

# Advancing super resolution microscopy for quantitative in-vivo imaging of chromatin nanodomains

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# Outline of the talk

Introduction to fluorescence nanoscopy

Probabilistic modeling approaches to fluorescence nanoscopy

Approach I: Enhance nanoscopy with deep generative models

Approach II: Integrated single photon counting and widefield single molecule imaging

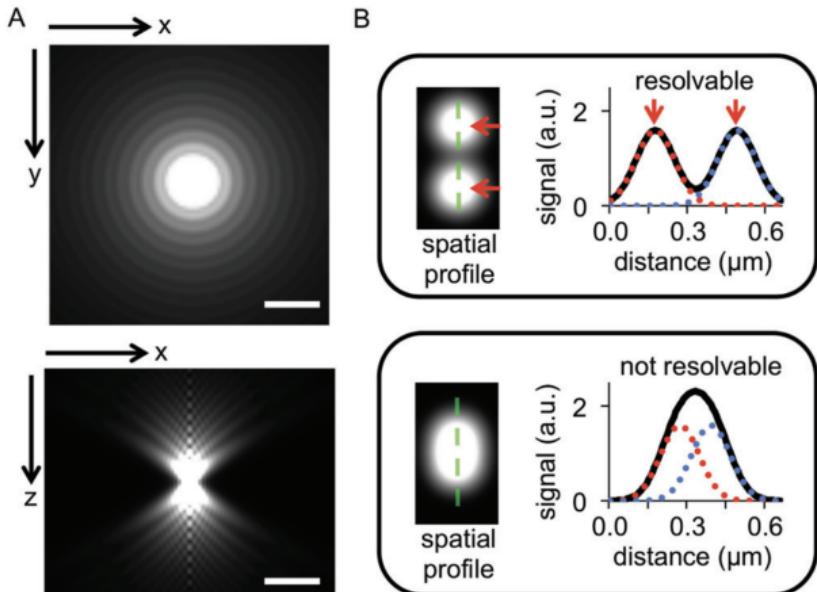
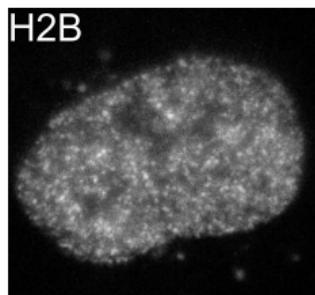
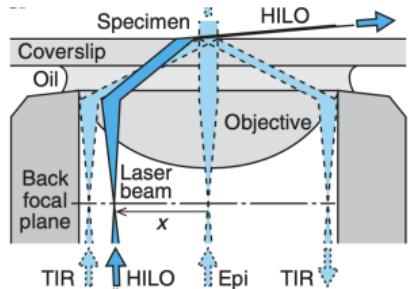
Super-resolution of nucleosome nanodomains *in-vivo*

Interaction of transcriptional condensates with nucleosome nanodomains

# Introduction to fluorescence nanoscopy

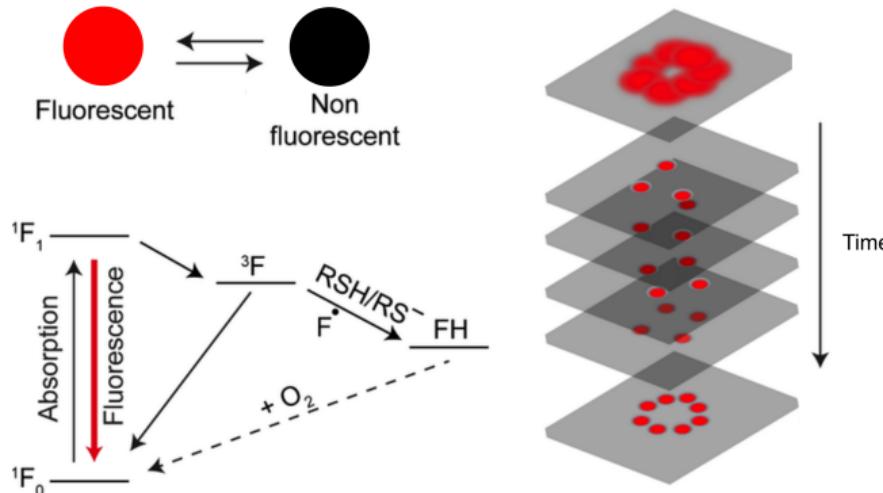
# Fluorescence microscopy and the diffraction limit

- Minimal resolvable distance  $d \sim \text{wavelength}$



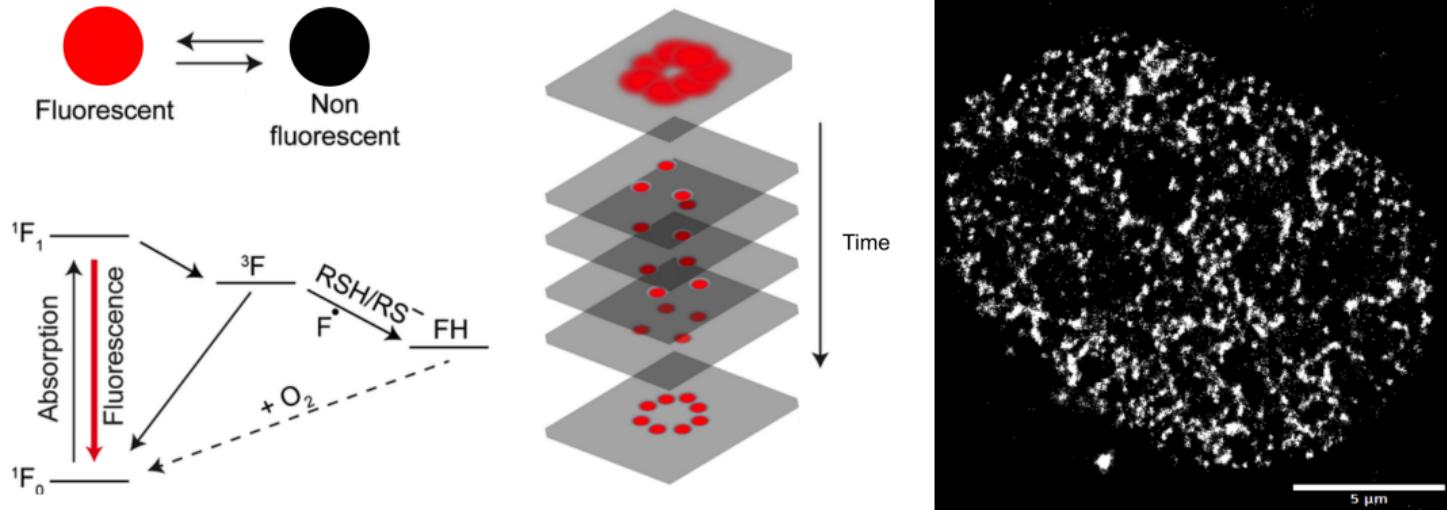
Herbert et al. Microscopy and Microanalysis.

