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ESC7: Single molecule approaches

MOSBRI Lecture on Optical Tweezers

Katarzyna (Kasia) Tych

rijksuniversiteit groningen

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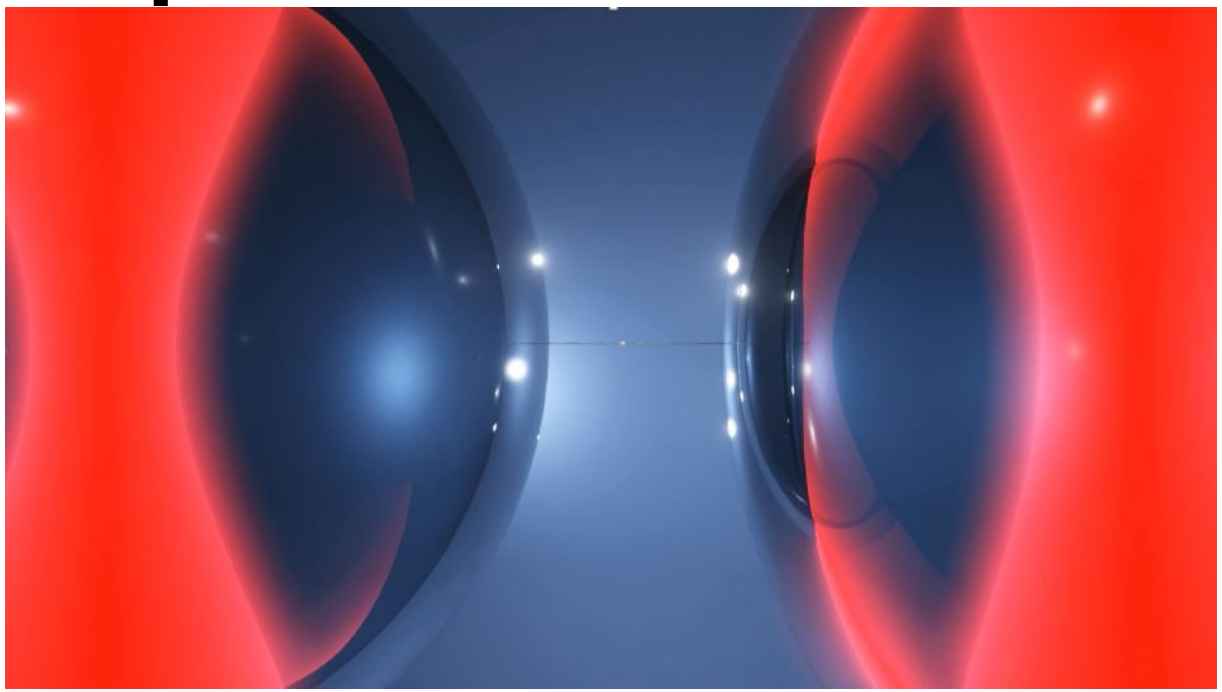
MOSBRI Lecture on Optical Tweezers



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Radiation pressure

Momentum

$$\boldsymbol{p} = m\boldsymbol{v}$$

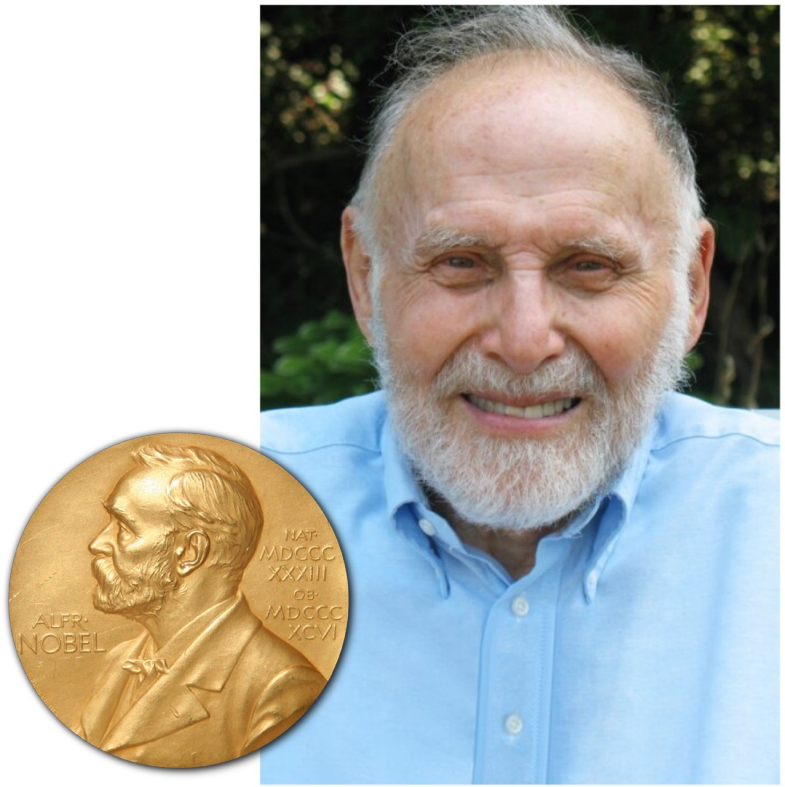
$$\boldsymbol{p} = \frac{h}{\lambda}$$

Second Law

$$\boldsymbol{F} = m\boldsymbol{a}$$

$$\boldsymbol{F} = \frac{d\boldsymbol{p}}{dt}$$

First Demonstration of Optical Tweezers



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LETTERS

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Trapping of Atoms by Resonance Radiation Pressure

A. Ashkin
Bell Telephone Laboratories, Holmdel, New Jersey 07733
(Received 17 October 1977)

A method of stably trapping, cooling, and manipulating atoms on a continuous-wave basis is proposed using resonance radiation pressure forces. Use of highly focused laser beams and atomic beam injection should give a very deep trap for confining single atoms or gases at temperatures $\sim 10^{-6}$ °K. An analysis of the saturation properties of radiation pressure forces is given.

A method of optically trapping and cooling atoms on a continuous-wave (cw) basis is proposed based on radiation pressure forces. The new trap geometry provides stable confinement, optical damping, and means for optical manipulation of trapped atoms. Injection into the trap is from an atomic beam. The radiation pressure trapping forces used are the scattering force due to spontaneous emission[1-4] and the ponderomotive force[5-9] which exists on the induced atomic dipole in an optical field gradient. It is known that the scattering force can increase,[1,2,4] decrease,[3] or deflect[2,10] atomic velocities. Dipole gradient forces can be attractive or repulsive giving optical self-defocusing or self-focusing[5] as well as novel beam interaction forces[6] and a possible means of accelerating atoms.[8] Proposals exist for optically trapping atoms dynamically[2] and statically.[9] This proposal, based on a new treatment of the saturation of these forces and a new geometry, results in a trap with remarkable properties. The trapping energy is more than two orders of magnitude greater than previous proposals,[9] it can accept $\sim 10^7$ atoms, cool them to about a single photon momentum ($\sim 10^{-6}$ °K), and hold them indefinitely even as single atoms. The technique should have wide application in experiments in atomic physics.

Consider the behavior of the proposed trap qualitatively. Light from two opposing TEM_{00} mode beams is focused at points Q_1 and Q_2 located symmetrically about point E [see Fig. 1(a)]. The beams grow in radius from w_0 to $13w_0$ in going

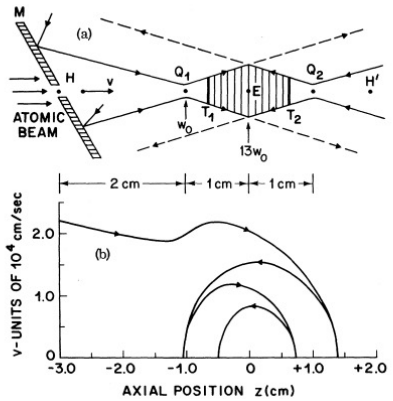
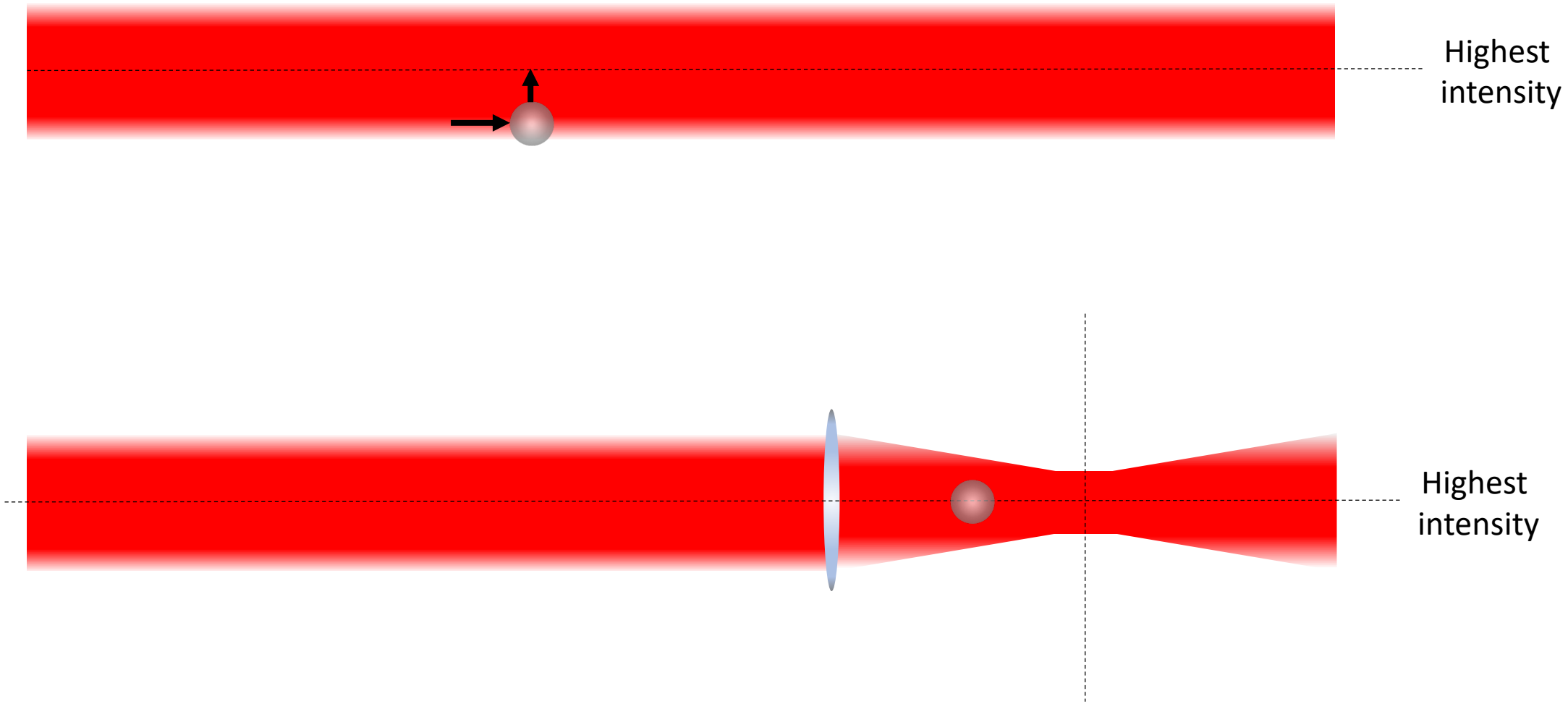


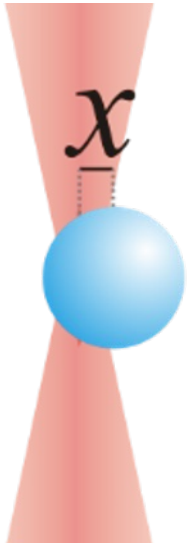
FIG. 1. (a) Sketch of the proposed optical trap for atoms; $w_0 \cong 12$ μm. (b) Calculated trajectory of an atom injected through H with $v = 2 \times 10^4$ cm/sec.

