

Physics of Life

PHYS-468

AFM

Atomic Force Microscopy

Henning Stahlberg,
LBEM, IPHYS, SB, EPFL



The Nobel Prize in Physics 1986

"for his fundamental work in electron optics, and for the design of the first electron microscope"

"for their design of the scanning tunneling microscope"



Ernst Ruska

🕒 1/2 of the prize

Federal Republic of Germany

Fritz-Haber-Institut
der Max-Planck-
Gesellschaft
Berlin, Federal
Republic of Germany

b. 1906
d. 1988



Gerd Binnig

🕒 1/4 of the prize

Federal Republic of Germany

IBM Zurich Research
Laboratory
Rüschlikon,
Switzerland

b. 1947



Heinrich Rohrer

🕒 1/4 of the prize

Switzerland

IBM Zurich Research
Laboratory
Rüschlikon,
Switzerland

b. 1933



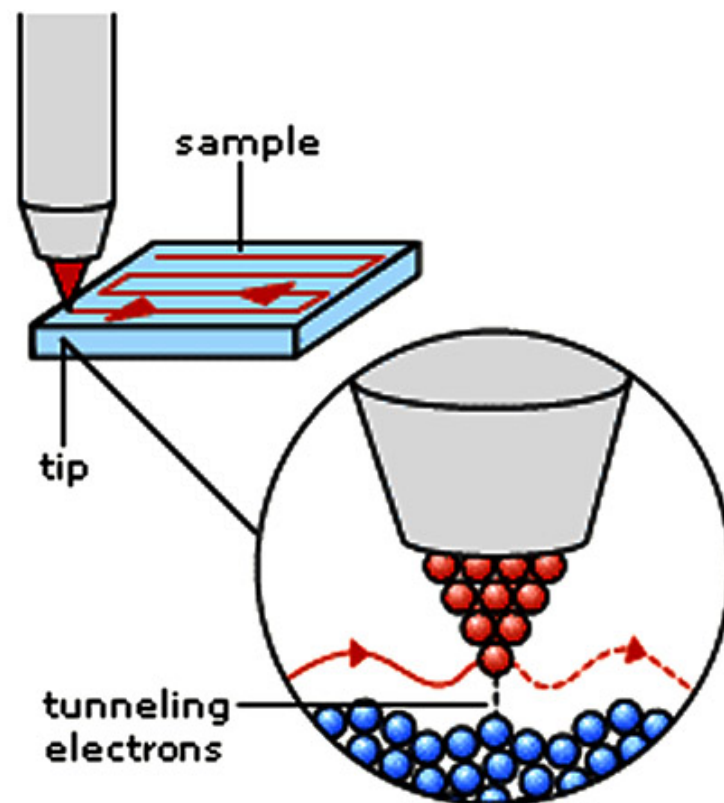
Nobel Laureates Heinrich Rohrer and Gerd Binnig

The Scanning Tunneling Microscope (STM)

In the STM, the structure of a surface is studied using a stylus that scans the surface at a fixed distance from it.

Currents Control the Surface

An extremely fine conducting probe is held close to the sample. Electrons tunnel between the surface and the stylus, producing an electrical signal. The stylus is extremely sharp, the tip being formed by one single atom. It slowly scans across the surface at a distance of only an atom's diameter. The stylus is raised and lowered in order to keep the signal constant and maintain the distance. This enables it to follow even the smallest details of the surface it is scanning. Recording the vertical movement of the stylus makes it possible to study the structure of the surface atom by atom. A profile of the surface is created, and from that a computer-generated contour map of the surface is produced.



Important in Many Sciences

The study of surfaces is an important part of physics, with particular applications in semiconductor physics and microelectronics. In chemistry, surface reactions also play an important part, for example in catalysis. The STM works best with conducting materials, but it is also possible to fix organic molecules on a surface and study their structures. For example, this technique has been used in the study of DNA molecules.

Invention of Atomic force microscope

► 2016 KAVLI PRIZE NANOSCIENCE

Recognized "for the invention and realization of atomic force microscopy, a breakthrough in measurement technology and nanosculpting that continues to have a transformative impact on nanoscience and technology."