# Stochastic optical reconstruction microscopy (STORM)



- ▶ STORM and similar nanoscopy techniques are diffraction-unlimited
- ▶ Photoswitching enables resolution of emitters below the diffraction limit

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# Nanoscopy by localizing isolated fluorescent emitters

- Modeling the point spread function permits sub-pixel localization

$$\mu_k = i_0 \int \int O(u, v) du dv + \lambda$$

$$i_0 = g_k \eta \zeta \Delta$$

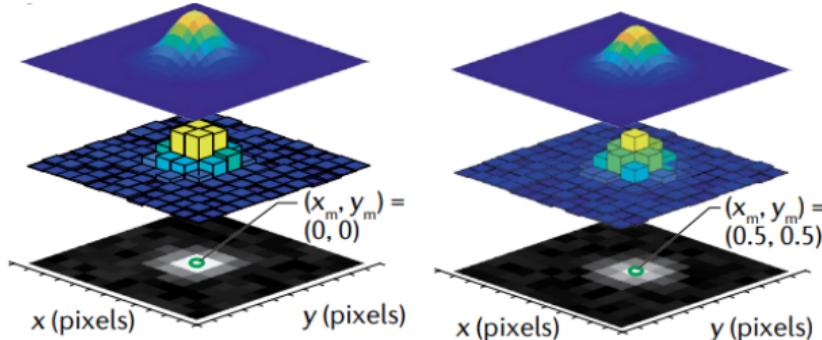
$g_k$  – pixel gain

$\eta$  – quantum efficiency

$\zeta$  – photon emission rate

$\Delta$  – exposure time

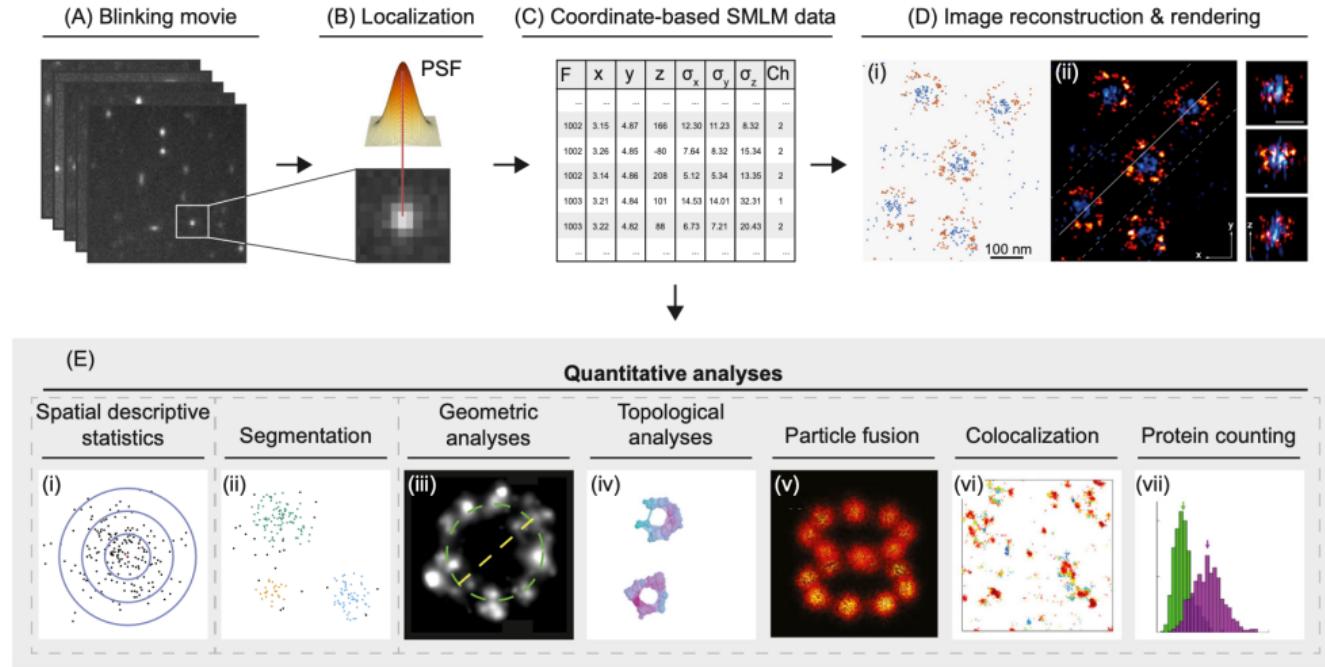
$\lambda$  – background rate



Maximum likelihood localization:

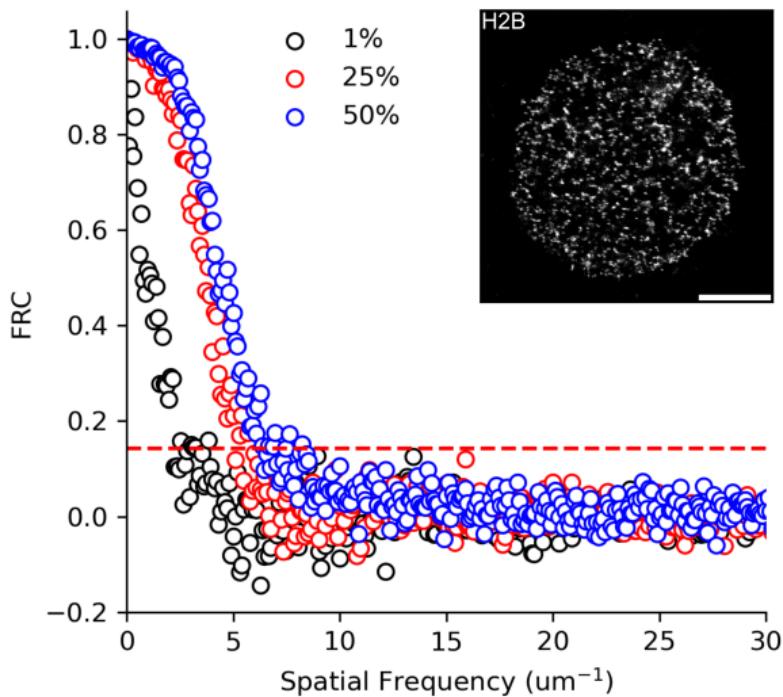
$$\theta^* = \operatorname{argmax}_{\theta} \prod_k p(\mathbf{x}_k | \theta) = \operatorname{argmin}_{\theta} - \sum_k \log p(\mathbf{x}_k | \theta)$$

# Applications of single molecule localization microscopy



Wu et al. Trends in Cell Biology. 30 (2020)

## Maximization of density, minimization of error

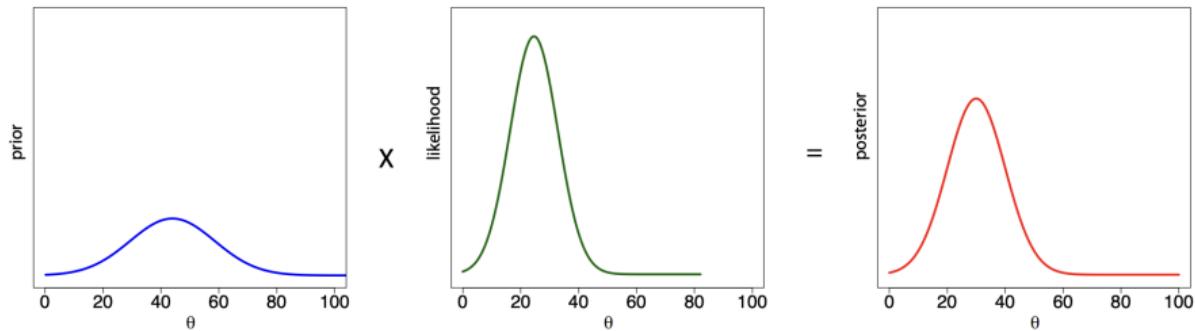


- ▶ **Maximize** density and in turn spatial/temporal resolution
- ▶ **Minimize** localization errors