Optical Tweezers



How to calibrate an optical tweezer

What we need for this

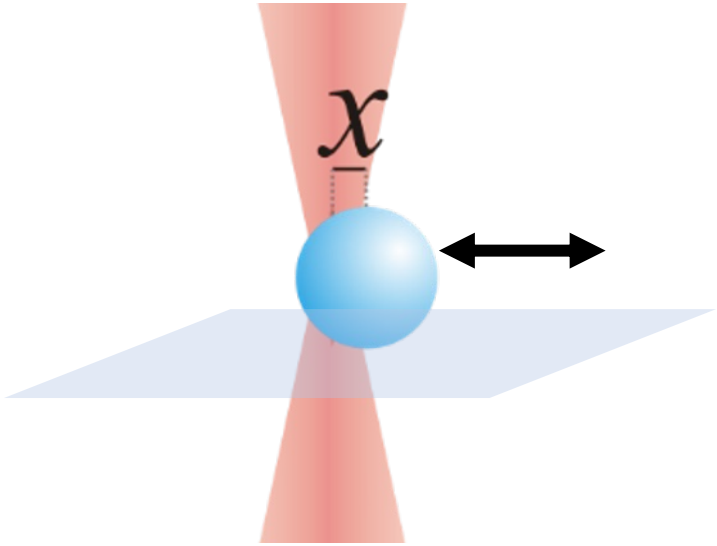


$$F = - k x$$

We need:

- The **trap stiffness**, *k*
- The **distance calibration**

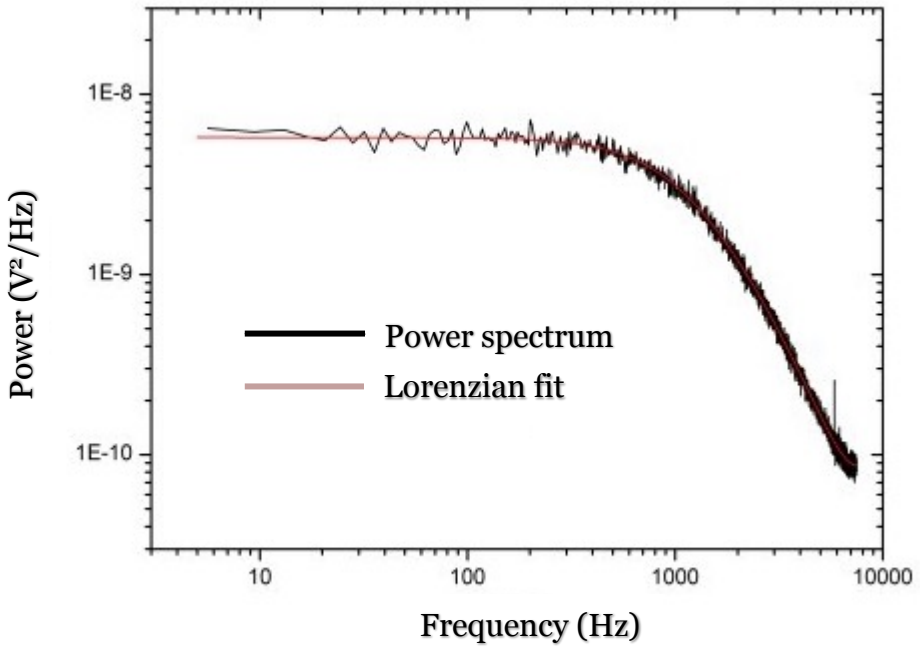
For distance calibration:



- Move the bead (stuck on the glass surface) by a set distance in nm
- Observe the voltage change on the photodetector (gives **nm/V**)

How to calibrate an optical tweezer

Trap stiffness in **pN/nm**: use **a power spectrum** (same as the thermal noise method for AFM)



$$f_c = \frac{k}{2\pi\gamma} \qquad \text{where:} \qquad \gamma = 6\pi\eta r$$

Advantages:

+ Simple
+ Does not depend on the position calibration

Disadvantages:

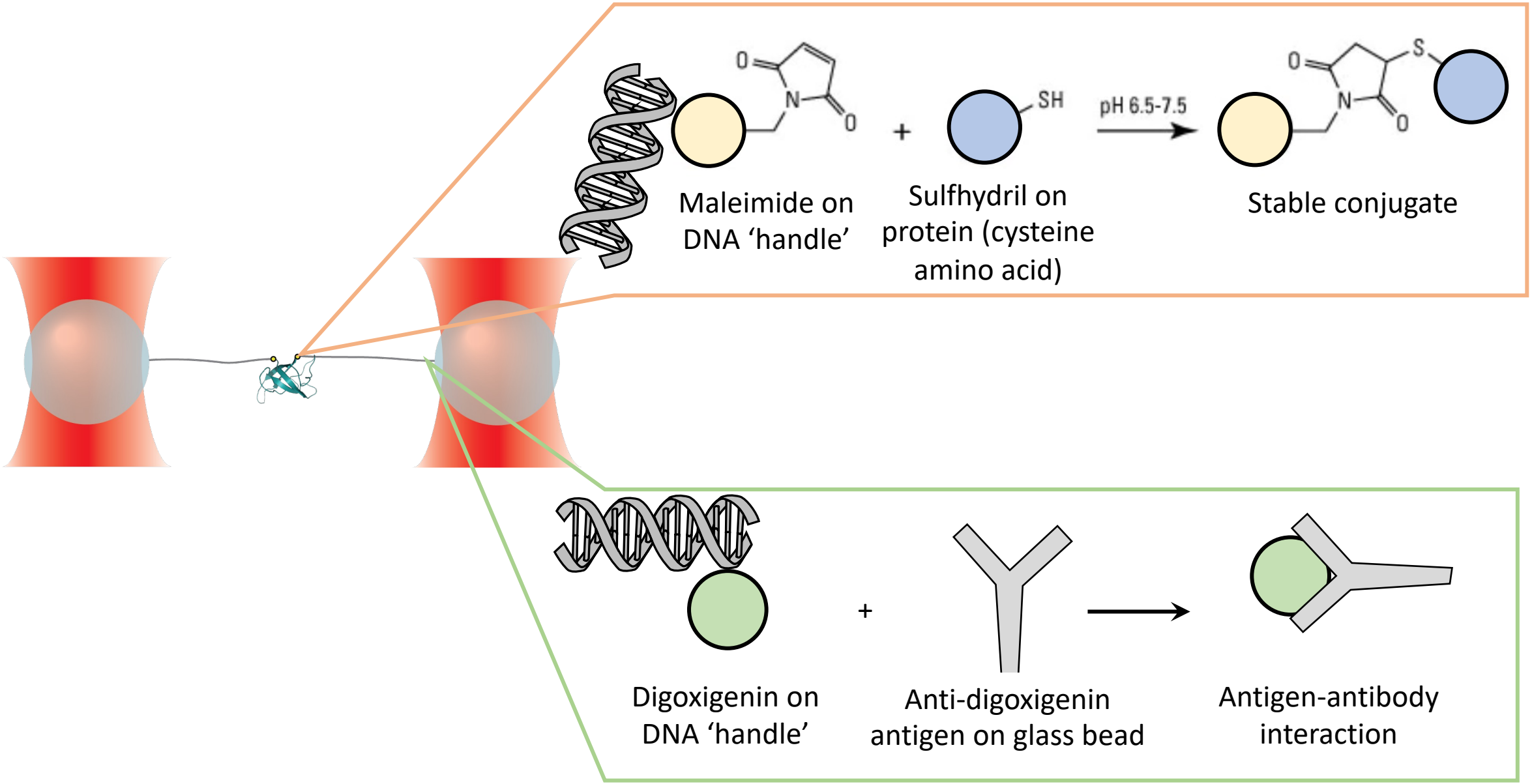
– High uncertainty (approx. 20%[1])
– Requires a detector with sufficient bandwidth

Neuman, Keir C., and Steven M. Block. *Review of scientific instruments* 75.9 (2004): 2787-2809.

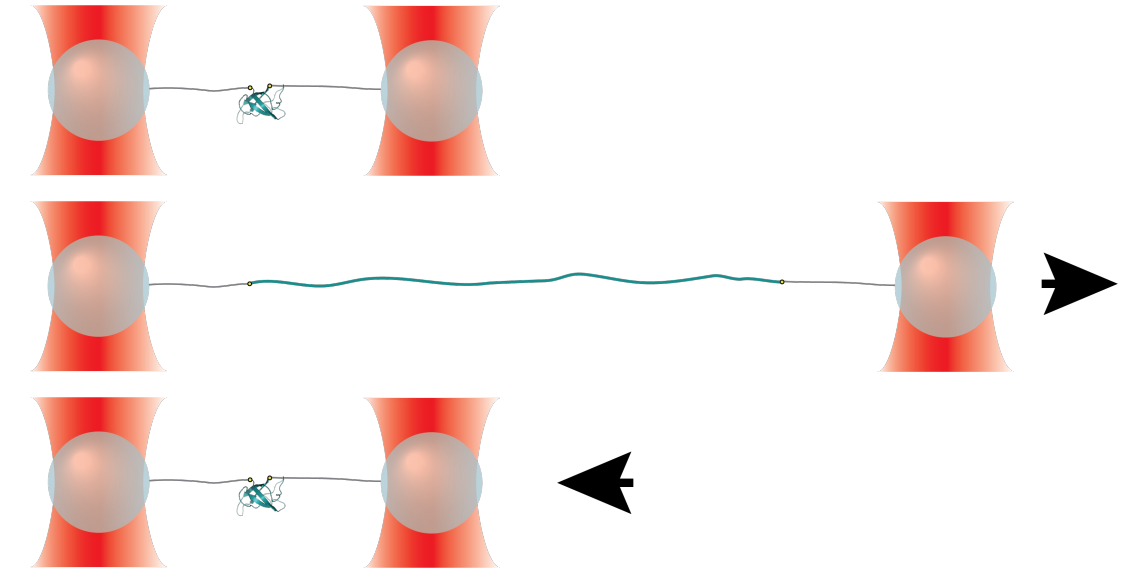
[1]Sarshar, M., W. T. Wong, and B. Anvari. *Journal of biomedical optics* 19.11 (2014): 115001–115001.

