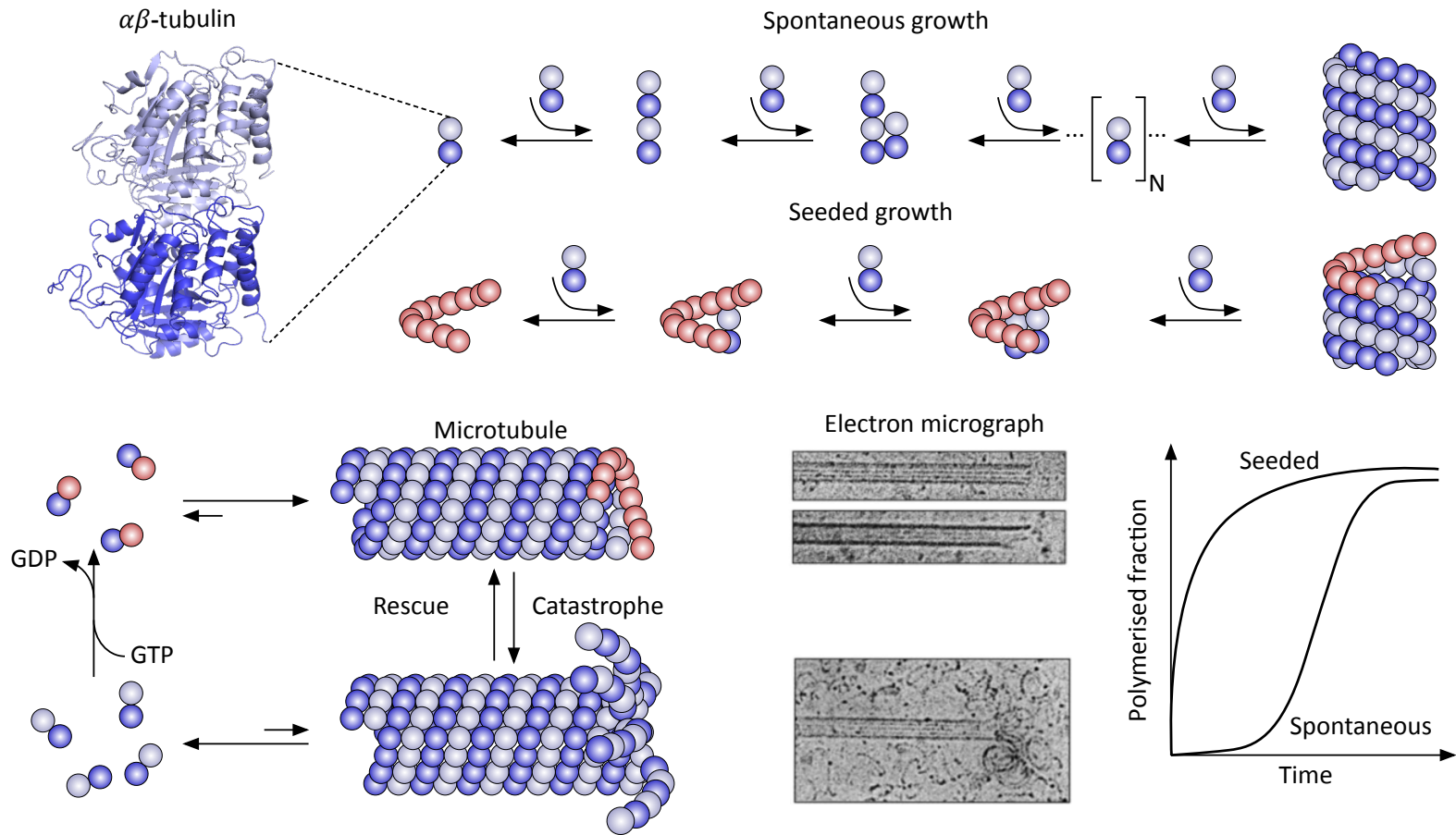


Label-free single molecule imaging with
interferometric scattering microscopy

Philipp Kukura

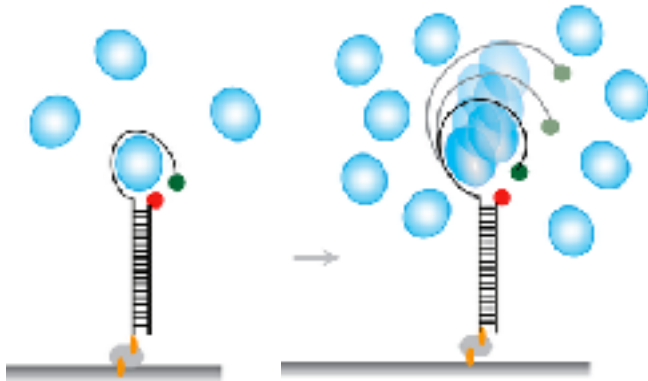
Physical and Theoretical Chemistry Laboratory, University of Oxford

How proteins work most of the time

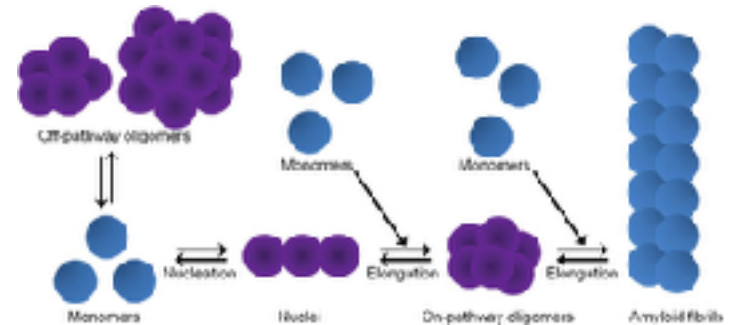


Some examples

Nucleation



Kim et al. Mol. Cell (2016)



Lorenzen et al. Essays Biochem (2014)

Microscopic to single molecule dynamics



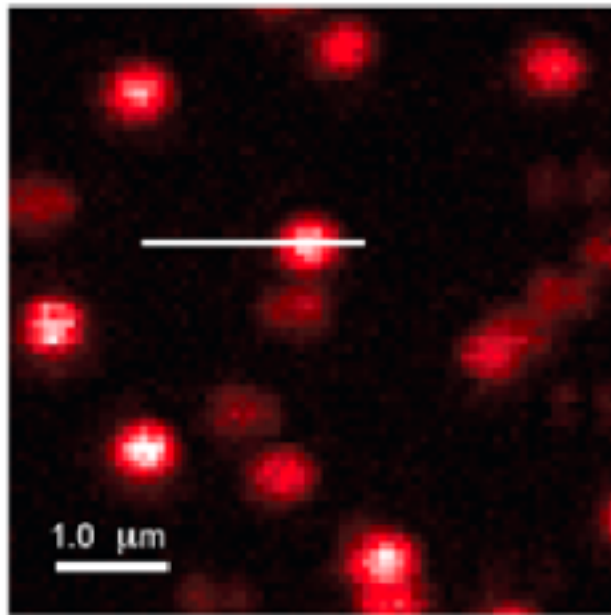
Zakharov et al. BPJ (2015)

We would need to be able to see single molecules the way they are depicted here:

Dynamically, in the presence of many others and with nm precision

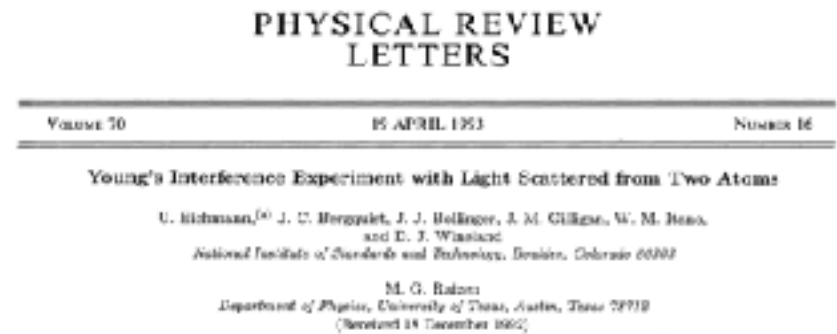
State-of-the-art in seeing small things

Single molecule fluorescence



Contrast, specificity, background rejection

Single molecule (ion) scattering?



