

# **Molecular Dynamics of the FUS Protein Fibril: Phosphorilation Effect**

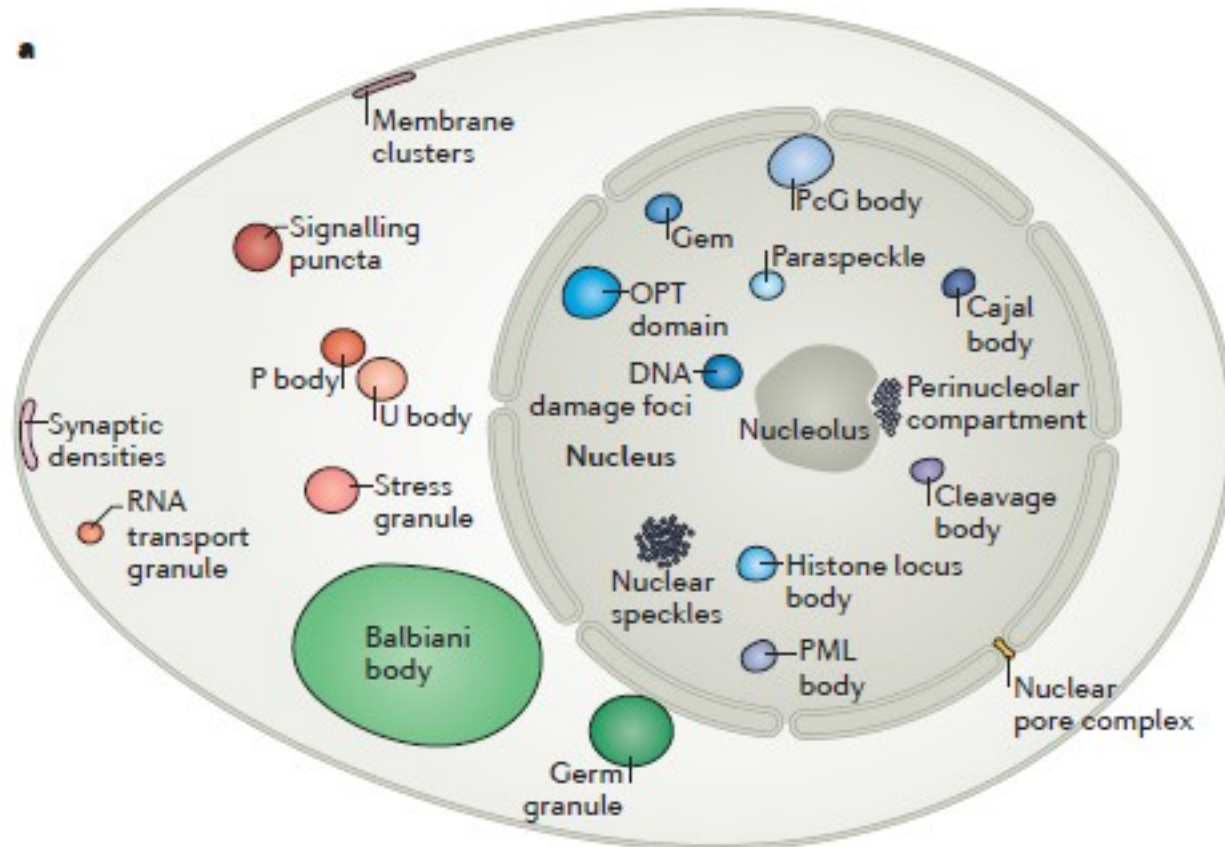
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**A. Poghosyan (Institute for Informatics and Automation problems, Yerevan)**

# Outline

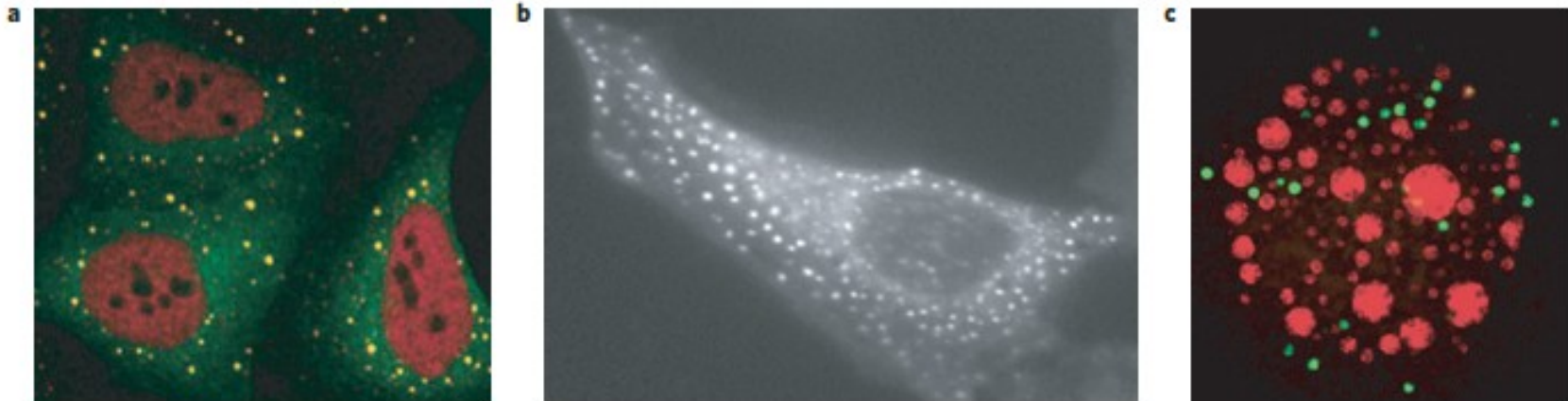
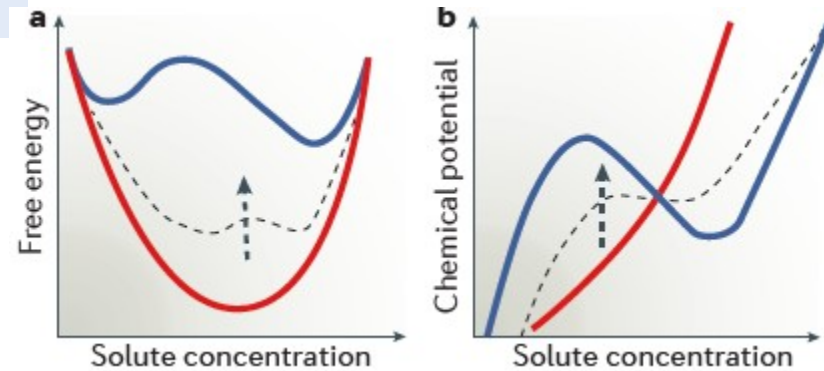
- Membraneless organelles
- Double-strand breaks and biomolecular condensate
- Biomolecular condensate and fibril stability
- FUS fibril stability and phosphorylation