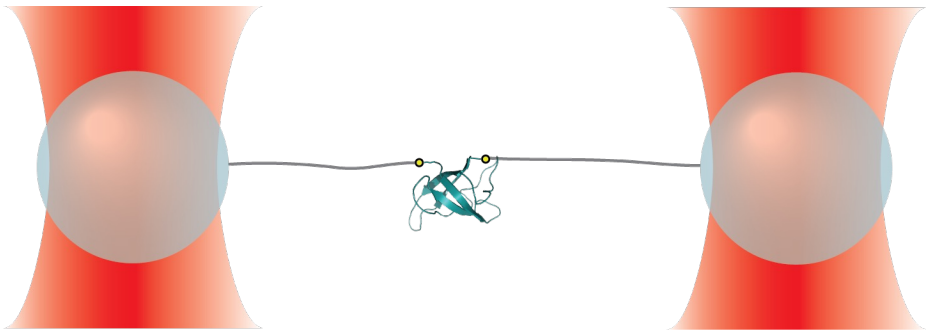
Studying proteins

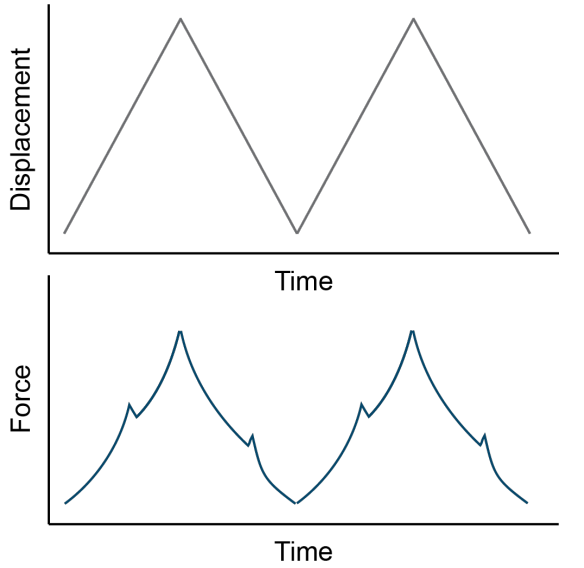
Using optical tweezers to probe proteins

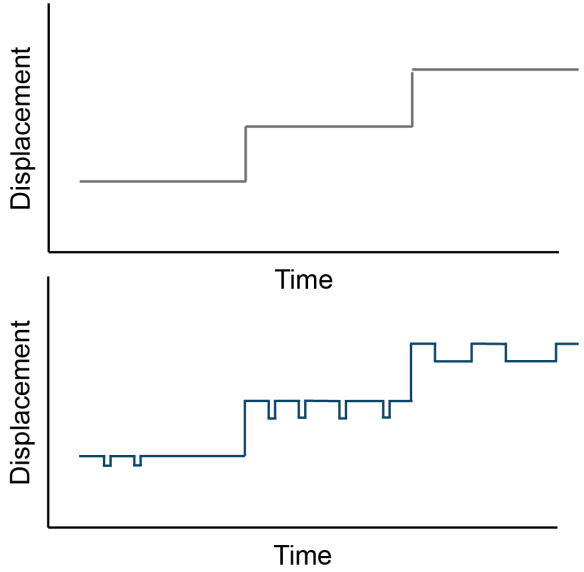


Using optical tweezers to probe proteins

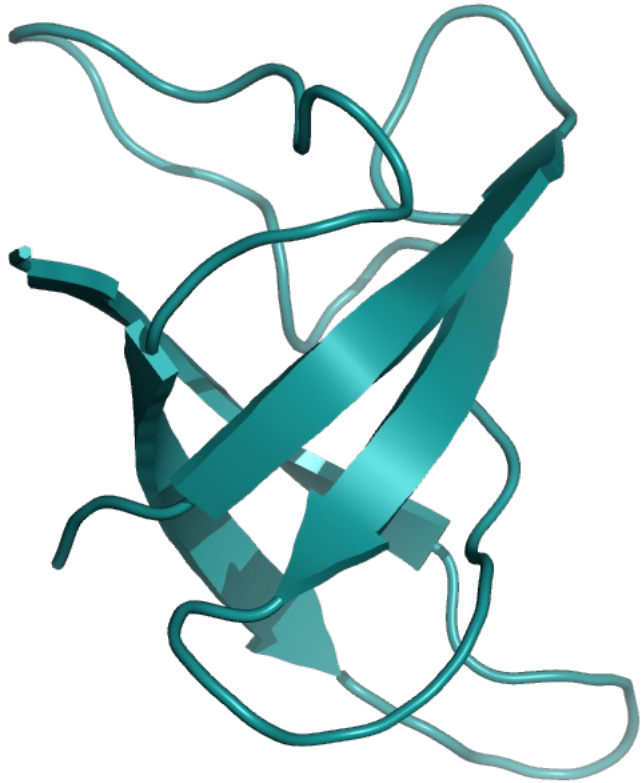






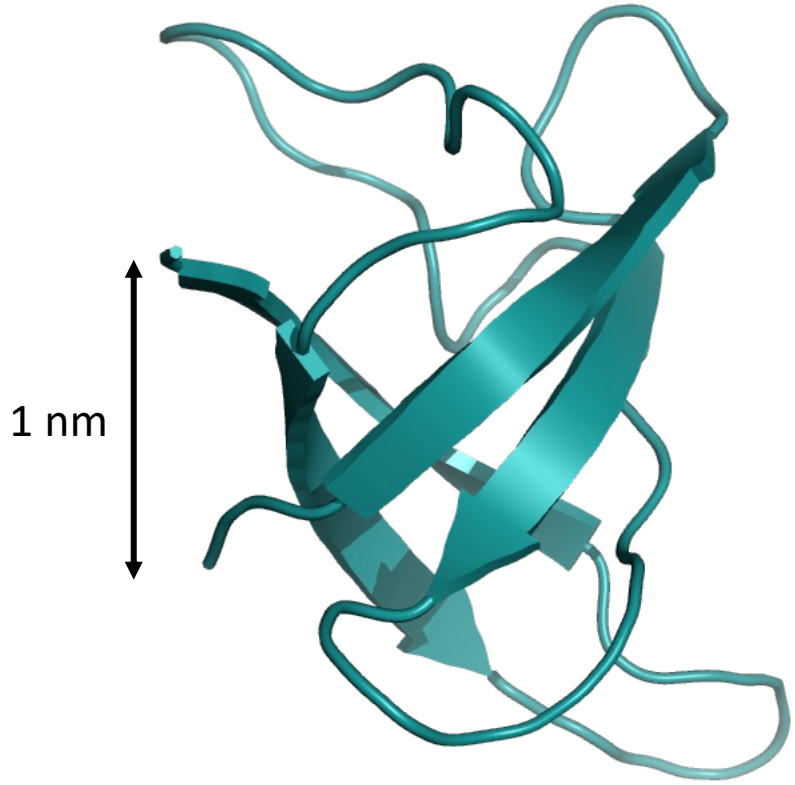


Protein folding/unfolding

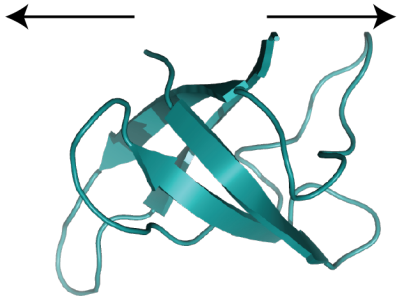


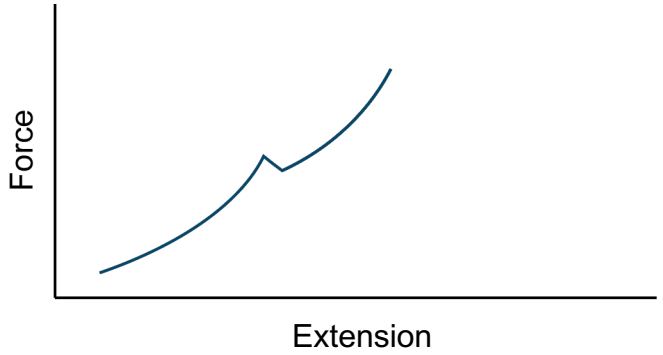
PDB: 1G6P

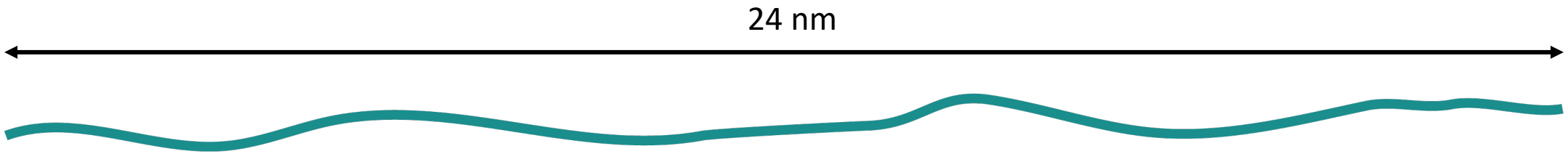
Protein folding/unfolding



Protein folding/unfolding







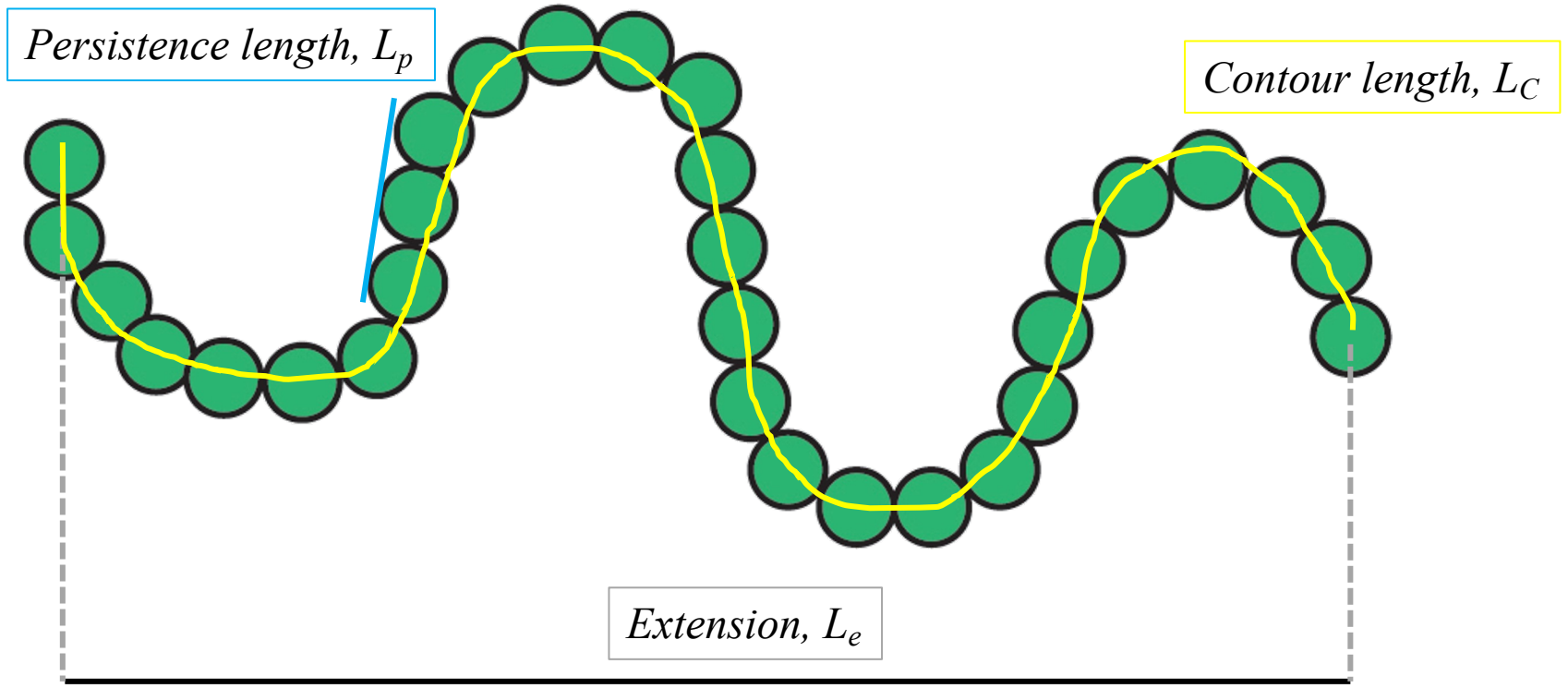
$$\Delta L_{C,expected} = (N \times 0.365nm) - L_{e,initial}$$