## Probabilistic modeling approaches to fluorescence nanoscopy

# The Bayesian calculation and variational inference

**Bayes Rule:**  $p(\theta|x) = \frac{p(x|\theta)p(\theta)}{\int p(x,\theta)d\theta} \propto p(x|\theta)p(\theta)$



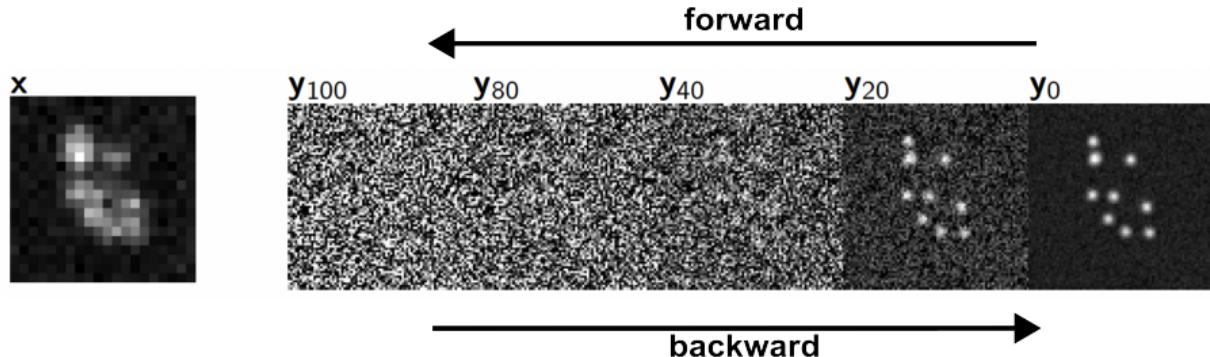
- ▶  $p(\theta|x)$  is can be hard to obtain
- ▶ Variational inference: fit a model distribution  $p_\psi(\theta|x)$
- ▶  $\psi$  can be a multivariate Gaussian, neural network, etc.

## Approach I: Resolution enhancement with a diffusion model

**Objective:** Infer of a high resolution image  $\mathbf{y}_0$  from low resolution  $\mathbf{x}$

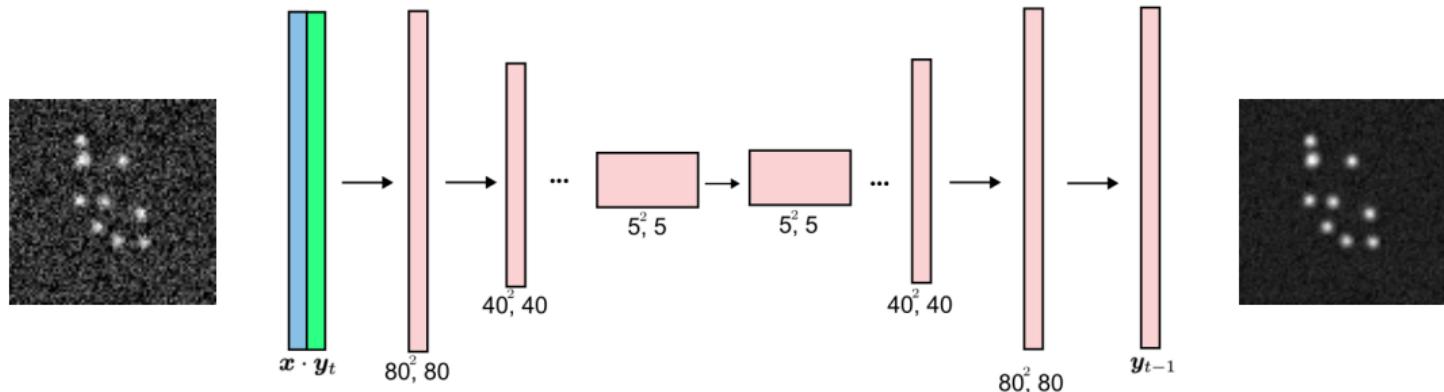
- ▶ A diffusion model can approximate the posterior distribution  $p_\psi(\mathbf{y}_0|\mathbf{x})$

$$q(\mathbf{y}_t|\mathbf{y}_{t-1}) = \mathcal{N} \left( \sqrt{1 - \beta_t} \mathbf{y}_{t-1}, \beta_t I \right)$$



$$p_\psi(\mathbf{y}_{t-1}|\mathbf{y}_t, \mathbf{x}) = \mathcal{N} (\mu_\psi(\mathbf{y}_t, \gamma_t), \beta_t I)$$

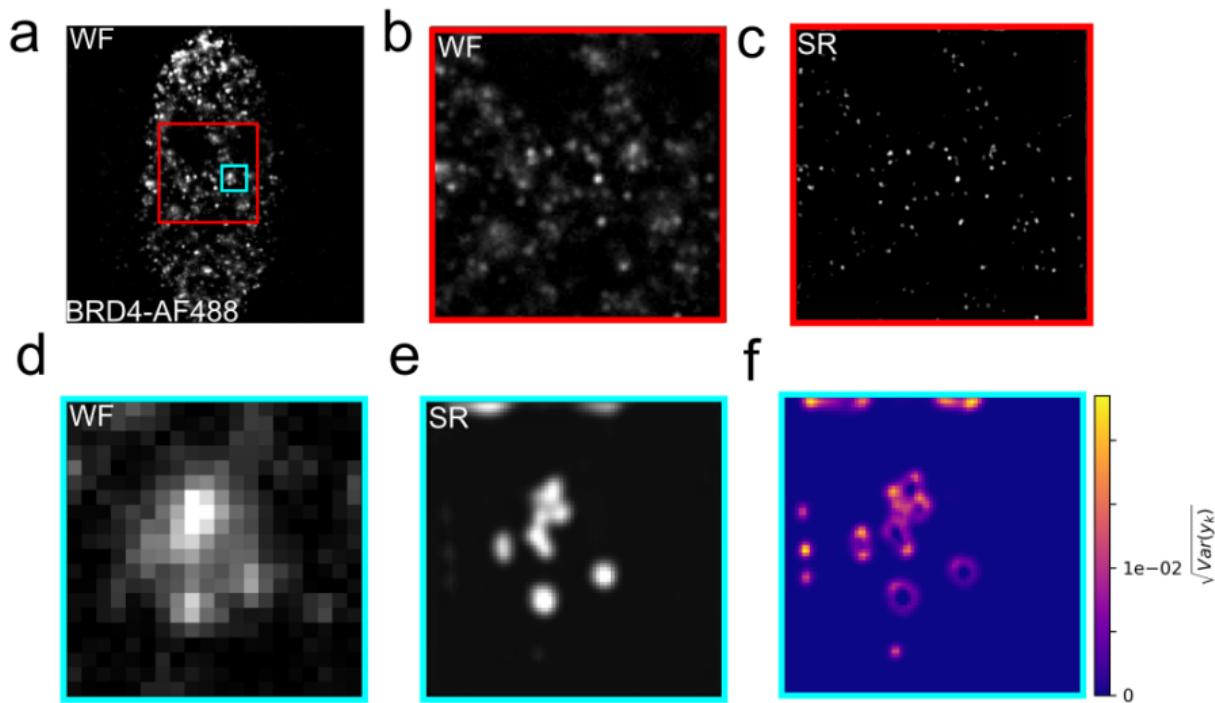
## Approach I: Resolution enhancement with a diffusion model