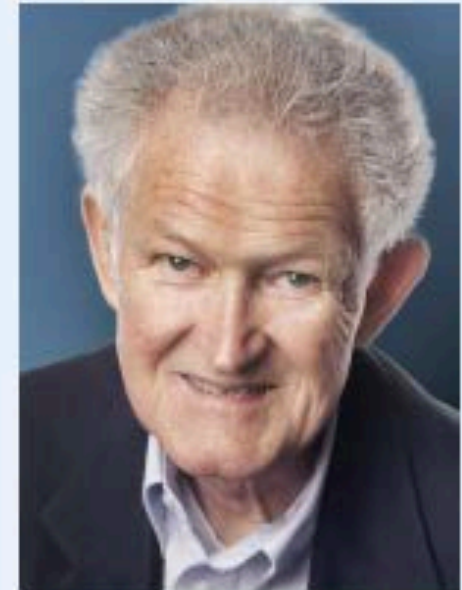
Gerd Binnig

*Former member of IBM Zurich
Research Laboratory, Switzerland*



Christoph Gerber

University of Basel, Switzerland

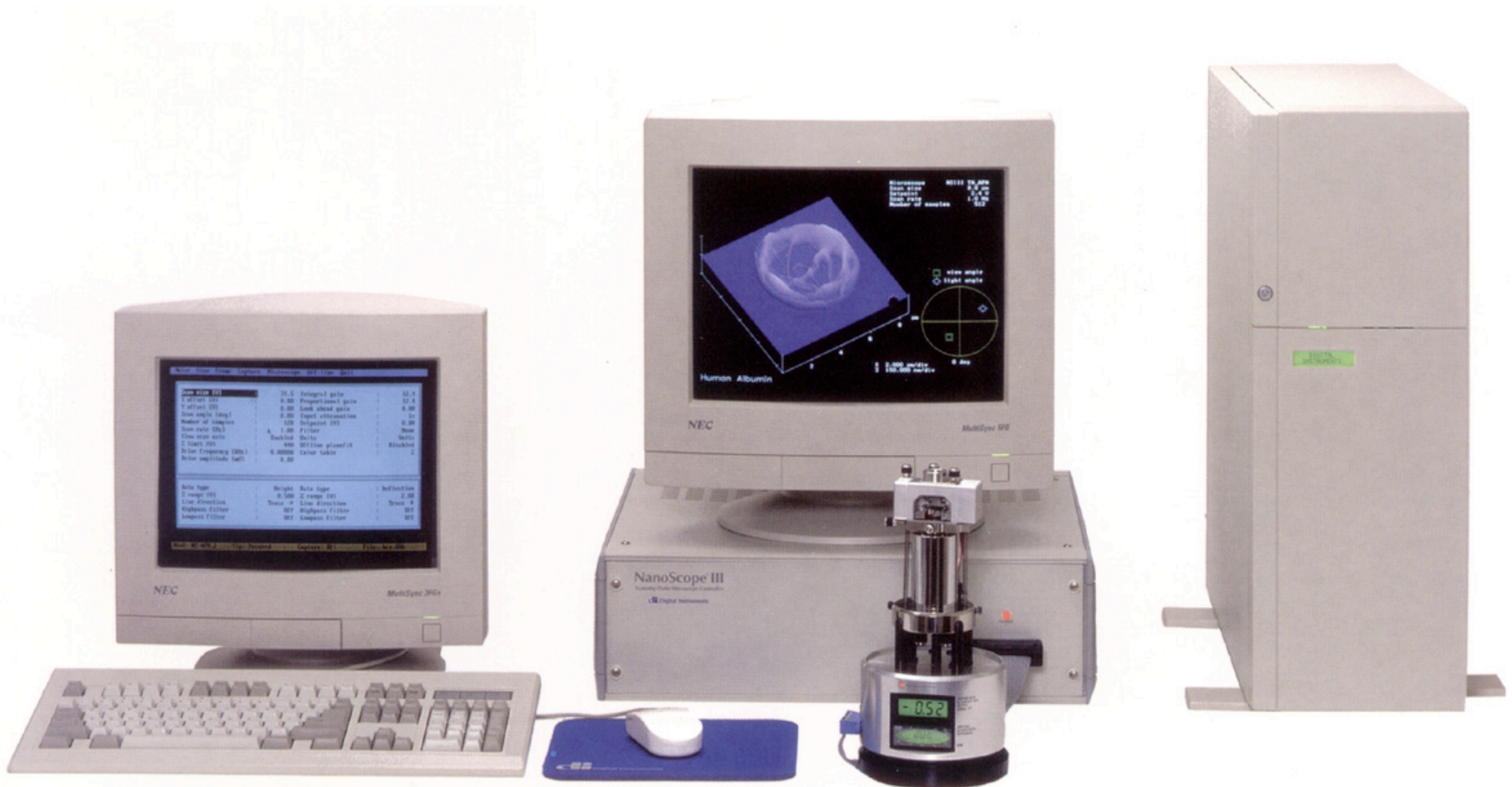


Calvin Quate

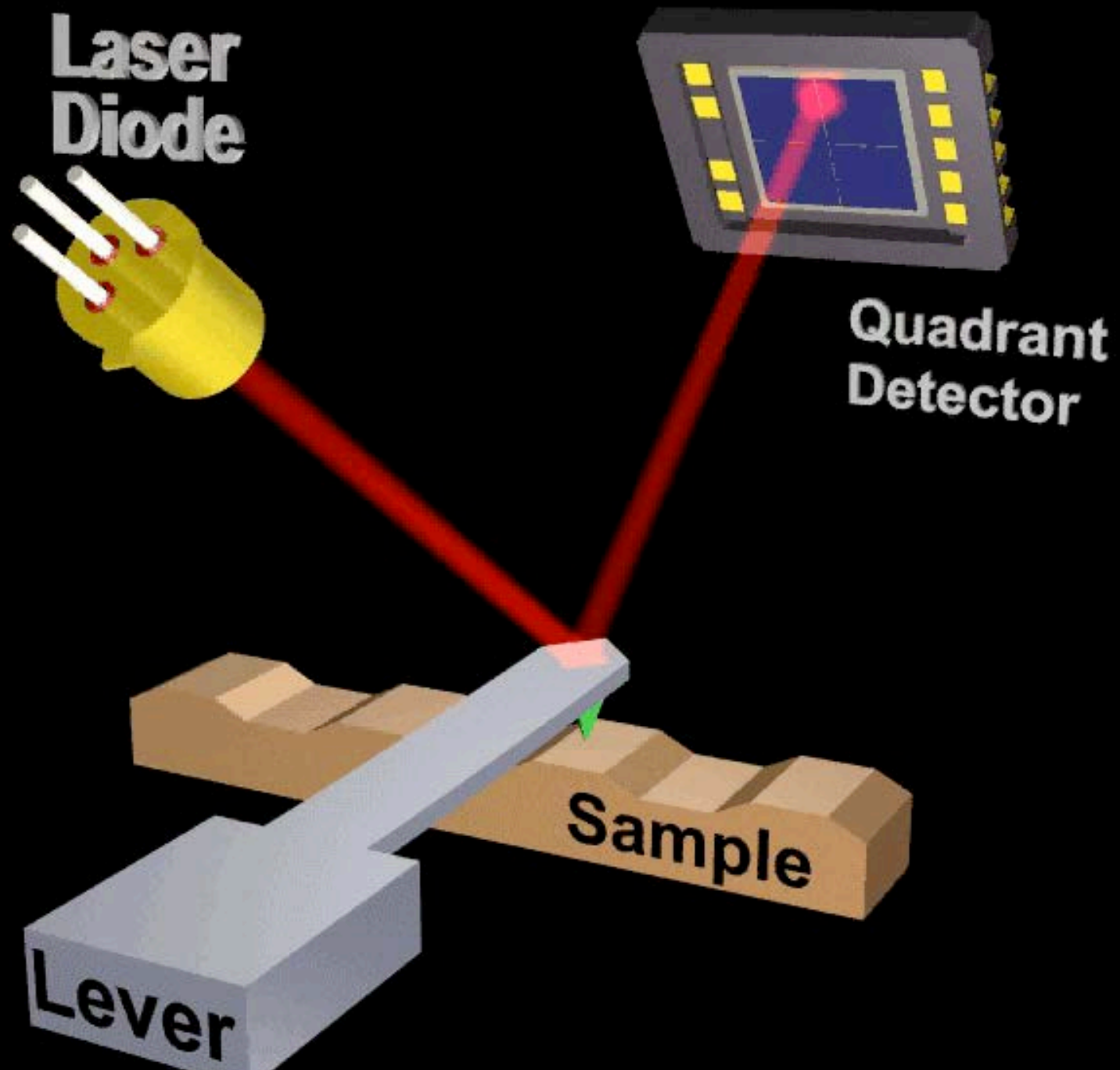
Stanford University, USA

Atomic Force Microscope (AFM)

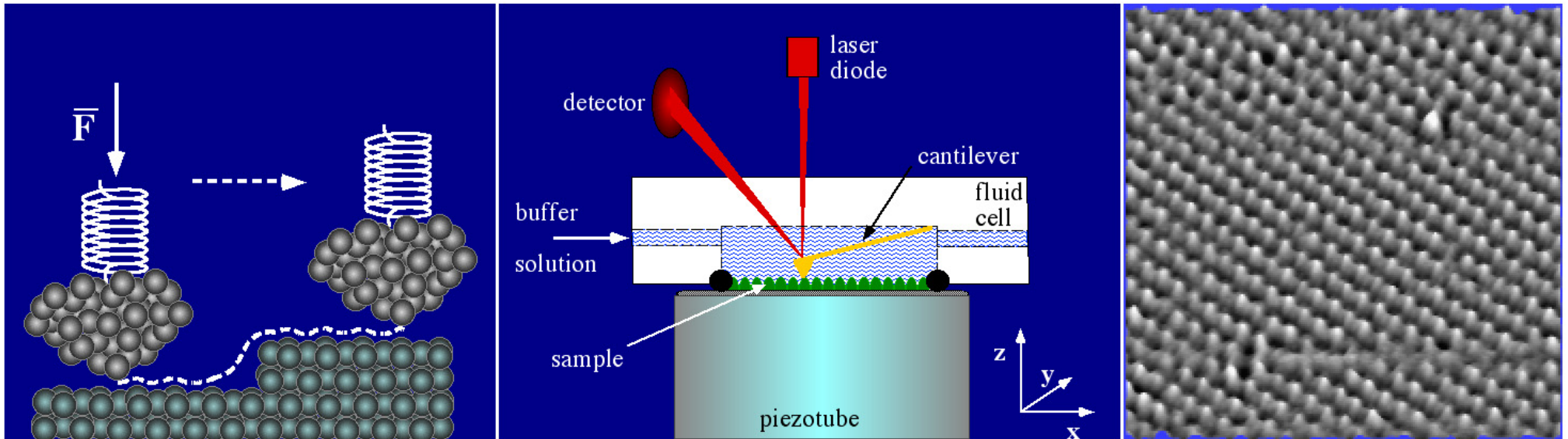