$N = number\ of\ amino\ acids\ between\ the\ two\ attachment\ points$

$0.365\ nm = average\ length\ of\ a\ single\ amino\ acid$

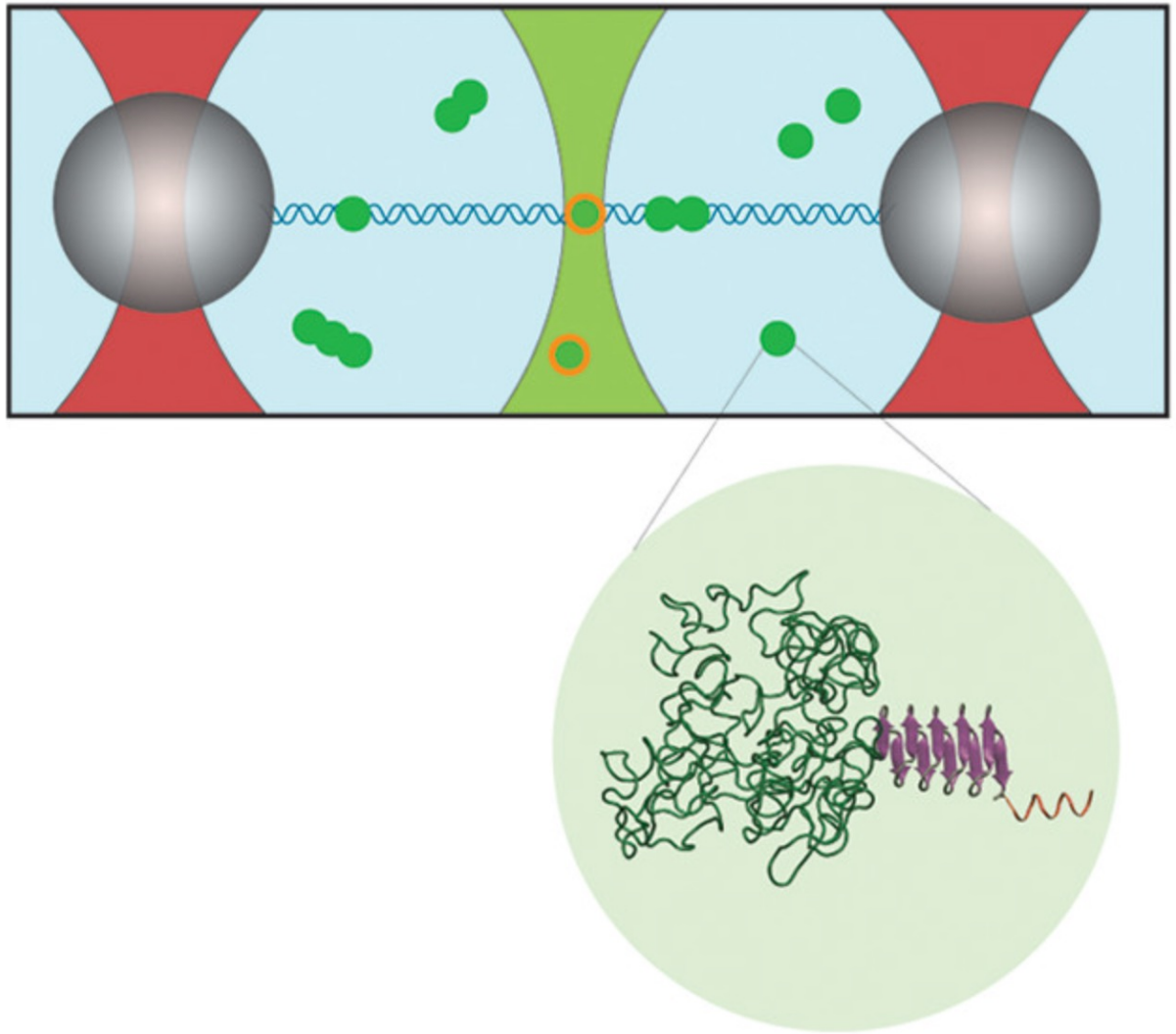
Final length **change** will be 24 nm - 1 nm = **23 nm**

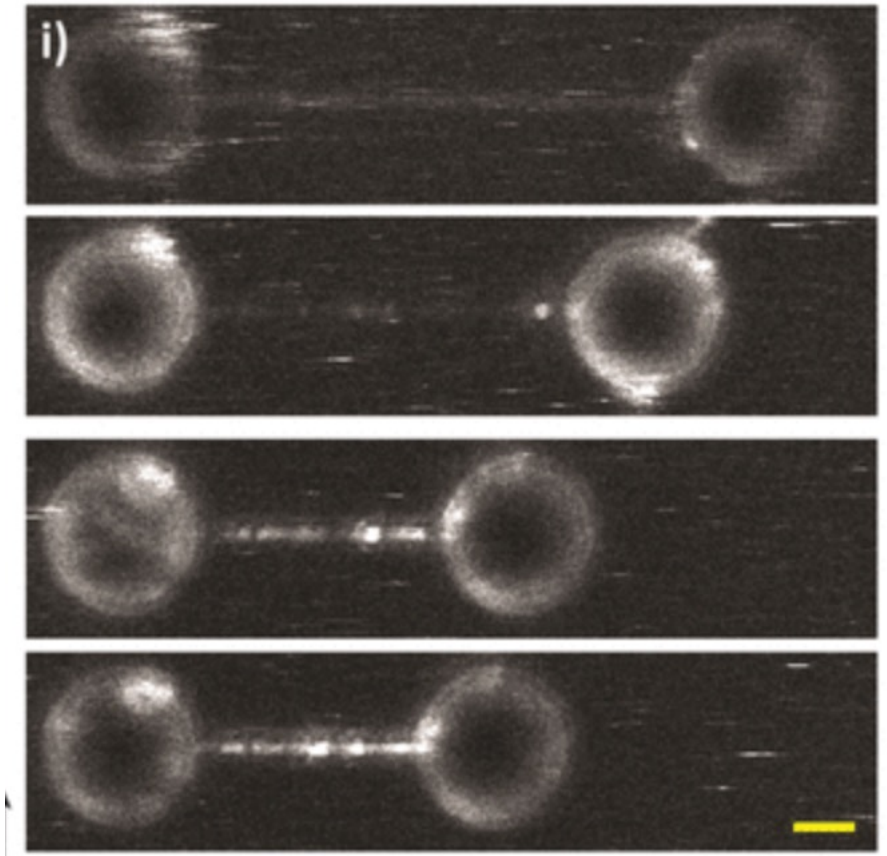
The Worm-Like-Chain Model



$$F = \frac{k_B T}{L_p}\left(\frac{1}{4(1-\frac{L_e}{L_c})} - \frac{1}{4} + \frac{L_e}{L_c}\right)$$

Protein – DNA interactions





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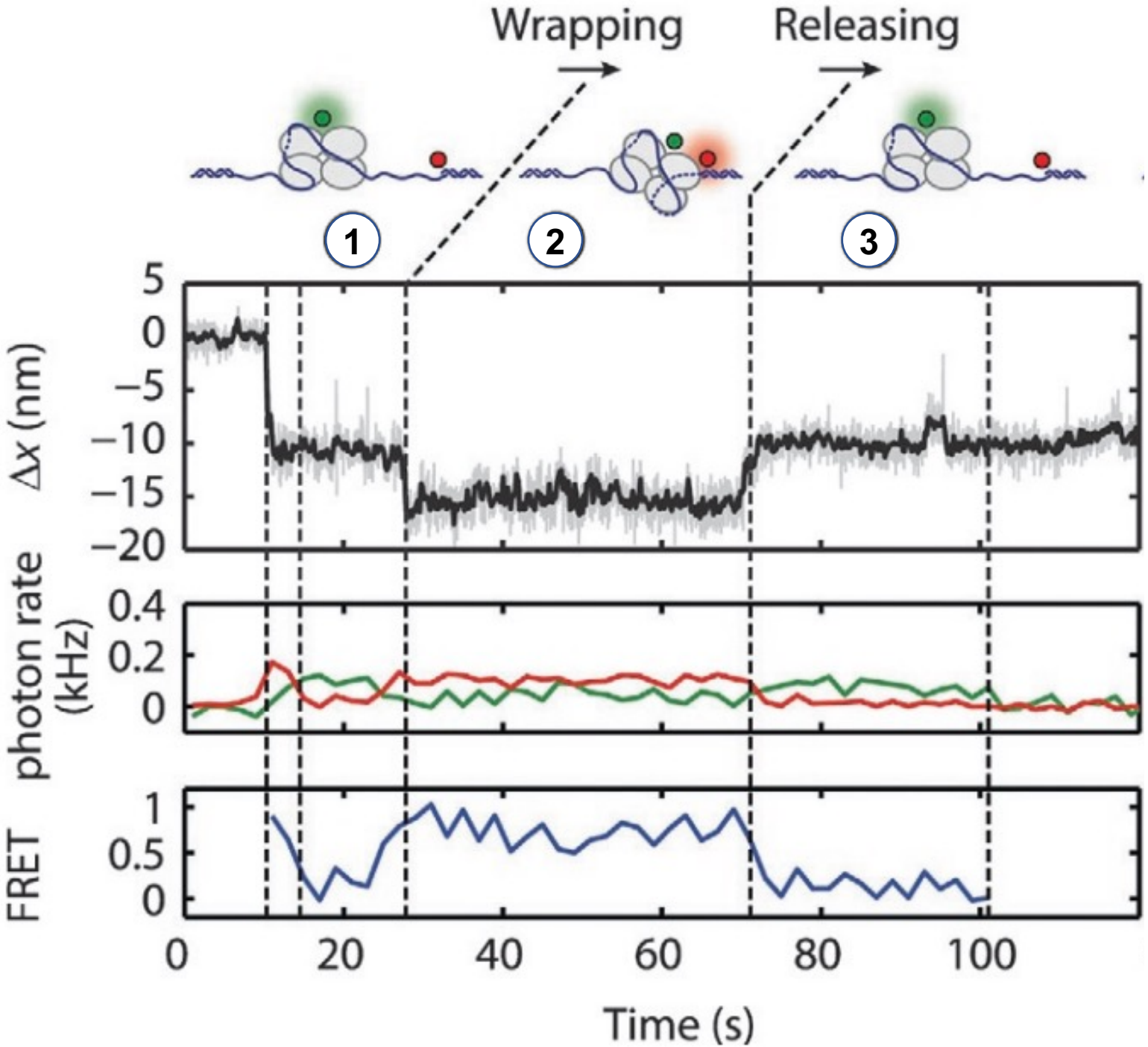
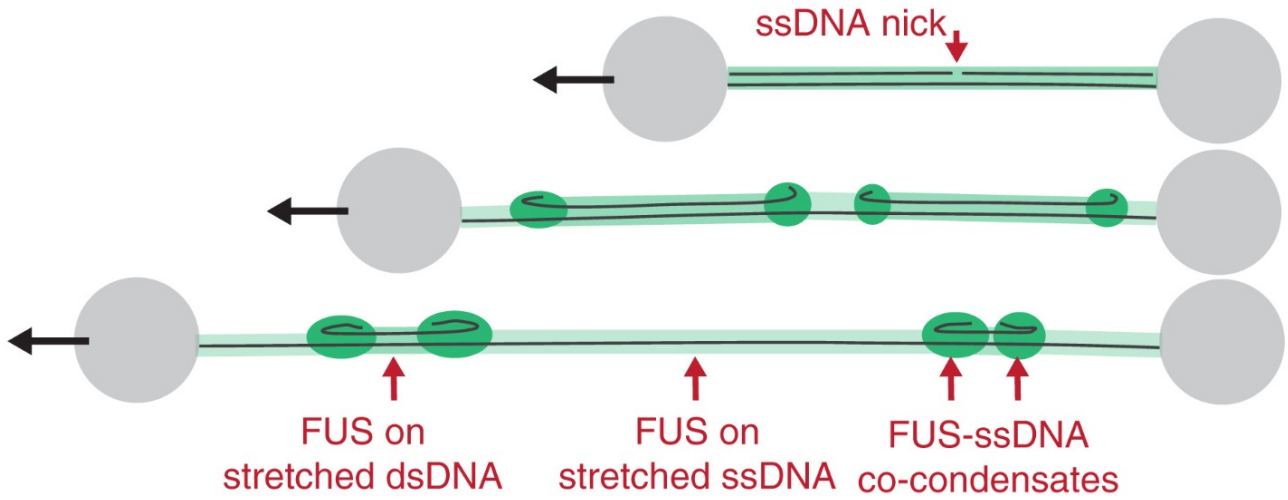


