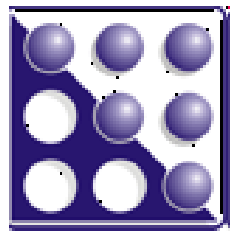


NOTES ON NANO(BIO)TECHNOLOGY

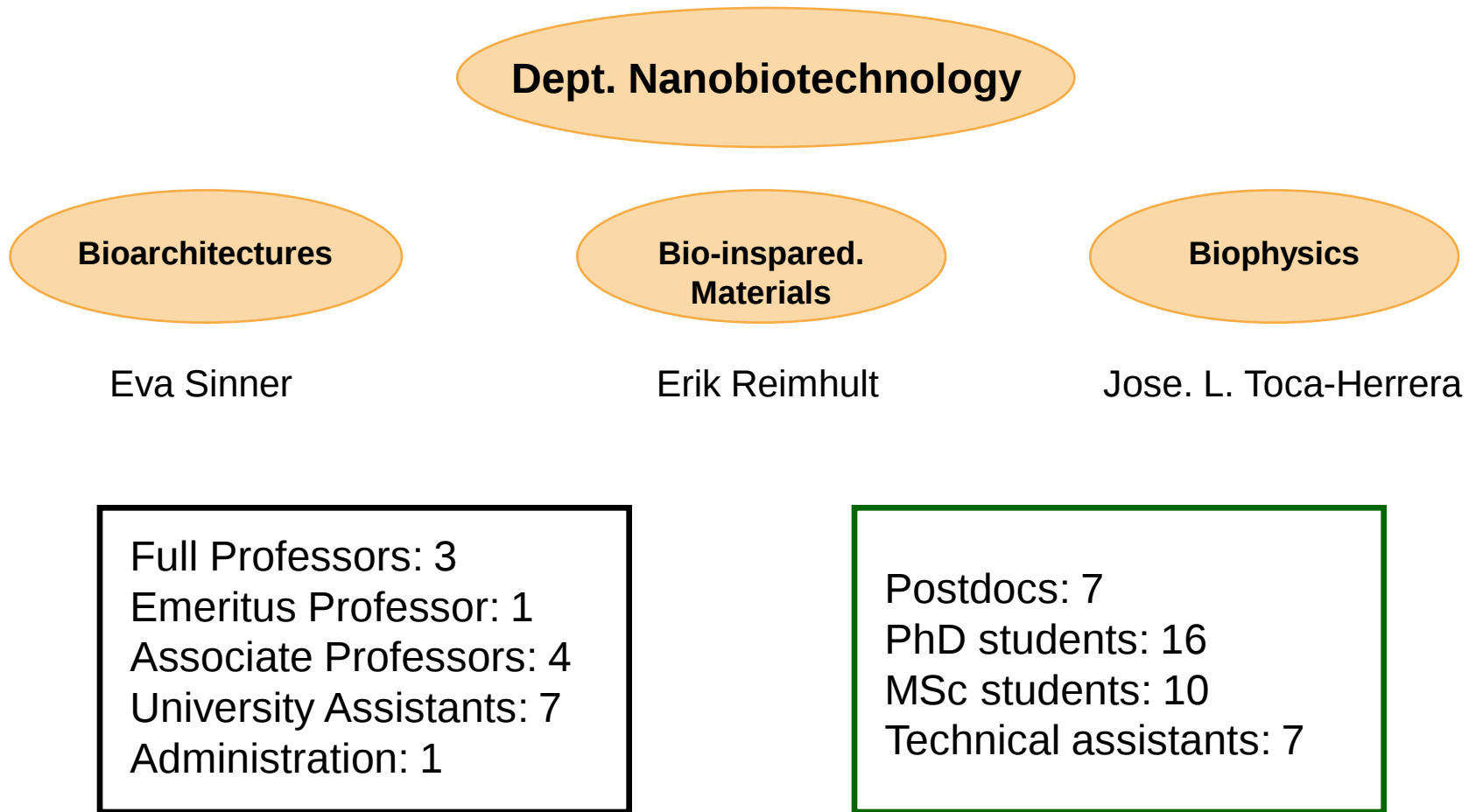
José L. Toca-Herrera

*Institute for Biophysics
Department of Nanobiotechnology (DNBT)
BOKU- University of Natural Resources and Life Sciences
Muthgasse 11, A-1190 Vienna, AUSTRIA*



Vienna (Mödling) – 16/10/2013

Who are we since Sept 2010 - organisation

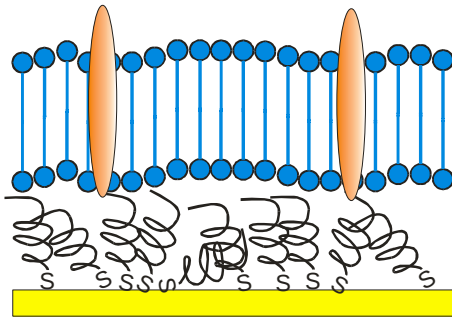


We are also hosting PhD and MSc students of other universities or institutes!

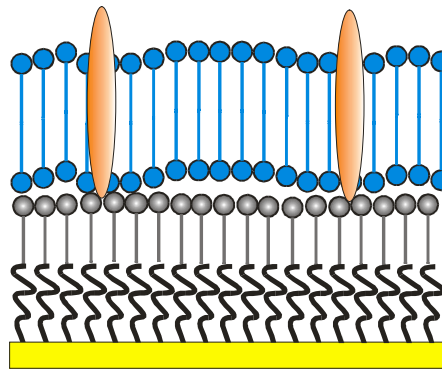
DNBT – Research Eva Sinner



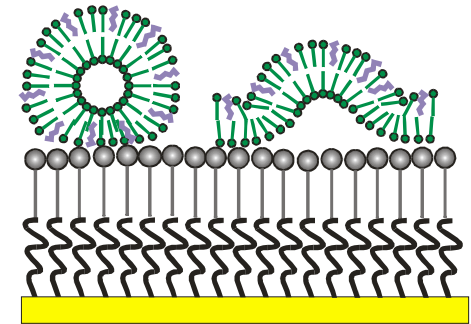
- Synthetic biology is the engineering of biology: the synthesis of complex, biologically based (or inspired) systems which display functions that do not exist in nature



- Peptide P19
- CHO membrane (with *hPepT1*)



- Octadecanethiol
- Lipid
- CHO membrane (with *hPepT1*)

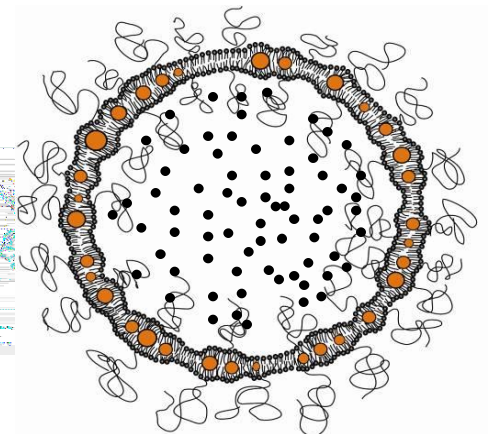
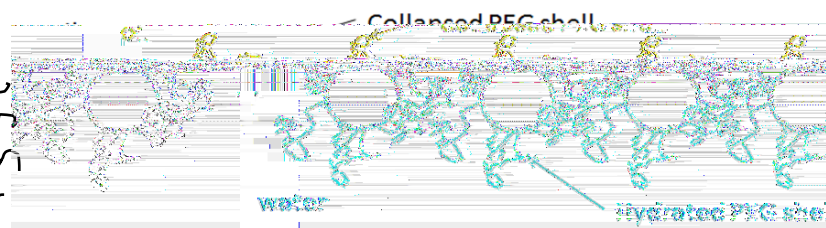
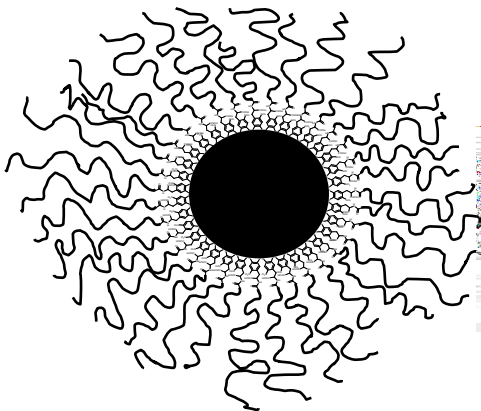


- Octadecanethiol
- Lipid
- PC/Cholesterol vesicles

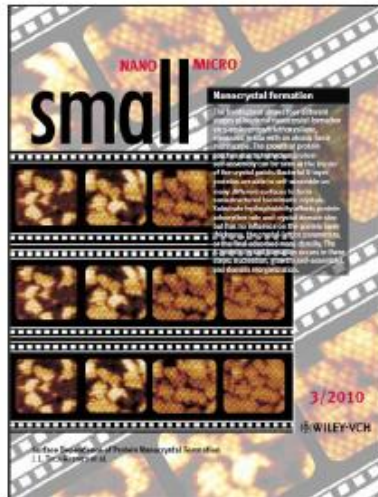
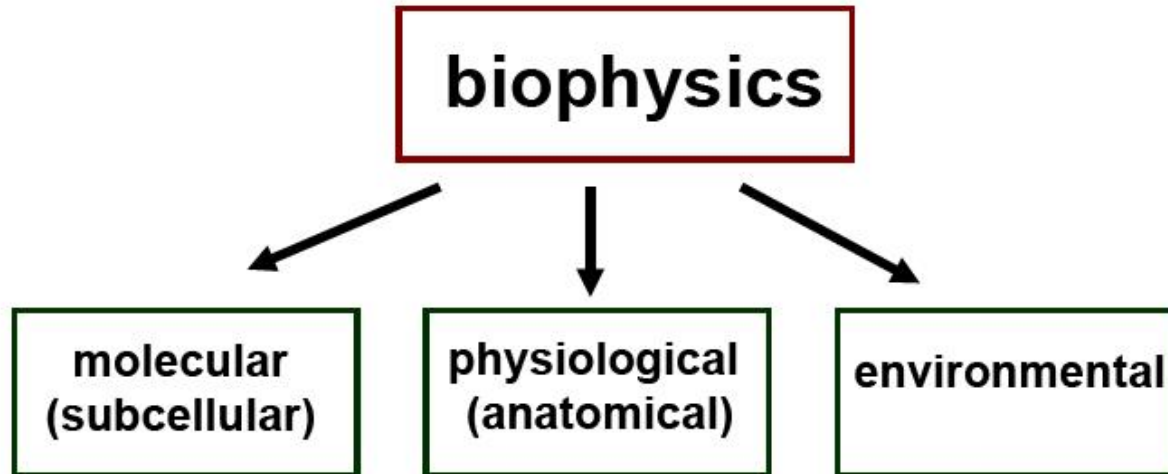
DNBT – Research Erik reimhult



- Supramolecular (bio)materials - nanoscale building blocks enables controlled interfacial assembly
- (Bioinspired) liquid-liquid interfaces allow energy minimization by attaining ordering of adsorbed nanoparticles
- Dispersed nanoparticles can be used as antennas for external actuation of interfacial (membrane) properties without causing structural or environmental degradation



DNBT – Research José L. Toca-Herrera



Biophysics is an interdisciplinary science where physics, biology, chemistry and mathematics all meet

Where are we since sept 2010 ?



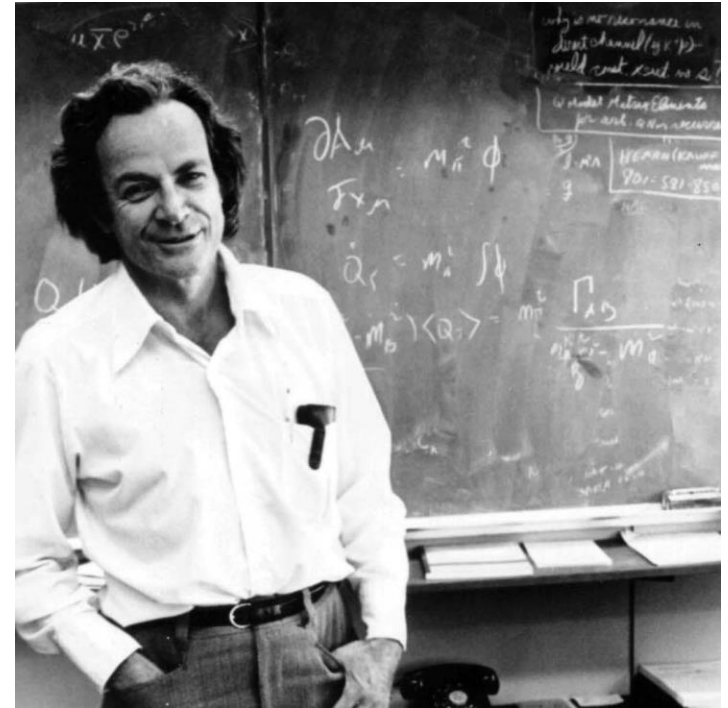
Here !!



Muthgasse 11 (2nd floor), A-1190 Vienna

NANO – When?

I want to build a billion tiny factories, models of each other, which are manufacturing simultaneously. . . The principles of physics, as far as I can see, do not speak against the possibility of maneuvering things atom by atom. It is not an attempt to violate any laws; it is something, in principle, that can be done; but in practice, it has not been done because we are too big.
— Richard Feynman (1959), Nobel Prize winner in physics



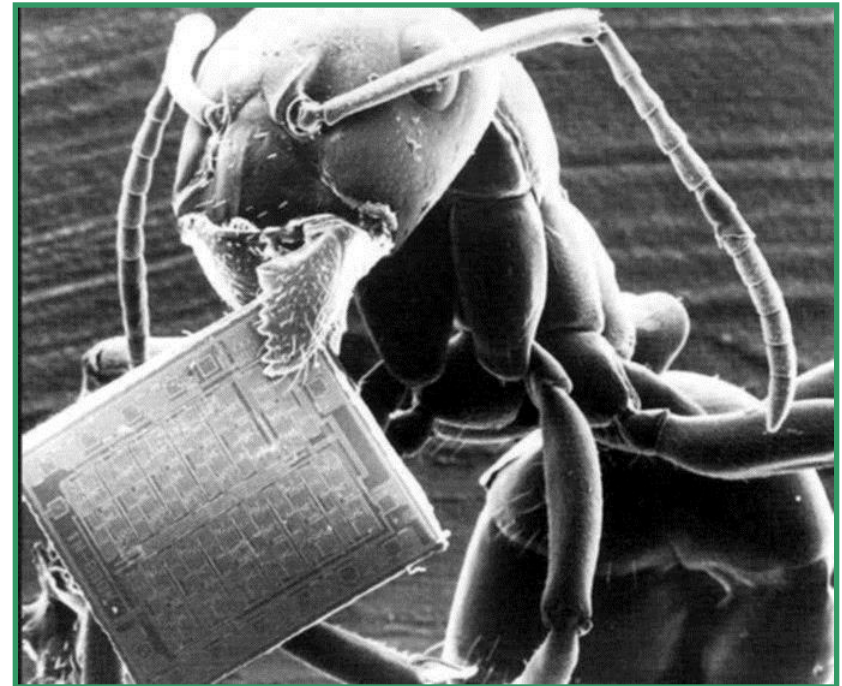
Possible consequences: scanning tunneling microscope and scanning probe microscope, quantum computers....