**Membraneless organelles**, Banani, S., Lee, H., Hyman, A. et al. Nat. Rev. Mol. Cell. Biol. **18**, 285 (2017).



# Liquid-liquid phase separation, Brangwynne, C., Tompa, P. & Pappu, R. Nature Phys. **11**, 899 (2015)

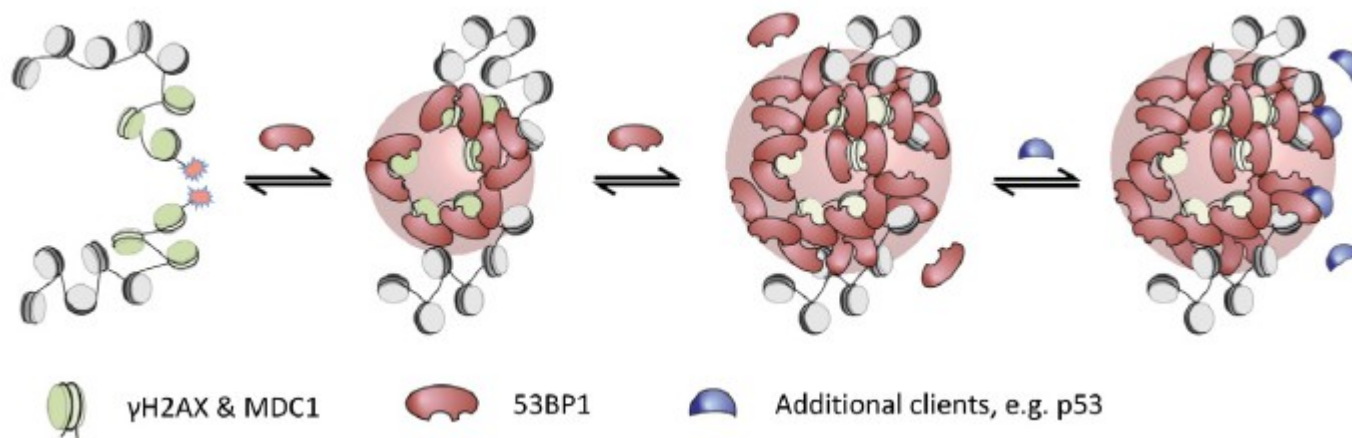
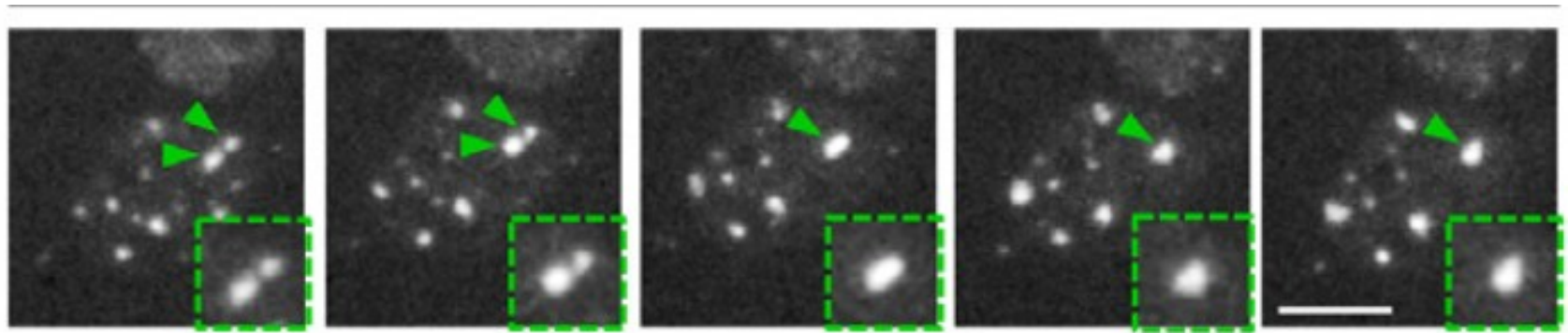
$$\frac{F}{k_B T} = \frac{\phi}{N} \ln \frac{\phi}{2} + (1 - \phi) \ln(1 - \phi) - \alpha(\sigma \phi)^{3/2}$$



**Figure 1 | Examples of membrane-less bodies in cells. a**, P bodies (yellow) in tissue culture cells (adapted from ref. 63, NPG). **b**, Purinosomes (adapted from ref. 3, AAAS). **c**, Nucleoli (red) and histone locus bodies (green) in the nucleus of a large *X. laevis* oocyte (adapted from ref. 14, NPG).

