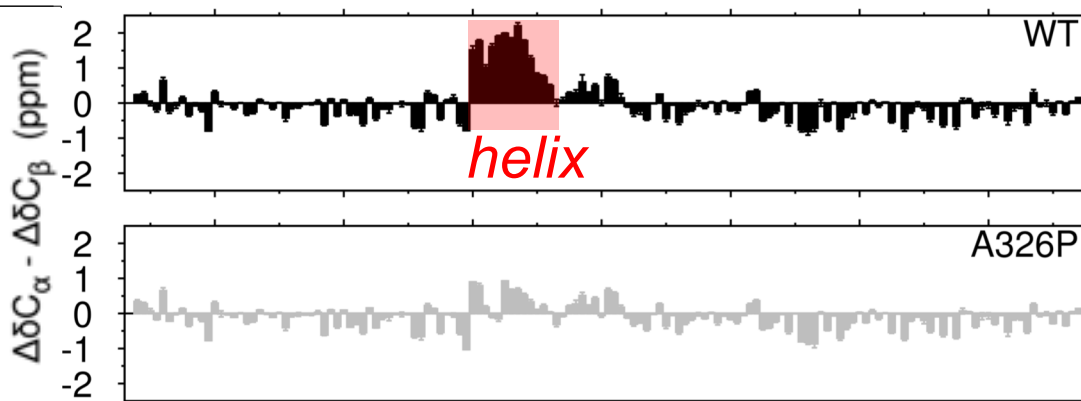
Requires helical region...

Helical region is cooperatively formed



TDP-43 Phase Separation

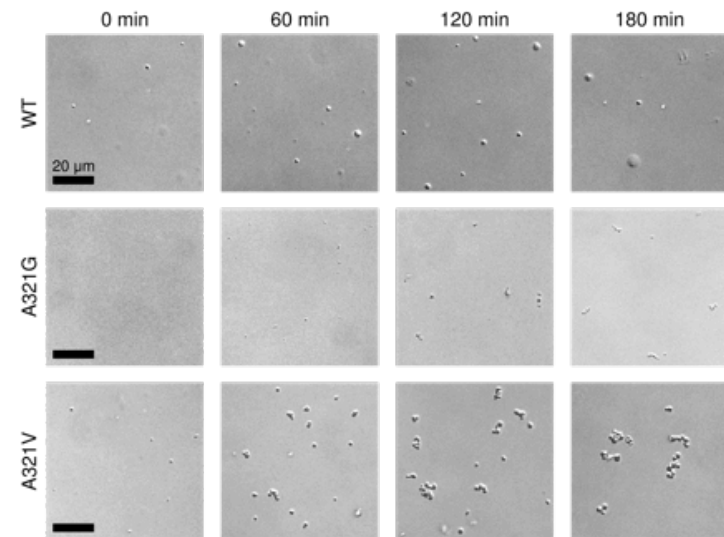
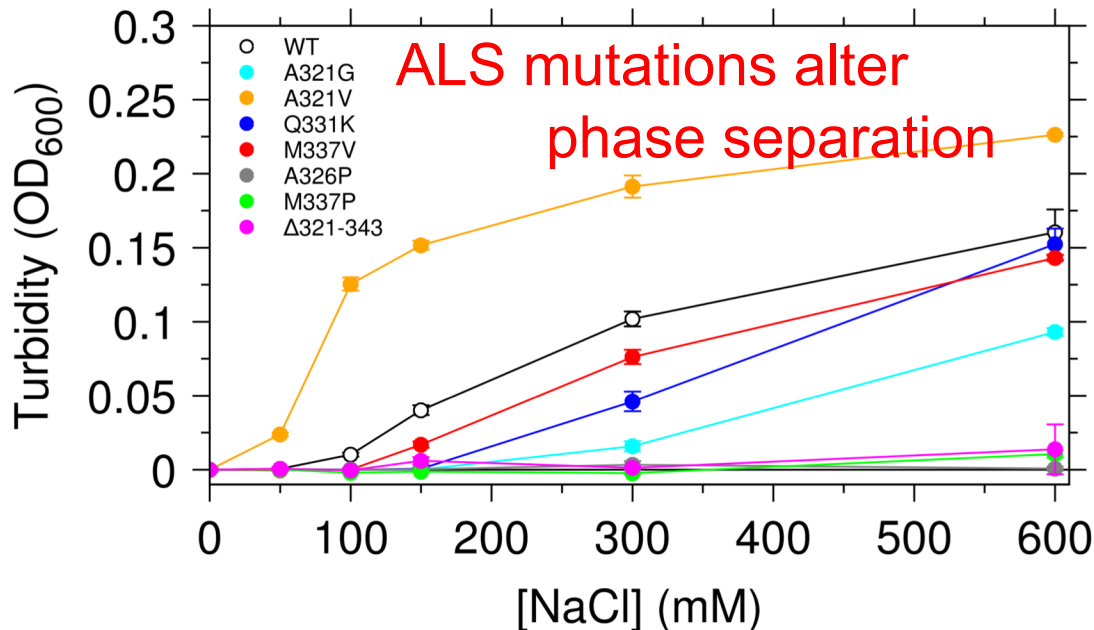
TDP-43 CTD contains **helical** region