Link to the lecture: <http://www.youtube.com/watch?v=4eRCygdW--c>

Definition of NanoBiotechnology

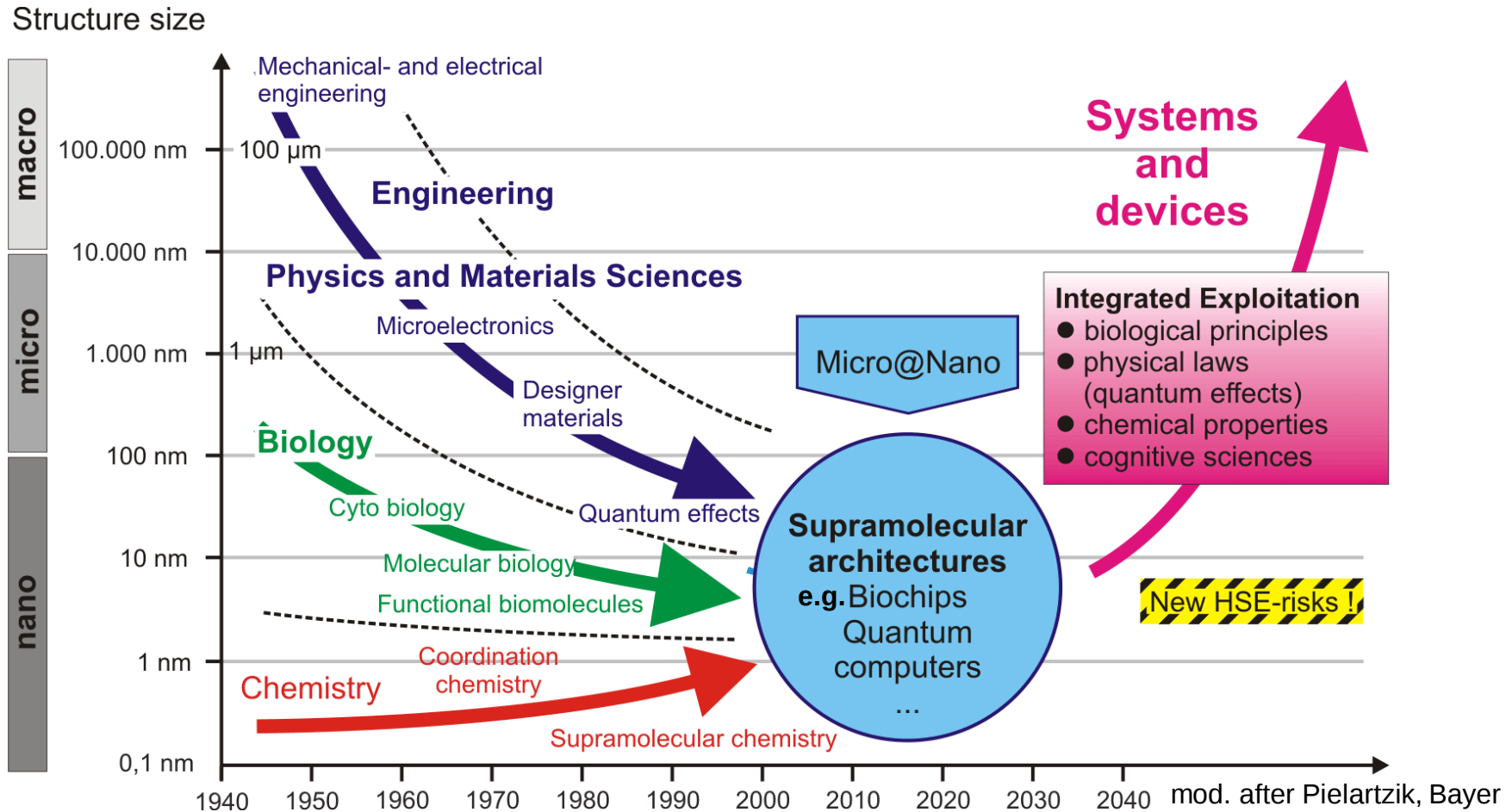
Nanobiotechnology involves the processing, fabrication and packaging of **organic** or **biomaterial** devices or assemblies in which the dimension of at least one functional component lies between 1 and 100nm.

Nanobiotechnology is characterized by its highly inter-disciplinary nature and features a close collaboration between life-scientists, physical scientists, and engineers.



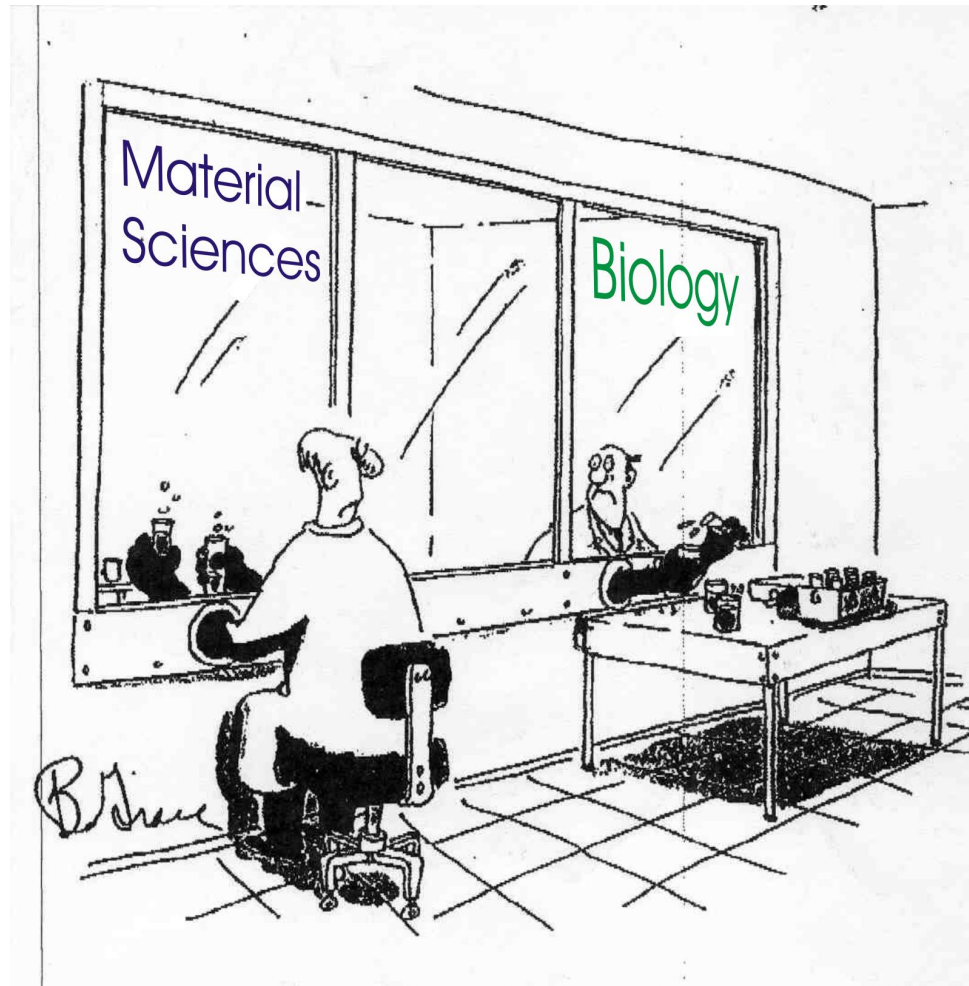
courtesy of FEI-Company, NL

Converging Technologies

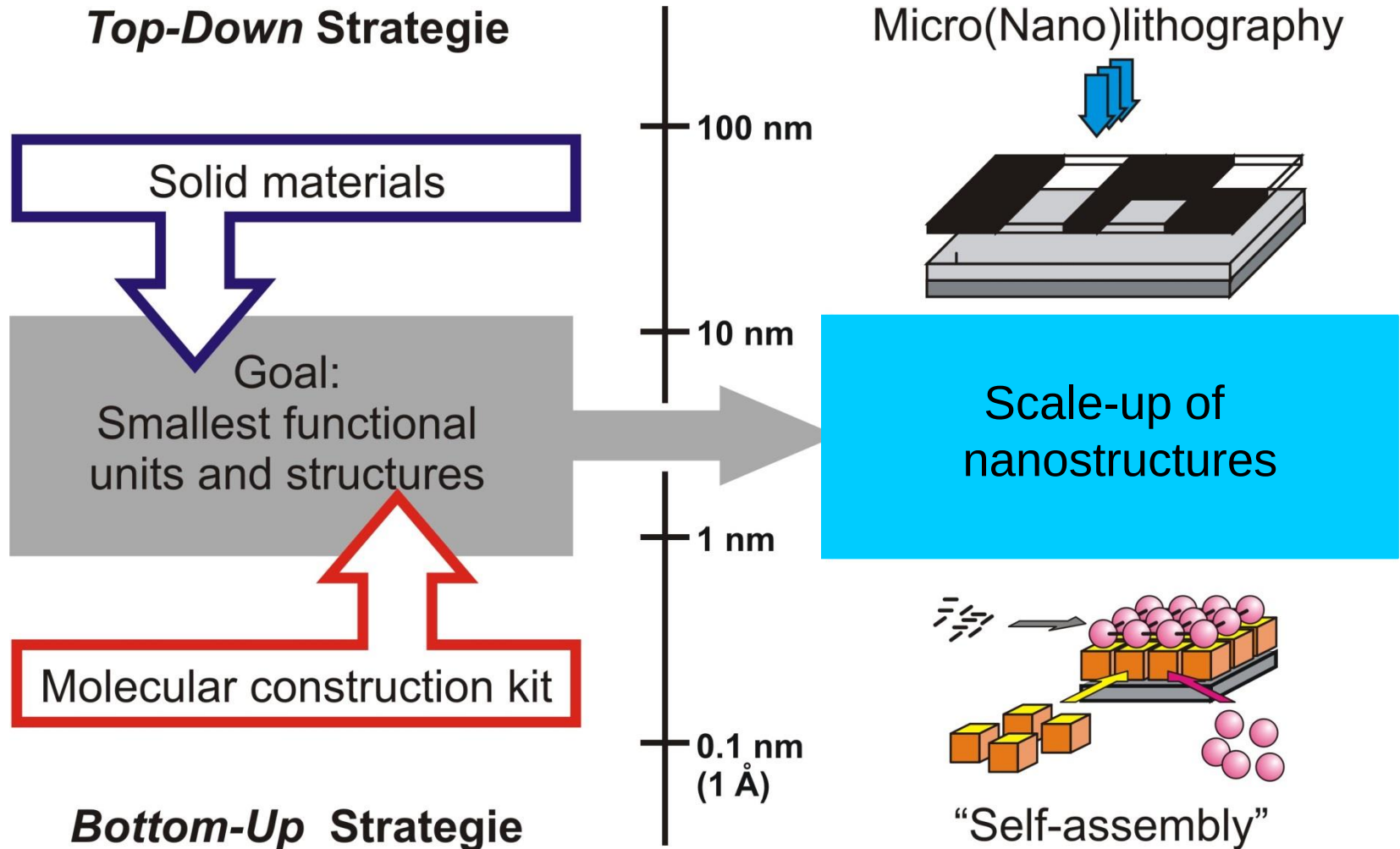


**Nano(bio)technology is not a „rebranding“ of older science !
Its influence is **revolutionary** rather than evolutionary.**

Finally, we can say that **Nanobiotechnology** is an **Interdisciplinary** Field Crossing the Boundaries of Established Disciplines



Nanosciences and Nanotechnology



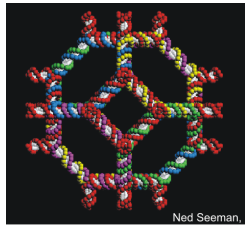
Generating Supramolecular Structures

Molecular LEGO™

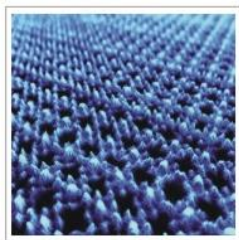


- Supramolecular design
- Self-assembly of complex structure
 - nature builds complexity in a hierarchical way
 - sequential assembly strategies
- Patterning elements
- Functionalization of supramolecular structures
- Quality control and characterization of structures

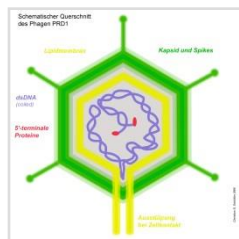
Basic Structures (Patterning Elements) for Generating Complex Supramolecular Structures



- DNA



- Monomolecular crystalline bacterial cell surface layers (S-layers)



- Phage proteins



- Membrane proteins

In our department we basically give importance to **basic building blocks (in a biomolecular construction kit)**

- Biological molecules (e.g. proteins, lipids, glycans, nucleic acids)
- Chemically or genetically modified molecules
- Chemically synthesized molecules

We also look for understanding the principles behind self assembly and biological processes

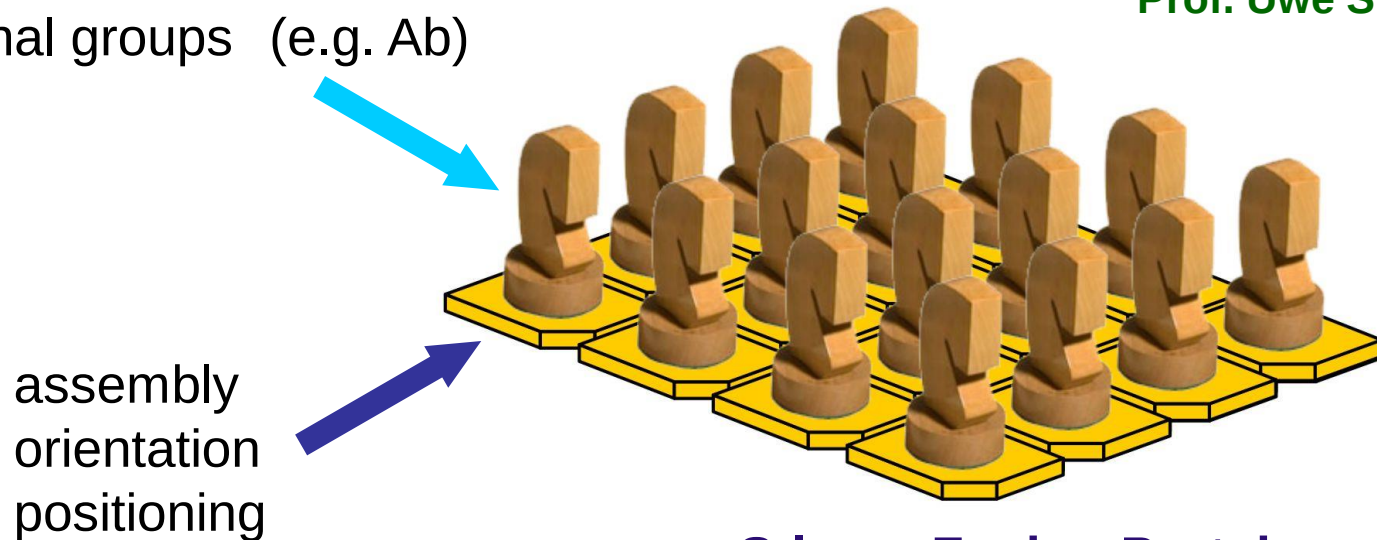
SOME REAL EXAMPLES FROM THE LAB

Our Department has experience on nanobiotechnology using surface protein layers



Prof. Uwe Sleytr

functional groups (e.g. Ab)