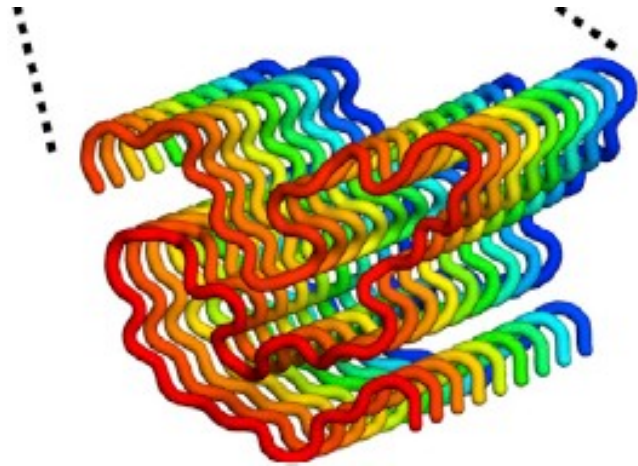
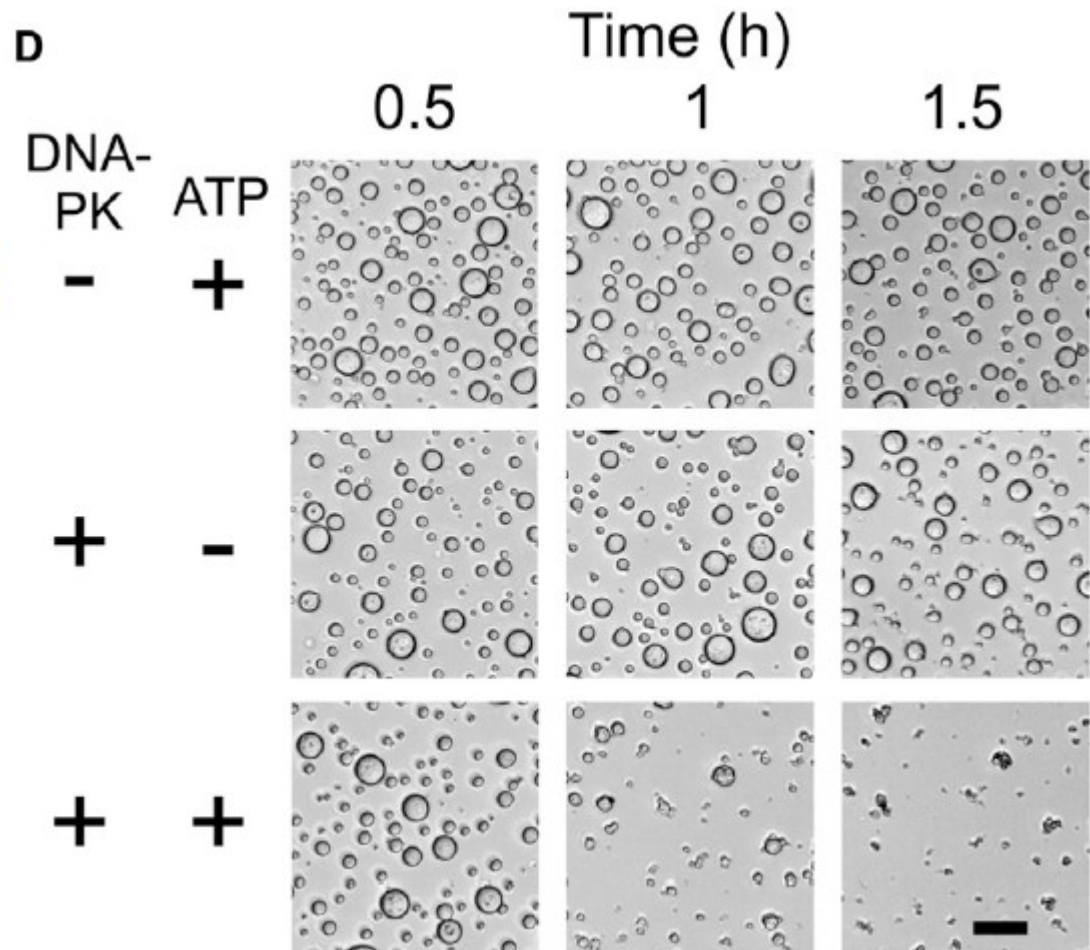
# Phase separation of 53BP1 determines liquid-like behavior of DNA repair compartments, Kilic S., et al. EMBO J. **38**, e101379(2019)

- The 53BP1 protein clusters exhibit the droplet-like behavior



# FUS fibril and stability of biomolecular condensate

Murray D. T., et al. Cell. 2017 Oct 19;171(3):615-627



# Molecular dynamics (MD)

$$m_i \frac{d^2 \mathbf{r}_i}{dt^2} = -m_i \gamma_i \frac{d\mathbf{r}_i}{dt} + \mathbf{F}_i(\mathbf{r}) + \overset{\circ}{\mathbf{r}}_i$$

$$\mathbf{v}' = \mathbf{v}(t - \frac{1}{2}\Delta t) + \frac{1}{m}\mathbf{F}(t)\Delta t$$

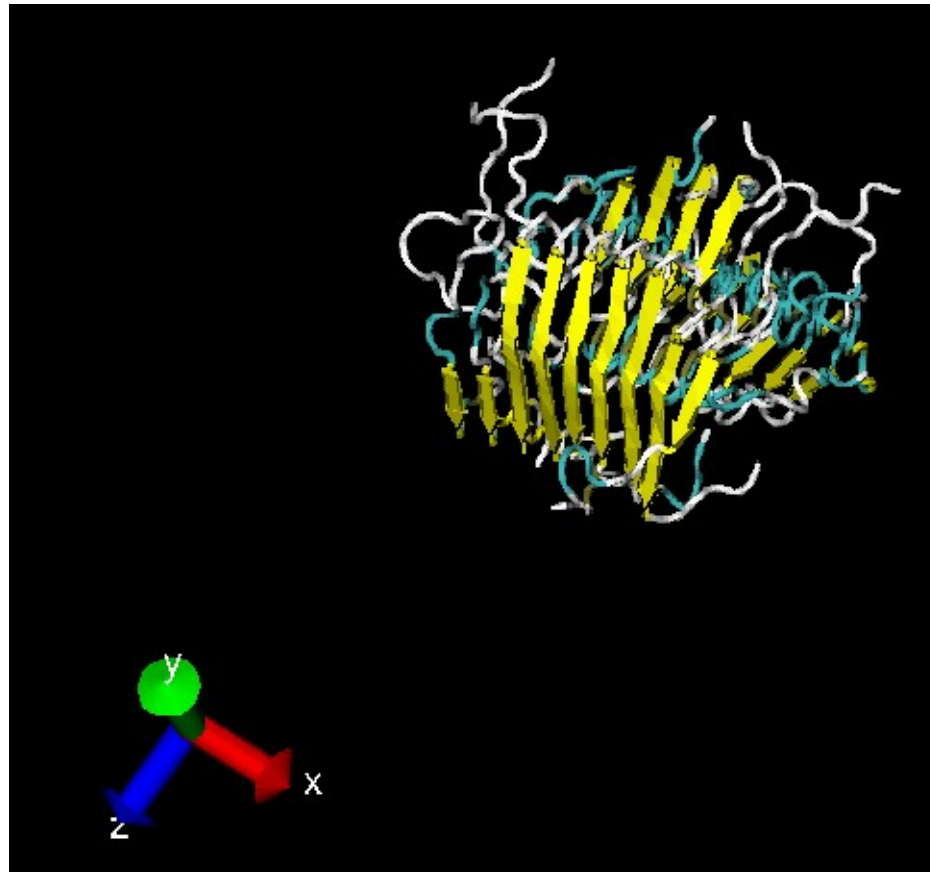
$$\Delta \mathbf{v} = -\alpha \mathbf{v}'(t + \frac{1}{2}\Delta t) + \sqrt{\frac{k_B T}{m} \alpha(2 - \alpha)} \mathbf{r}^G_i$$