A deep neural network estimates the gradient of the reverse process

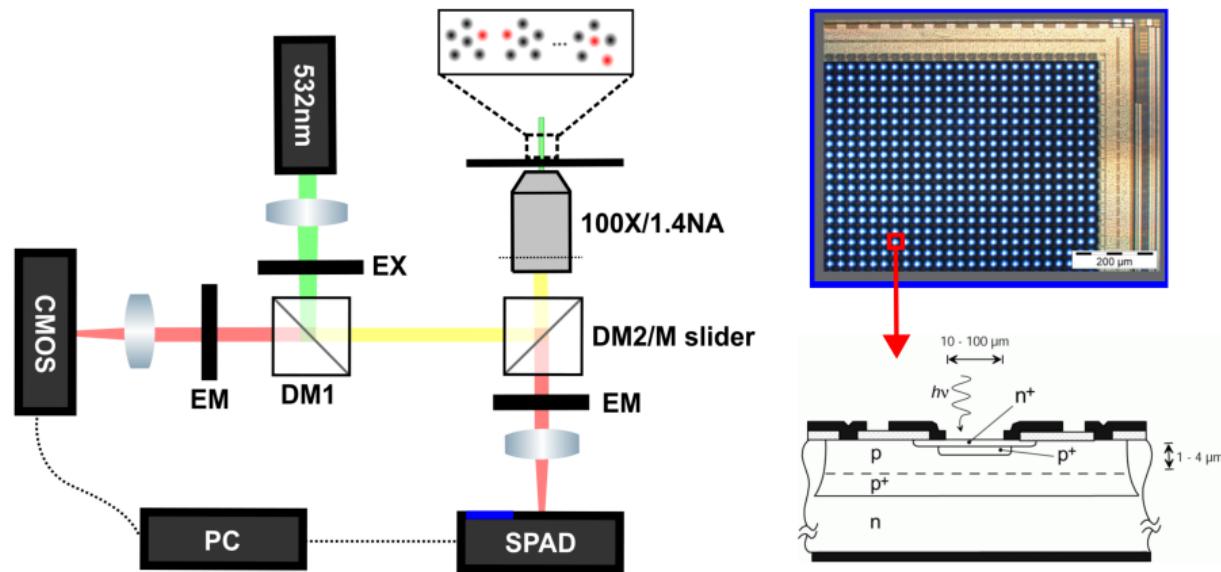
$$\mathbf{y}_{t-1} = \frac{1}{\sqrt{1 - \beta_t}} (\mathbf{y}_t + \beta_t s_\psi(\mathbf{y}_t)) + \sqrt{\beta_t} \xi \quad \xi \sim \mathcal{N}(0, I)$$