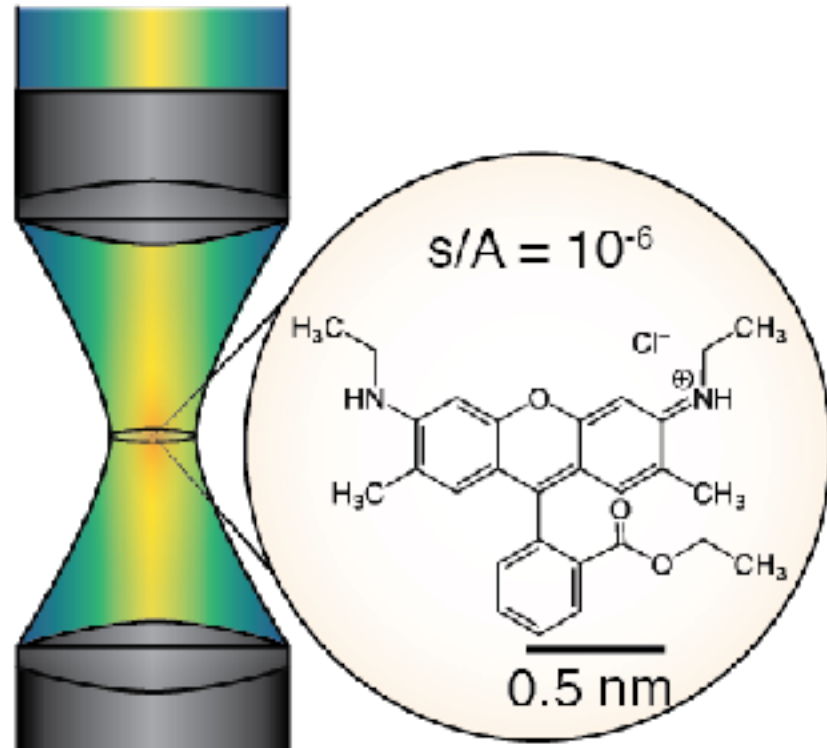
Scattering just as good?

The fundamental problem: molecular size vs. wavelength

300 years ago



Still true today

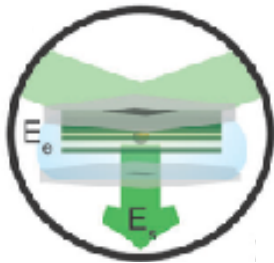
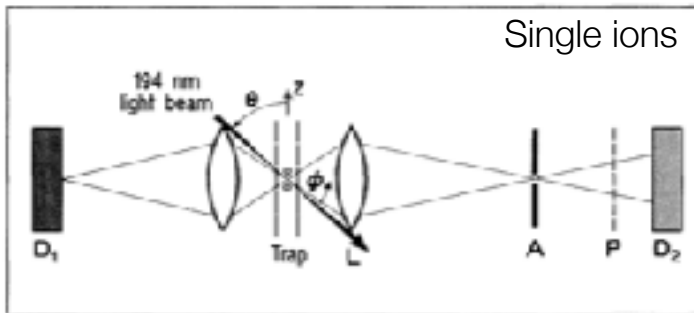


While there are techniques that can **resolve** better than the diffraction limit...

The diffraction limit still holds in terms of focusing

Light scattering

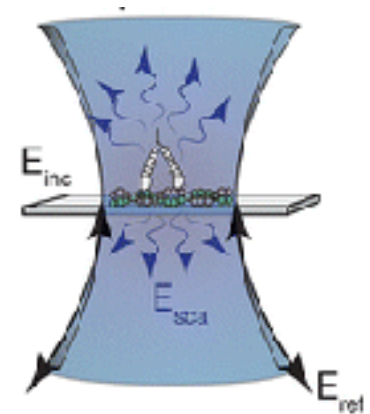
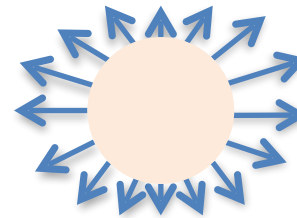
Dark-field imaging



Detection limit: ~20 nm gold

Scattering cross section

$$\sigma = |s|^2 \propto V^2 \left| n_m \frac{n_p - n_m}{n_p + 2n_m} \right|^2$$



Strong size dependence

BUT $\sigma_{20 \text{ nm gold}} \sim 10^6 \sigma_{\text{protein}}$

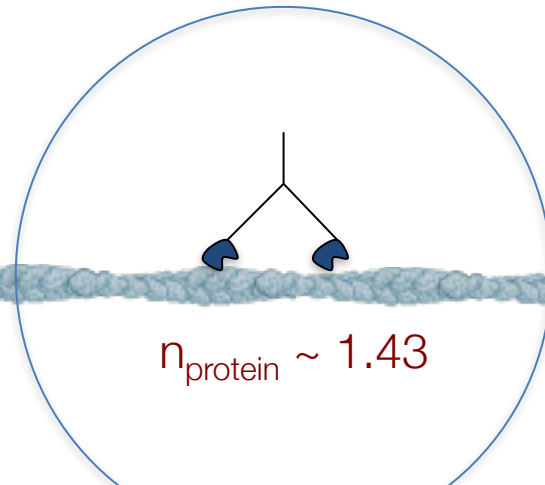
Thinking about it differently

We can all see this:

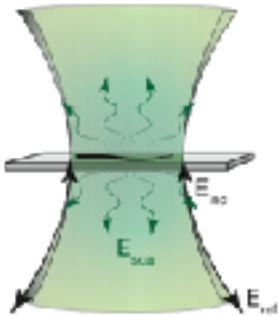


So why not this?

$$n_{\text{water}} = 1.33$$



Interferometric scattering microscopy (iSCAT)



Combine scattered & reflected light:

$$|E_s + E_r|^2 = |E_i|^2 [r^2 + |s|^2 - 2r|s| \sin \phi]$$

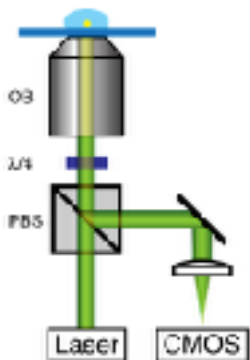
Vasicek (1961) Opt. Spectrosc. 11, 128
Curtis (1964) J. Cell Biol. 20, 199