S-layer Fusion Proteins

providing a highly ordered functional surface in nanometer-scale

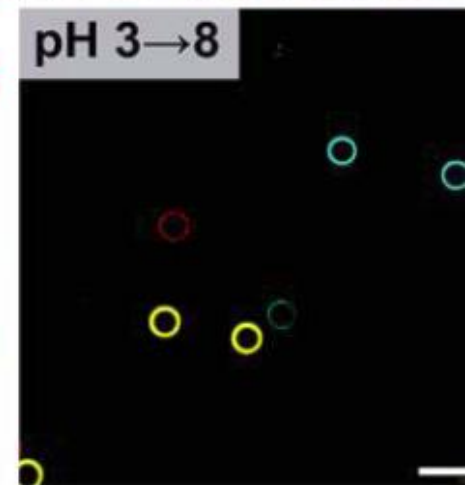
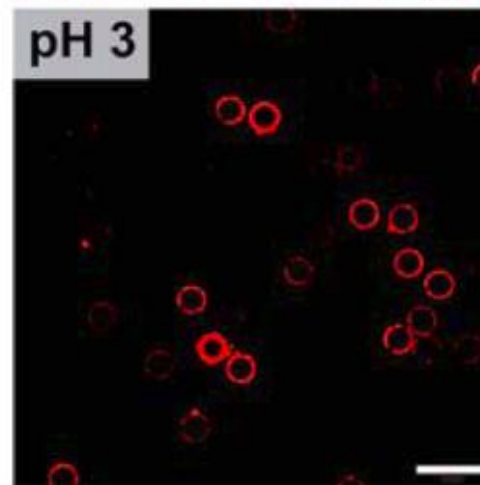
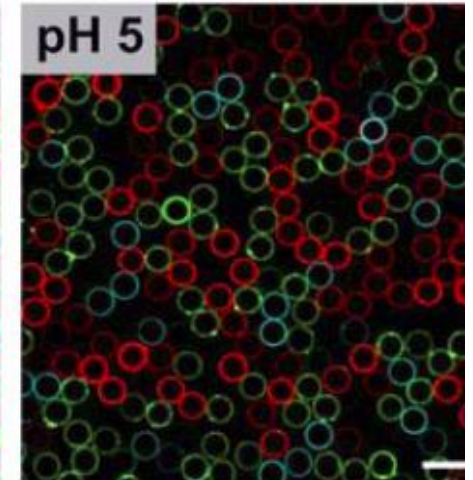
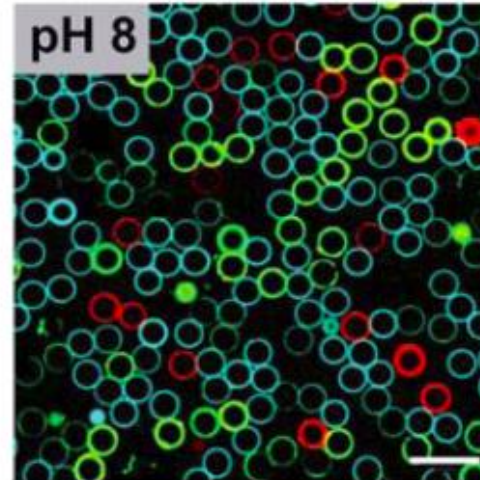
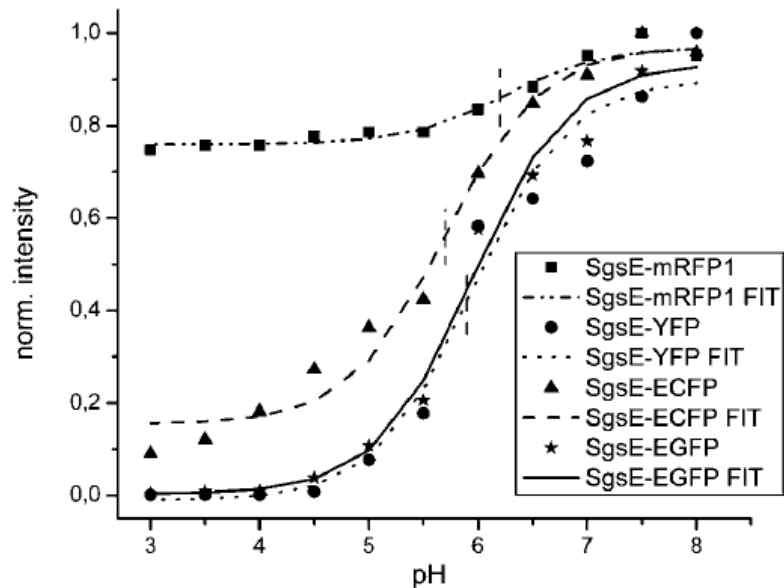
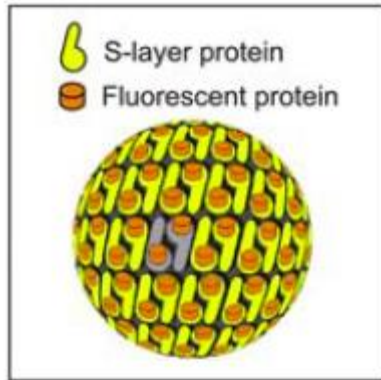


Fluorescence microscopy

Flow cytometry



Preparing particles that are sensitive to changes in pH



AFMs am DNBT... (surface analysis, mechanics and molecular forces)



Scanning probe microscope I

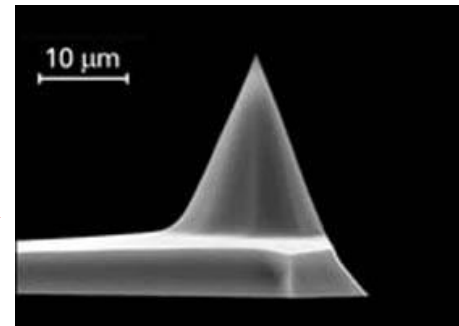
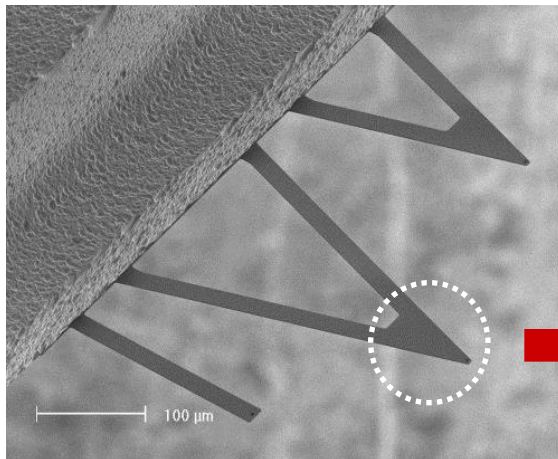
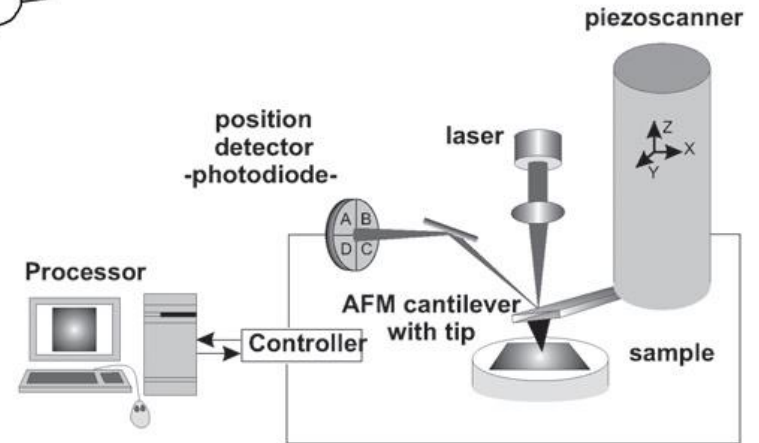
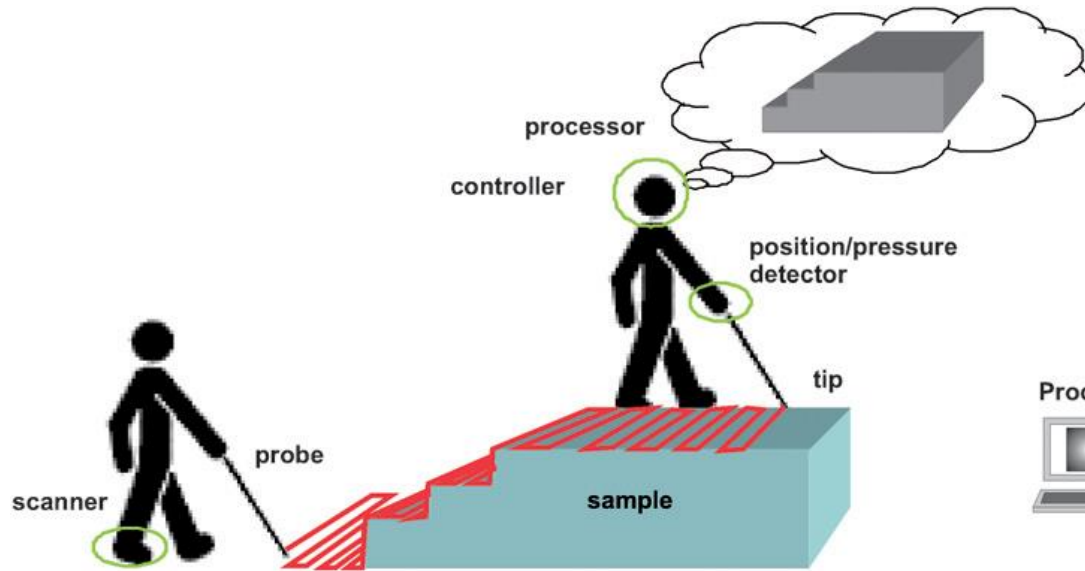


Scanning probe microscope II

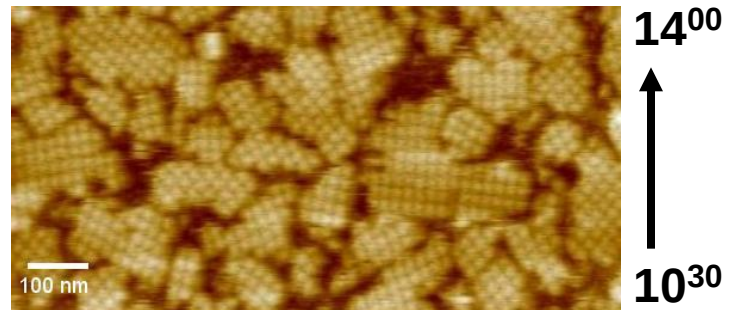
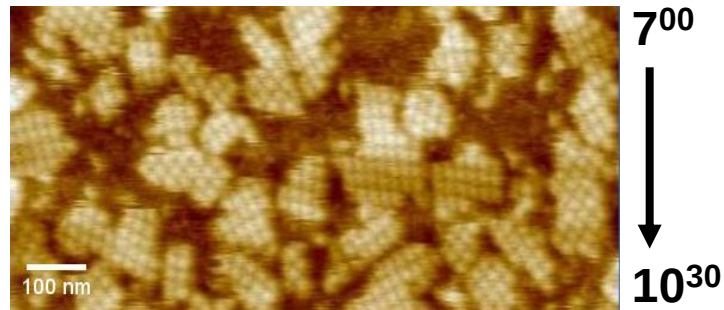
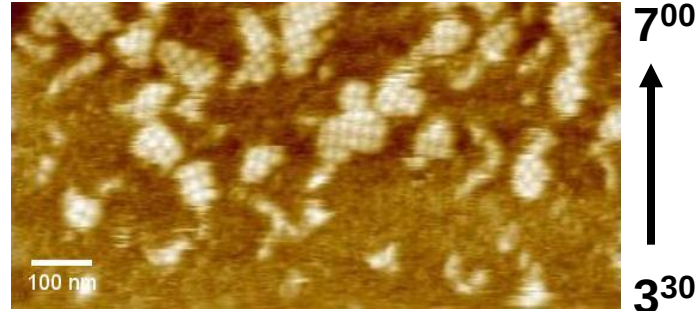
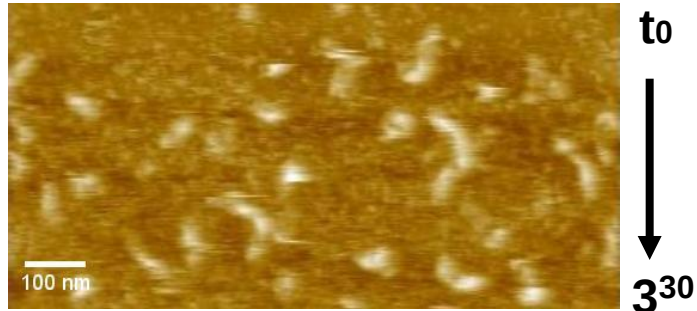


Third SPM will arrived soon!

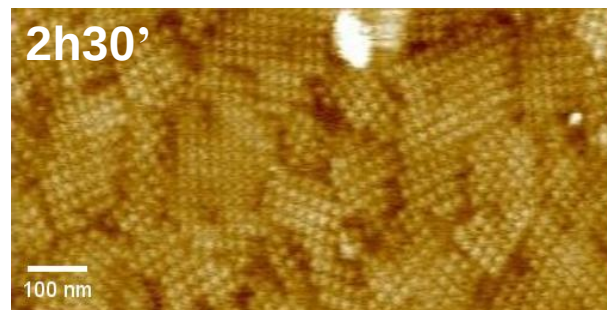
This thing called AFM...