# Super resolution of BRD4 protein in a HeLa cell

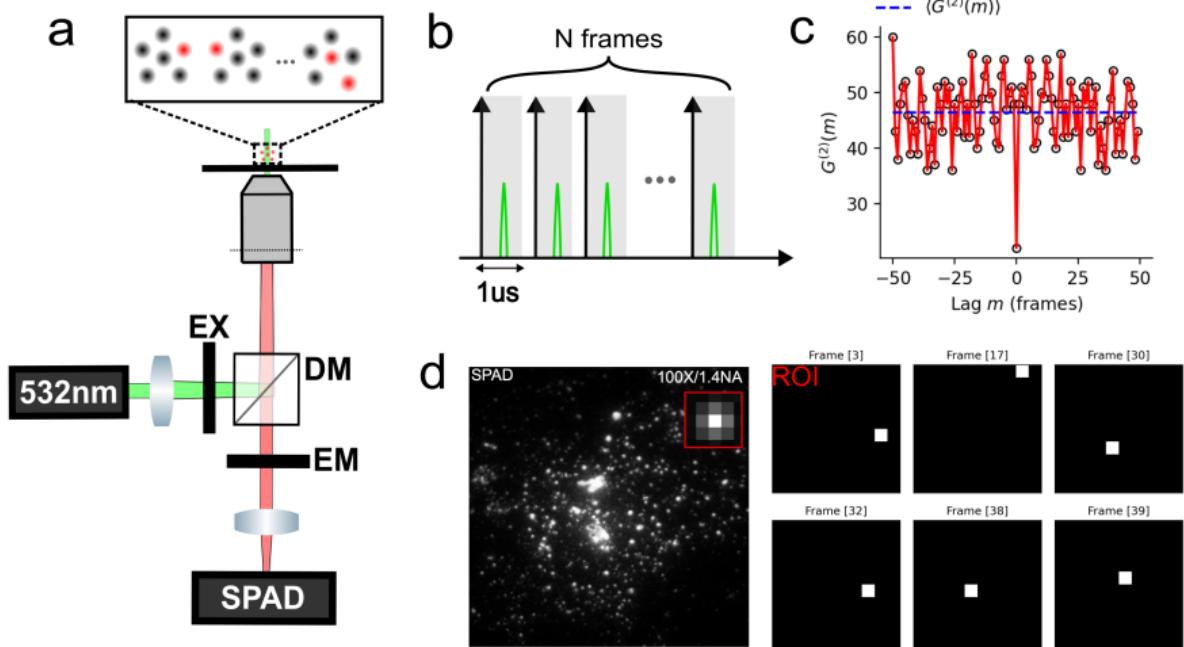


## Approach II: Integrated single photon counting and widefield single molecule imaging

- ▶ Single photon avalanche diode (SPAD) arrays give us new modeling approaches

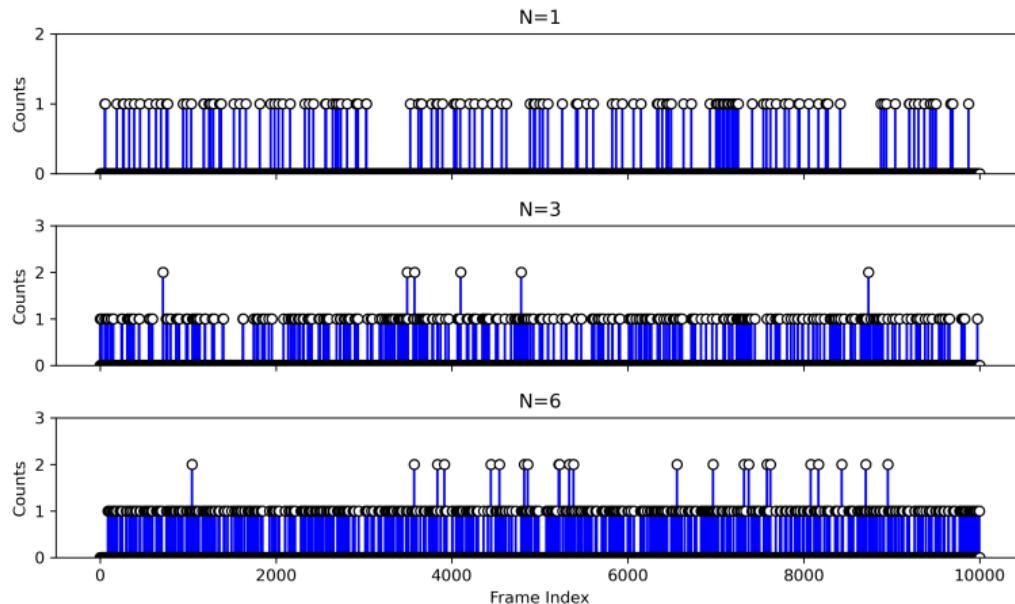


# Imaging Qdot655 photon by photon



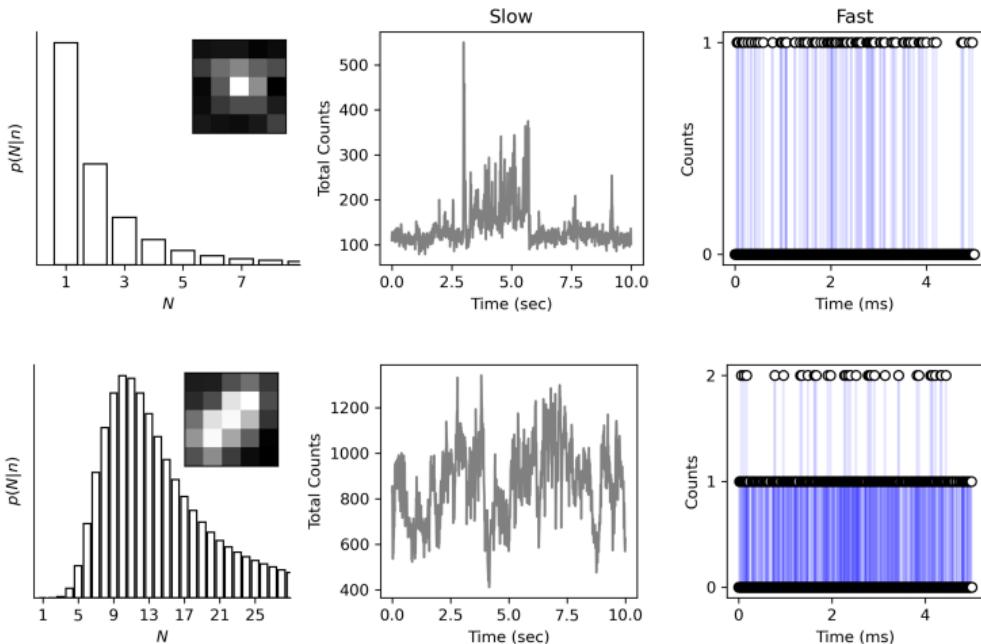
- ▶ 532nm picosecond pulsed laser pulsed at 500kHz to excite fluorescent quantum dots

## Poisson-Binomial photon count data (simulation)



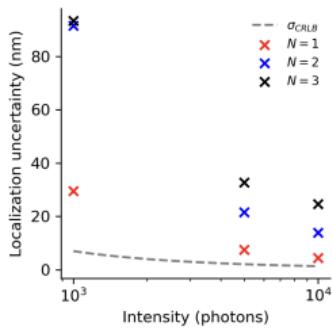
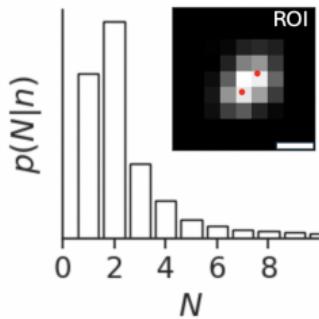
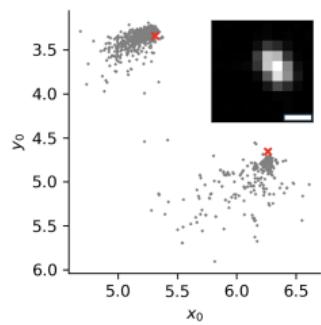
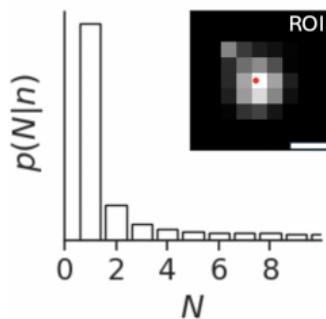
- ▶ Likelihood  $\mathcal{L}$  is a mixture of counts from  $N$  single photon sources, and background noise
- ▶ A simple form of a Hidden Markov Model (HMM)

# Discrimination of single and multiple quantum dots



- ▶ Likelihood  $\mathcal{L} = \text{Poisson}(\lambda) * \text{Binomial}(N, \zeta)$
- ▶ A simple form of a Hidden Markov Model (HMM)

# Constrained multi-emitter localization with photon counting



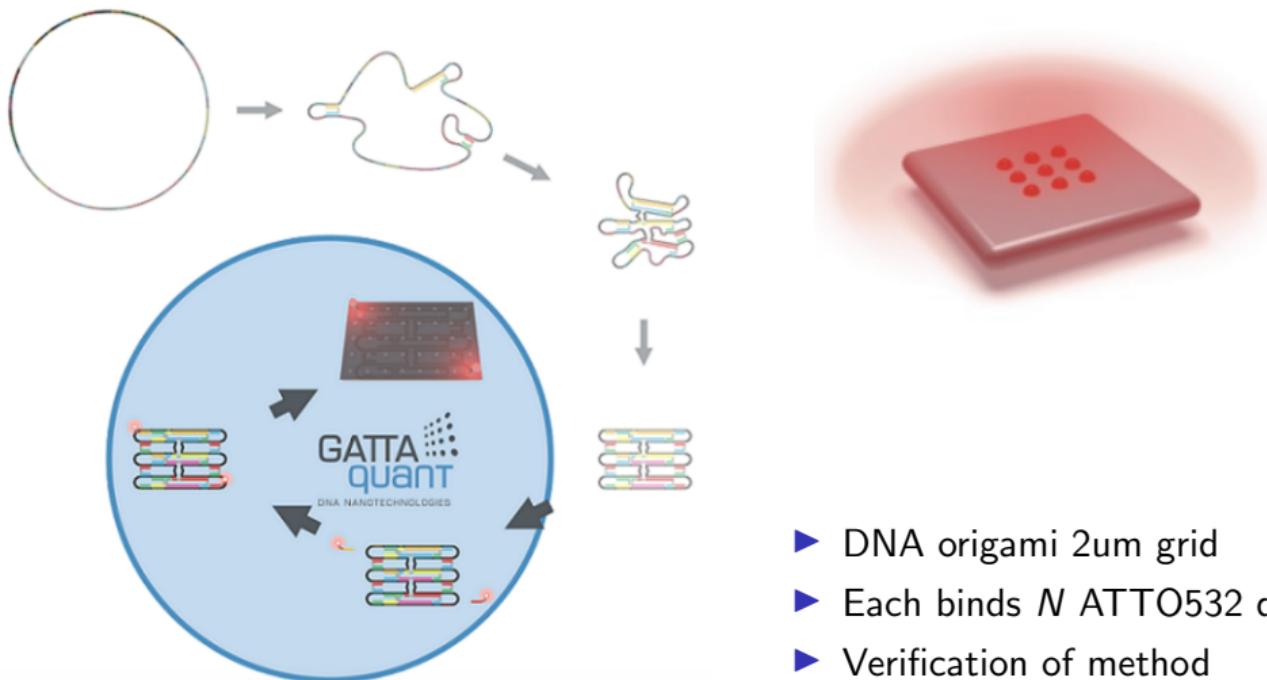
Can obtain a posterior on  $N$ :

$$\mathcal{L} = \text{Poisson}(\lambda) * \text{Binomial}(N, \zeta)$$

$$p(N|n) \propto \int_0^1 \mathcal{L}(n|N, \zeta) p(\zeta) d\zeta$$

- ▶ Posterior  $\rightarrow$  parameterization of multi-emitter fitting
- ▶ Approaches lower bound on localization error at high counts