Signal for a small scatterer:

$$\text{Contrast} = 1 - \frac{2|s| \sin \phi}{r}$$

High sensitivity: weaker size dependence (V vs V²)

Lindfors, *et al.* (2004) PRL, 93, 037401
Kukura, *et al.* (2010) JPCL, 1, 3323



Shot-noise limited SNR

$$\frac{\text{Contrast}}{\text{Background fluctuations}} = \text{Contrast} \sqrt{N}$$

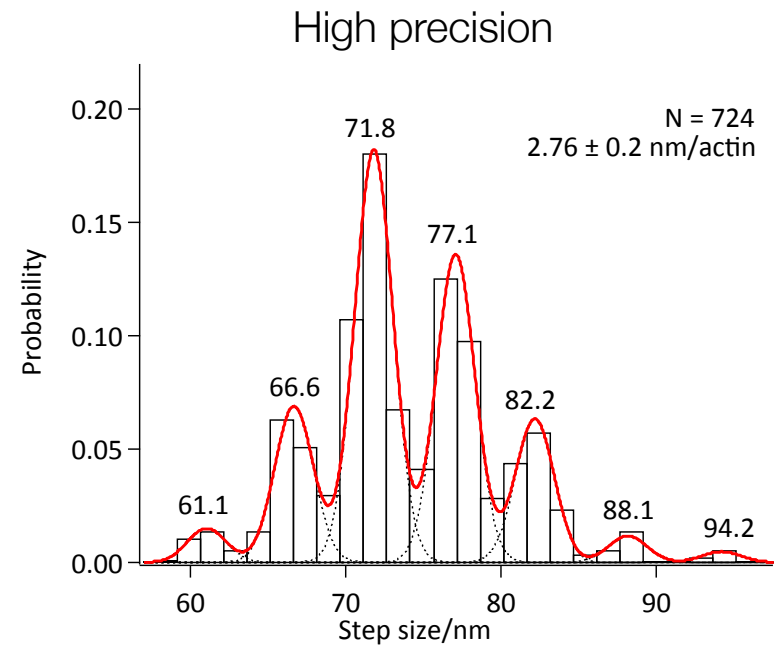
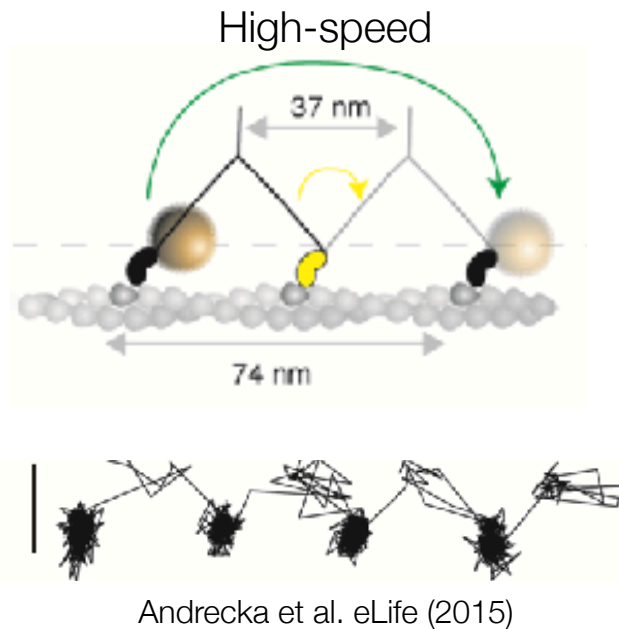
Simultaneous high localisation precision and time-resolution