$$\mathbf{r}(t + \Delta t) = \mathbf{r}(t) + \left( \mathbf{v}' + \frac{1}{2}\Delta \mathbf{v} \right) \Delta t$$

$$\mathbf{v}(t + \frac{1}{2}\Delta t) = \mathbf{v}' + \Delta \mathbf{v}$$

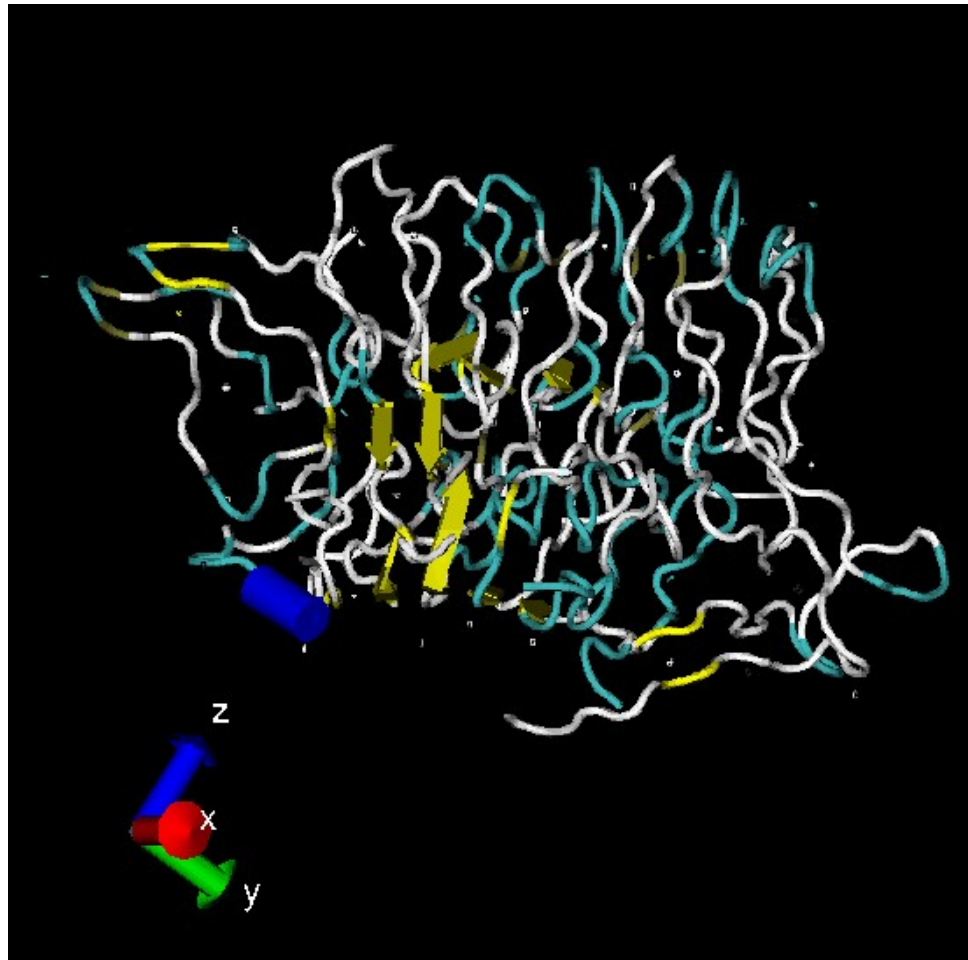
$$\alpha = 1 - e^{-\gamma \Delta t}$$

# MD simulation, 150 ns, CHARMM ff, 0.5M NaCl, without phosphorylation (WT)

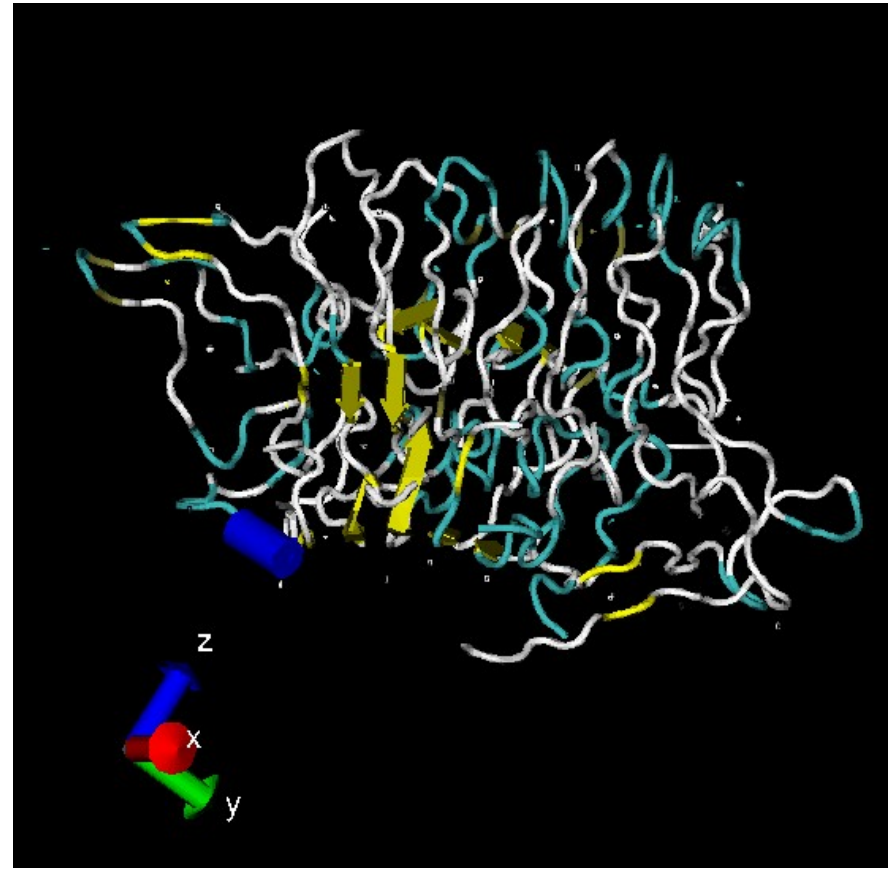
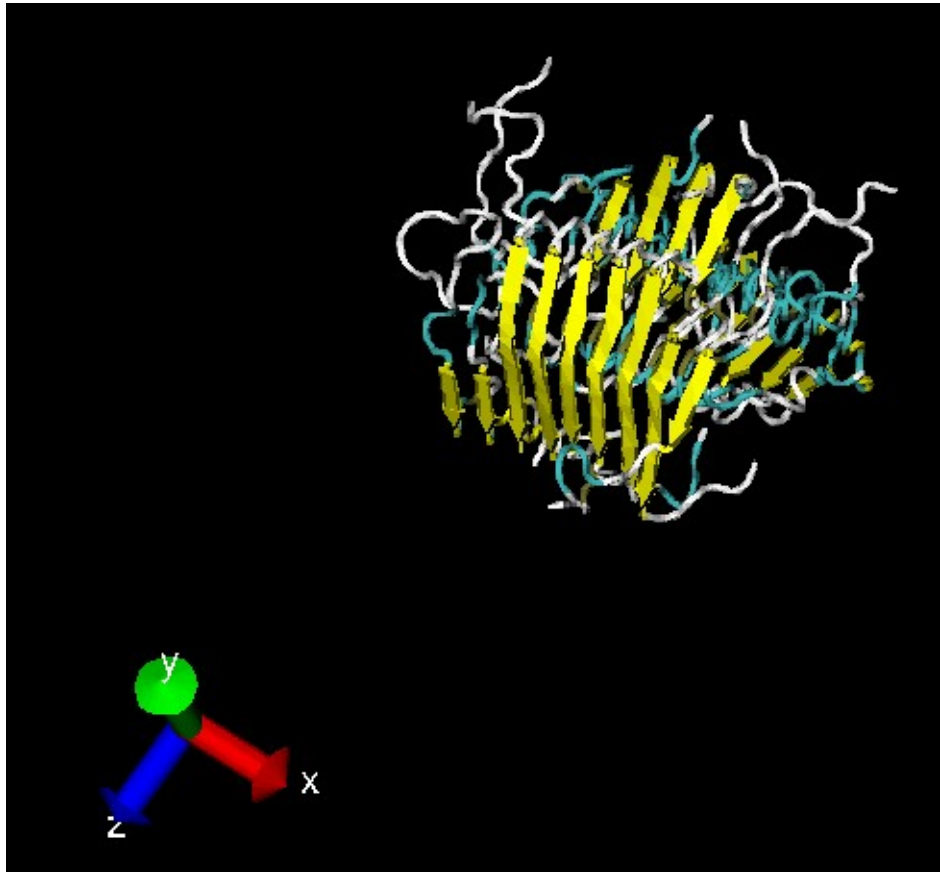