## Counting ATTO532 dye bound to DNA origamis

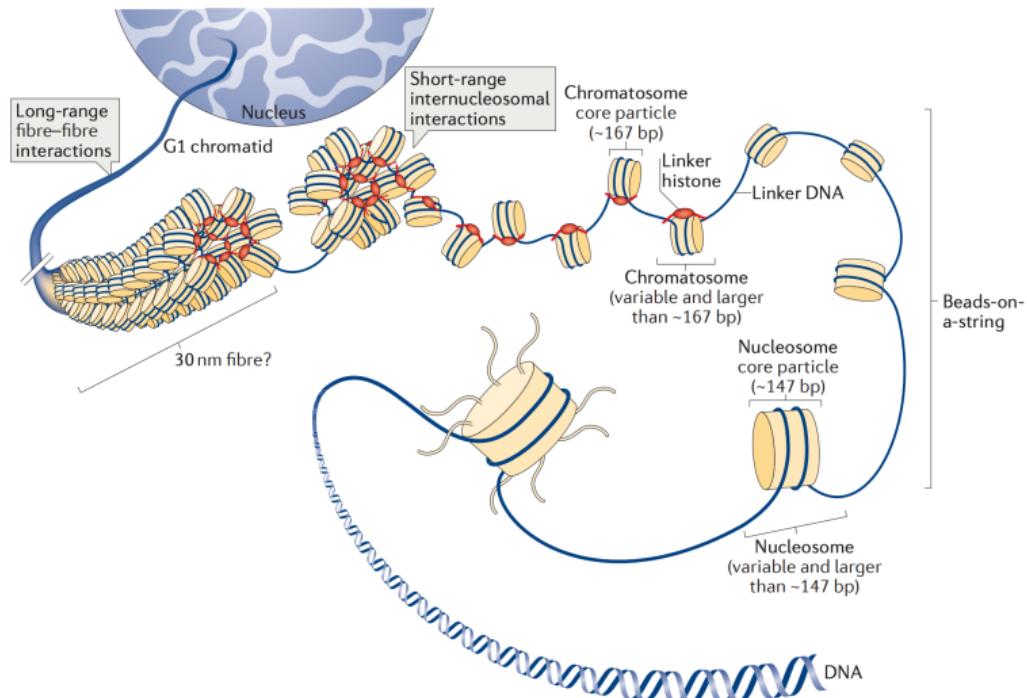


- ▶ DNA origami 2um grid
- ▶ Each binds  $N$  ATTO532 dyes
- ▶ Verification of method

Courtesy of GATTAquant DNA Nanotech

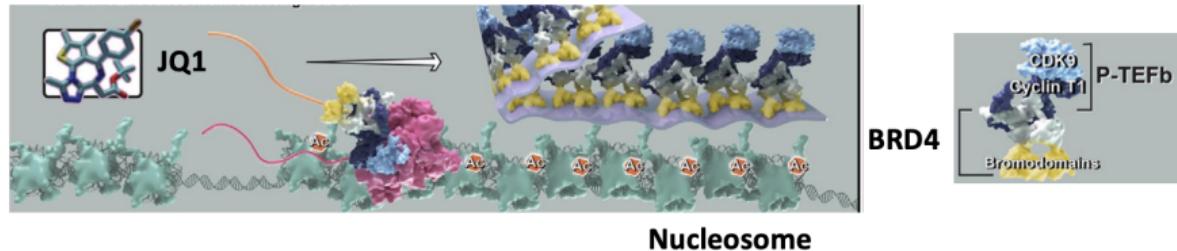
## Super-resolution of nucleosome nanodomains *in-vivo*

# Hierarchical structure of chromatin

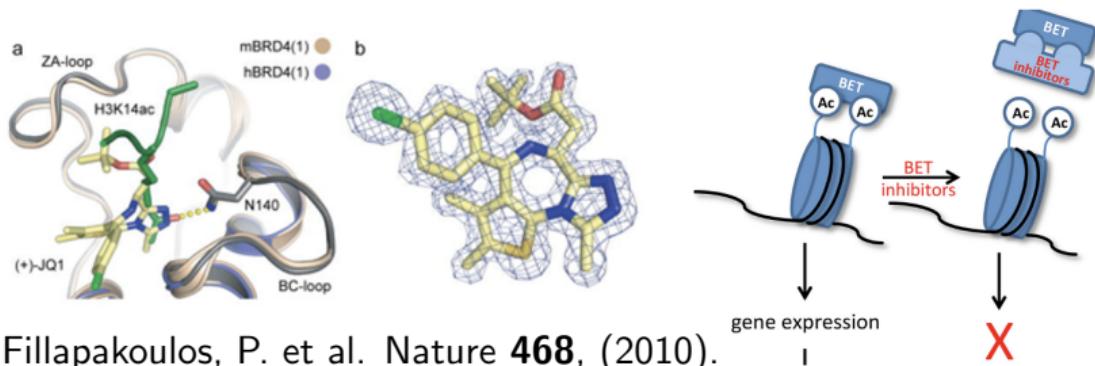


Fyodorov, D. et al. Nat Rev Mol Cell Biol **19**, (2018).

# Bromodomain protein 4 (BRD4) binds acetylated chromatin

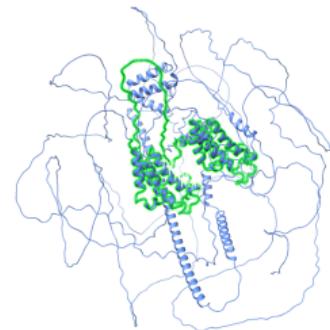
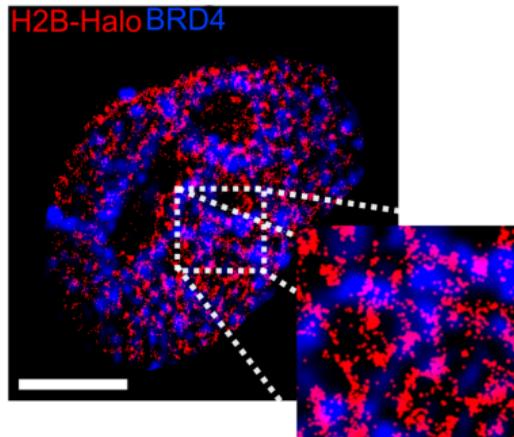


Zheng, B. et al. Molecular Cell **16**, (2023).