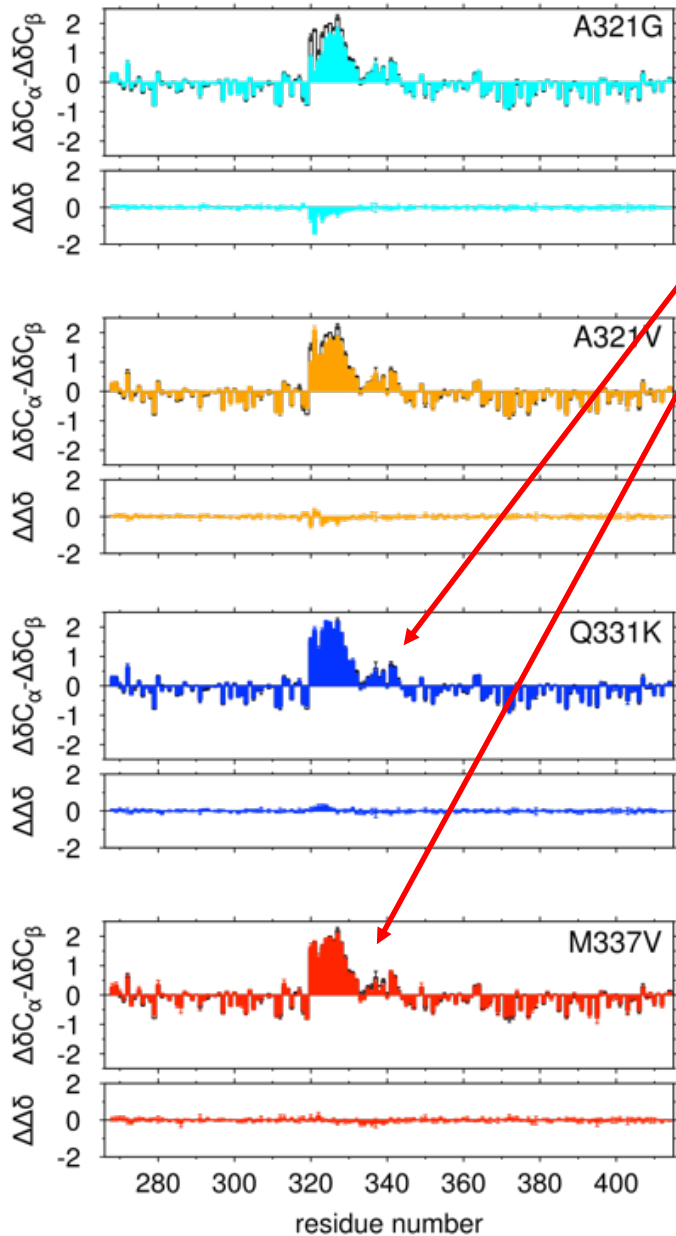
Requires helical region...