Bacterial crystals on silanes



time	SiO ₂	OTS	APTS
5'	X	31	21
15'	33	77	68
30'	62	96	83
1h	80	99	85
2h30'	85	99	95
>12h	98	100	100



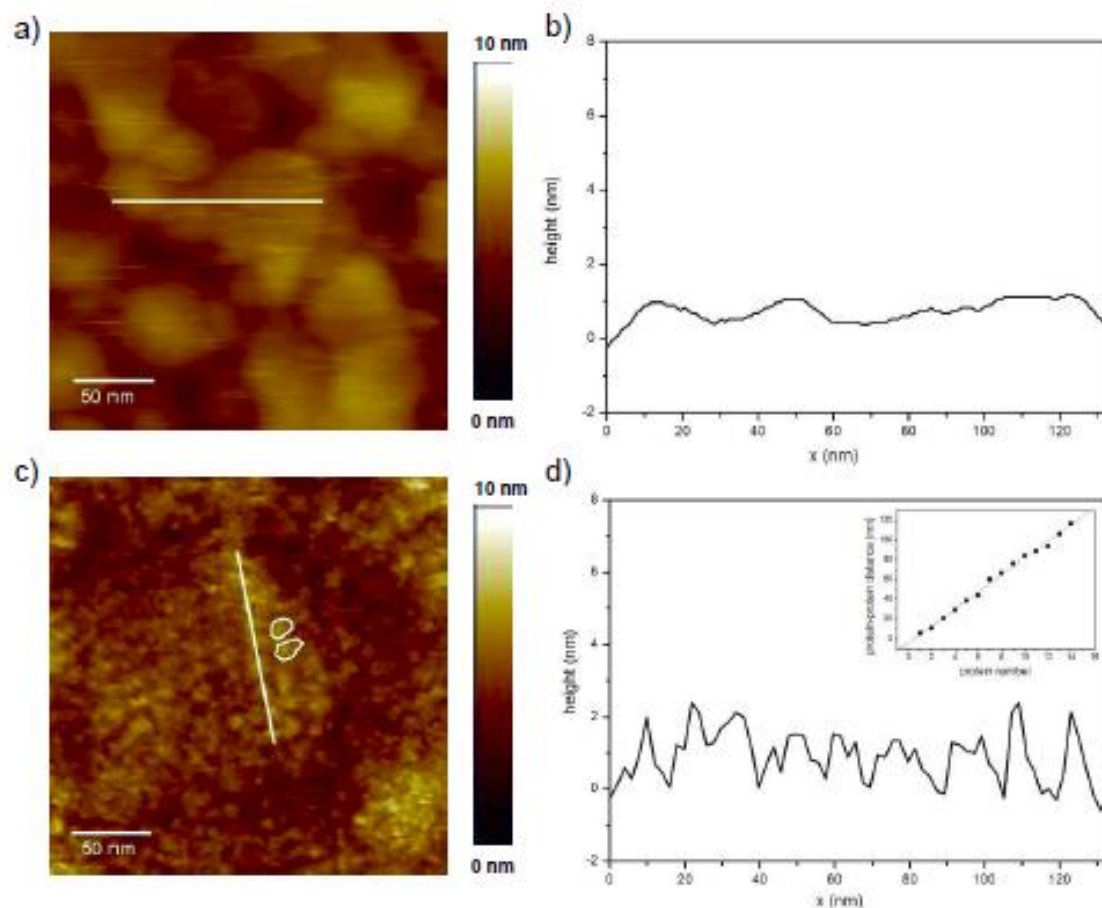
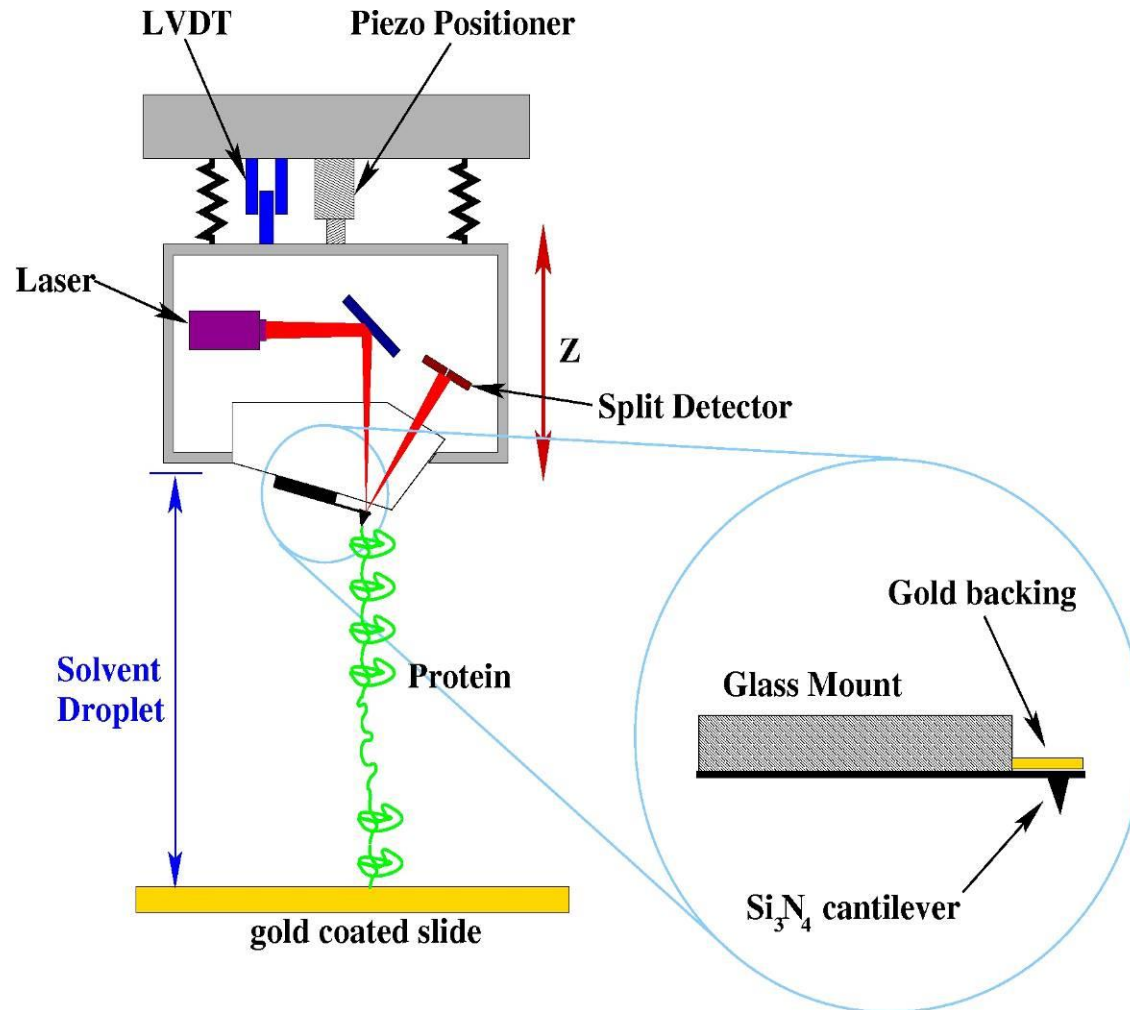
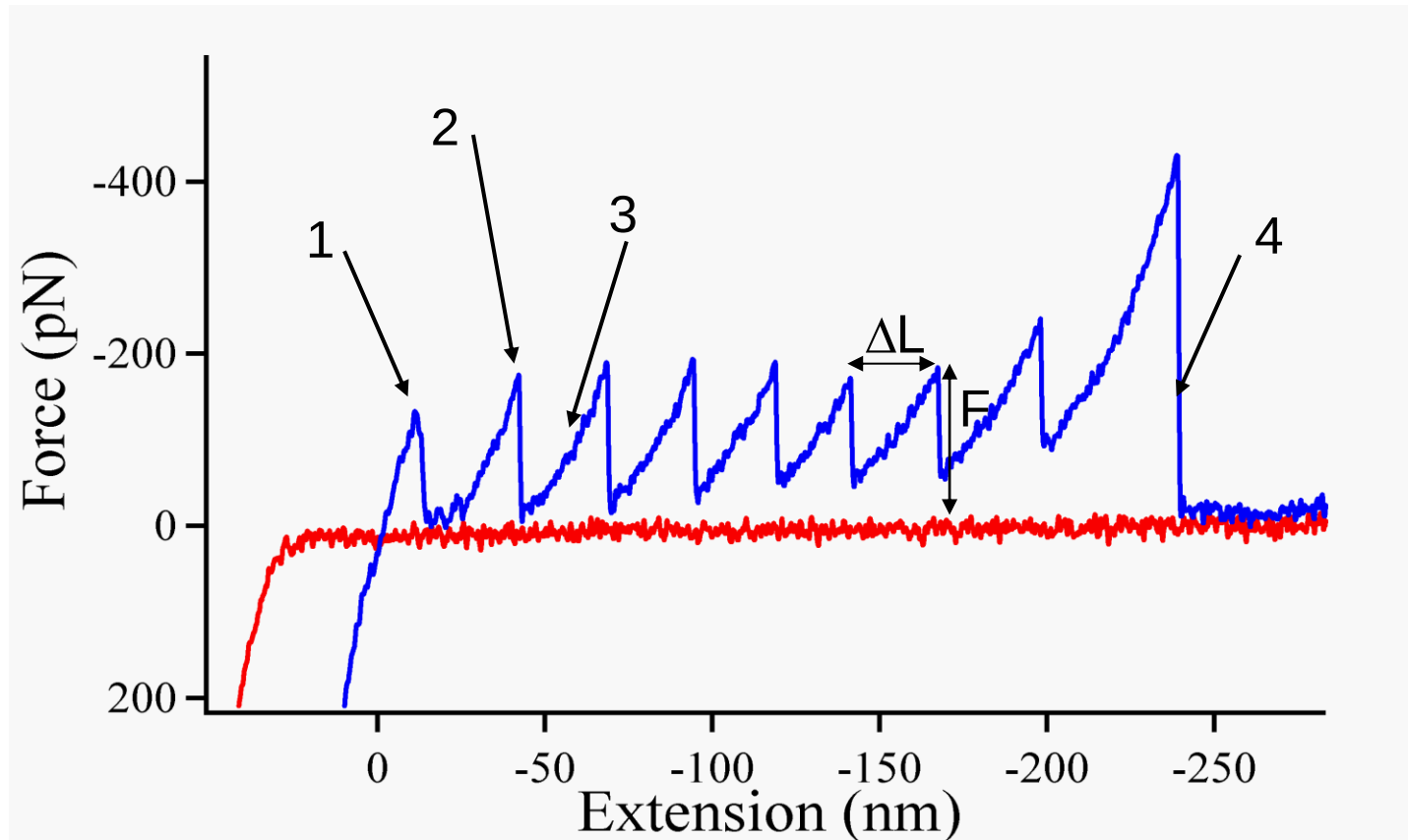
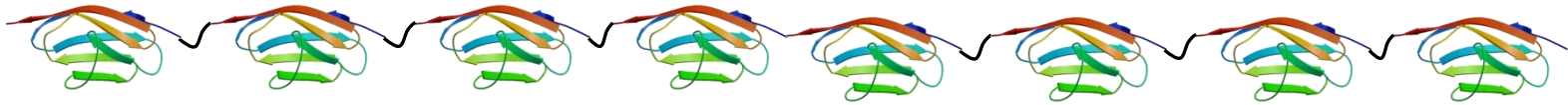


Figure 7.6. a) AFM height image (250 x 250 nm²) of glutaraldehyde functionalized gold substrate. The white cross section shows the profile of gold/glutaraldehyde surface that is plotted in figure b), c) AFM height image (250 x 250 nm²) of immobilized HSA with glutaraldehyde. The white circles indicate single HSA proteins and the white cross sections show the albumin profile which is plotted in d). The profile analysis carried out at different points of the surface show that the average height of HSA molecules is 1.8 nm. The inset in figure d) shows the protein-protein distance as a function of protein number. The data were fitted with a linear equation. The slope gives information about HSA width. (These analyses were carried out at 50 different points).

AFM as a mechanical machine (on proteins)

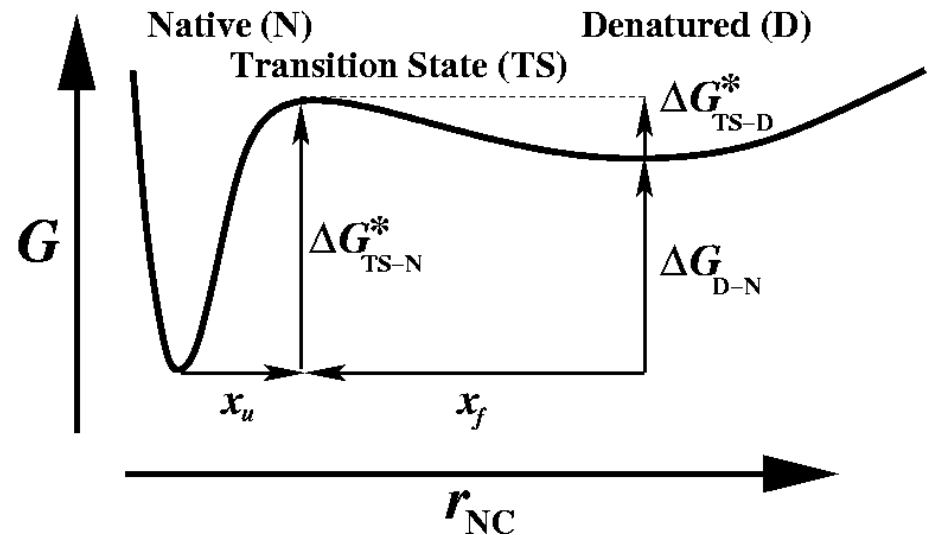




1. Non-specific adhesion
2. Unfolding of one domain
3. Unfolded protein stretching
4. Protein detaches

AFM as a mechanical machine: the AFM offers...

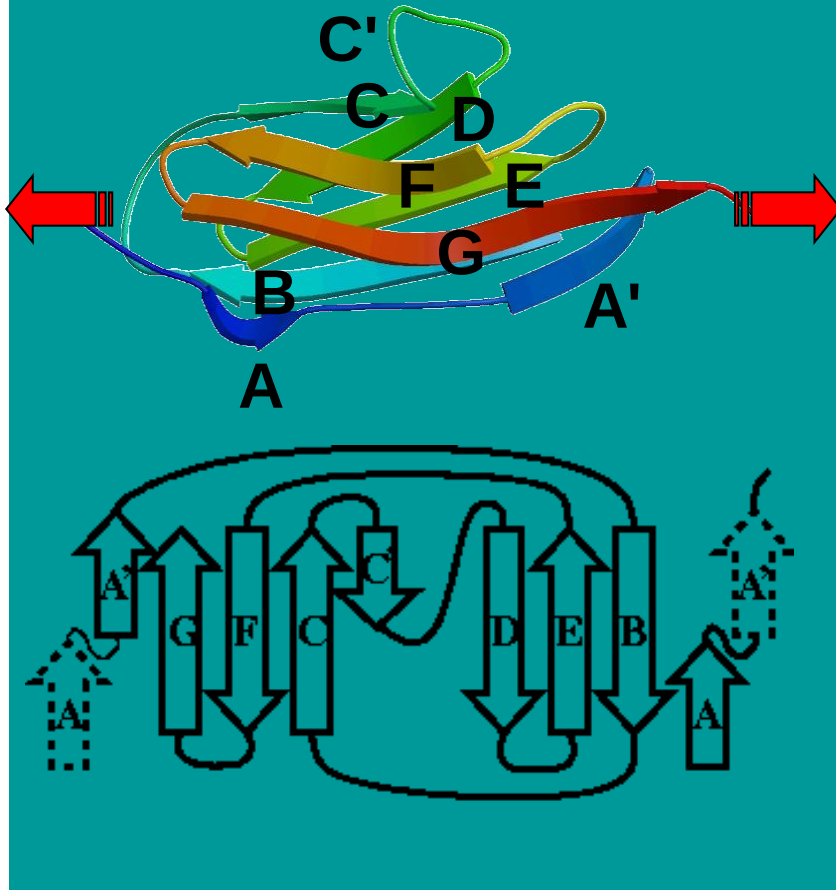
- Alternative to conventional methods of denaturation (e.g. heat, acid, chemical denaturant).
- Single molecule experiment.
- Well defined reaction coordinate.
- Direct comparison with all-atom MD simulation.
- Possibility to observe rare events