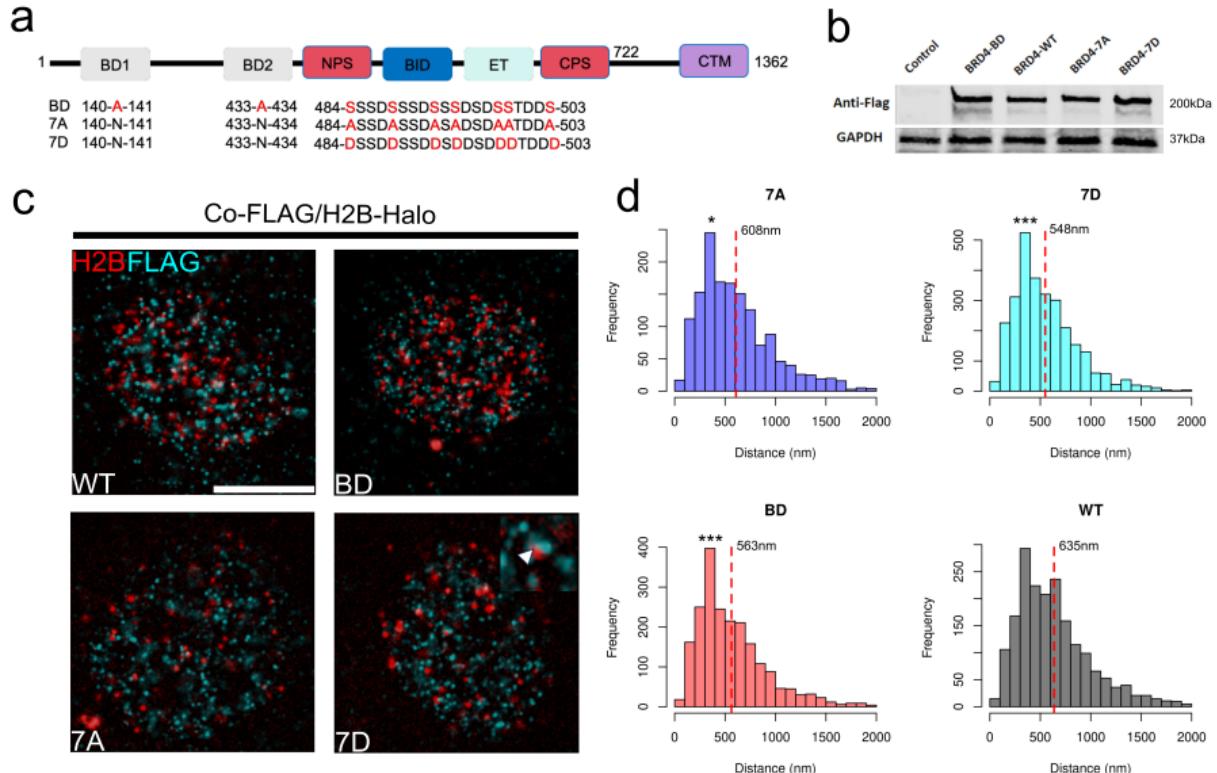


Fillapakoulos, P. et al. Nature **468**, (2010).

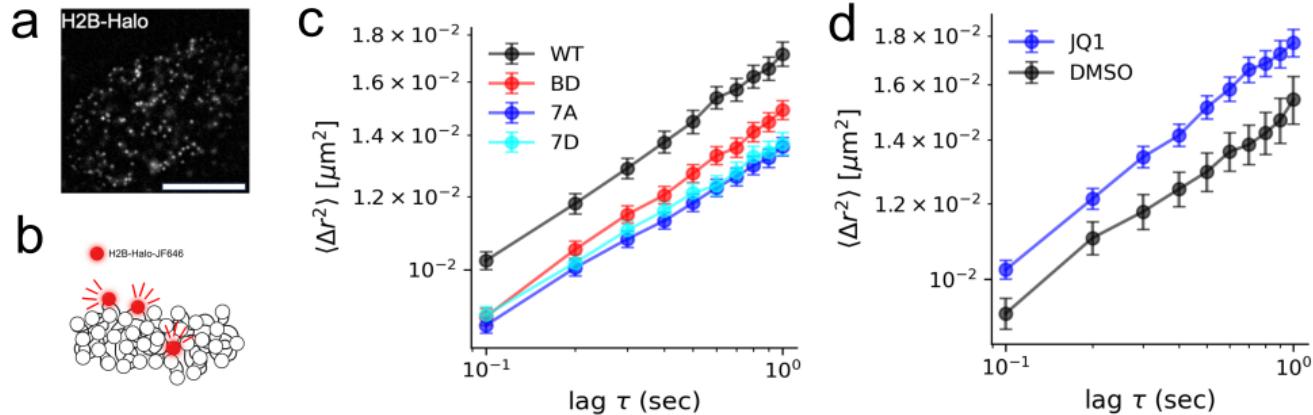
# BRD4 mutations to probe effects on chromatin structure