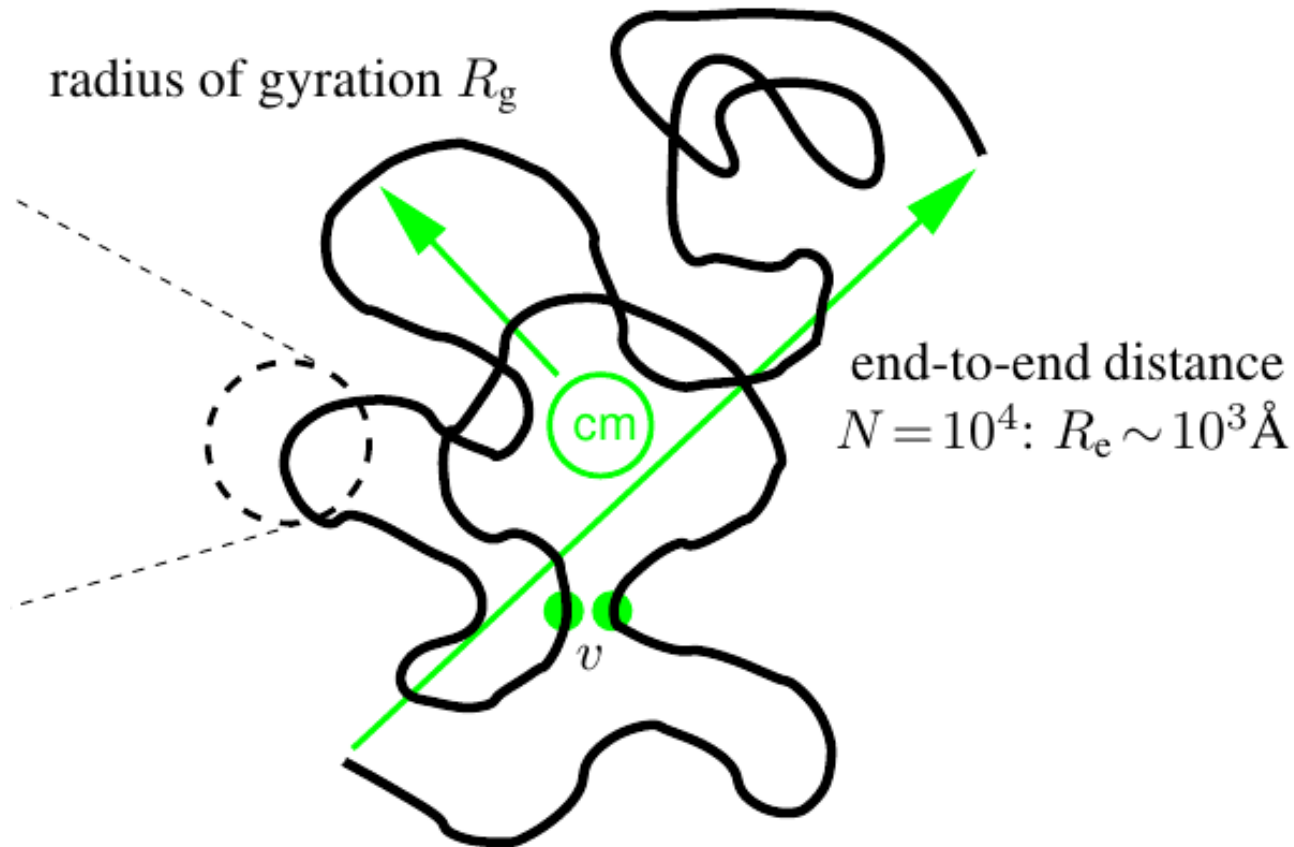
# MD simulation, 150 ns, CHARMM ff, 0.5M NaCl, phosphorilated