ALS A321V: prone to *liquid* to aggregate conversion

Helical region is cooperatively formed

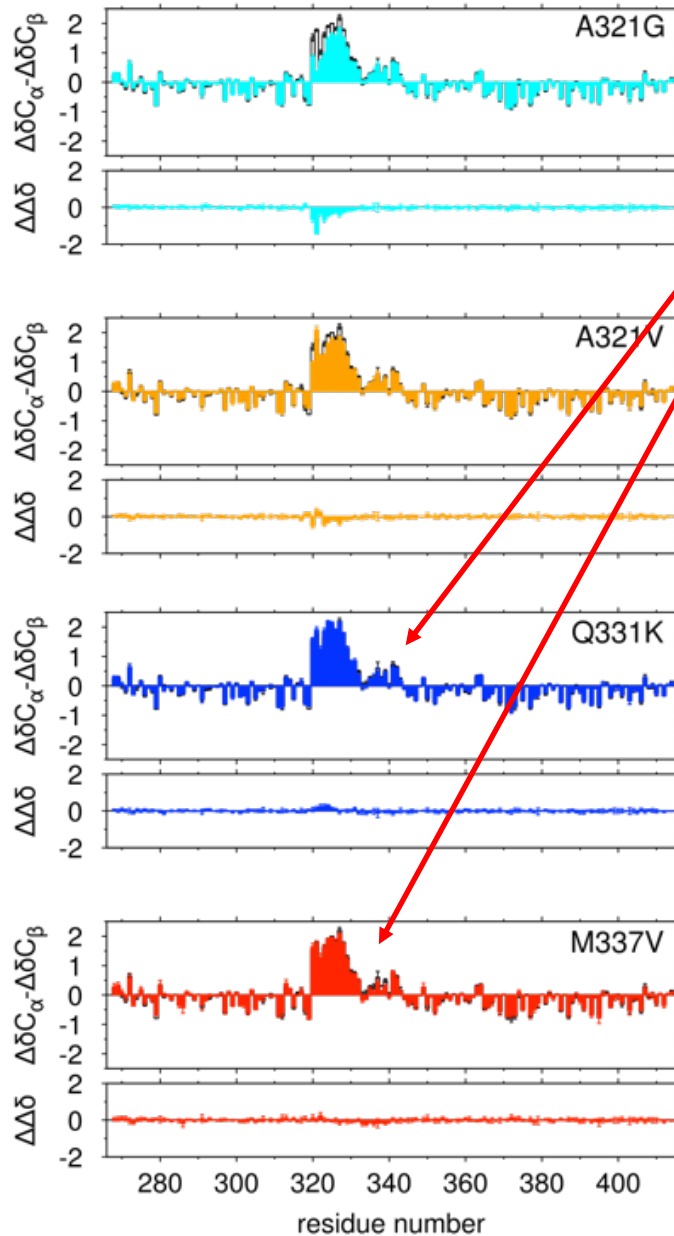


TDP-43 helical structure

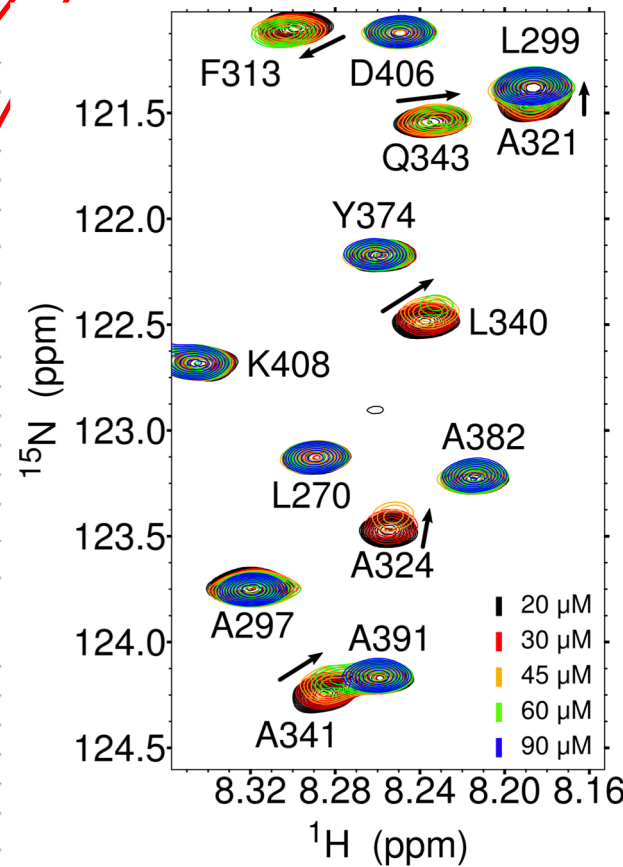


Disruption of helical structure of monomer?
*No change for Q331K or M337V
can't explain change in phase separation*

TDP-43 helix-helix assembly

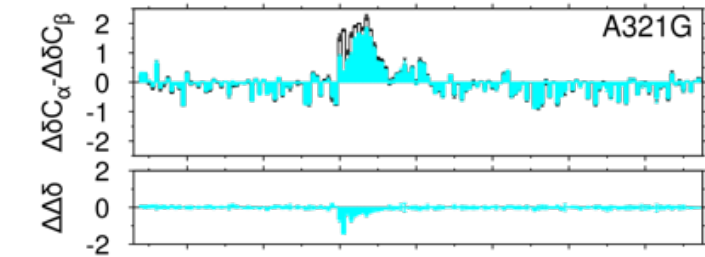


Disruption of helical structure of monomer?
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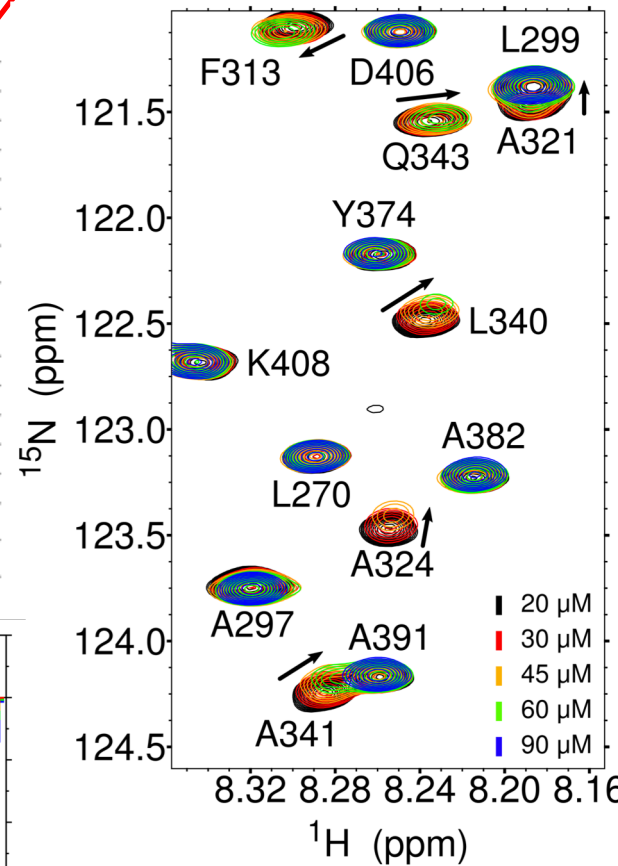
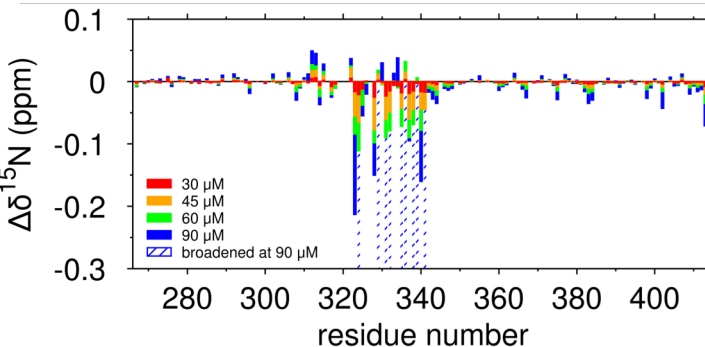
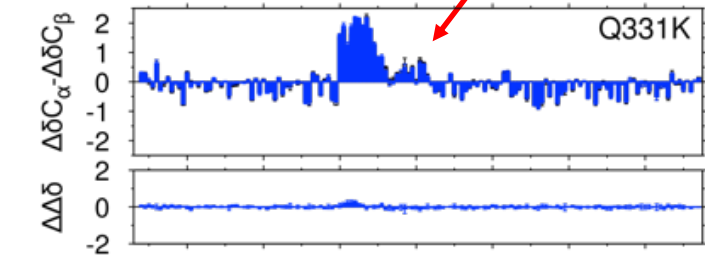
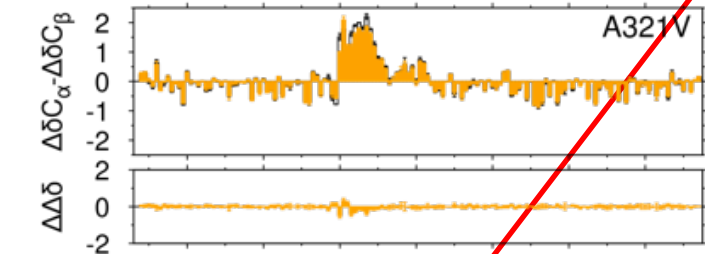