(The AFM is the younger brother of the STM)



Atomic force microscopy (AFM)



Atomic force microscopy (AFM)



Resolution:

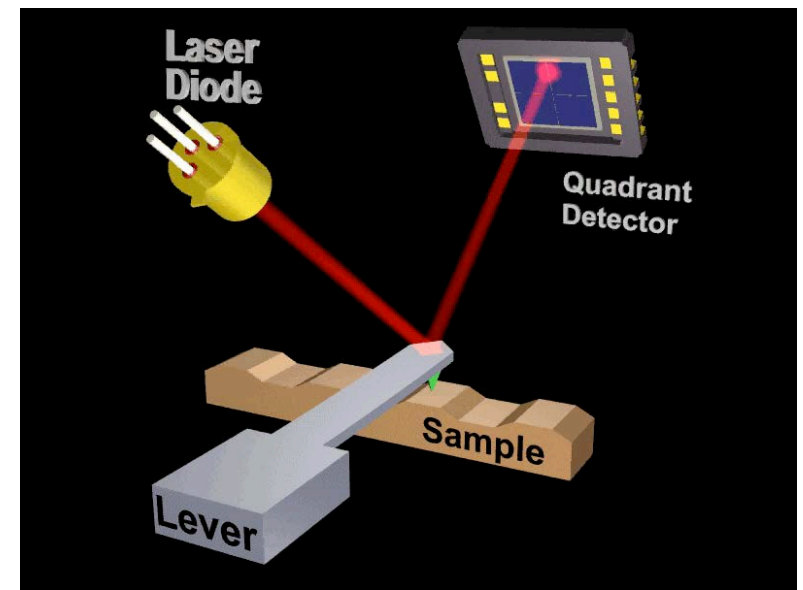
STM on Metals: 1 Å (X,Y,Z)