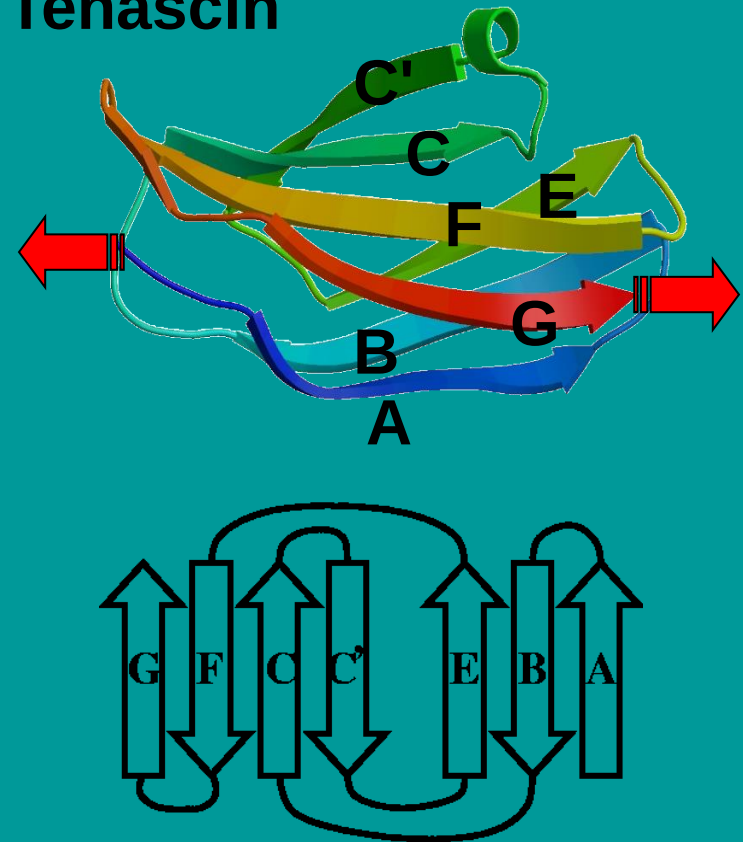
$$k_u(F) = \nu \kappa \exp(-\beta(\Delta G_{TS-N}^* - Fx_u)) \\ = k_u(0) \exp(\beta Fx_u)$$

Tenascin and titin I27 have a similar fold

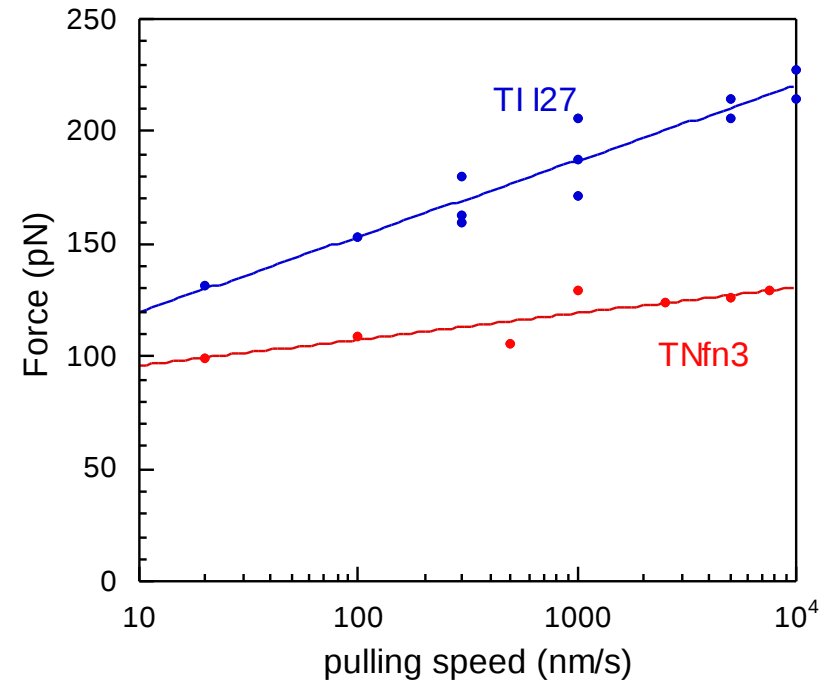
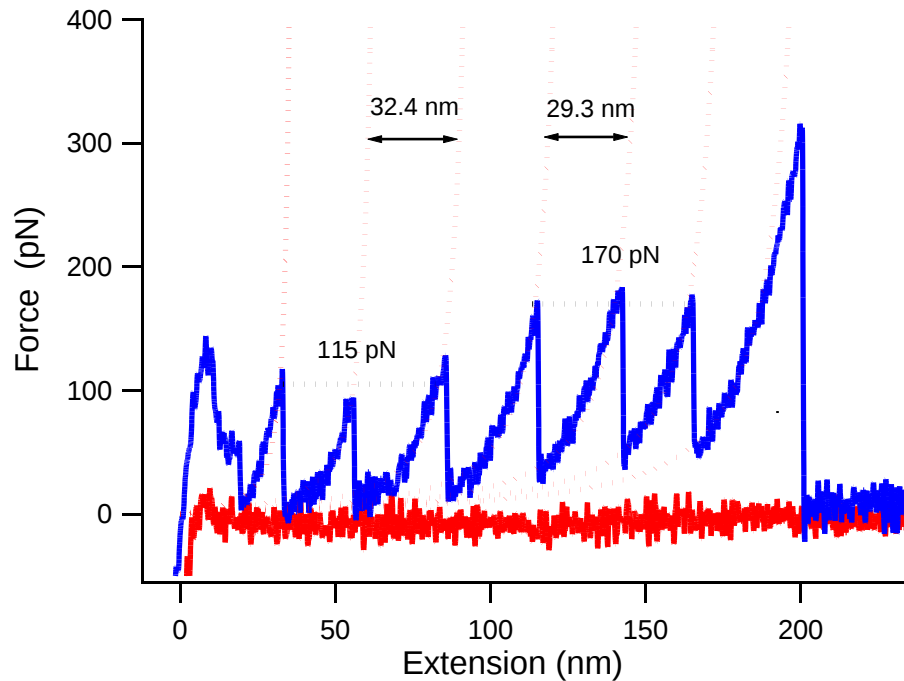
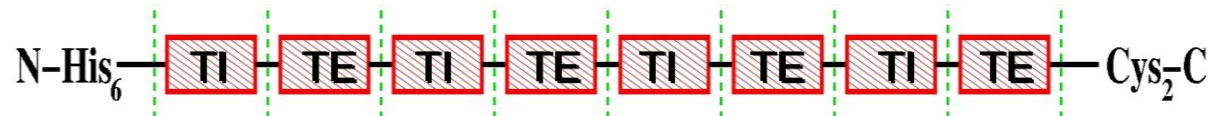
Titin I27



Tenascin



“Similar” proteins unfold mechanically in a different way



$$X_u(\text{tn}) = 0.7 \text{ nm}, X_u(\text{titin}) = 0.3 \text{ nm}$$

$$K_{\text{off}}(\text{tn}) = 8 \times 10^{-9} \text{ s}^{-1}, K_{\text{off}} = 4 \times 10^{-5} \text{ s}^{-1}$$

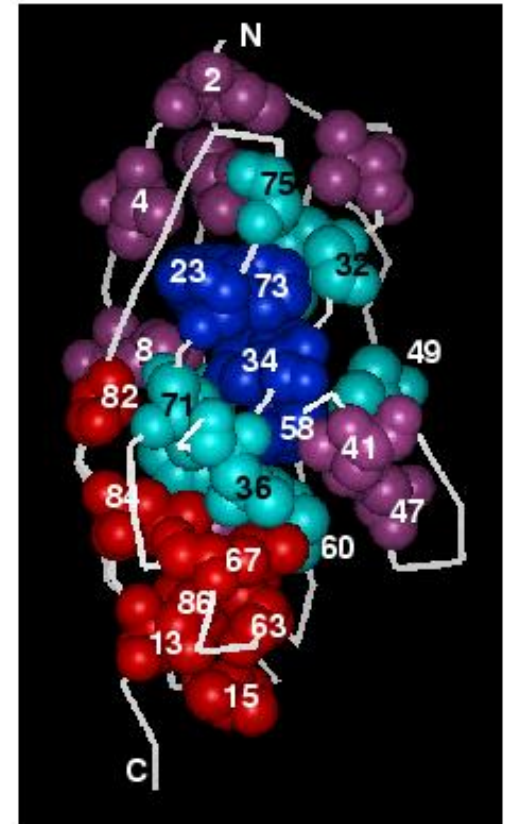
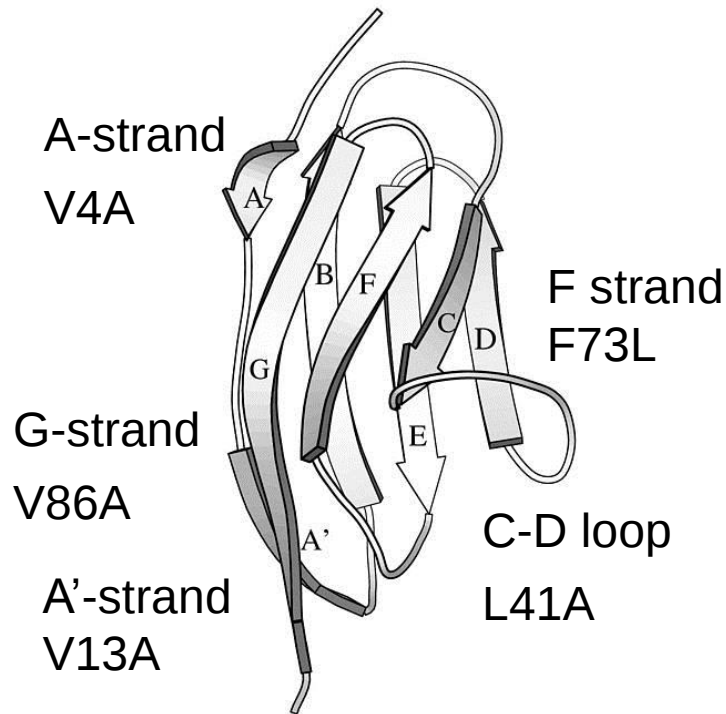
Protein Science, 11 (2002) 2179

PNAS 99 (2002) 12143

Nature, 442 (2003) 446

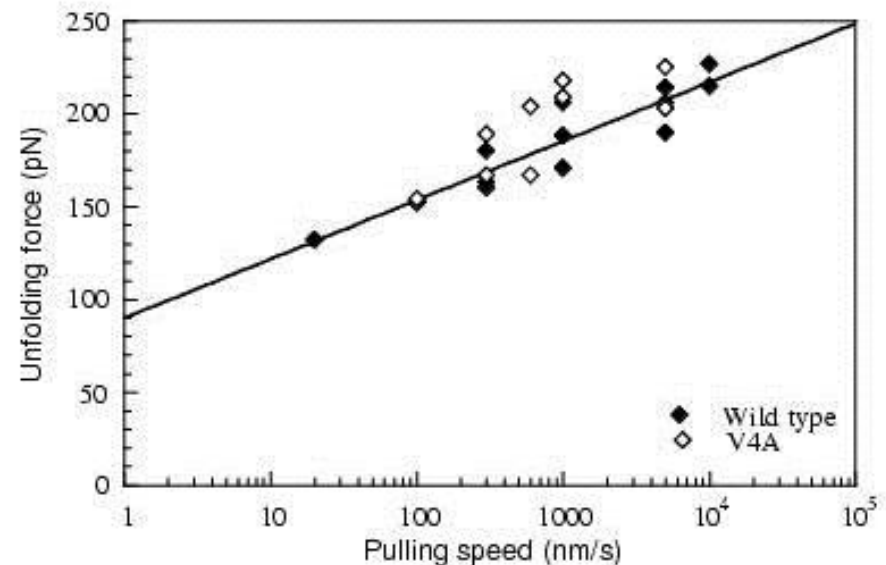
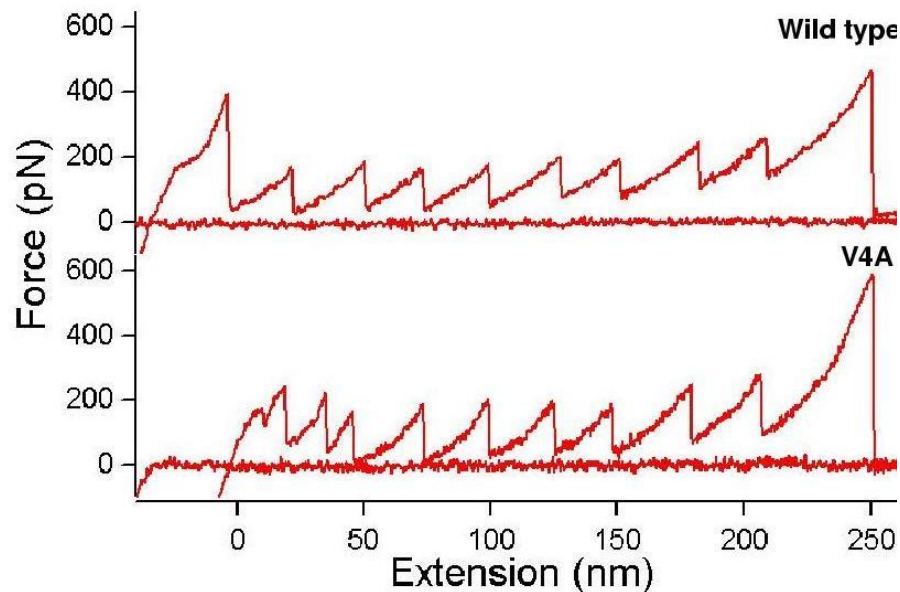
Choice of mutants is critical and deliver information about protein stability

Conservative, non-disruptive, significantly destabilising

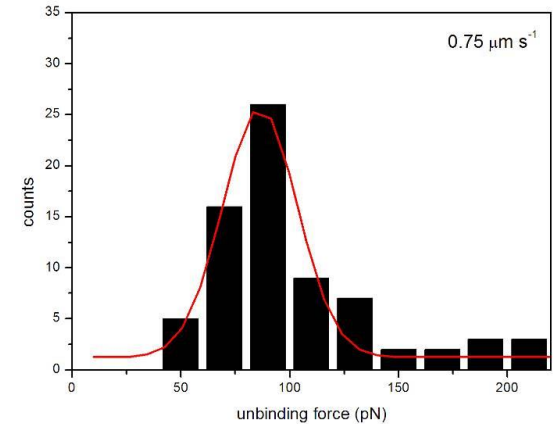
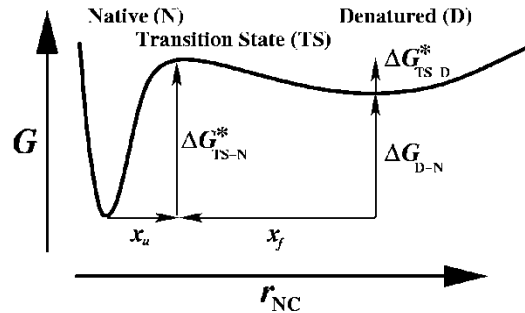
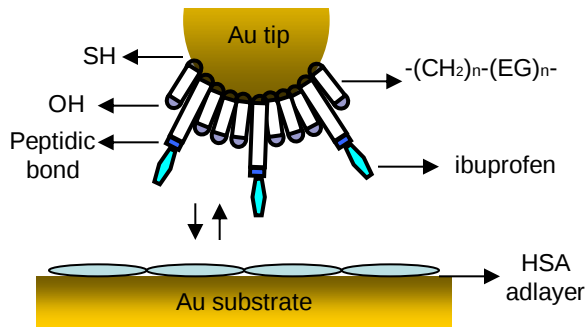