Suksombat, S., *et al*., eLIFE, 4, e08193, 2015



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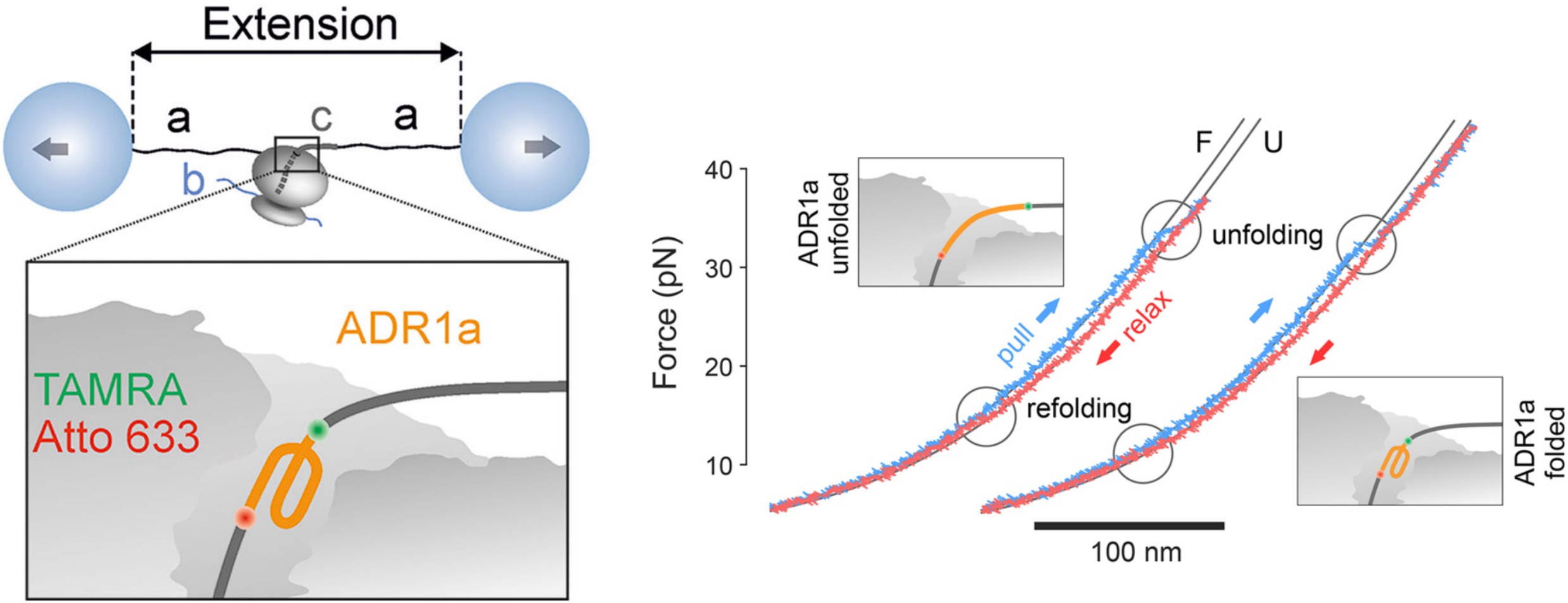
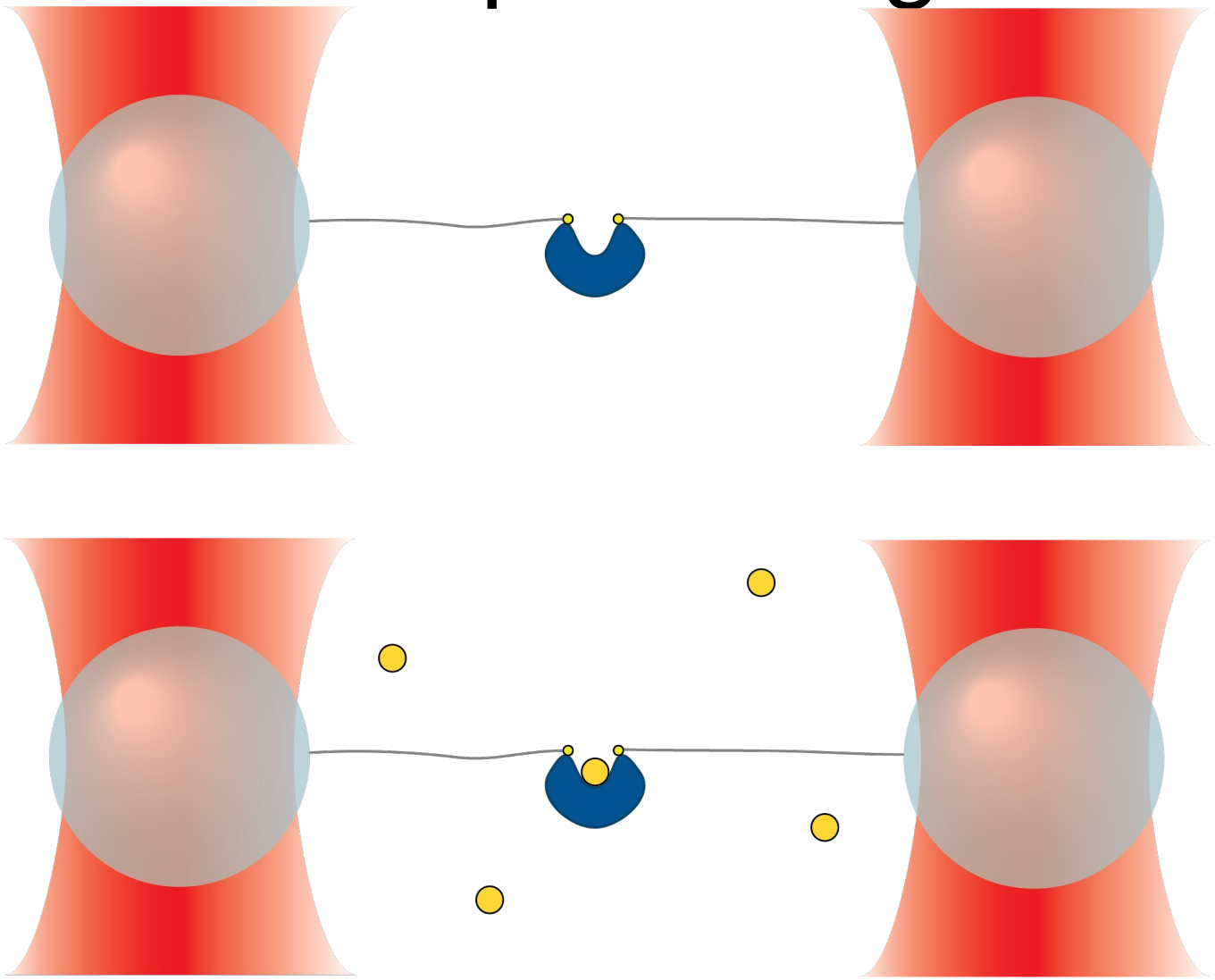
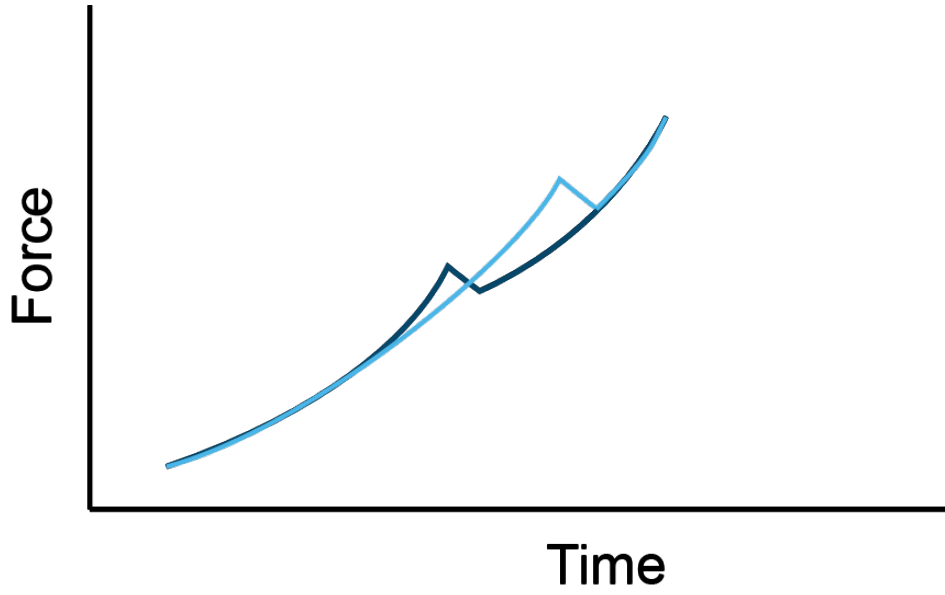


F. Wruck, *et al.*, Communications Biology volume 4, Article number: 523 (2021)

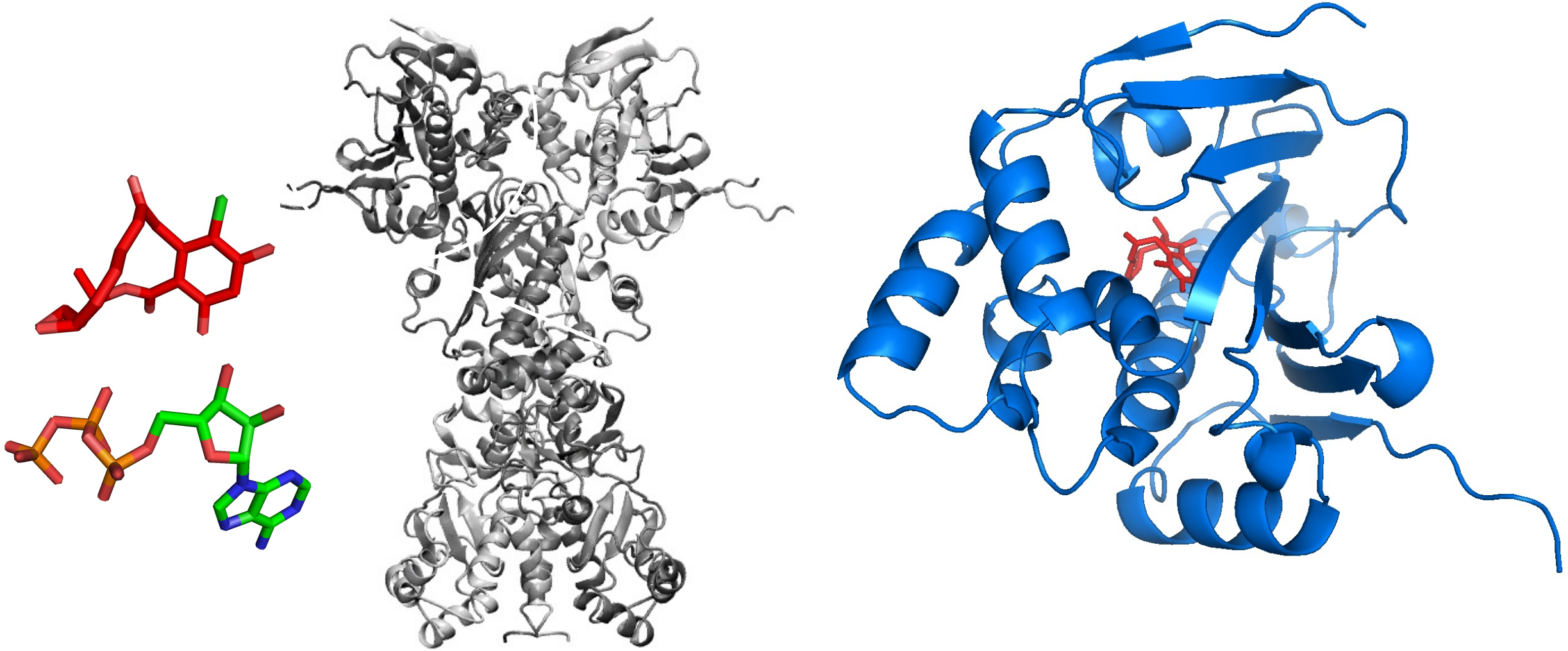
Protein-protein or protein-ligand interactions