AFM on Proteins: 5 Å (X,Y), 1 Å (Z)

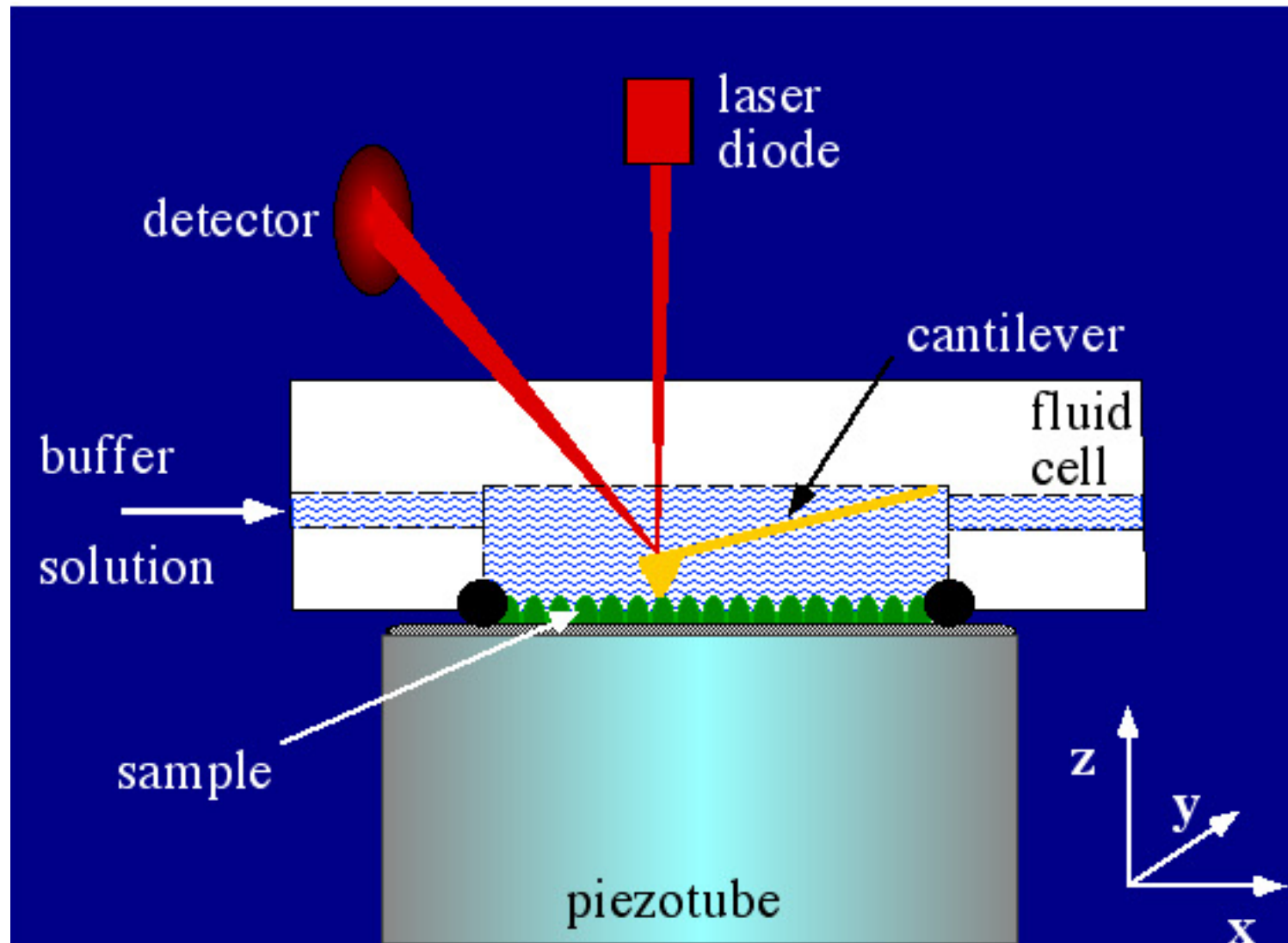
Signal Source:

STM: Electric current between tip and sample.