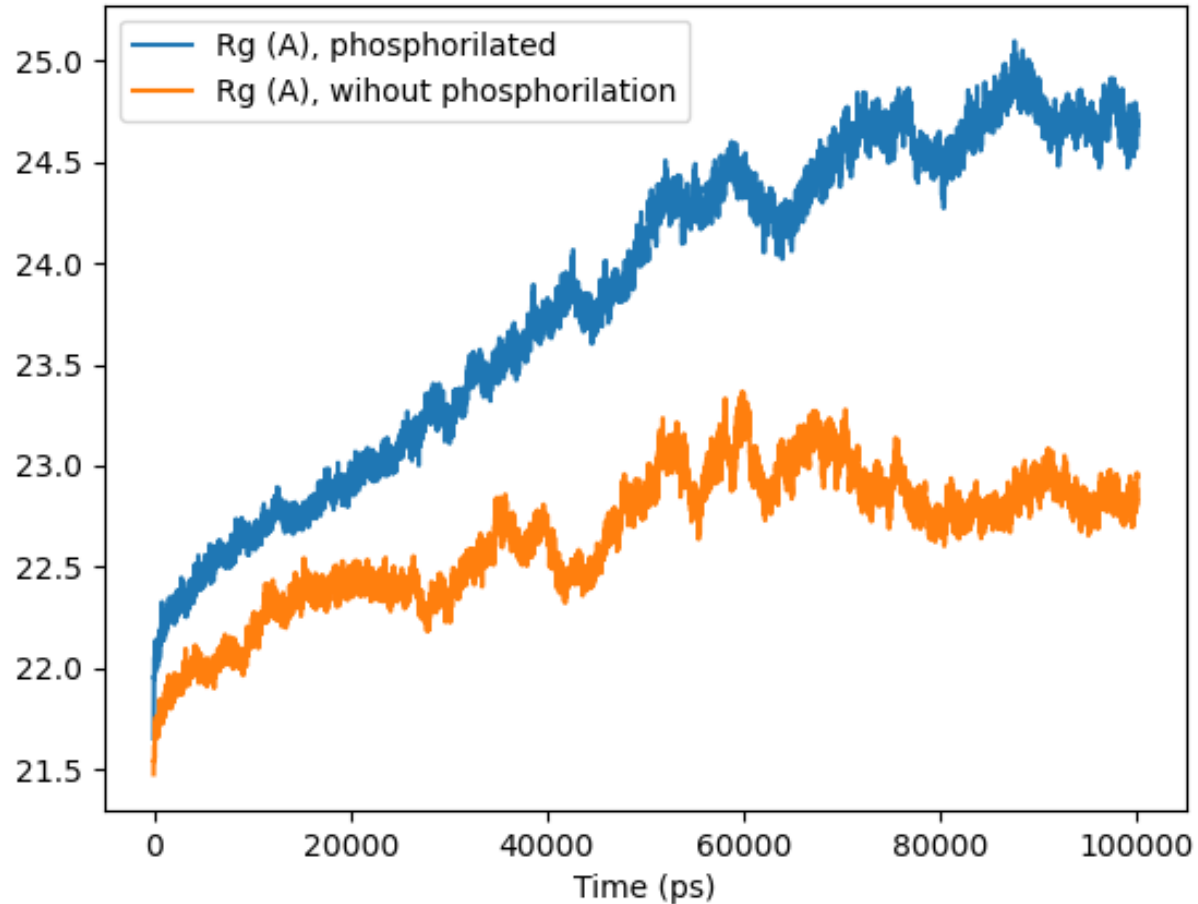
# Let's compare ...