Kukura, *et al.* (2009). Nat. Methods, 6, 923

For ideal SNR: suggests 'arbitrary' speed and sensitivity

You can also go for precision instead of speed

Myosin 5



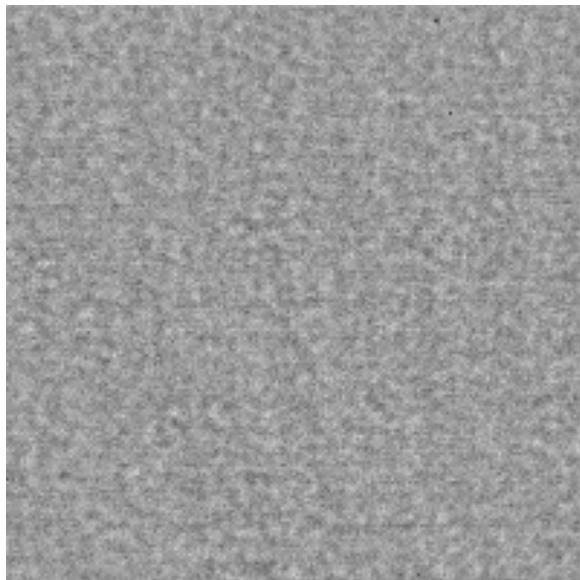
100 Hz with <0.5 nm precision

You cannot only see gold particles: you can see anything

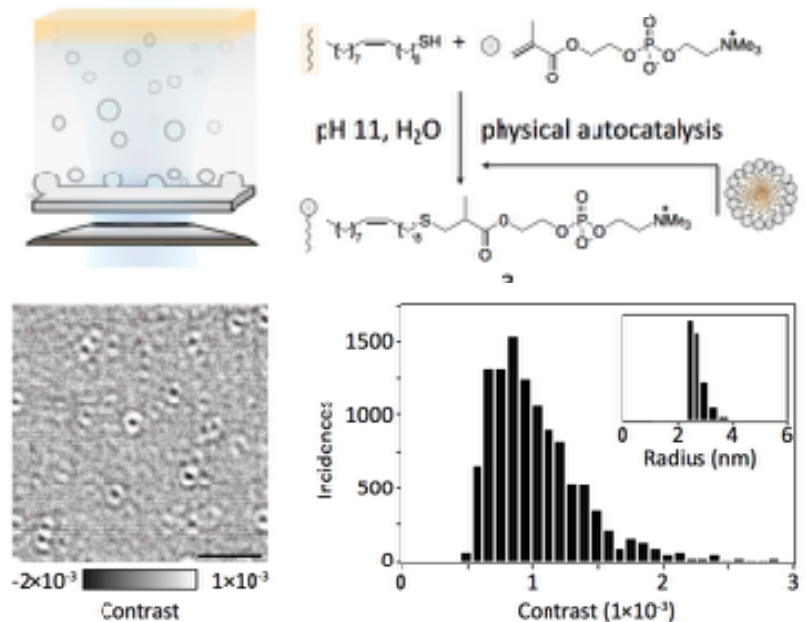
Scattering cross section is given by

$$\sigma = |s|^2 \propto V^2 \left| n_m \frac{n_p - n_m}{n_p + 2n_m} \right|^2$$

Lipid rafts

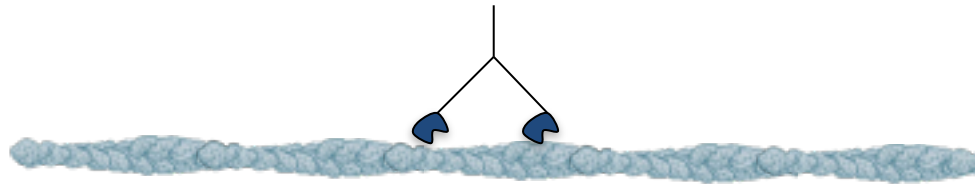


Micelles and vesicles

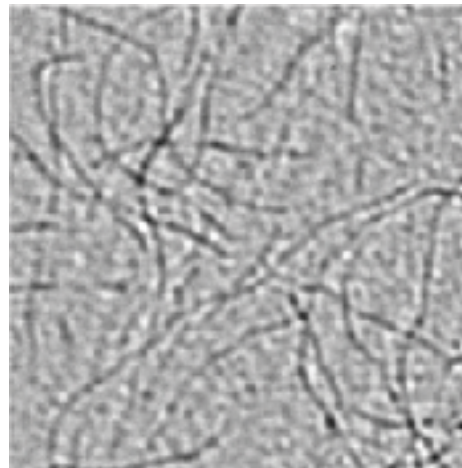


From micelles to single molecules

Myosin 5 bound to actin



Actin filaments on glass



0.98  1.02
Normalised reflected intensity

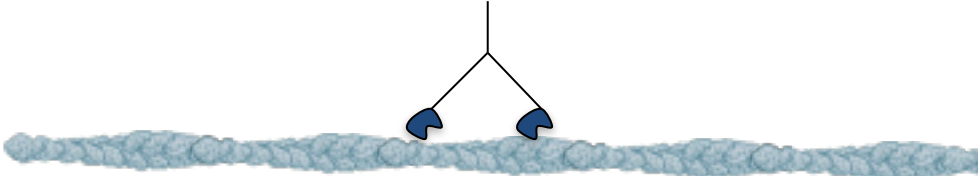
But with this much background, how do I see the molecule I am interested in?



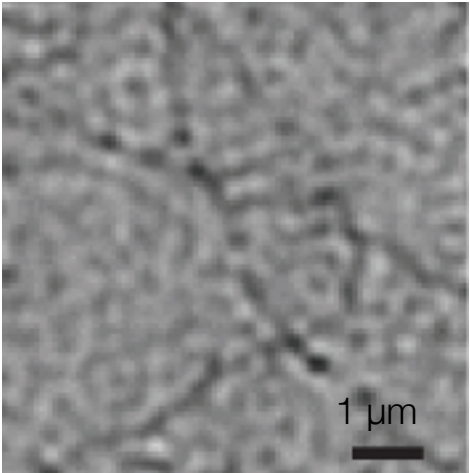
Where is Odlaw?



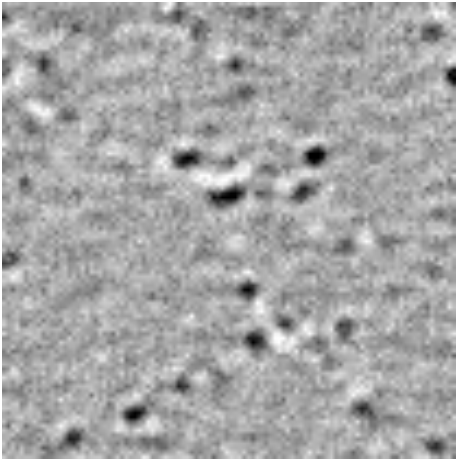
Myosin 5 binds and walks



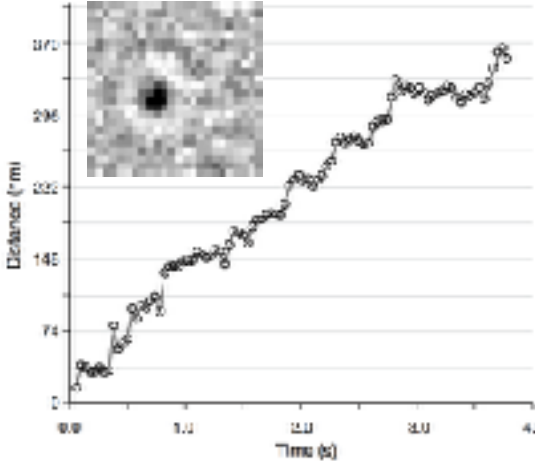
Actin on glass



Background subtracted



Nanometric tracking



Ortega-Arroyo et al Nano Letters (2014) 2065

All-optical, label-free detection of a single, unlabelled protein

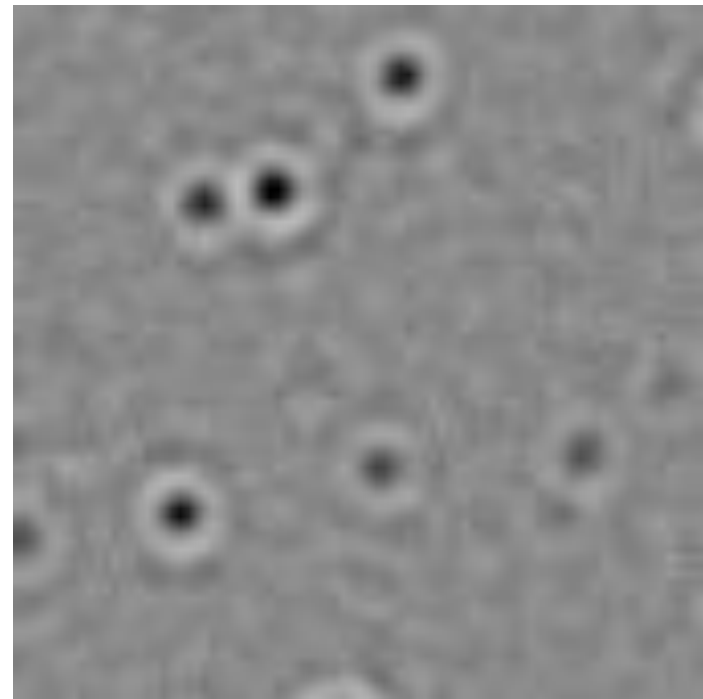
Really becoming shot noise limited

Two years later: Non-specific binding of a similar-sized protein to a bare glass surface