Detection and quantification of protein-protein or protein-ligand interactions



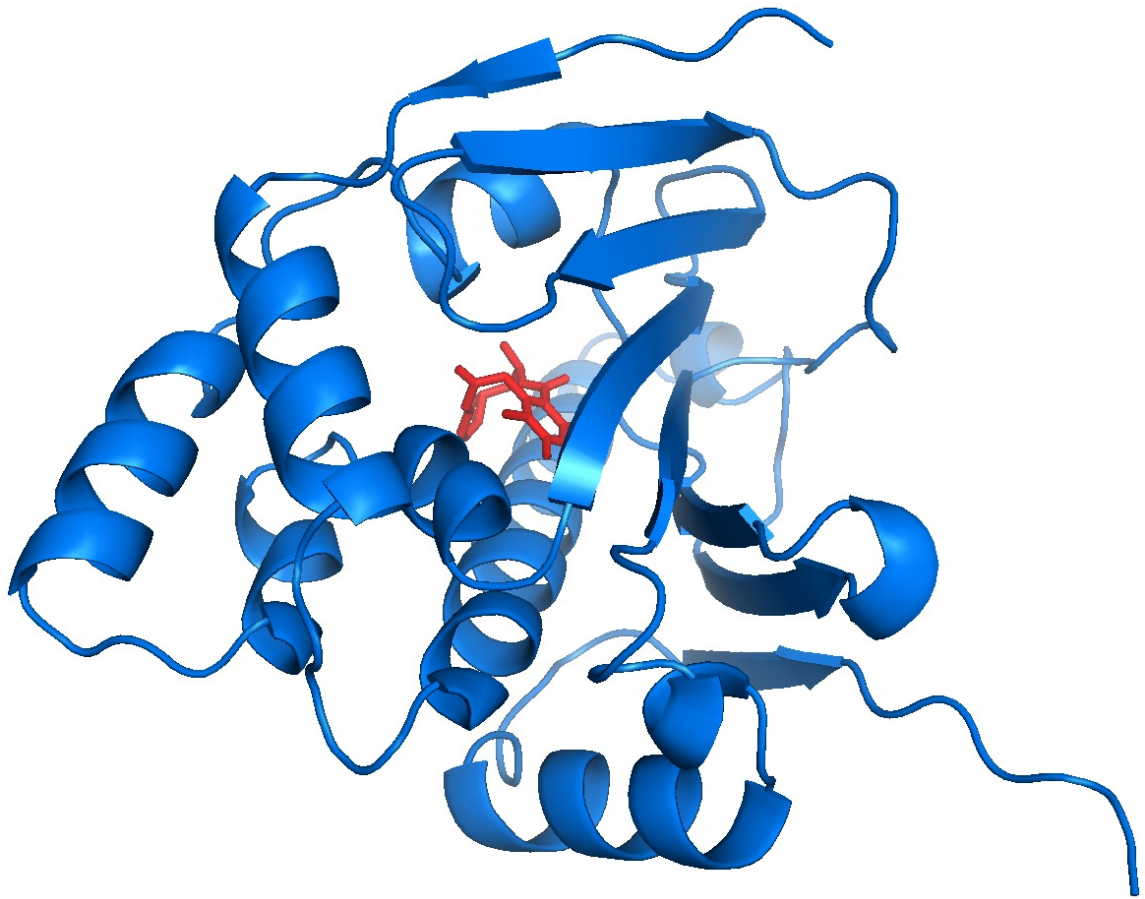


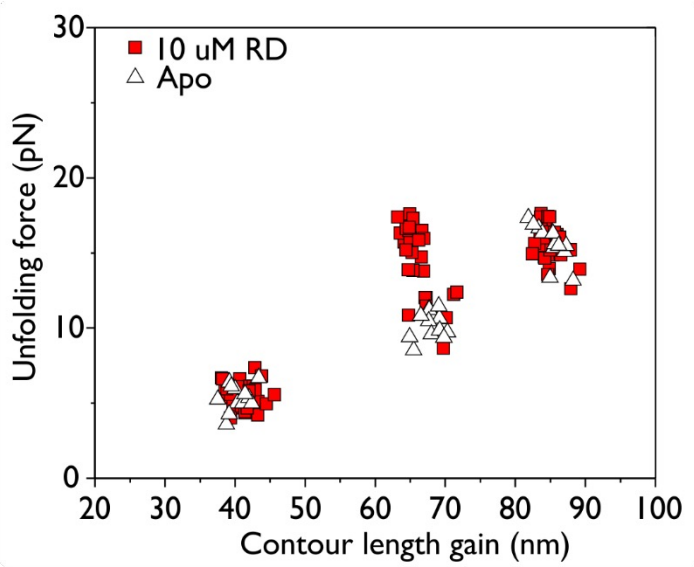
Radicicol and Hsp90



PDB: 1BGQ

Radicicol and Hsp90



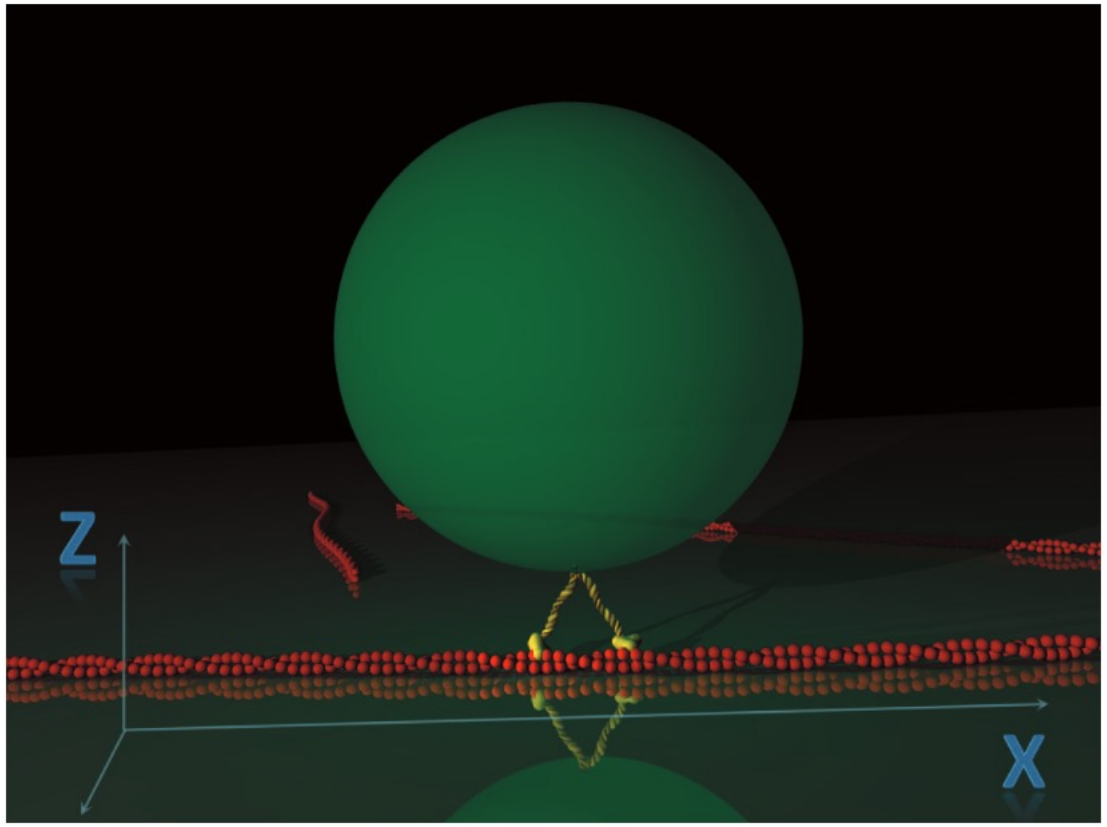


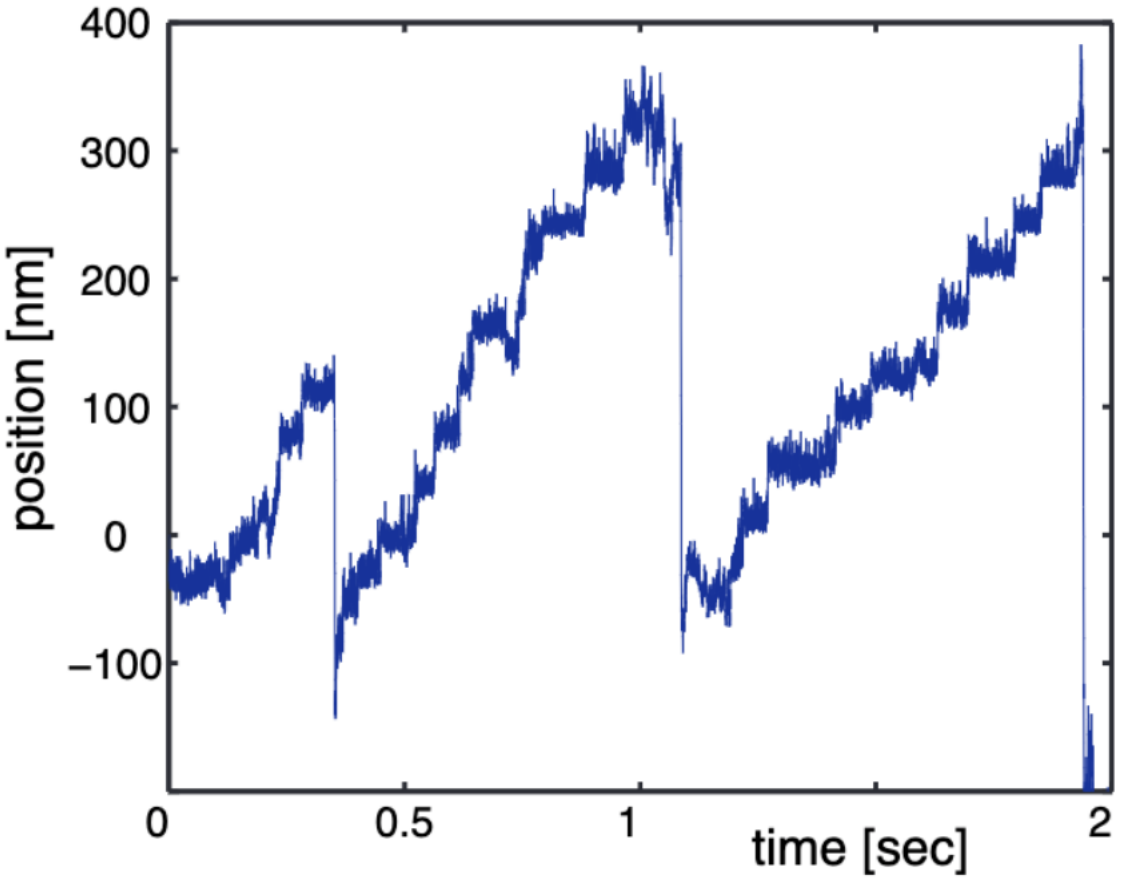
PDB: 1BGQ

H. Girstmair, F. Tippel, A. Lopez, K. Tych, *et al*. Nature Communications 10(1), 2019

Function-related motions of proteins

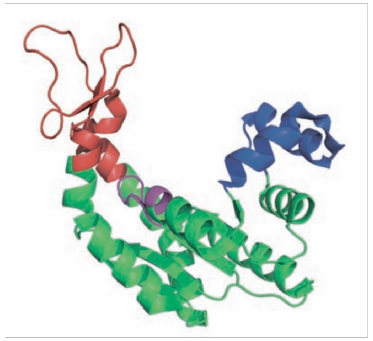
Direct observation of function-related motions