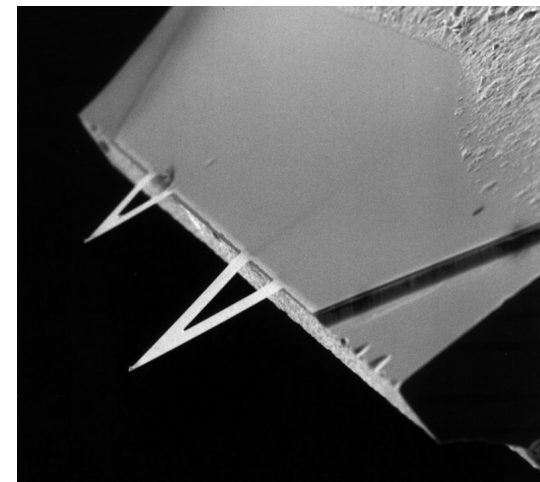
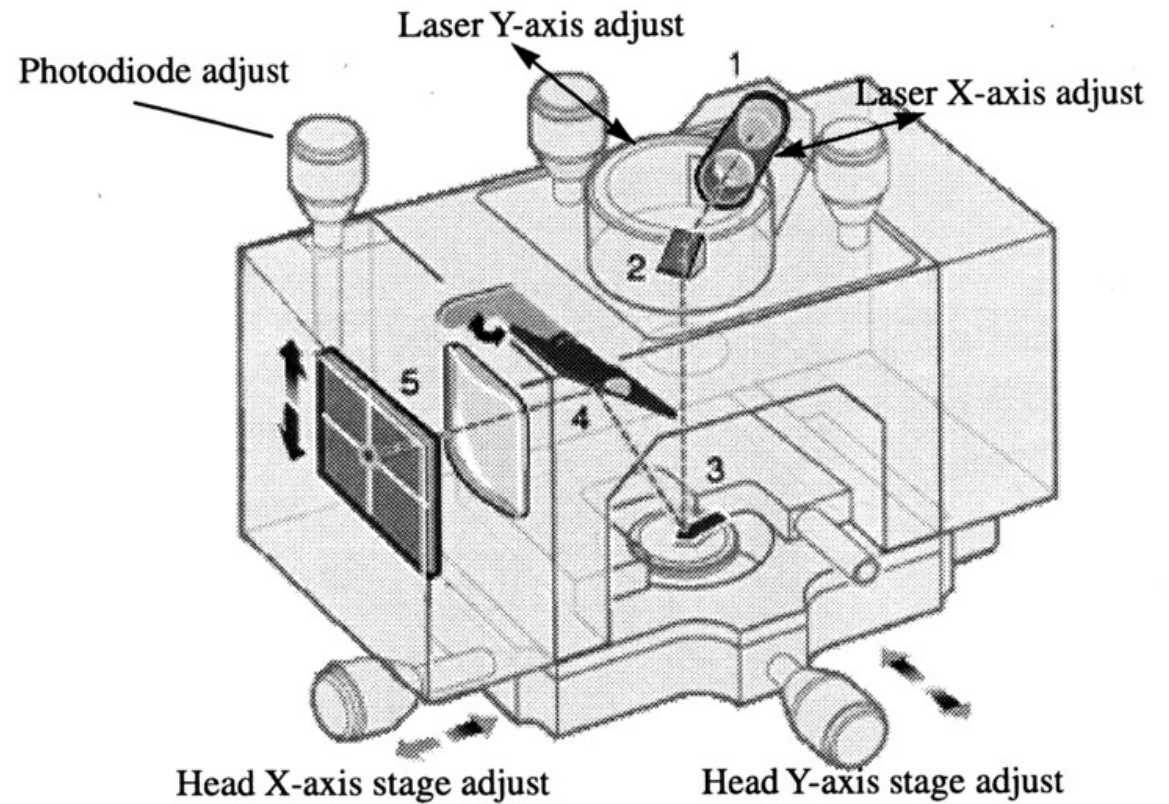
AFM: Physical bending of the cantilever.