# Radius of gyration as a measure of space occupied by a polymer

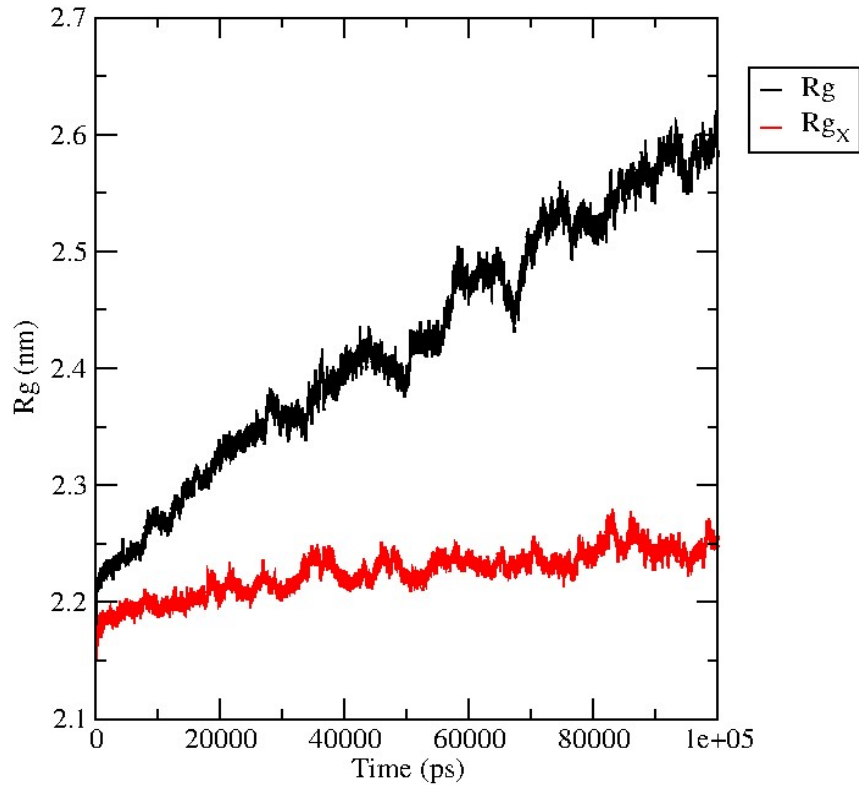


# Radius of gyration vs time (0.5 M NaCl)

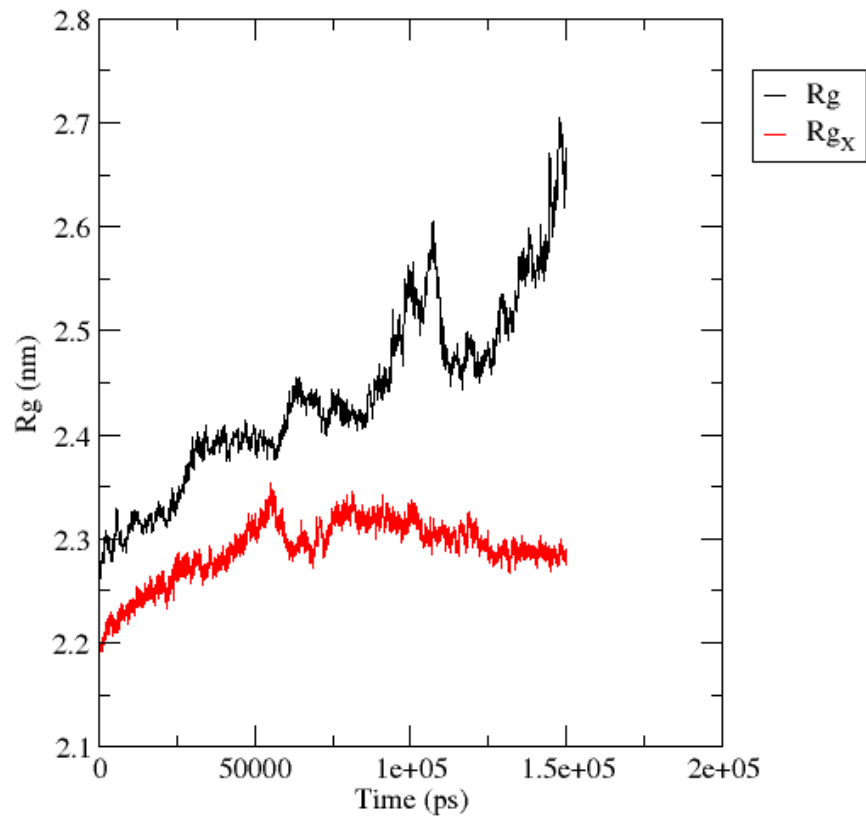


# Radius of gyration vs time (no salt vs 0.15 M NaCl)

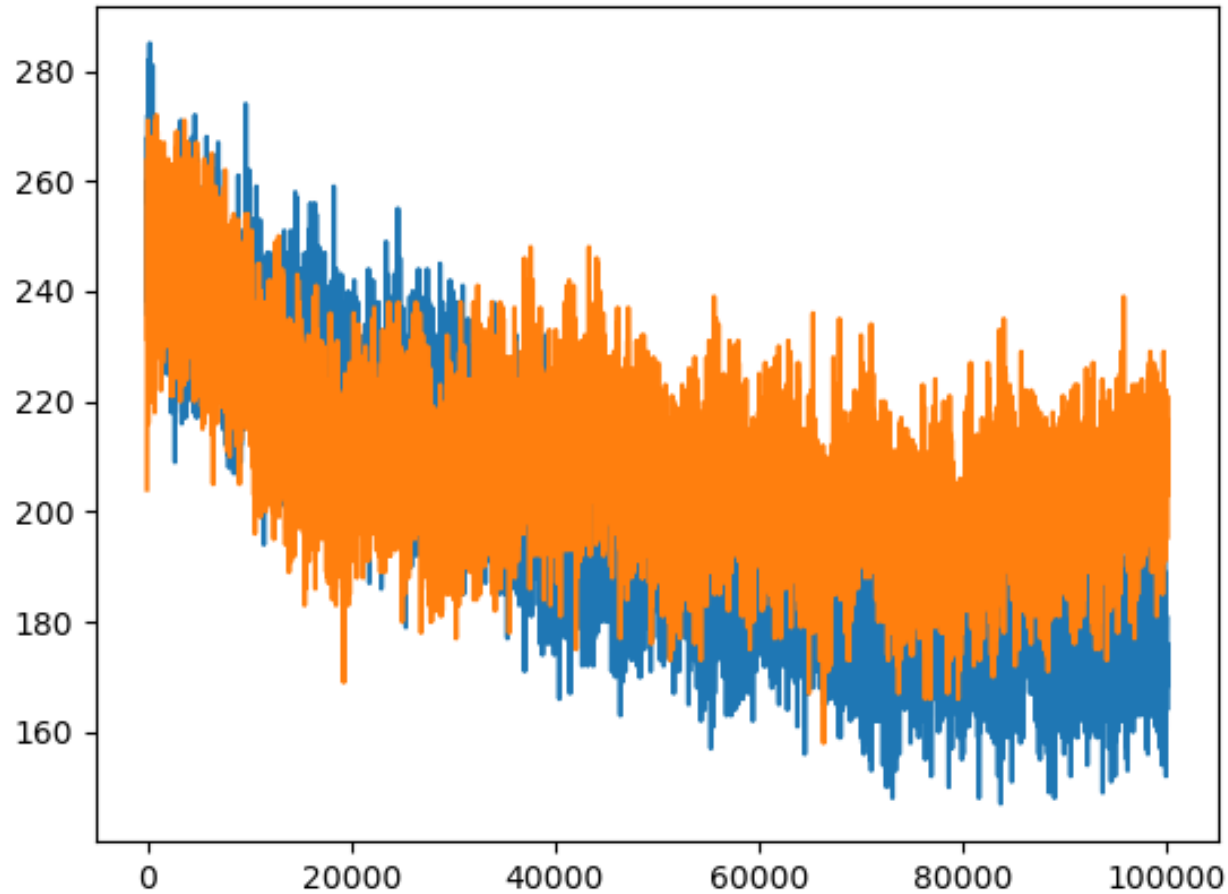
Radius of gyration (total and around axes)



Radius of gyration (total and around axes)

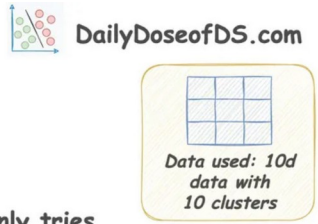


# The number of intra-molecular hydrogen bonds vs time

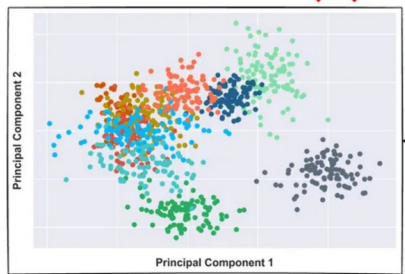


# Dimensionality reduction: t-SNE algorithm

## PCA vs. t-SNE



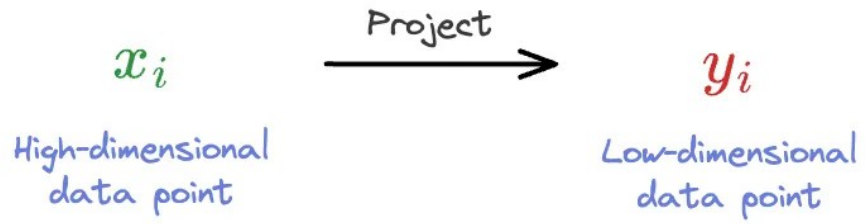
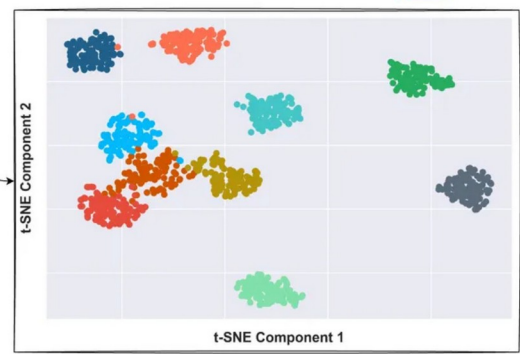
### PCA Projection ✗