But we noticed:
Wild type TDP-43
self interacts at low
salt (without phase
separation)

TDP-43 helix-helix assembly



Disruption of helical structure of monomer?
*No change for Q331K or M337V,
can't explain change in phase separation*

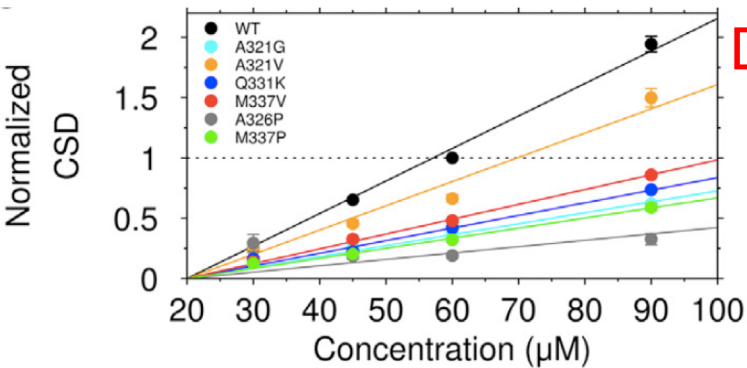


But we noticed:

Wild type TDP-43
self interacts at low
salt (without phase
separation)

Self interaction at the 321-340 region

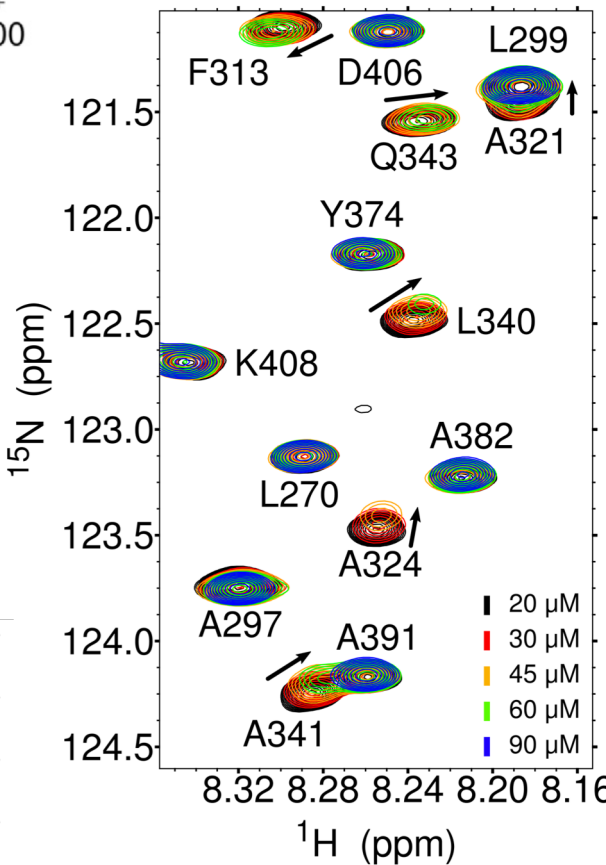
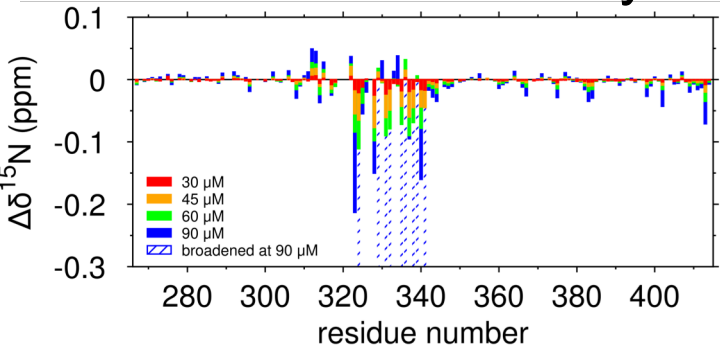
TDP-43 helix-helix assembly



Disruption of helical structure of monomer?
*No change for Q331K or M337V,
can't explain change in phase separation*

ALS mutations disrupt helix-helix interactions

- even those that don't disrupt monomer structure
- Structured, helix-helix contacts \rightarrow assembly



But we noticed:

Wild type TDP-43 self interacts at low salt (without phase separation)

Self interaction at the 321-340 region

TDP-43 helix-helix assembly

G335 and G338 discourage helical assembly?

Human TDP-43

IGMNF GAF S I N P A M M A A A Q A A L Q S S W G M M G M L A S Q Q N Q S G P S G N

||| |

Zebrafish TAR

---N F G N F N L I N P A M M A A A Q A A L Q S S W G M M G M L A --- Q Q N Q S G T S G T

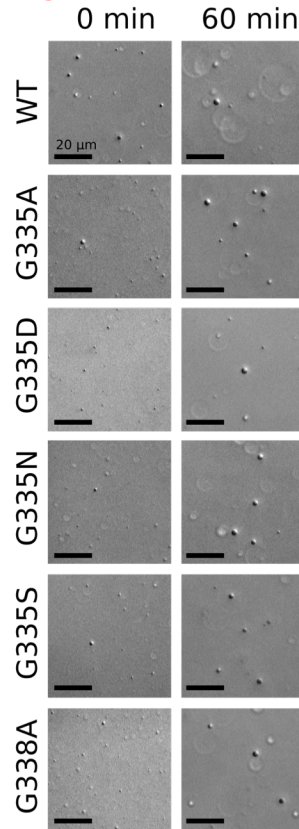
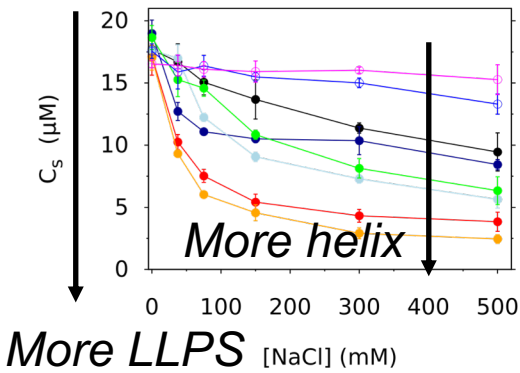
319 341