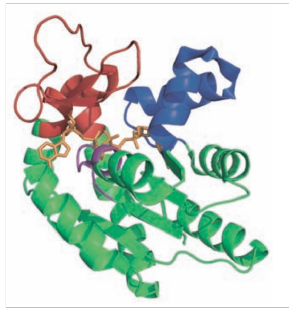


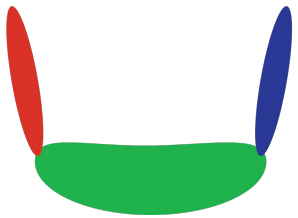


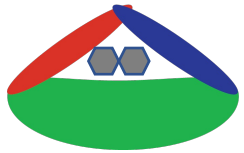
G. Capello, *et al.,* Myosin V stepping mechanism, *PNAS 104(39), 15328 – 15333,* 2007

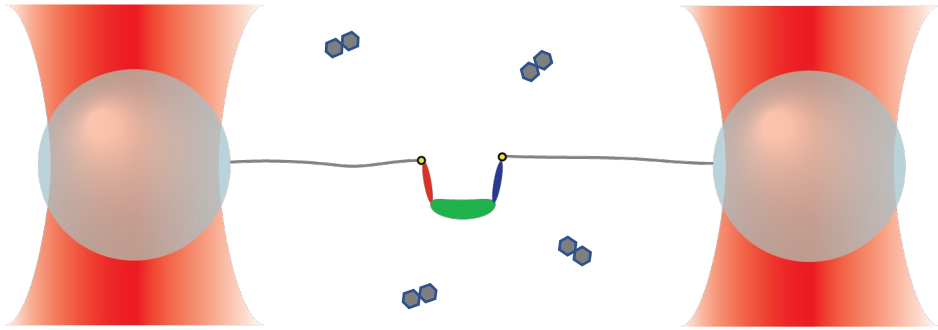
Direct observation of function-related motions

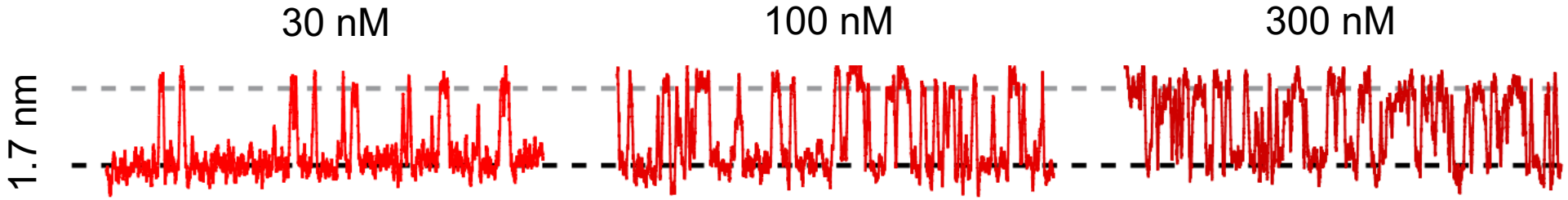






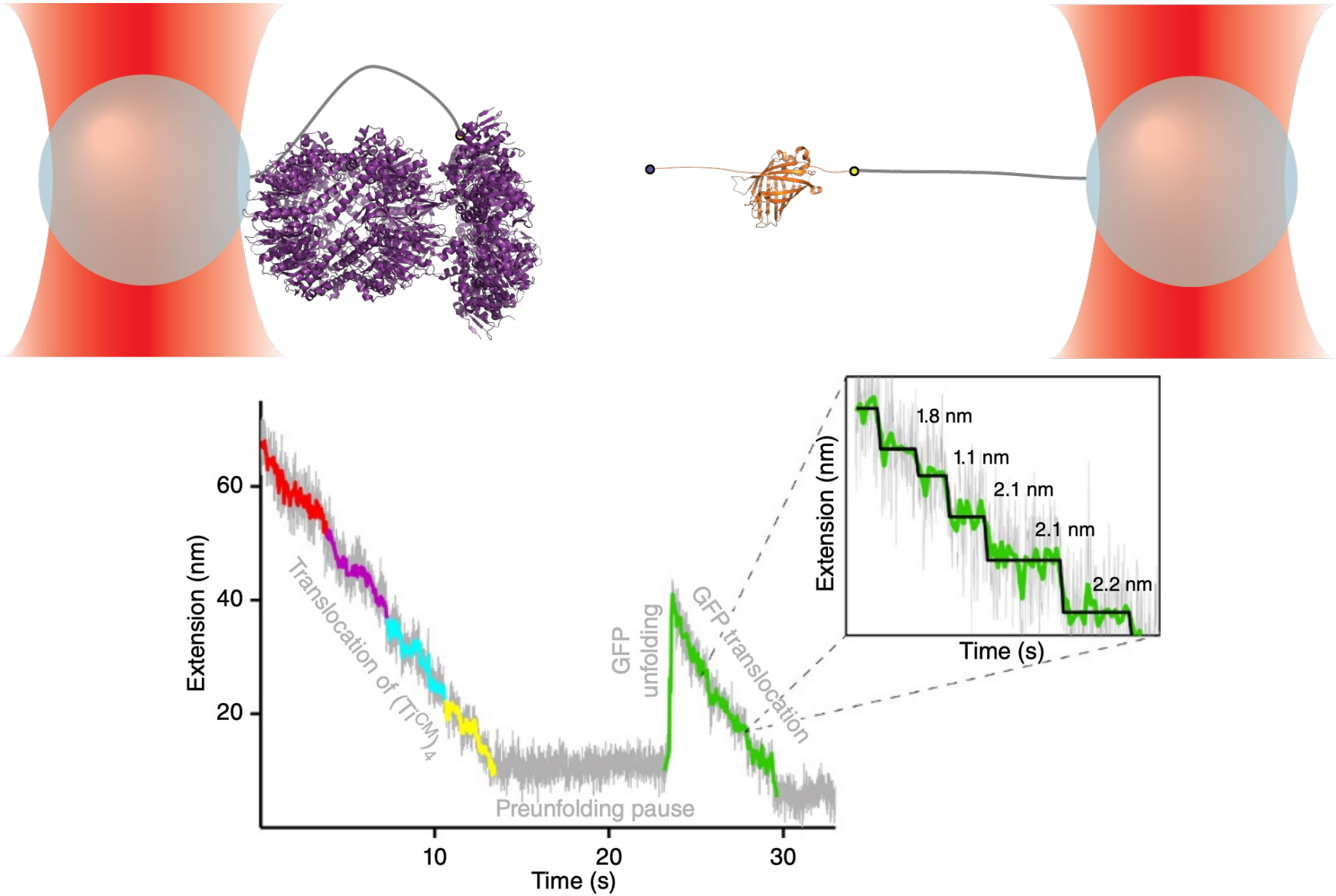






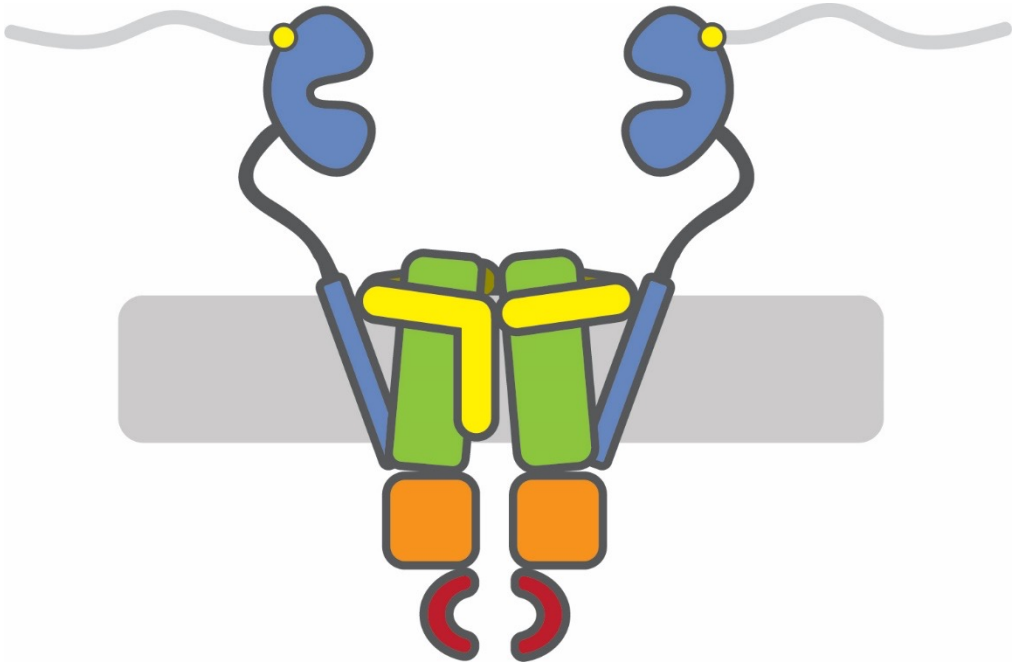
B. Pelz, *et al., Nature Communications* 2016 doi: 10.1038/ncomms10848

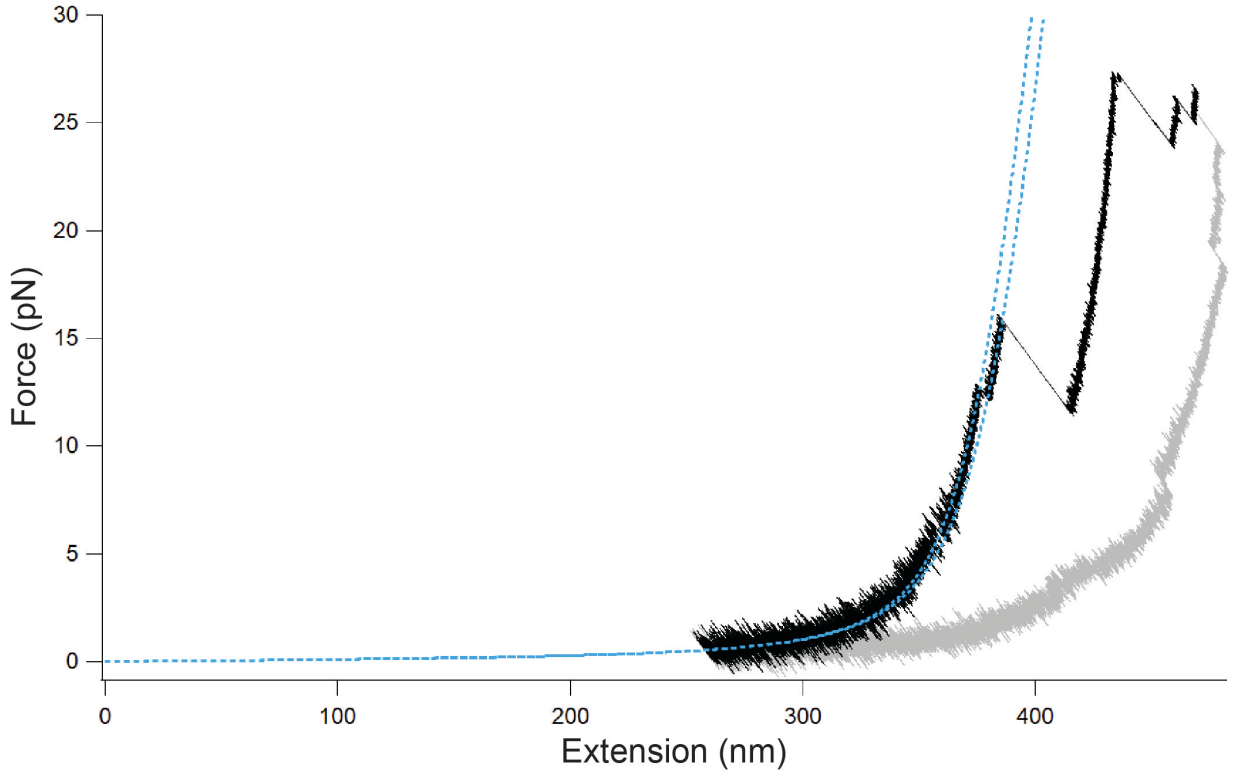
Direct observation of function-related motions