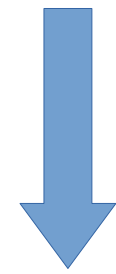
PCA only tries to retain max variance

### t-SNE Projection ✓

- retains max variance
- AND preserves the spatial structure



$$p_{j|i} = \frac{\exp(-\|\mathbf{x}_i - \mathbf{x}_j\|^2 / 2\sigma_i^2)}{\sum_{k \neq i} \exp(-\|\mathbf{x}_i - \mathbf{x}_k\|^2 / 2\sigma_i^2)}$$

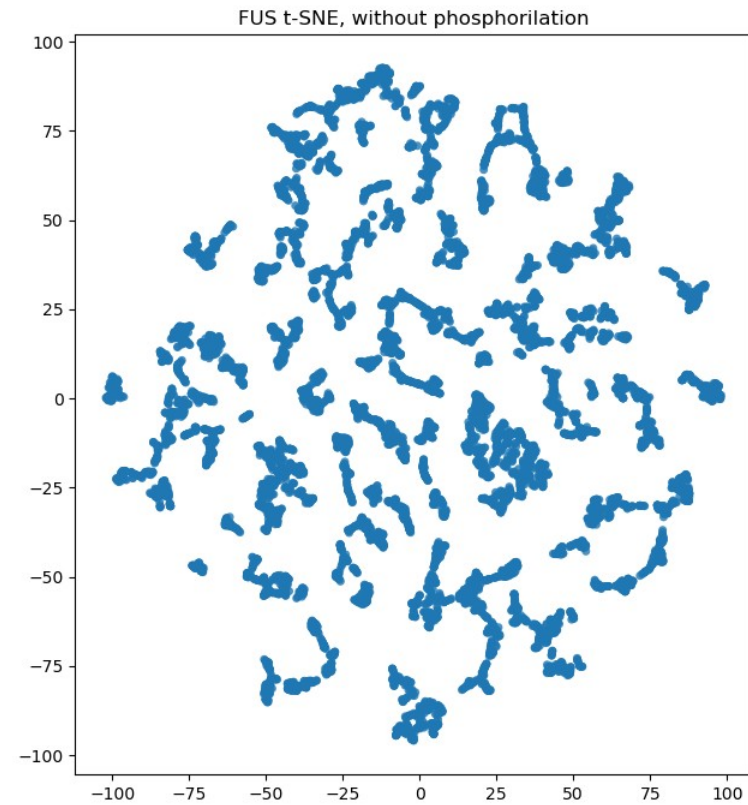
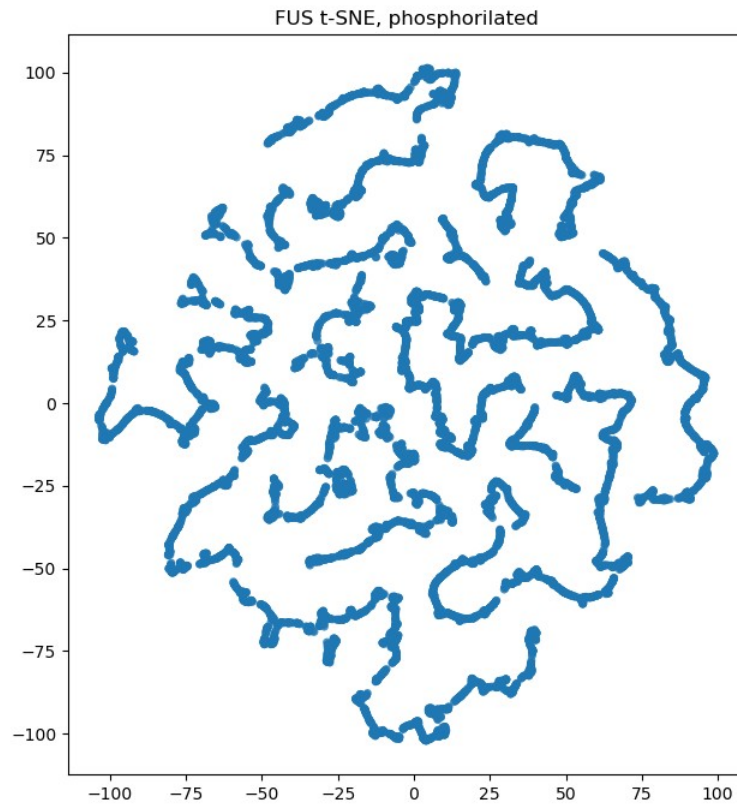


$$KL(P \parallel Q) = \sum_{i \neq j} p_{ij} \log \frac{p_{ij}}{q_{ij}}$$

$$q_{ij} = \frac{(1 + \|\mathbf{y}_i - \mathbf{y}_j\|^2)^{-1}}{\sum_k \sum_{l \neq k} (1 + \|\mathbf{y}_k - \mathbf{y}_l\|^2)^{-1}}$$

$$q_{j|i} = \frac{\exp(-\|y_i - y_j\|^2)}{\sum_{k \neq i} \exp(-\|y_i - y_k\|^2)}$$

# t-SNE (t-distributed stochastic neighbor embedding) projection: the effect of phosphorylation





# Conclusions:

- MD simulation confirmed the experimental results for the FUS fibril destabilization
- Dynamics of the the phosphorylated FUS fibril pass through a quasi-continuous manifolds of states separated by free energy barriers
- The manifolds of states that the WT FUS fibril passes through are more compact than the phosphorylated ones.

# Conclusions:

- MD simulation confirmed the experimental results for the FUS fibril destabilization for different salt concentrations
- Dynamics of the the phosphorylated FUS fibril pass through many basins of attraction separated (probably) by free energy barriers
- The basins of attraction that the WT FUS fibril passes through are more compact than the phosphorylated ones.

**Thank you for  
your attention**