Evidence from mutation

When we pull a protein with a destabilising mutation in the A strand (V4A) it does not affect the unfolding forces at all



Forces between single molecules

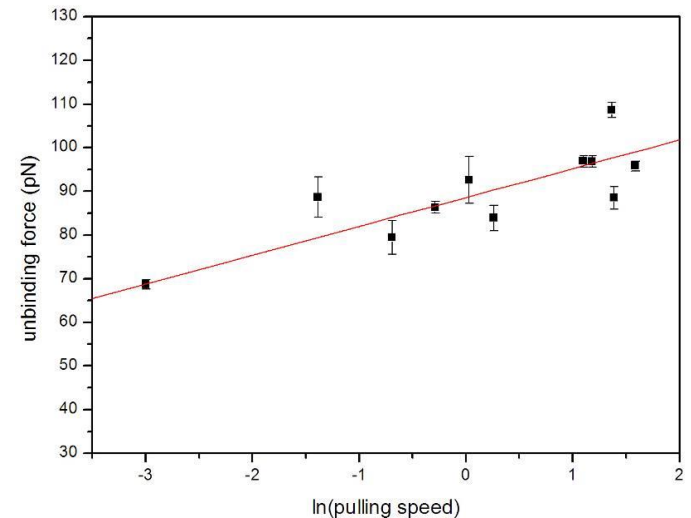


$$F = \left(\frac{k_b T}{x_u} \right) \ln \left(\frac{x_u k_e}{k_b T K_{off}} \right) + \left(\frac{k_b T}{x_u} \right) \ln v$$

$$x_u = 0.6 \text{ nm}$$

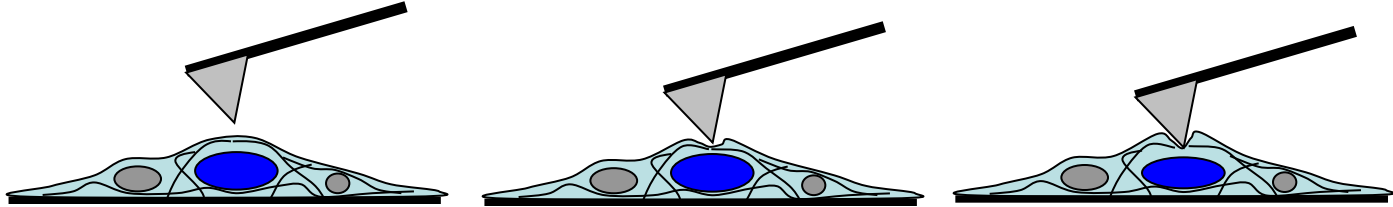
$$K_{off} = 0.055 \text{ s}^{-1}$$

Possibility of molecular recognition !!

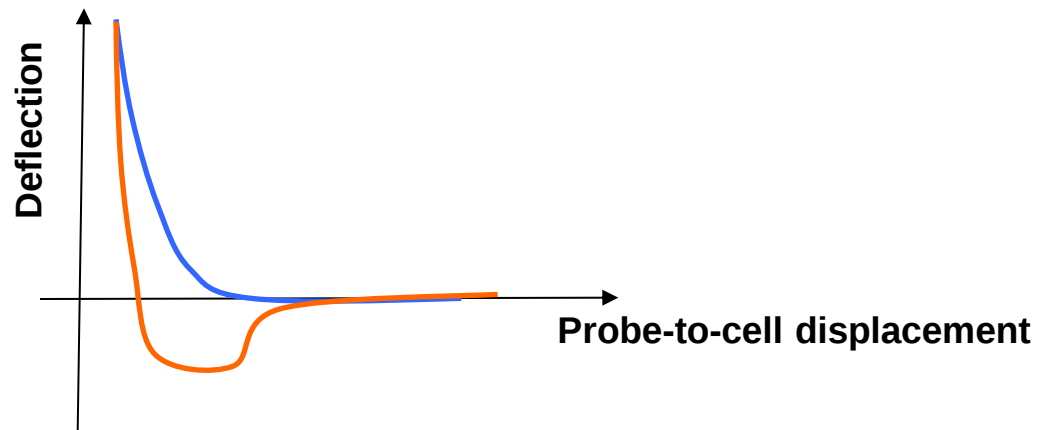
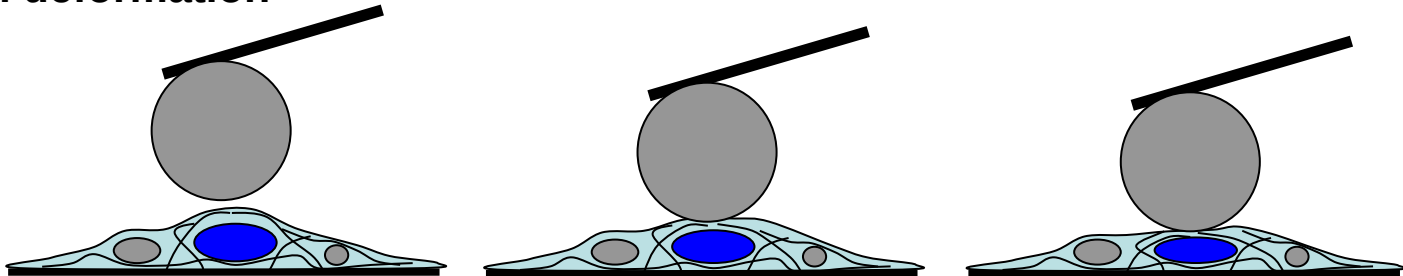


AFM – mechanical machine on cells

Local deformation



Global deformation



MOTIVATION !!

- Alternative AFM-based approach that takes into account

Cell complexity

3D heterogeneity

- Use it as a diagnostic tool for cell type/malfunction ???

correlation mechanical properties – cell function ???

Force-distance based approach: cell elasticity

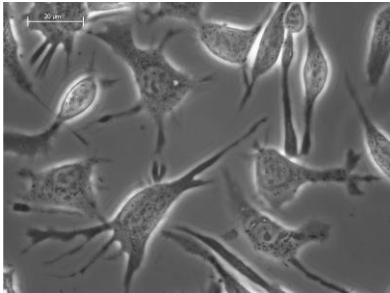


- small deformations (1-5%)
- cells = purely elastic bodies

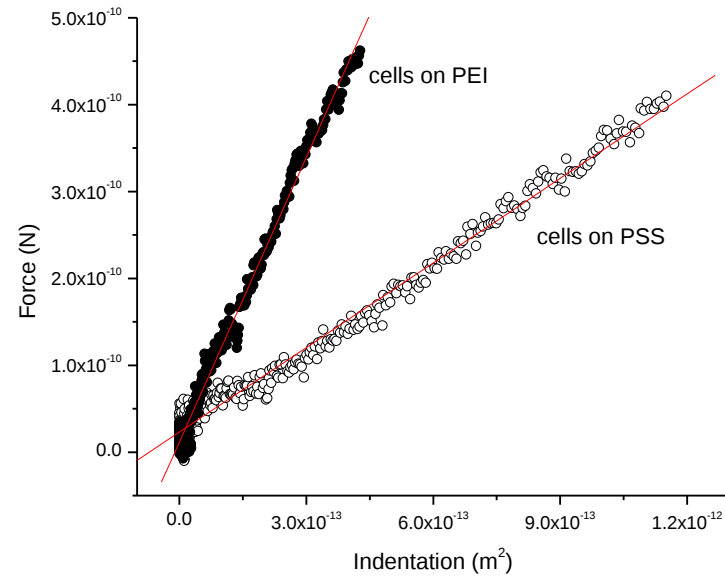
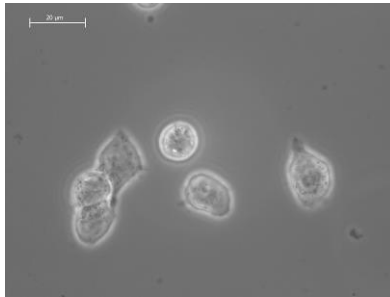
$$F = Cte * E * I^2$$

Force-distance based approach - HepG2 cells

PEI



PSS



- small deformations
- cells = purely elastic bodies

● 191 ± 14 Pa (PSS)

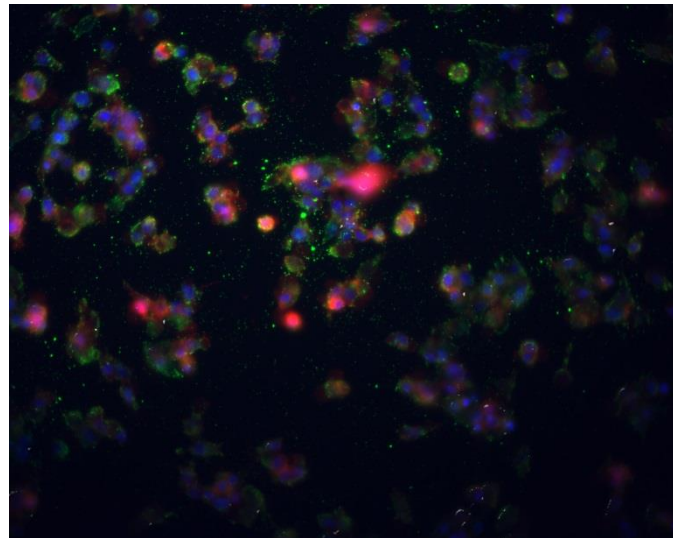
● 941 ± 58 Pa (PEI)

Substrate influences SHAP₂
SHAP₂ $\Rightarrow$ different
Young Modulus
 $\downarrow$
the membrane should
change its permeability

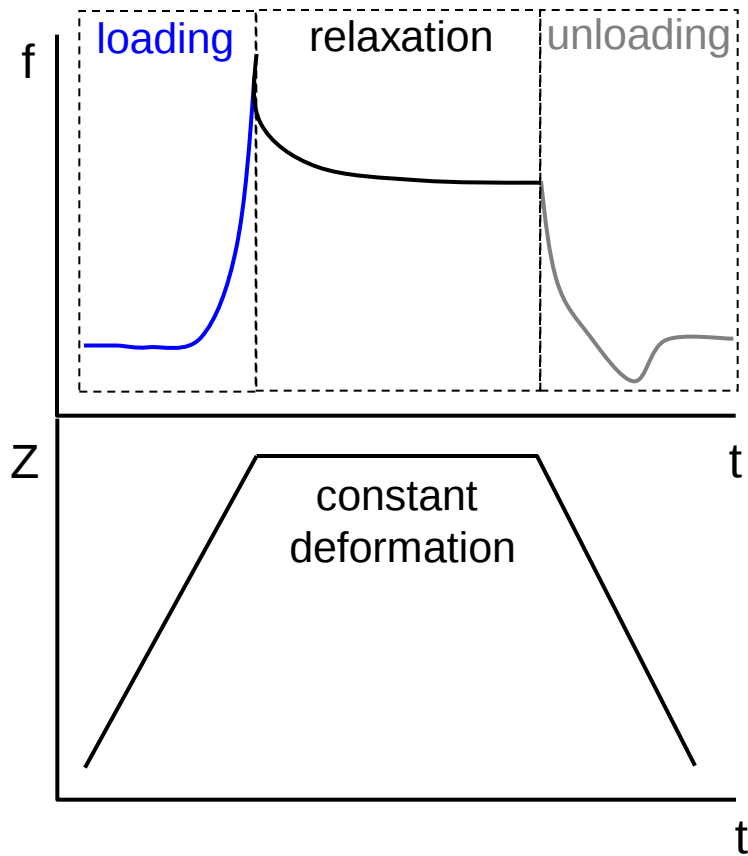
Particle uptake by Hep G2 cell
cultured on polystyrene sulfonate

Particle size: 49 nm and 240 nm

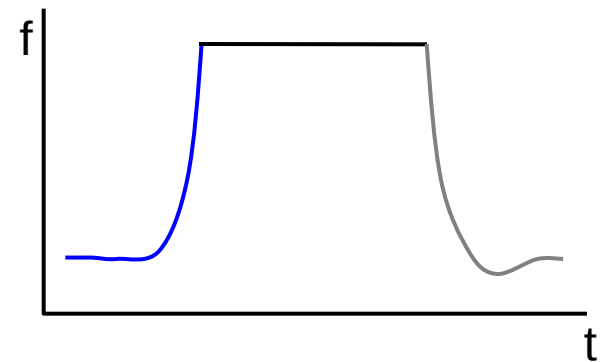
Research on going....



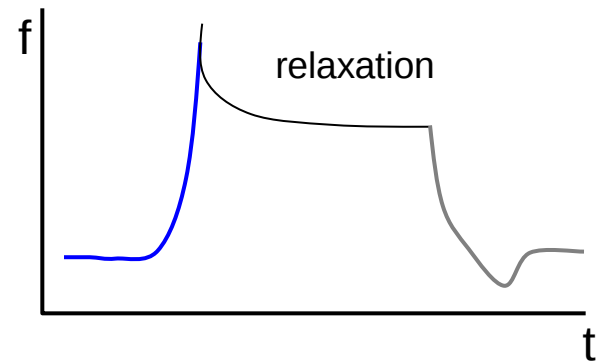
Force-time based approach: relaxation



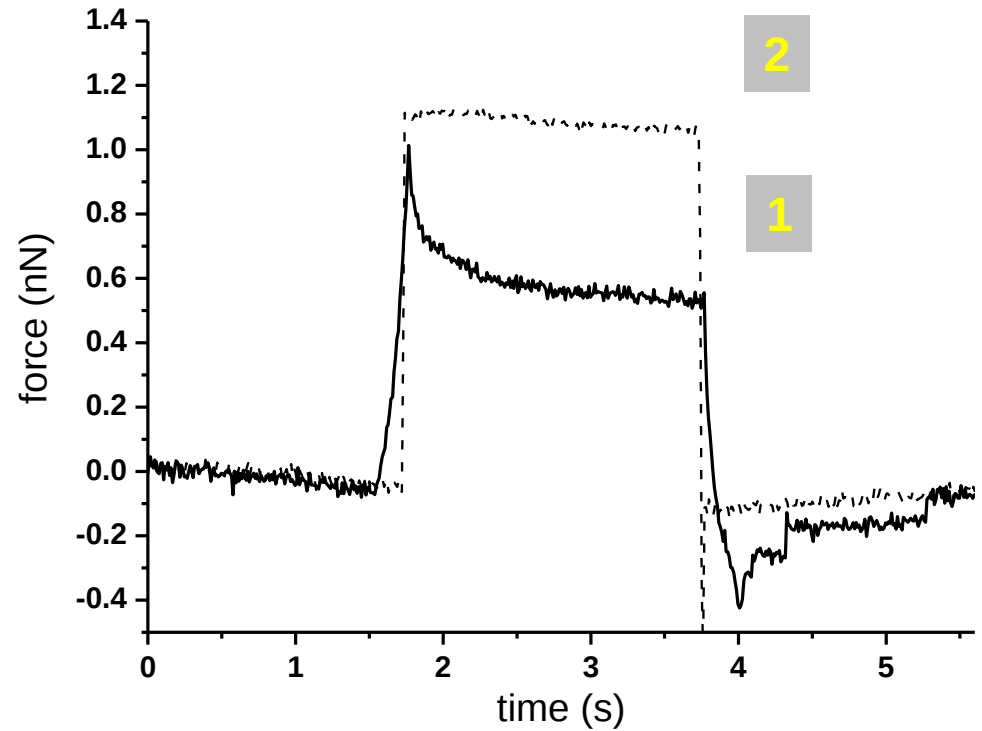
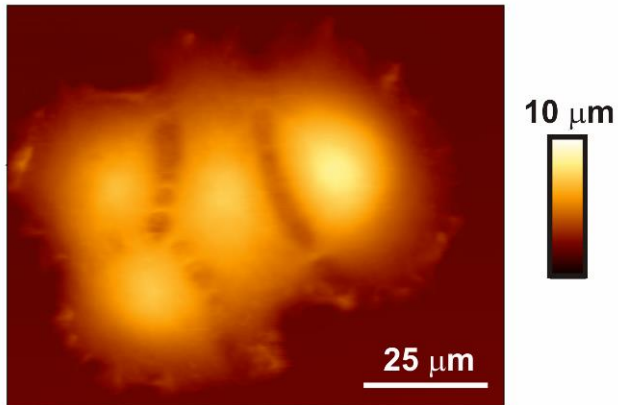
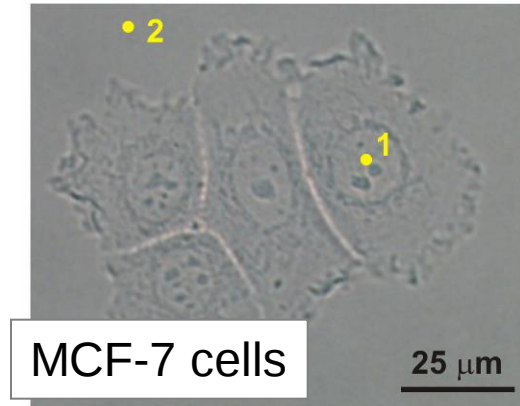
● purely elastic bodies