# BRD4 binding efficacy controls colocalization with nucleosome nanodomains

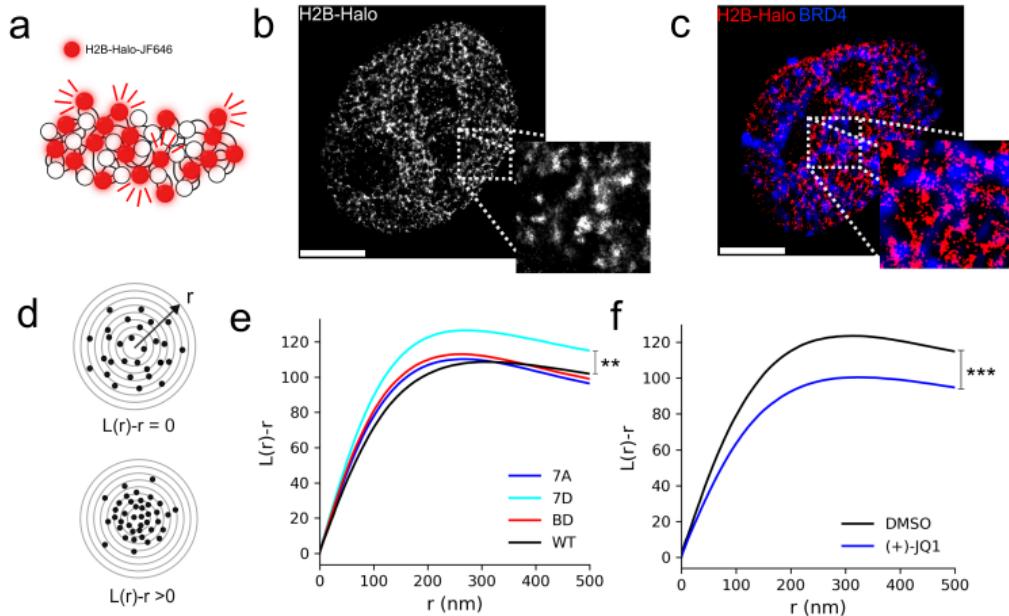


# BRD4 chromatin binding controls chromatin mobility



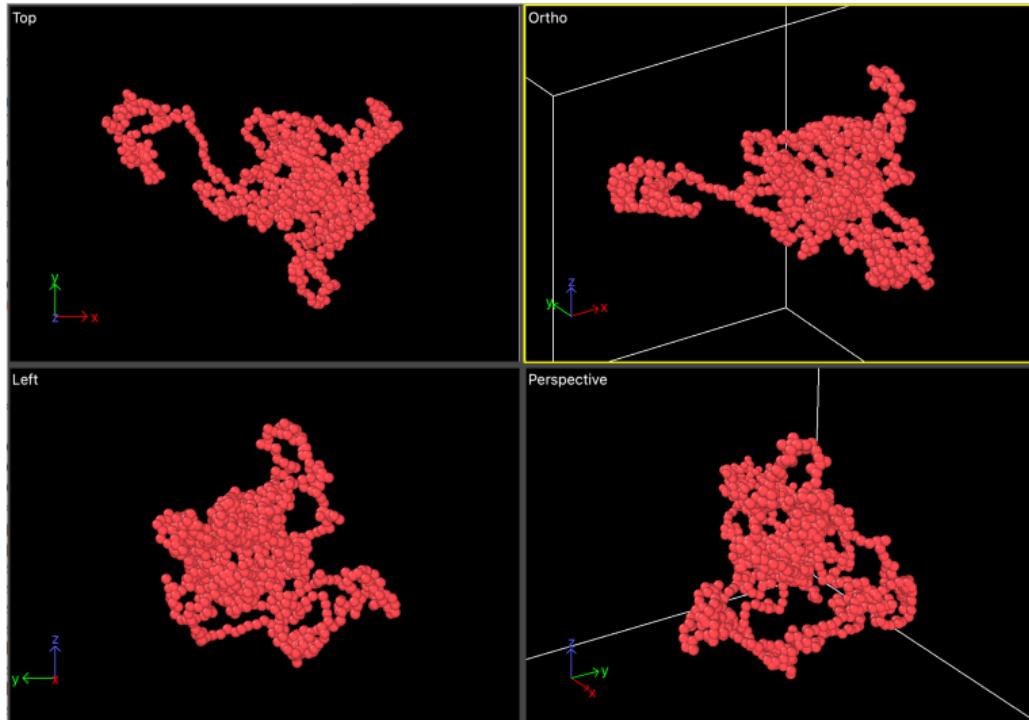
- ▶ H2B is sparsely labeled for particle tracking
- ▶ Reduced diffusion coefficient  $D$  in BRD4 mutants
- ▶ Increased  $D$  in cells exposed to (+)-JQ1

# BRD4 binding is necessary for maintenance of nucleosome nanodomains



- ▶ H2B is densely labeled for super-resolution imaging
- ▶ BRD4 chromatin binding activity controls nanodomain density

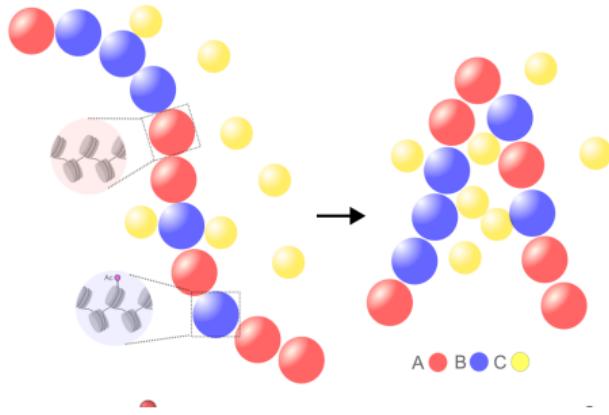
# Coarse grained molecular dynamics of chromatin at 310K



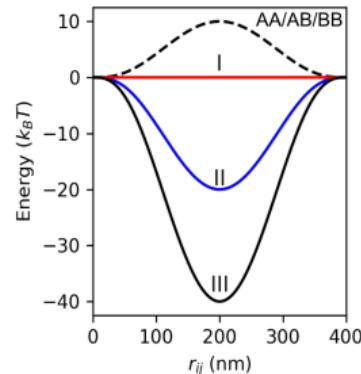
- ▶ 100kb chromatin beads connected by harmonic bonds (Rouse model)

# Coarse grained molecular dynamics of chromatin binders at 310K

a



b

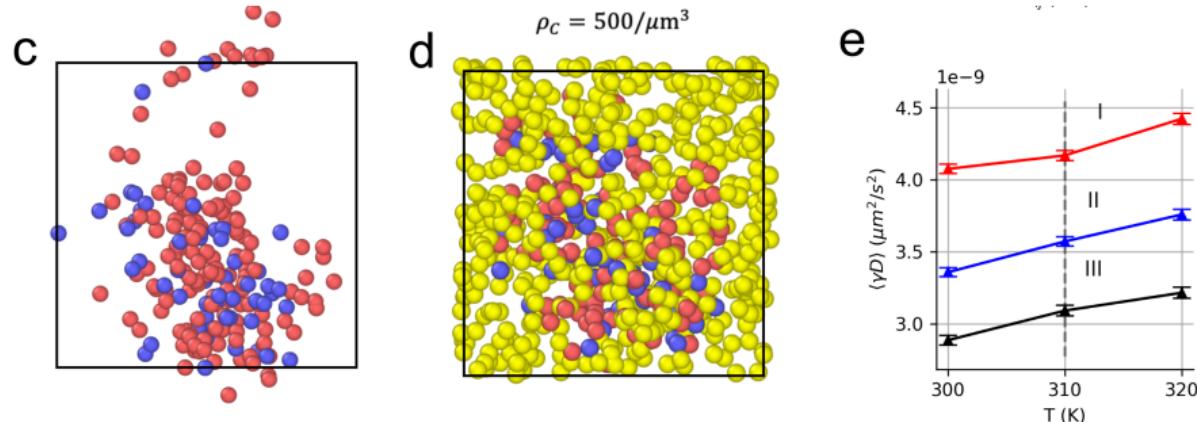


Chromatin chains interact with binders via the potential

$$U_{ij} = \epsilon \left( 1 - \left( \frac{|r_{ij}|}{R_0} \right)^2 \right)^3$$

- ▶ A (B) type particles represent unacetylated (acetylated) chromatin beads
- ▶ BRD4-like C particles bind B type particles with variable energies

# Multivalent chromatin binding reduces chromatin mobility



Integrate Brownian dynamics:  $\dot{r} = \gamma^{-1} \nabla U + \sqrt{2k_B T} \gamma^{-1/2} \xi$   $\gamma = 10^{-6}$

Stochastic forcing is a delta-correlated noise  $\xi \sim \mathcal{N}(0, 1)$ ,  $\langle \xi(t) \xi(t + \tau) \rangle = \delta(\tau)$

## Summary of contributions

- ▶ First generative model of super-resolution microscopy images from low-resolution inputs
- ▶ Applied SPAD array for counting fluorescent molecules in widefield microscopy
- ▶ First data supporting control of chromatin architecture by transcriptional condensates

## Selected Publications

- ▶ **Clayton Seitz**, Donghong Fu, Mengyuan Liu, Hailan Ma, and Jing Liu. *BRD4 phosphorylation regulates the structure of chromatin nanodomains.* Submitted. 2024
- ▶ **Clayton Seitz** and Jing Liu. *Uncertainty-aware localization microscopy by variational diffusion.* In Review. 2024
- ▶ **Clayton Seitz** and Jing Liu. *Quantum enhanced localization microscopy with a single photon avalanche diode array.* In Progress. 2024
- ▶ Maelle Locatelli<sup>†</sup>, Josh Lawrimore<sup>†</sup>, Hua Lin<sup>†</sup>, Sarvath Sanaullah, **Clayton Seitz**, Dave Segall, Paul Kefer, Salvador Moreno Naike, Benton Lietz, Rebecca Anderson, Julia Holmes, Chongli Yuan, George Holzwarth, Bloom Kerry, Jing Liu, Keith D Bonin, Pierre-Alexandre Vidi. *DNA damage reduces heterogeneity and coherence of chromatin motions.* PNAS 12 July 2022; 119 (29): 1-11
- ▶ Mengdi Zhang, **Clayton Seitz**, Garrick Chang, Fadil Iqbal, Hua Lin, and Jing Liu *A guide for single-particle chromatin tracking in live cell nuclei.* Cell Biology International 15 January 2022; 46 (5): 683-700

## Acknowledgements



(left to right) Charles Park, Garrick Chang, Jing Liu, David Buchanan, Mengyuan Liu, Hailan Ma



Norbert Scherer



Donghong Fu

Thank you!