DNA binding
protein

G335 G338

TDP-43 helix-helix assembly

G335 and G338 discourage helical assembly

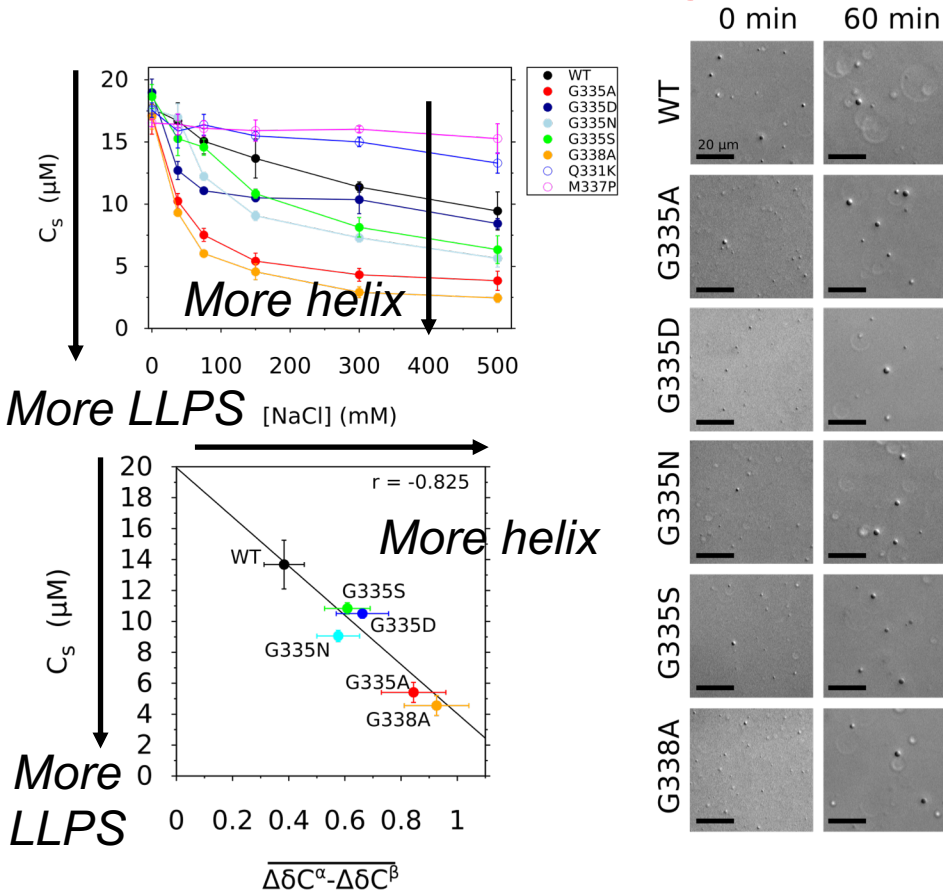


G335A, G338A, and other variants enhance helix-helix interaction and LLPS *in vitro*

Conicella and Dignon et al., *in prep*

TDP-43 helix-helix assembly

G335 and G338 discourage helical assembly

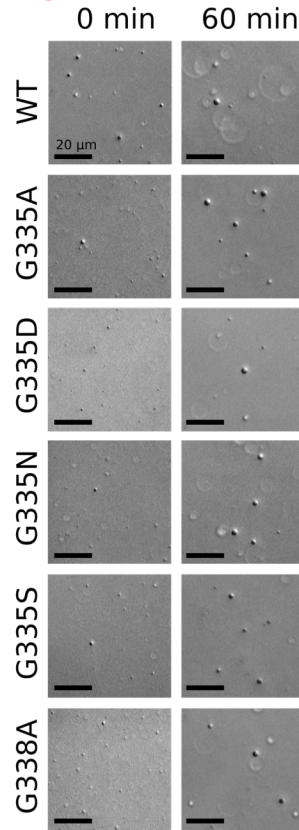
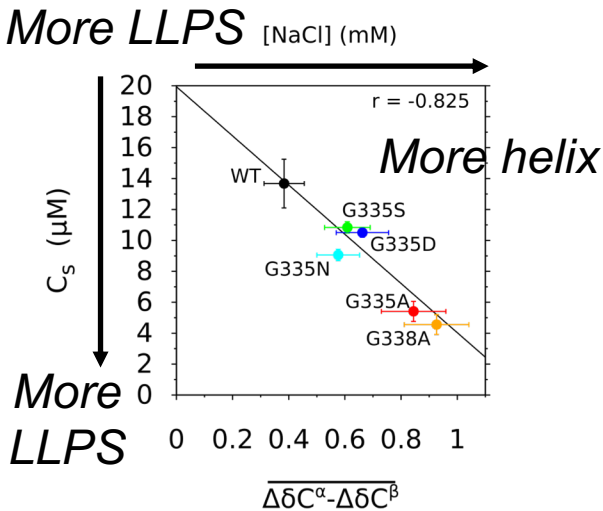
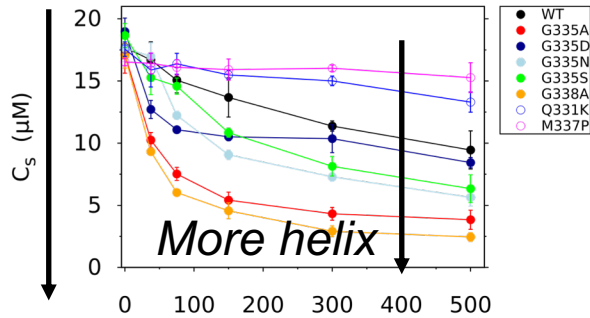