HSP 16.5



396 kDa



Real time (effective 6 Hz), 50 kW/cm², 240 nM

Let's think about this a little more carefully

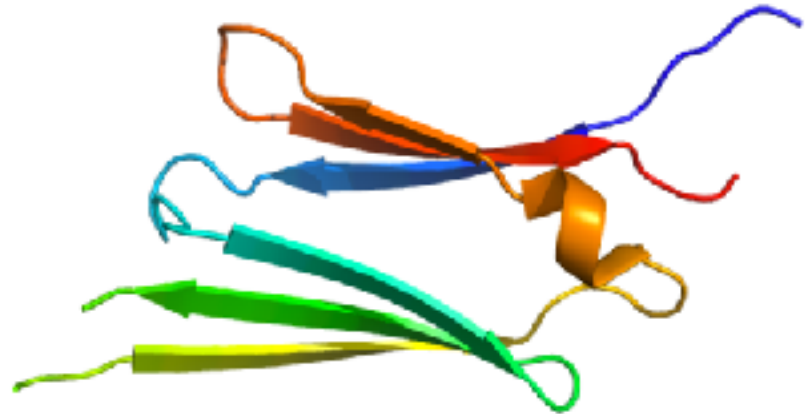
Proteins are made of amino acids

Which all have the same polarisabilities

Which means the signal should be

PROPORTIONAL TO MASS

$$\sigma = |s|^2 \propto V^2 \left| n_m \frac{n_p - n_m}{n_p + 2n_m} \right|^2$$

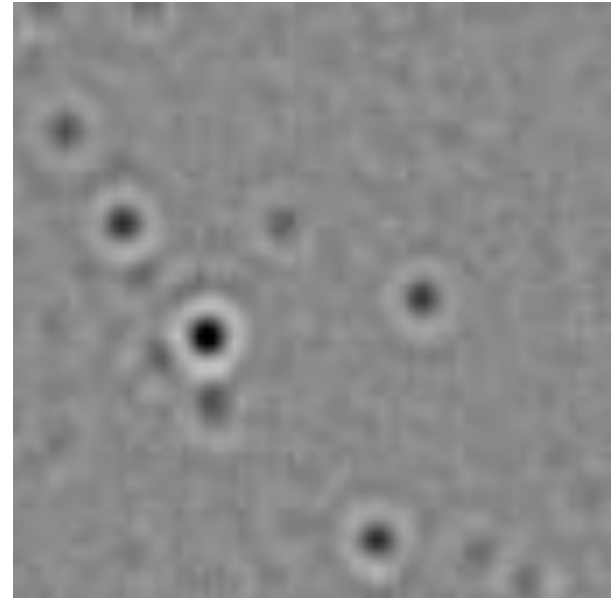
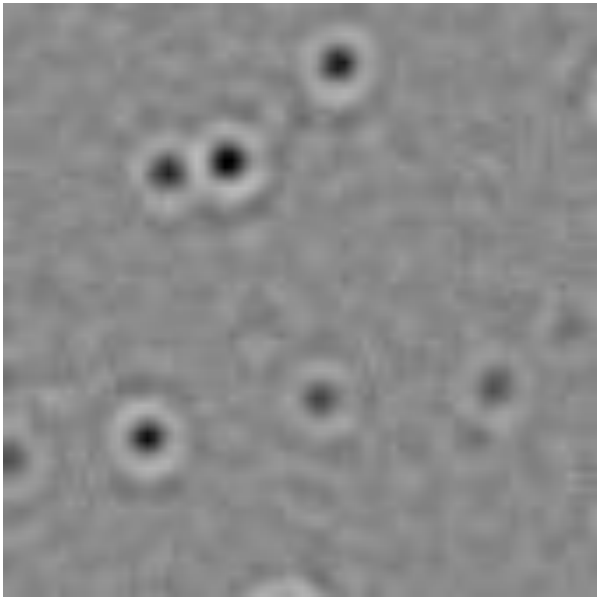
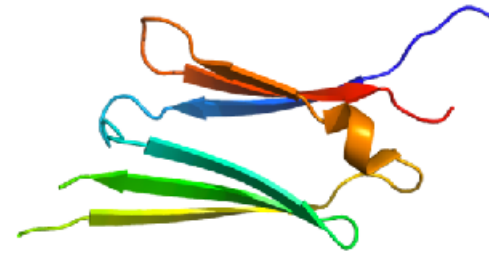


From mono-disperse to poly-disperse

HSP 16.5: Stable 24mer



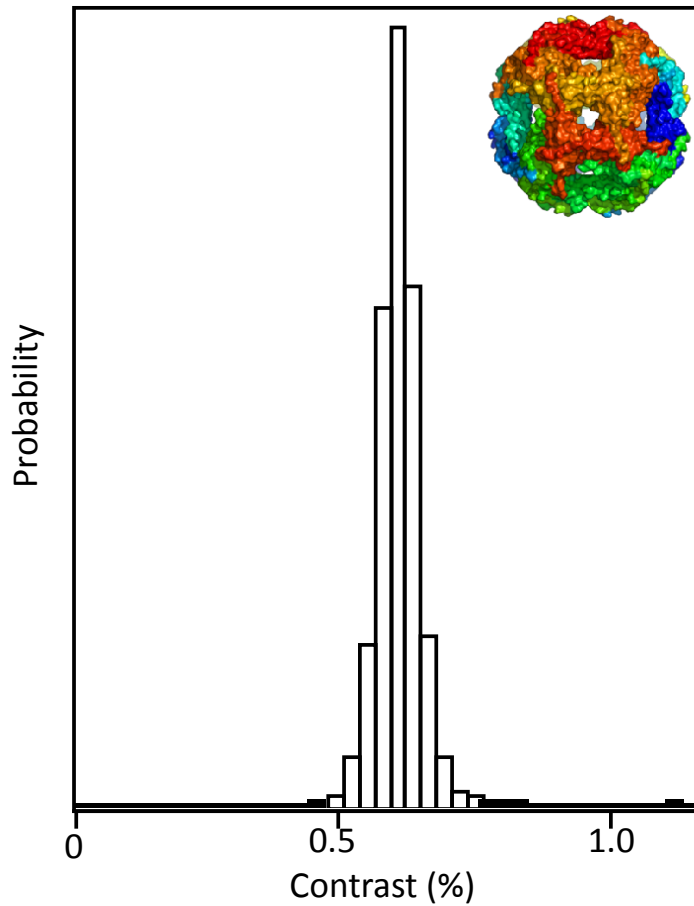
HSP 27: Highly dynamic oligomer



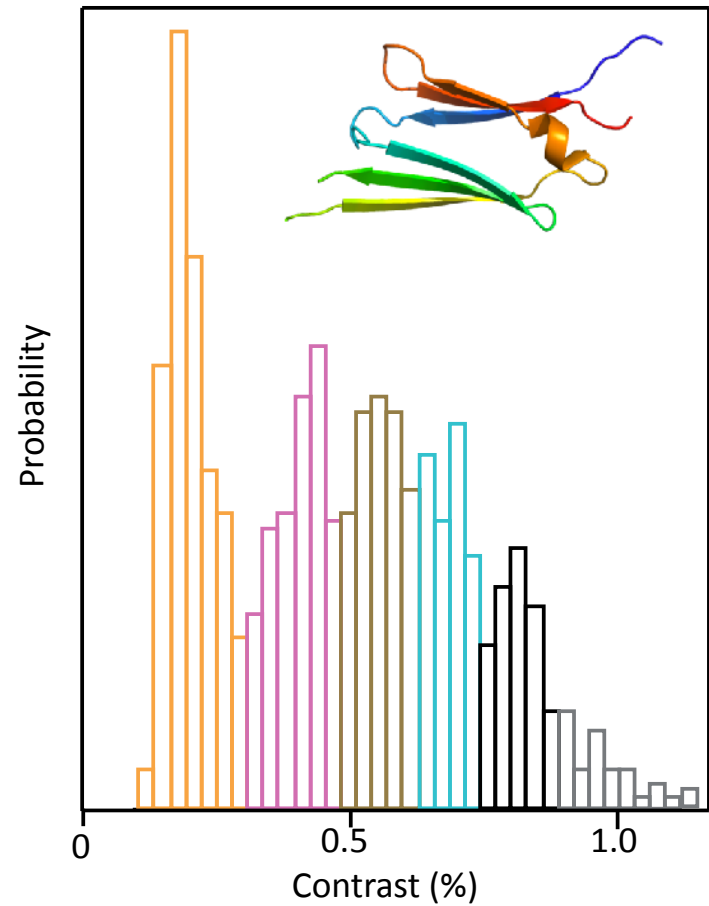
Real time (effective 6 Hz), 50 kW/cm², [monomer] = 240 nM