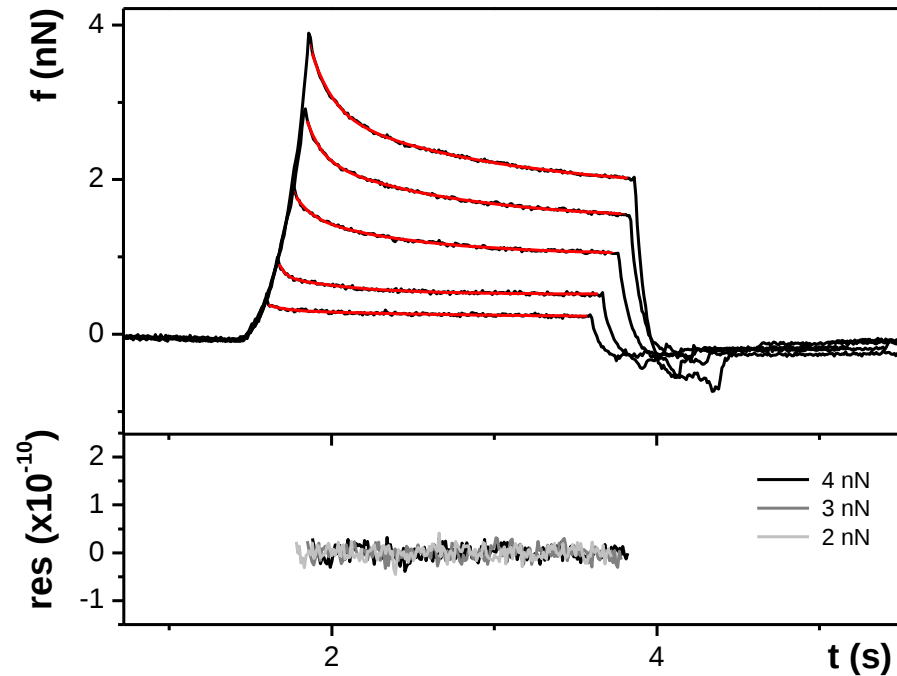
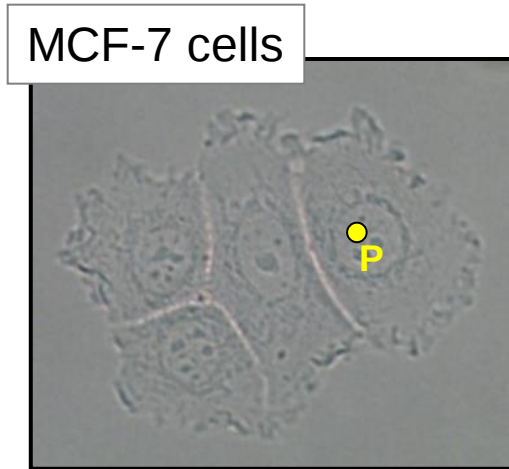
● viscoelastic bodies



Force-time based experiments: how do MCF-7 cells relax



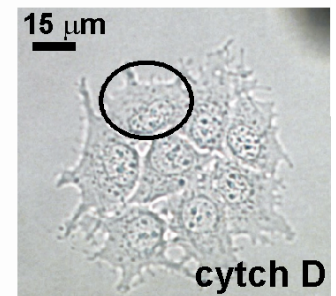
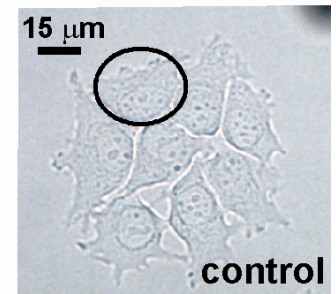
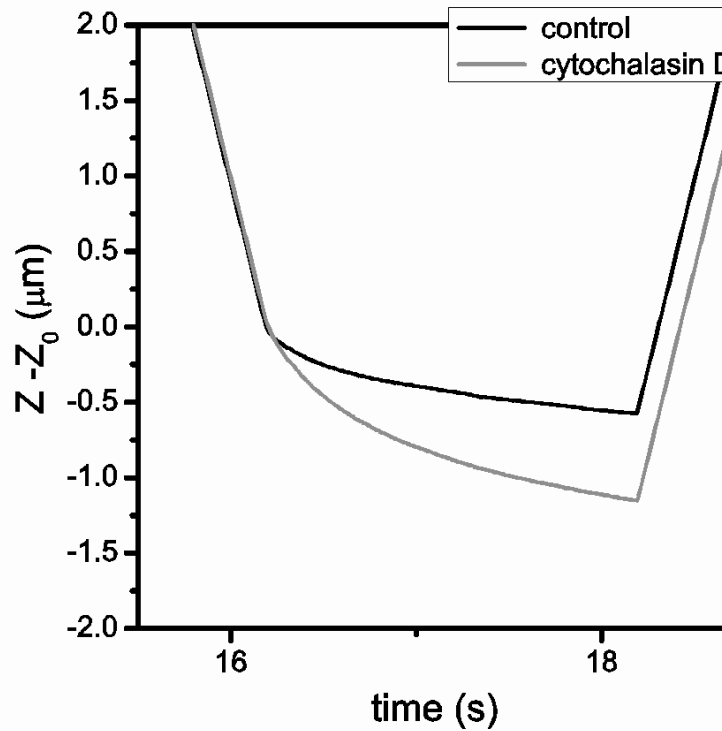
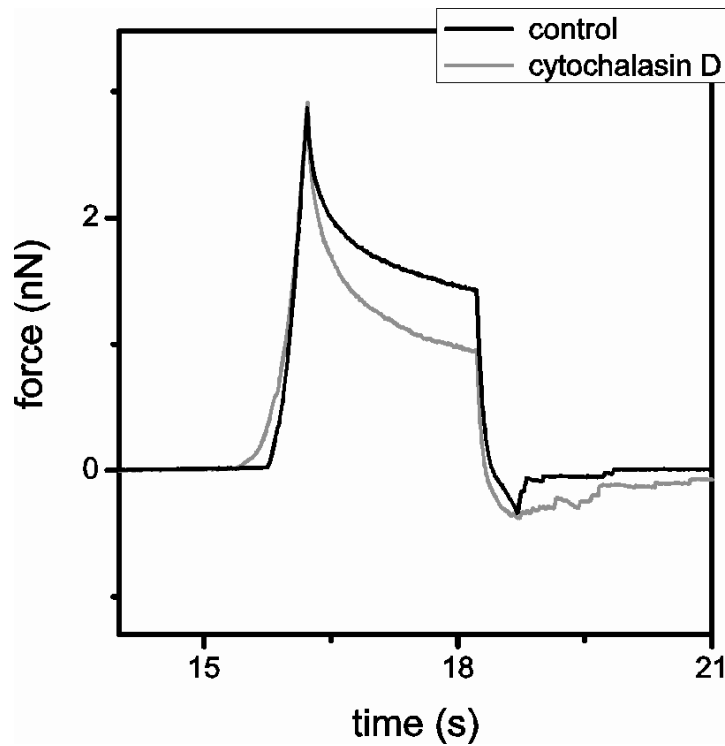
Force-time based experiments: bi-exponential behaviour



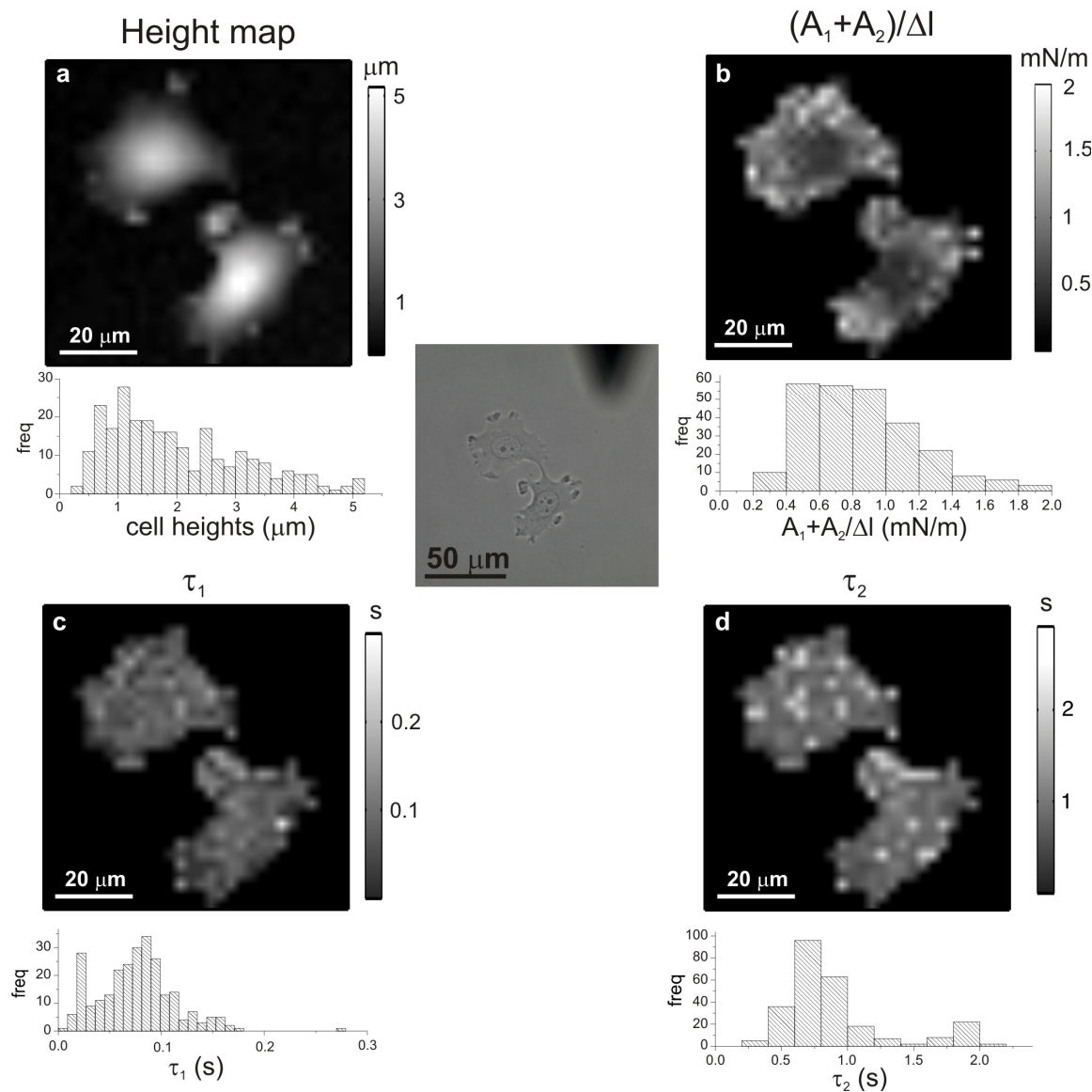
- bimodal decays: the proposed model fits reasonably well ($r > 0.8$)
- two simultaneously-occurring processes are detected

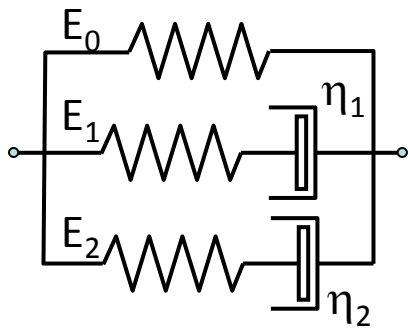
Stress relaxation and creep – actin-depolymerizing drug

Cytochalasin D disrupts the actin cytoskeleton
(E2 and η_2 should be more affected)



Stress Relaxation Microscopy (STREM): imaging decay parameters





Zener's model (Riande E. et al, *Polymer viscoelasticity, Stress and strain in practice*. Marcel Dekker 2000)

For a constant strain/deformation

$$\ddot{\sigma} + A\dot{\sigma} + B\sigma = r_0\dot{\varepsilon}_0$$

and the solution gives

$$\sigma(t) = E_0\varepsilon_0 + A_1e^{-t/\tau_1} + A_2e^{-t/\tau_2}$$

$$\tau_1 = \frac{\eta_1}{E_1}, \tau_2 = \frac{\eta_2}{E_2}$$

STRESS RELAXATION



$$A_1, A_2, \tau_1, \tau_2, \varepsilon_0$$

For a constant stress

$$r_2\ddot{\varepsilon} + r_1\dot{\varepsilon} + r_0\varepsilon = B\sigma_0$$

and the solution gives

$$\varepsilon(t) = \frac{\sigma_0}{G_1} + C_1e^{-x_1t} + C_2e^{-x_2t}$$

$$x_1 = \frac{-r_1 + \sqrt{r_1^2 - 4r_0r_2}}{2r_2}, x_2 = \frac{-r_1 - \sqrt{r_1^2 - 4r_0r_2}}{2r_2}$$