G335A, G338A, and other variants enhance helix-helix interaction and LLPS *in vitro*

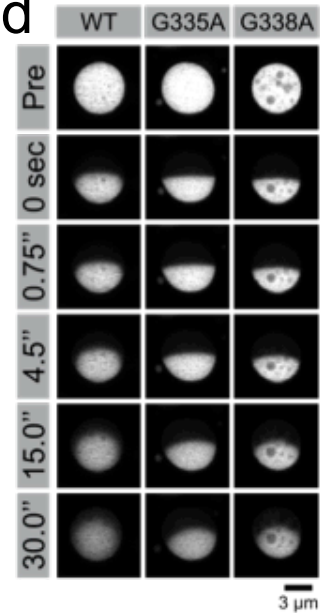
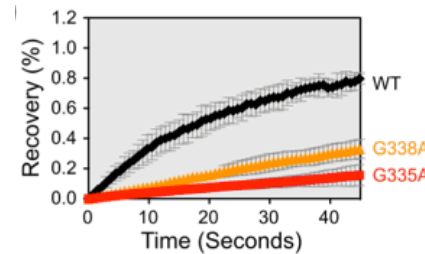
Conicella and Dignon et al., *in prep*

TDP-43 helix-helix assembly

G335 and G338 discourage helical assembly



G335A, G338A, and other variants decrease fluidity of TDP-43 reporter droplets in cell



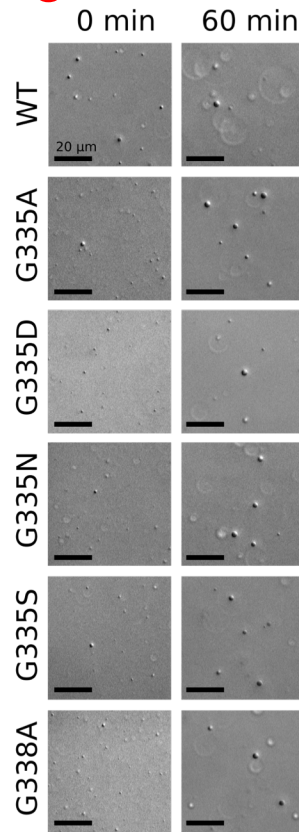
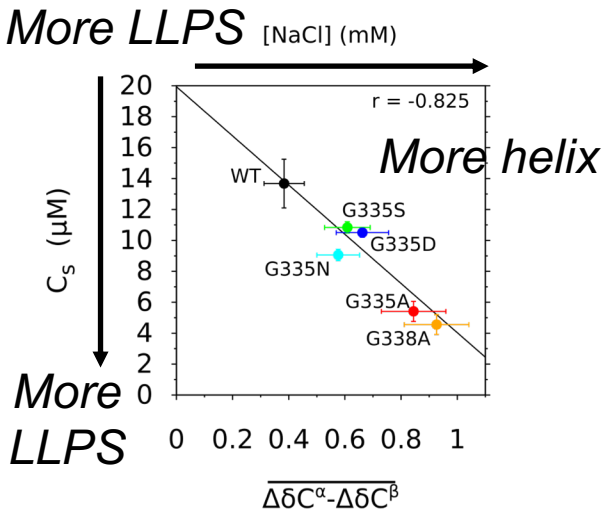
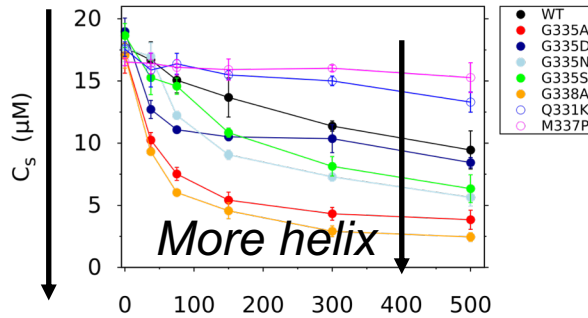
Broder Schmidt
(Stanford)

G335A, G338A, and other variants enhance helix-helix interaction and LLPS *in vitro*

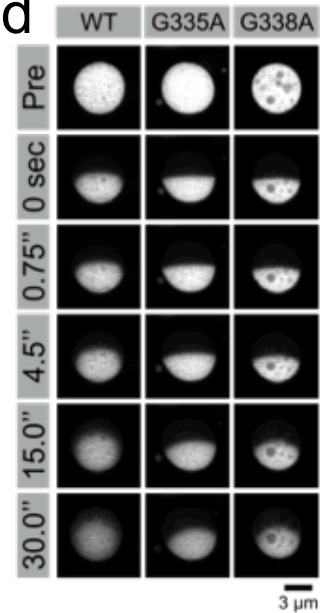
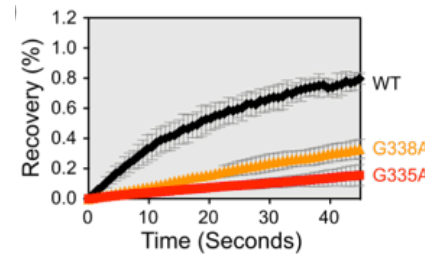
Conicella and Dignon et al., *in prep*