From mono-disperse to poly-disperse

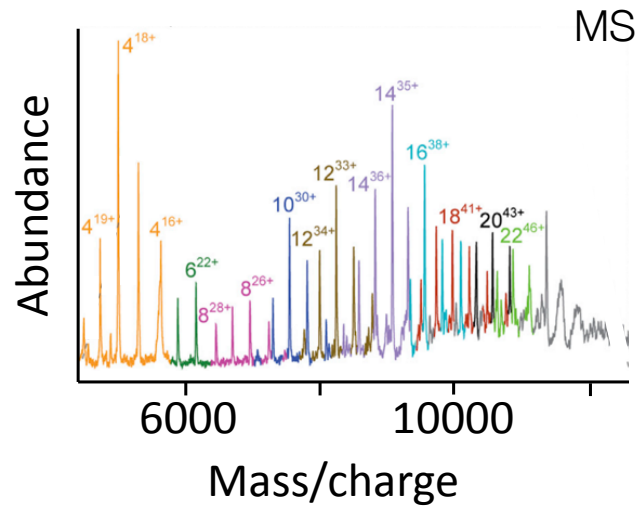
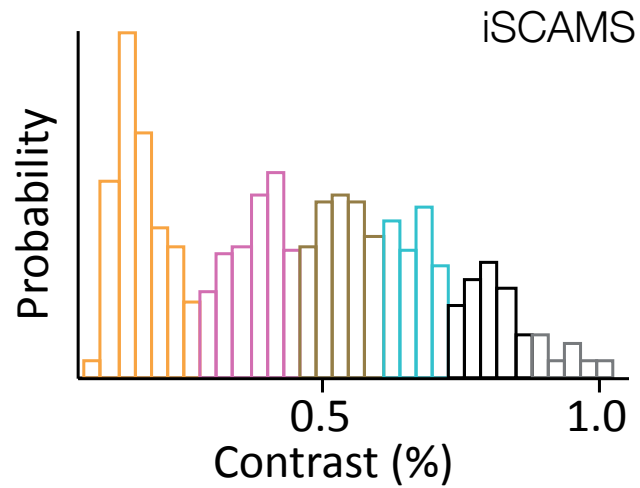
HSP 16.5: Stable 24mer



HSP 27: Highly dynamic oligomer

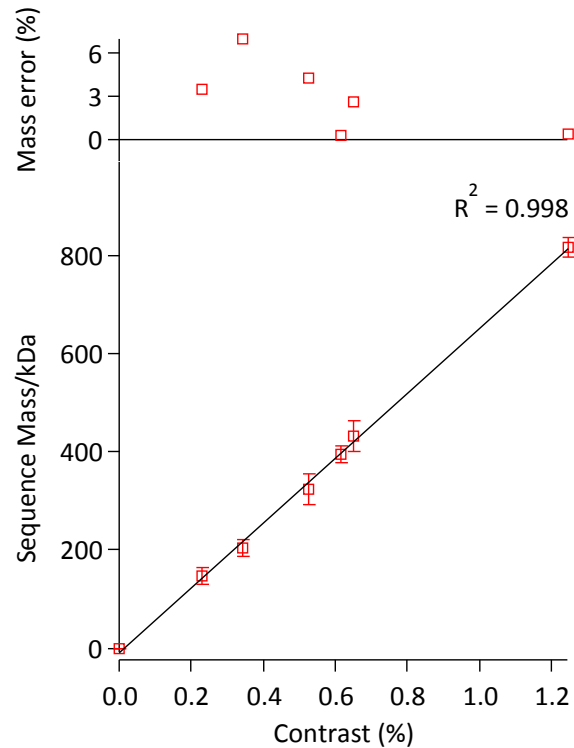


From monodisperse to polydisperse

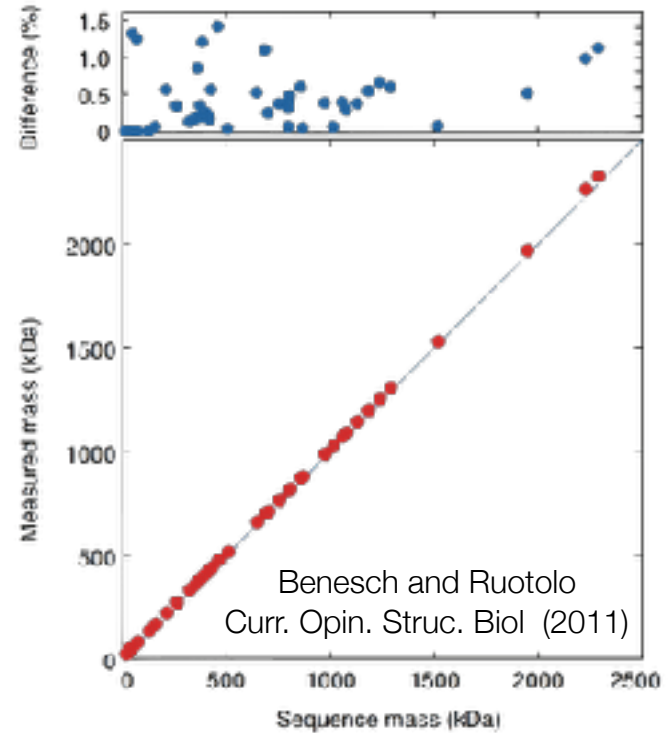


Interferometric scattering mass spectrometry (iSCAMS)?

iSCAMS



Native mass spectrometry



Comparable mass accuracy (<5%)

Protein-drug interactions

NATURE MEDICINE | SPOONFUL OF MEDICINE

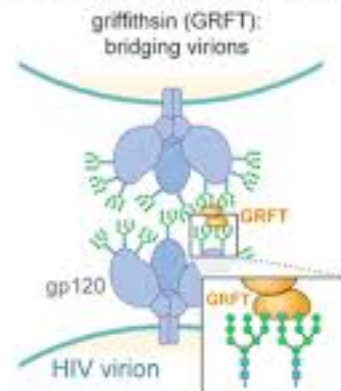
The Daily Dose – HIV protection goes bananas