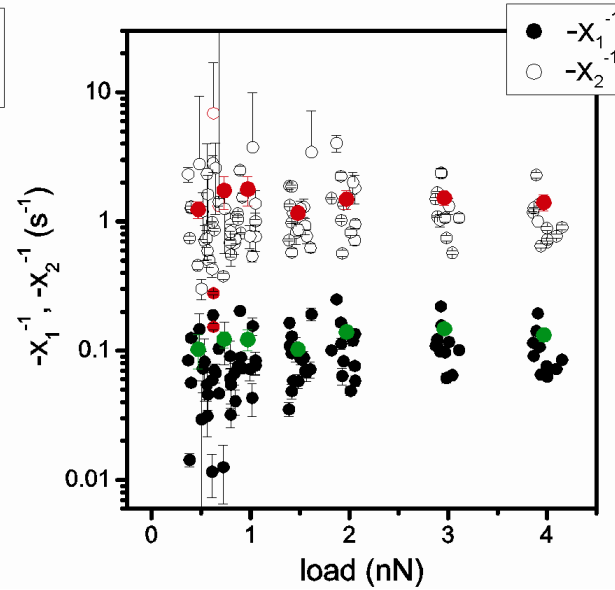
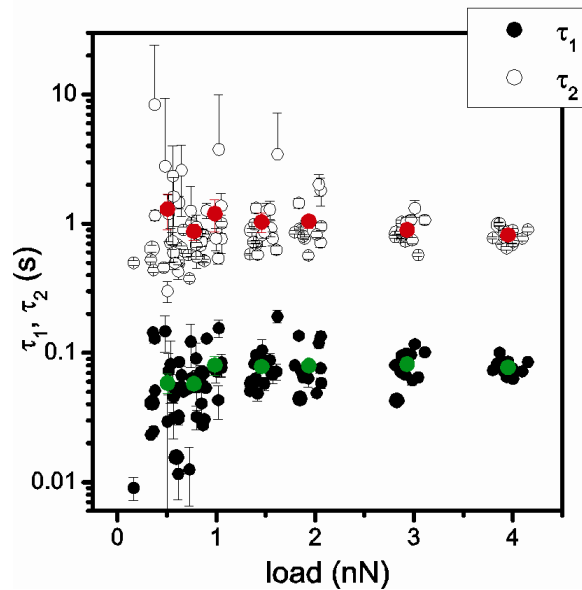
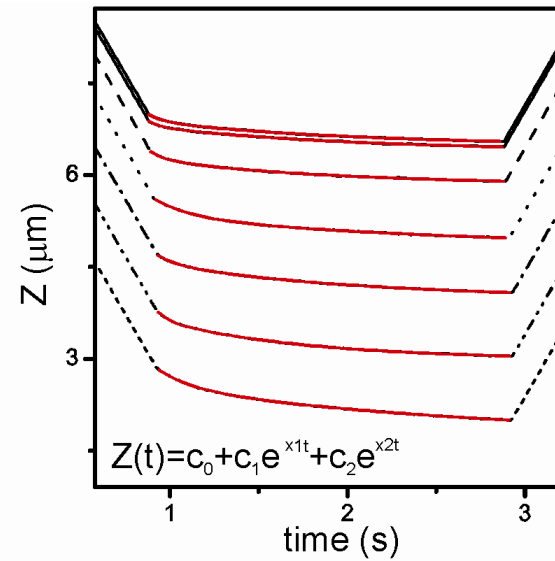
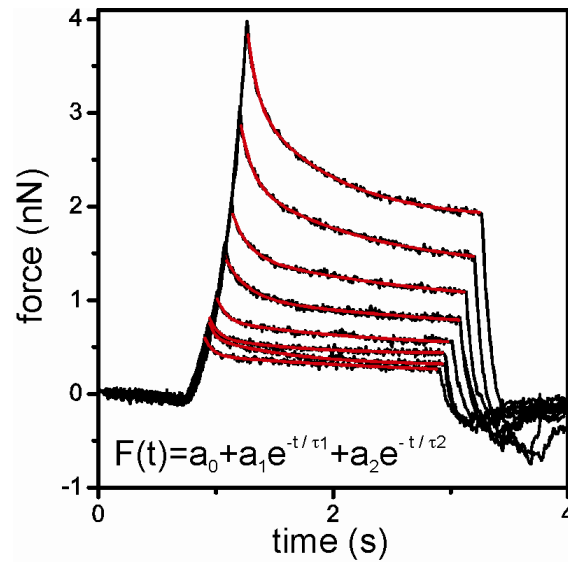
CREEP



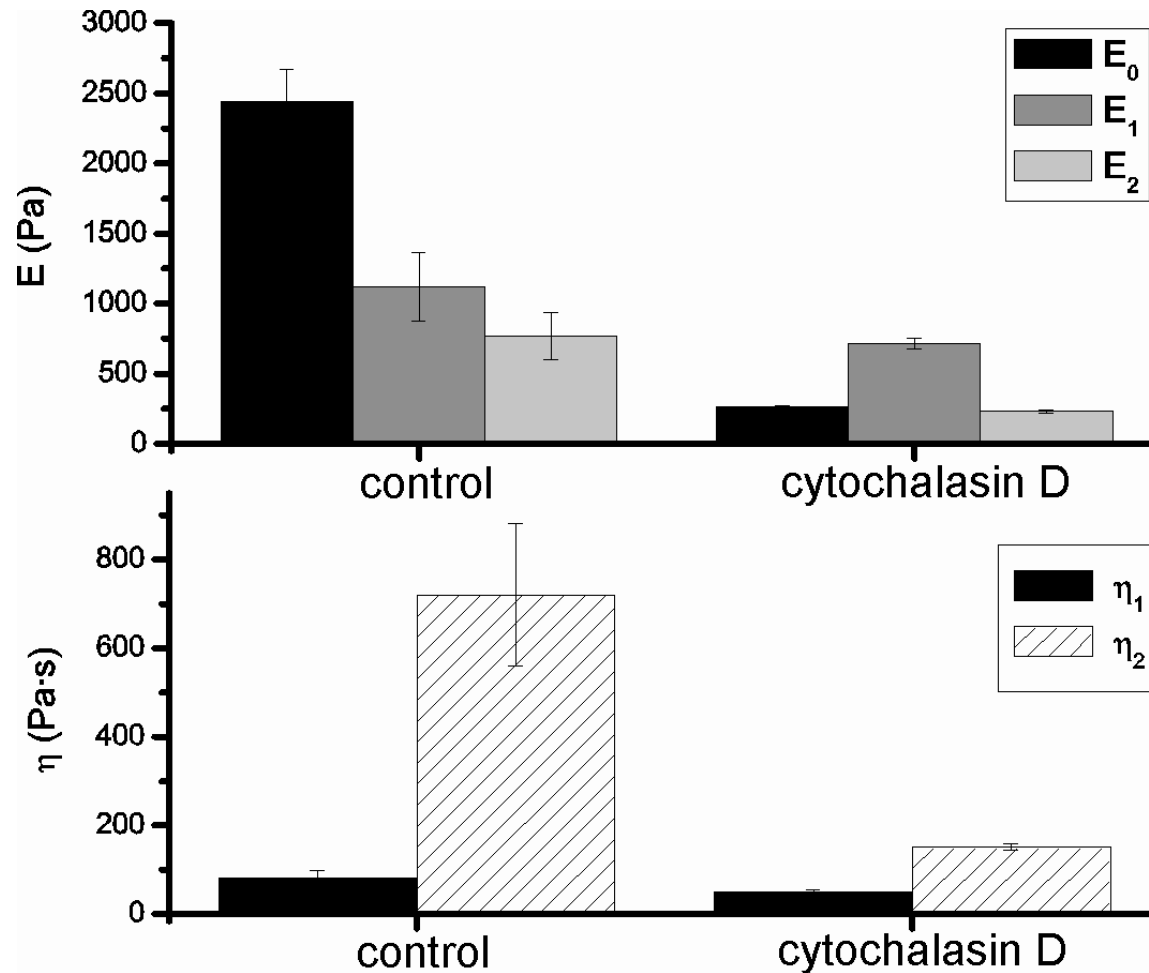
$$C_1, C_2, x_1, x_2, \sigma_0$$

Elastic modulus, relaxation time and viscosity ???

Force-time and height-time based experiments

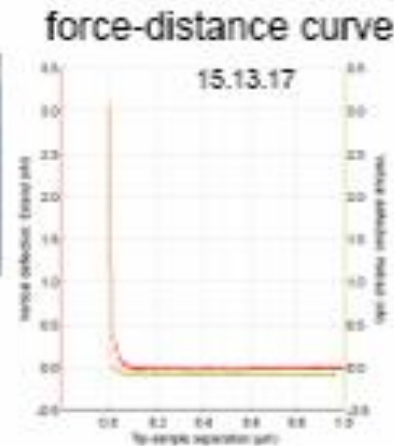
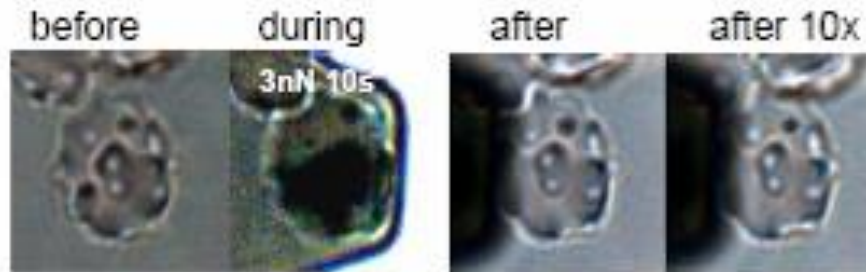


Stress relaxation and creep – actin-depolymerizing drug



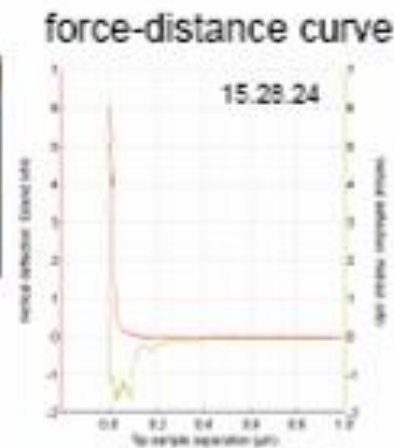
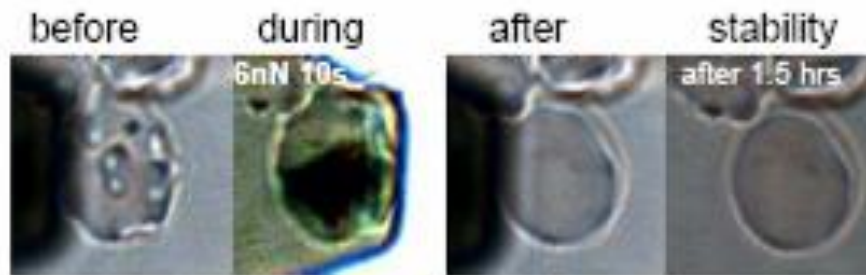
We are happy: This is nice and problematic at the same time!

Making RBC look younger – inducing cell shape change



summary

3 nN for 10s,
repeated 10x,
may not cause
shape change
(shape changes
were sometimes
observed at 3 nN)



summary

6 nN for 10s
causes shape
change
(positive control
for the 3 nN
experiment)

What could be going on...

-echinocytes were formed by storage of RBCs in plasma, followed by rinsing with phosphate buffered saline

-application of 6 nN or more causes a shape change
-application of 3 nN or less typically does not
- same effect is observed when the ATP-dependent translocases are inhibited (with vanadate)

-the smoother cell shapes are stable for periods of several hours

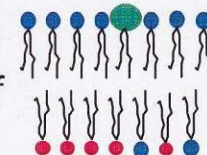
Red blood cells and their shapes:

Healthy red blood cells in vivo have a biconcave disc shape.

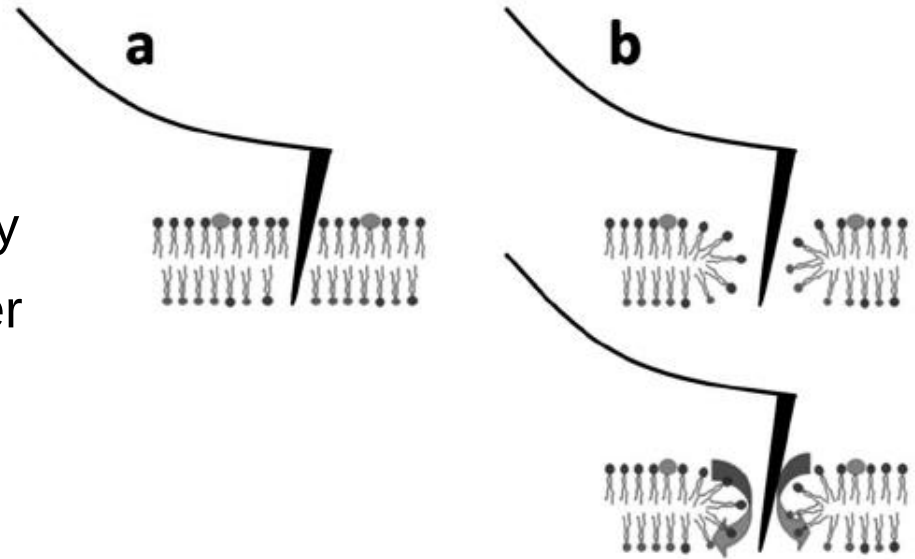
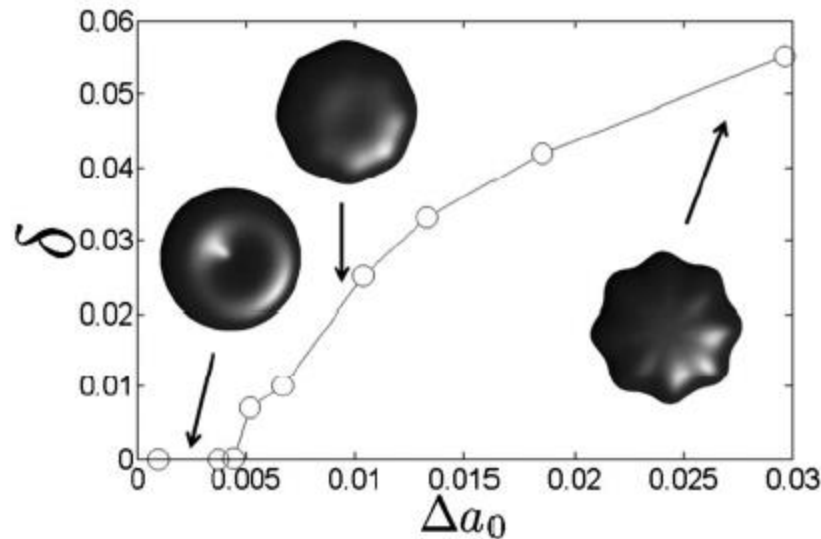


photograph
(light
microscope)

The disc shape is associated with minimisation of the bending energy^{1,2} that arises because the lipid bilayer is asymmetric. The relative areas of the inner and outer monolayers also affects cell shape^{3,4}.



The disc shape is associated with minimisation of the bending energy that arises because the lipid bilayer is asymmetric



$$E_e = \frac{\kappa}{2} \int_{S_0} (\lambda_1 \lambda_2 - 1)^2 dS_0 + \frac{\mu}{2} \int_{S_0} \frac{(\lambda_1 - \lambda_2)^2}{2\lambda_1 \lambda_2} dS_0$$

$$E_b = \frac{\kappa}{2} \int_S (H - c_0)^2 dS + \frac{\kappa_A \pi}{2AD^2} (\Delta A - \Delta A_0)^2$$

Conclusions are boring...there are
not any today!

The people who contributed to this presentation...



Dr. Susana Moreno-Flores



Dr. Birgit Kainz



Dr. Rafael Benitez



Dr. Maria Vivanco



Mag. Batirtze Prats



Dr. Kathryn Melzak

Thank you for listening!!!