TDP-43 helix-helix assembly

G335 and G338 discourage helical assembly

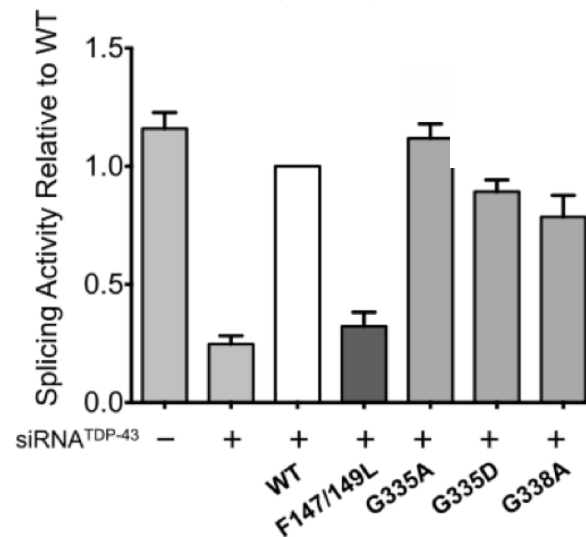


G335A, G338A, and other variants decrease fluidity of TDP-43 reporter droplets in cell



G335A, G338A, and other variants enhance helix-helix interaction and LLPS *in vitro*

Conicella and Dignon et al., *in prep*



G335A enhances splicing activity of TDP-43 (Yuna Ayala, SLU)

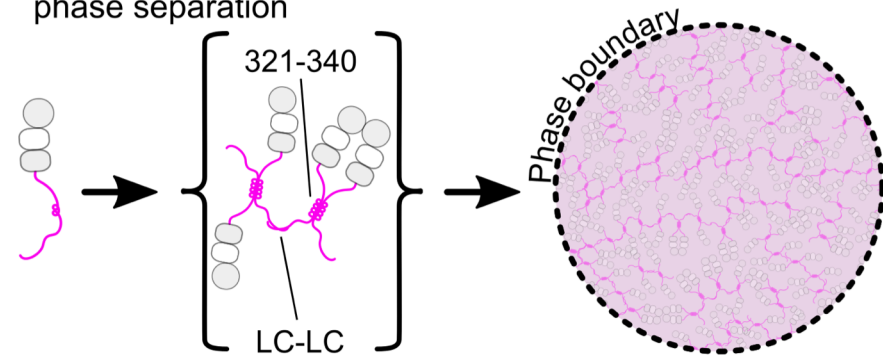
Seeing inside granules

TDP-43: helical regions

- boost disordered region LLPS
- extend/enhance upon assembly

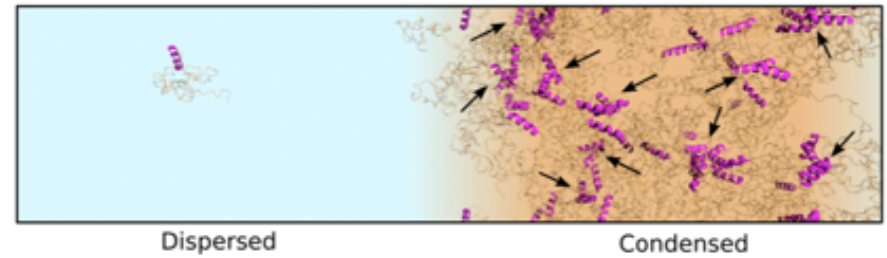
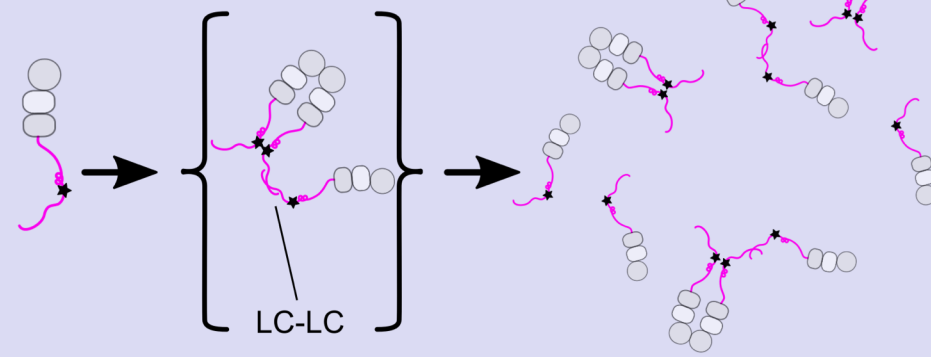
WT TDP-43