15 Mar 2010 | 12:00 EDT | Posted by [Christian Torres](#) | Category: [Daily Dose](#)

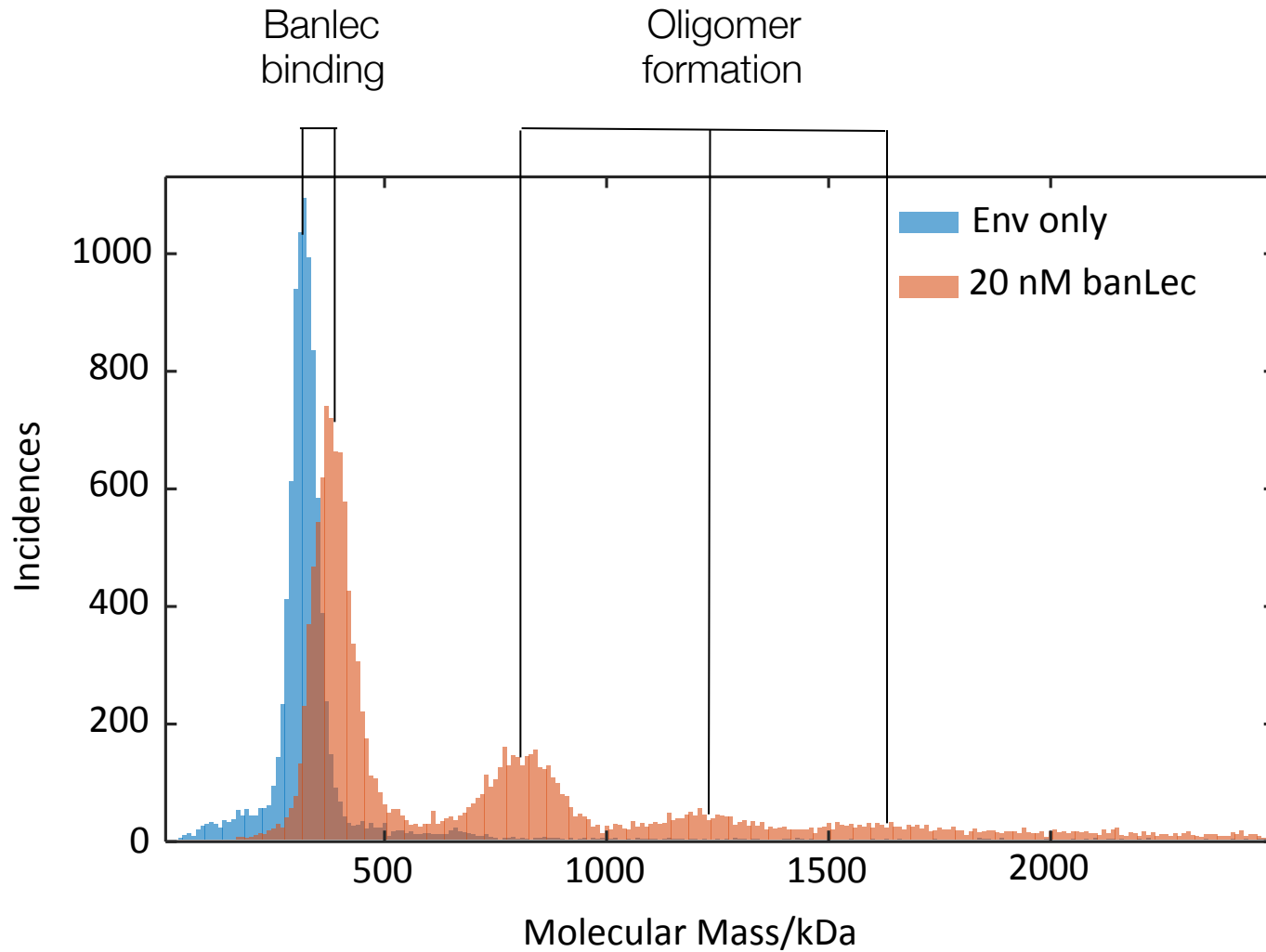
— Bananas, already a beacon of safe sex practices, might have a new role in the fight against HIV. According to [researchers](#), the fruit's sugar-binding proteins called lectins, which attach to molecules on the outside of the HIV virus, are comparable to two current anti-HIV drugs in blocking the virus from infecting cells. Banana lectin (BanLec for short) would be cheaper to produce and less likely to create selection for resistance than existing meds, the study authors [say](#).



Antiviral non-human lectins:

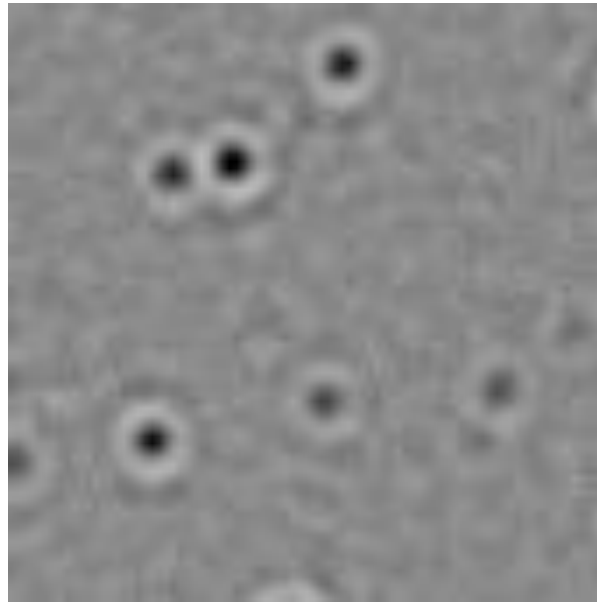


Direct observation of drug-induced protein aggregation



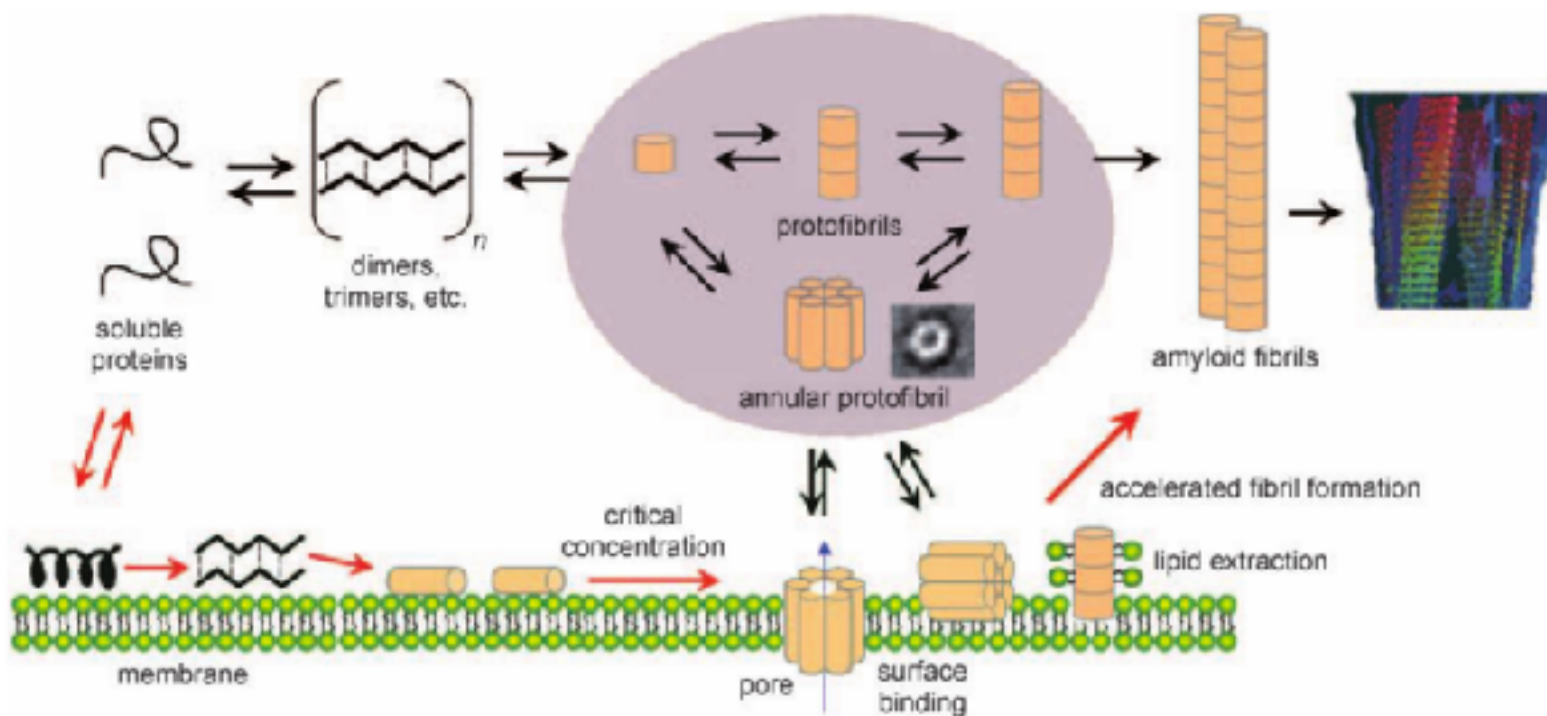
From mass spectrometry to mass imaging

Same approach to super-resolution as PALM/
STORM is valid here as well



150 ms exposure time, 3.5 nm localisation precision

Example 1: Synuclein aggregation on membranes



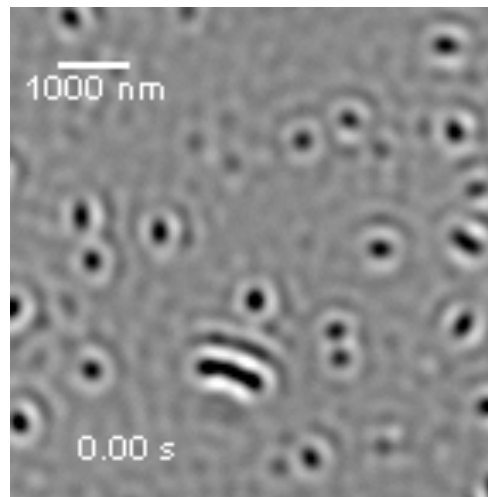
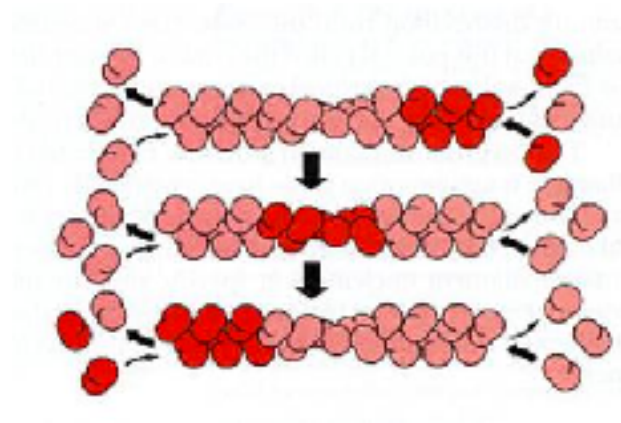
Example 1: α -Synuclein aggregation on membranes

Real-time imaging

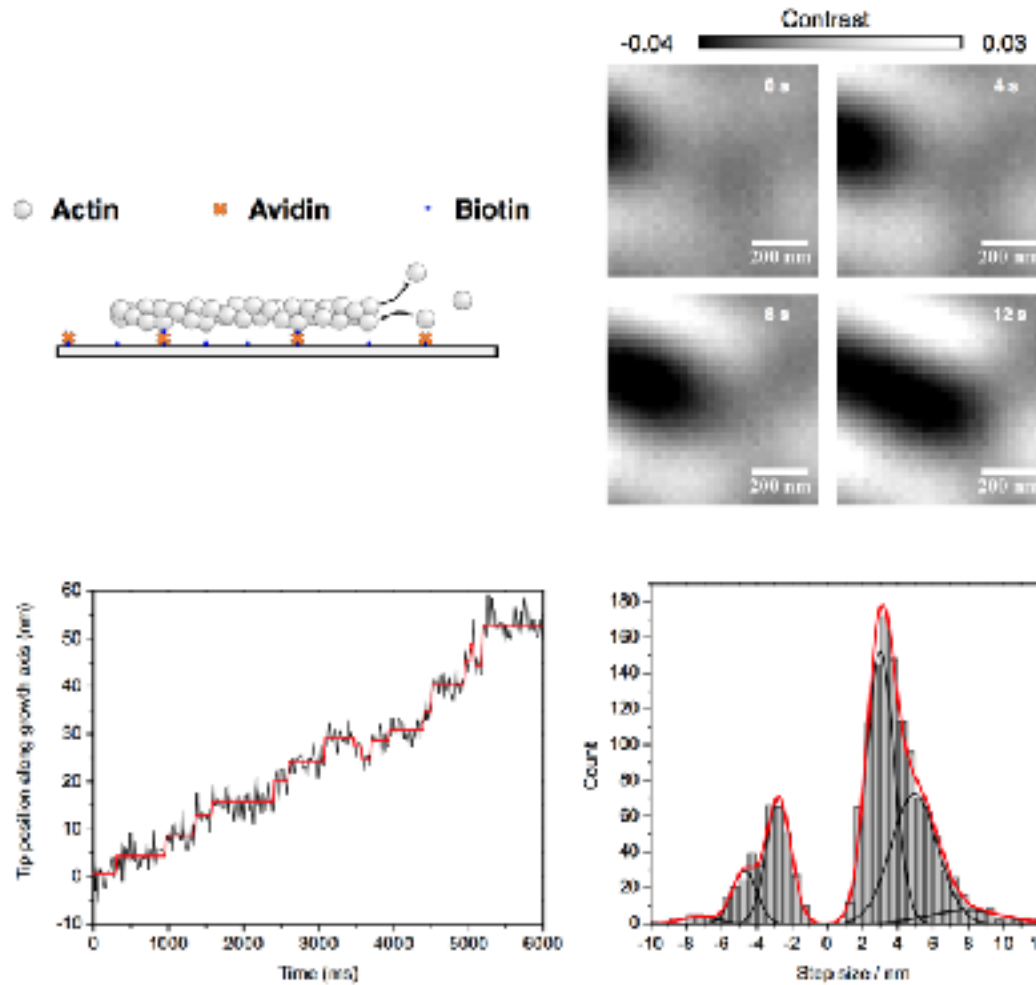


DOPC/DOPS membrane, 50 μ M α -synuclein, 35 fps

Example 2: actin polymerisation



Example 2: actin polymerisation



Justin Benesch

Weston Struwe

Jim Sellers & Harry Takagi

Cedric Eichmann & Phil Selenko

'GANDAM'



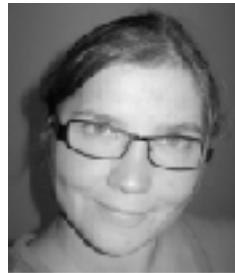
Gavin Young



Daniel Cole



Adam Fineberg



Joanna Andrecka



Nicolas Hundt