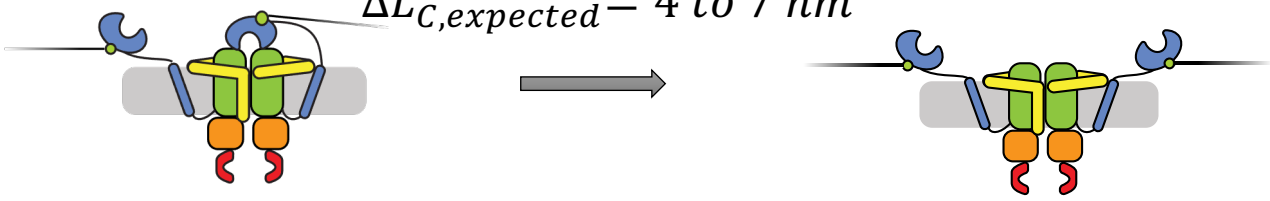
P. Rodriguez-Aliaga, *et al., Nature Structural and Molecular Biology* 2016 doi: 10.1038/nsmb.3298

Membrane proteins

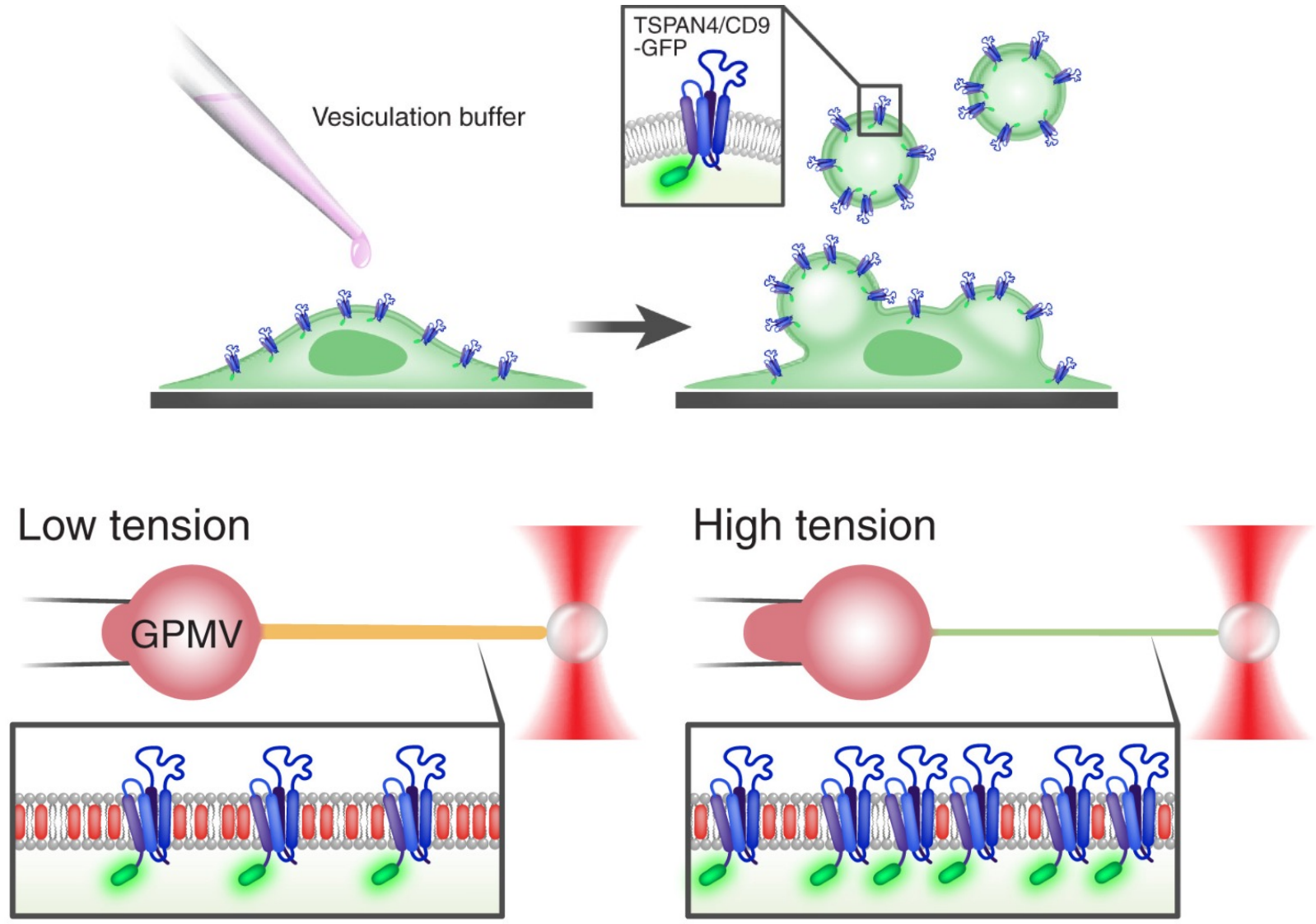




$\Delta L_{C,expected} = 4\ to\ 7\ nm$



https://www.biorxiv.org/content/10.1101/2023.09.01.555951v1



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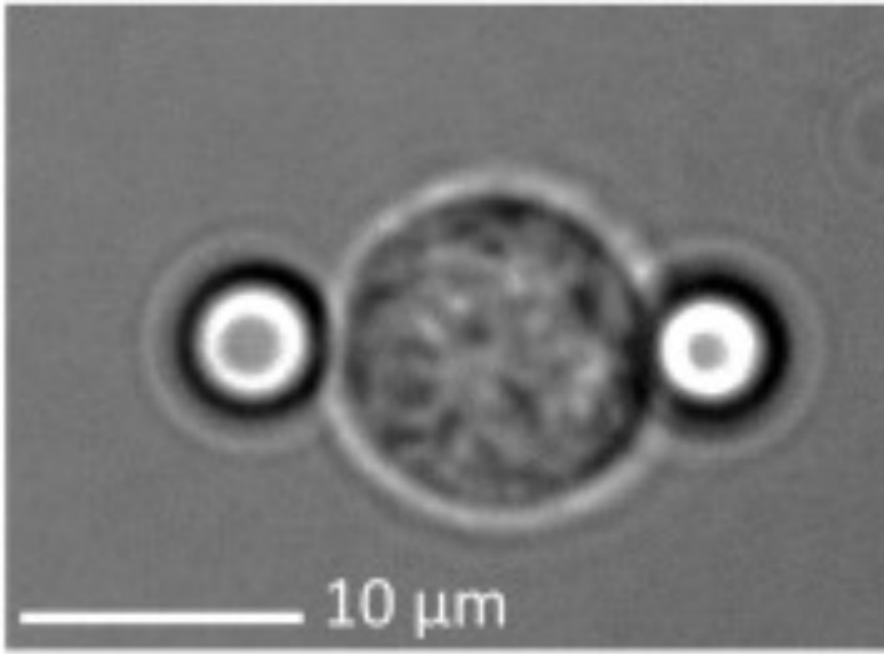
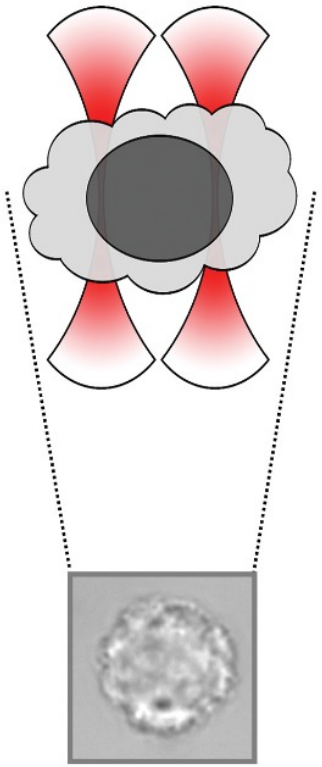
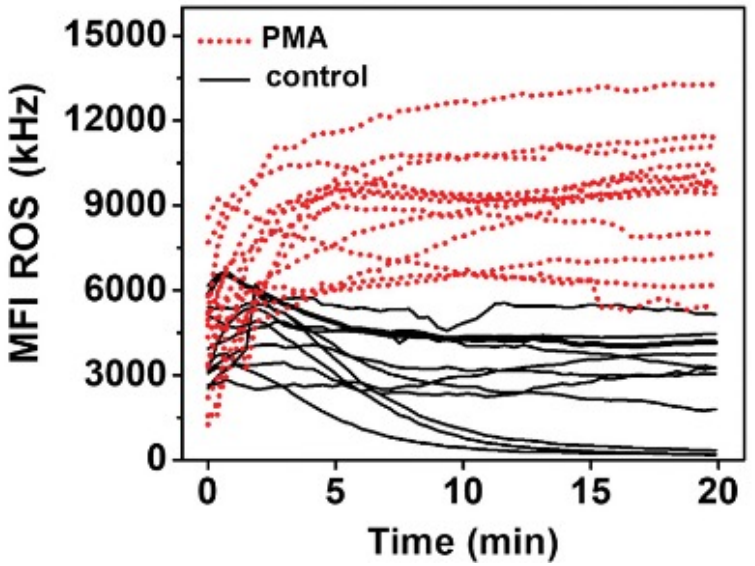
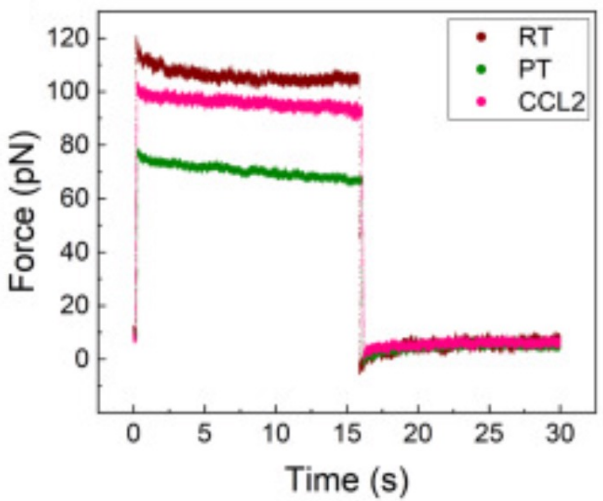
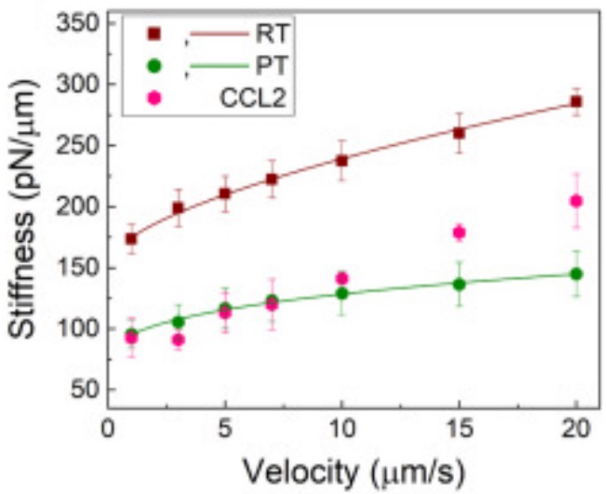
Cell mechanics











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G. Vasse *et al.,* Single Cell Reactomics: Real-Time Single-Cell Activation Kinetics of Optically Trapped Macrophages, *Small methods 5(4), 2021*

Summary