C-terminal domain contacts mediate liquid-liquid phase separation



ALS-mutant TDP-43

Reduced liquid-liquid phase separation or enhanced aggregation



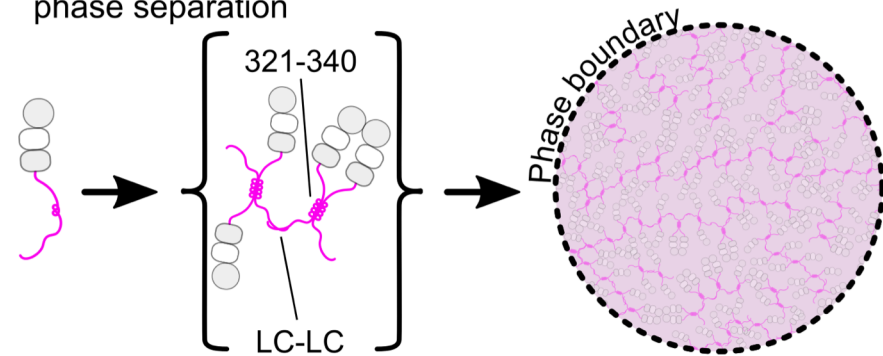
Seeing inside granules

TDP-43: helical regions

- boost disordered region LLPS
- extend/enhance upon assembly

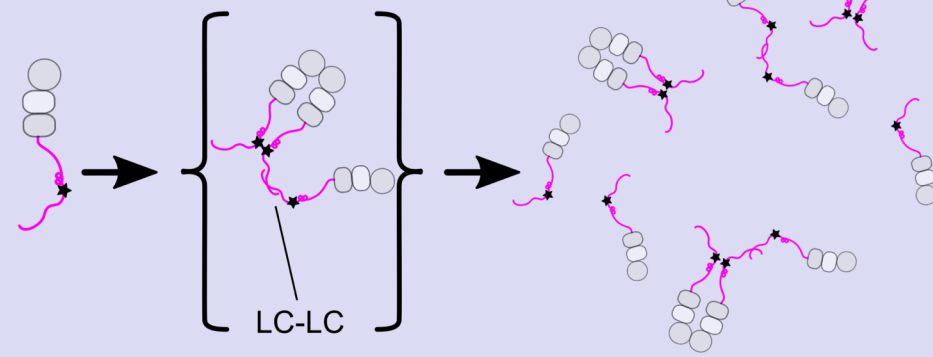
WT TDP-43

C-terminal domain contacts mediate liquid-liquid phase separation



ALS-mutant TDP-43

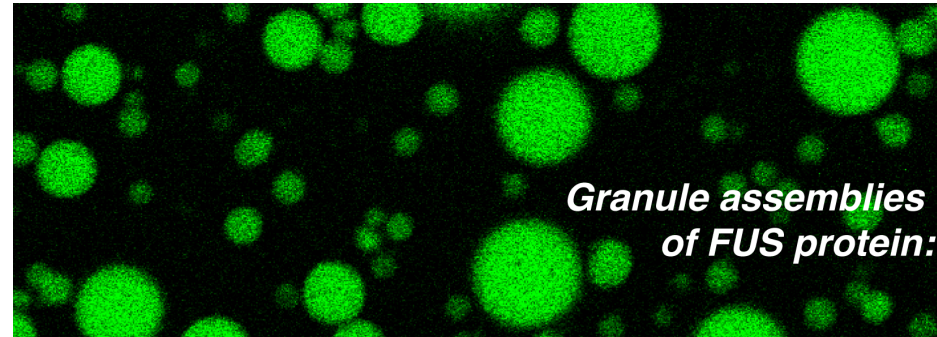
Reduced liquid-liquid phase separation or enhanced aggregation



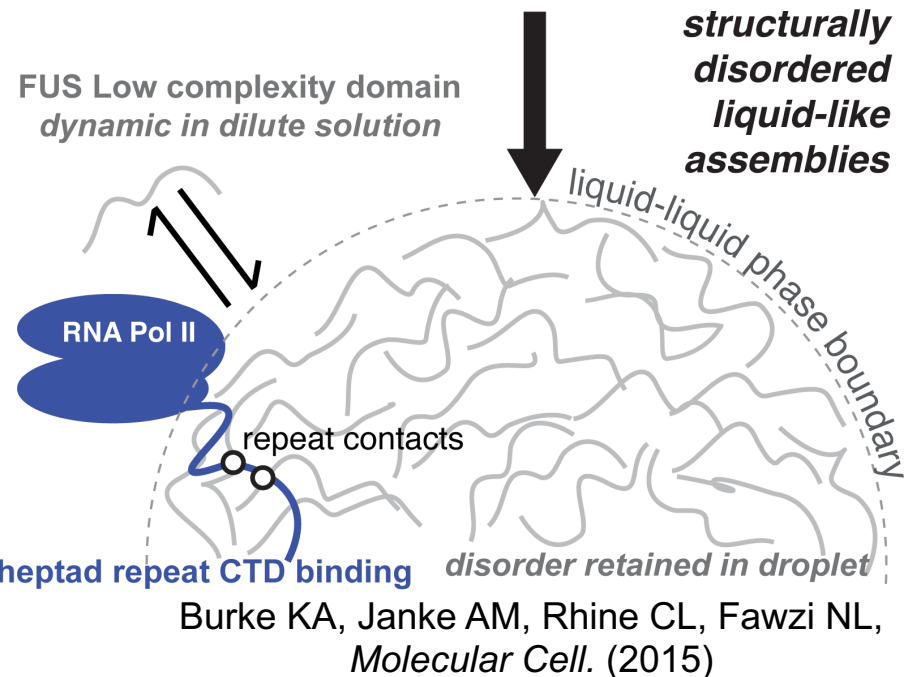
Conicella AE, Zerze GM, Mittal J, Fawzi NL, *Structure*. (2016)

FUS: disordered structure

- predominates even inside phase separated environment



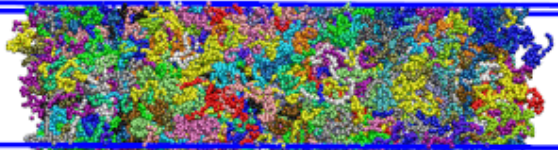
Granule assemblies of FUS protein:



A colorful molecular structure visualization showing various protein domains and interactions, with some parts highlighted in green, red, and blue. The title "Take aways, tools..." is overlaid on the right side of this image.

Take aways, tools...

- **NMR “sees” disorder domains at atomic scale**
 - Atomic details of interactions, structure, effect of mutations and post-translational modifications
- **Combining with microscopy to see micron-scale behavior**
- **Simulations predictive insight into structure**
 - *with Jeetain Mittal, Lehigh University*



- **CARS microscopy probes structure in droplets**
 - *with Sapun Parekh, MPI Polymer / UT Austin*



Take aways, principles...

- **Low complexity domains show predominant disorder**
 - Before and after liquid-liquid phase separation (LLPS)
 - Observed for proteins: FUS, TDP-43, and hnRNP A2
- **Structure can contribute to LLPS**
 - short helix-helix interaction embedded in TDP-43
 - Linear chain formation of TDP-43 N-terminal domain
 - But the primary contacts of LC domains are dynamic, distributed and degenerate
- **Disease mutations and post-translational modifications alter LLPS, aggregation, toxicity in cell**
 - Potential regulatory role and therapeutic opportunity
- **Titration of RNA (and salt) stimulates, then disfavors, select protein LLPS**

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