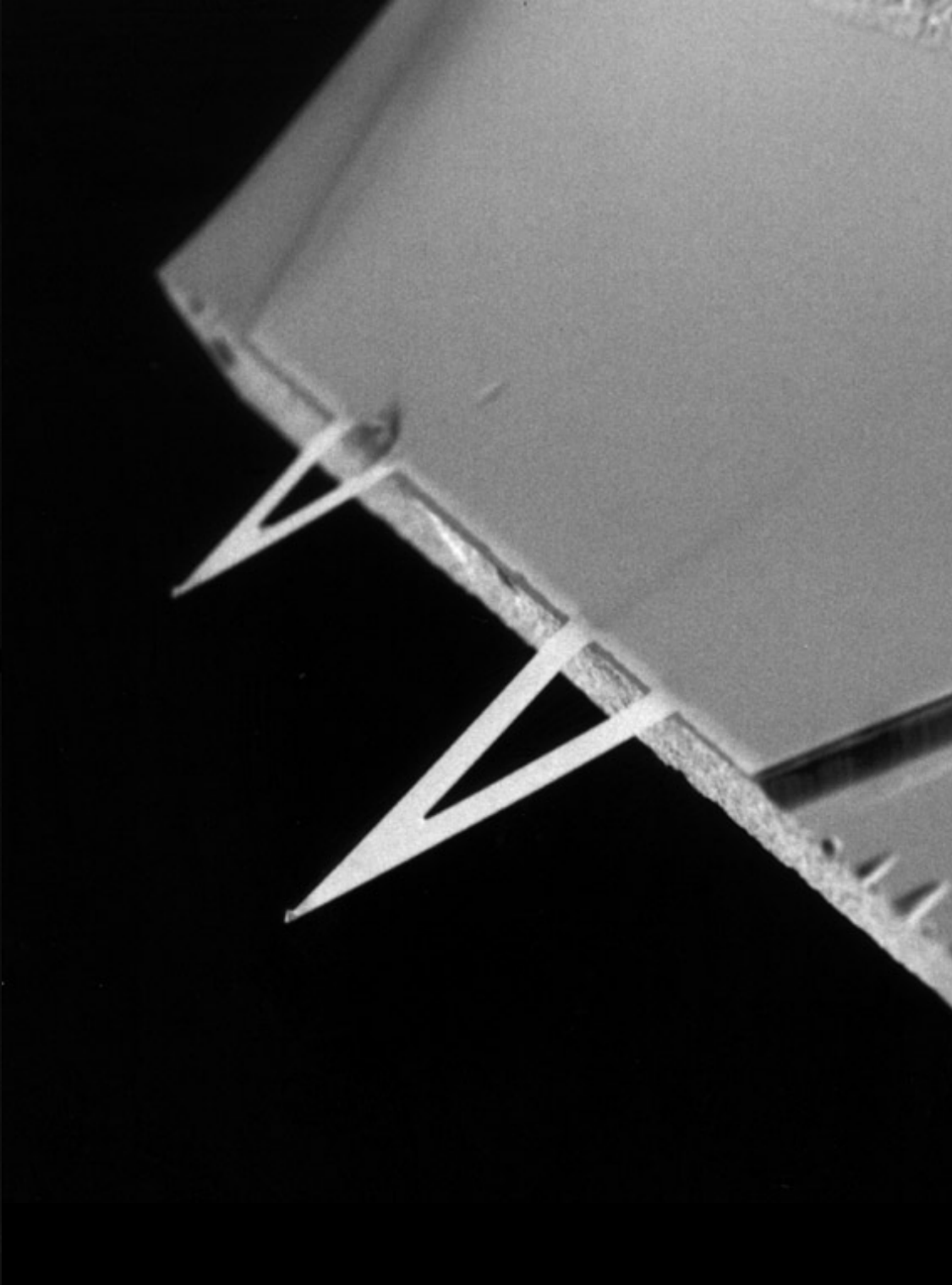
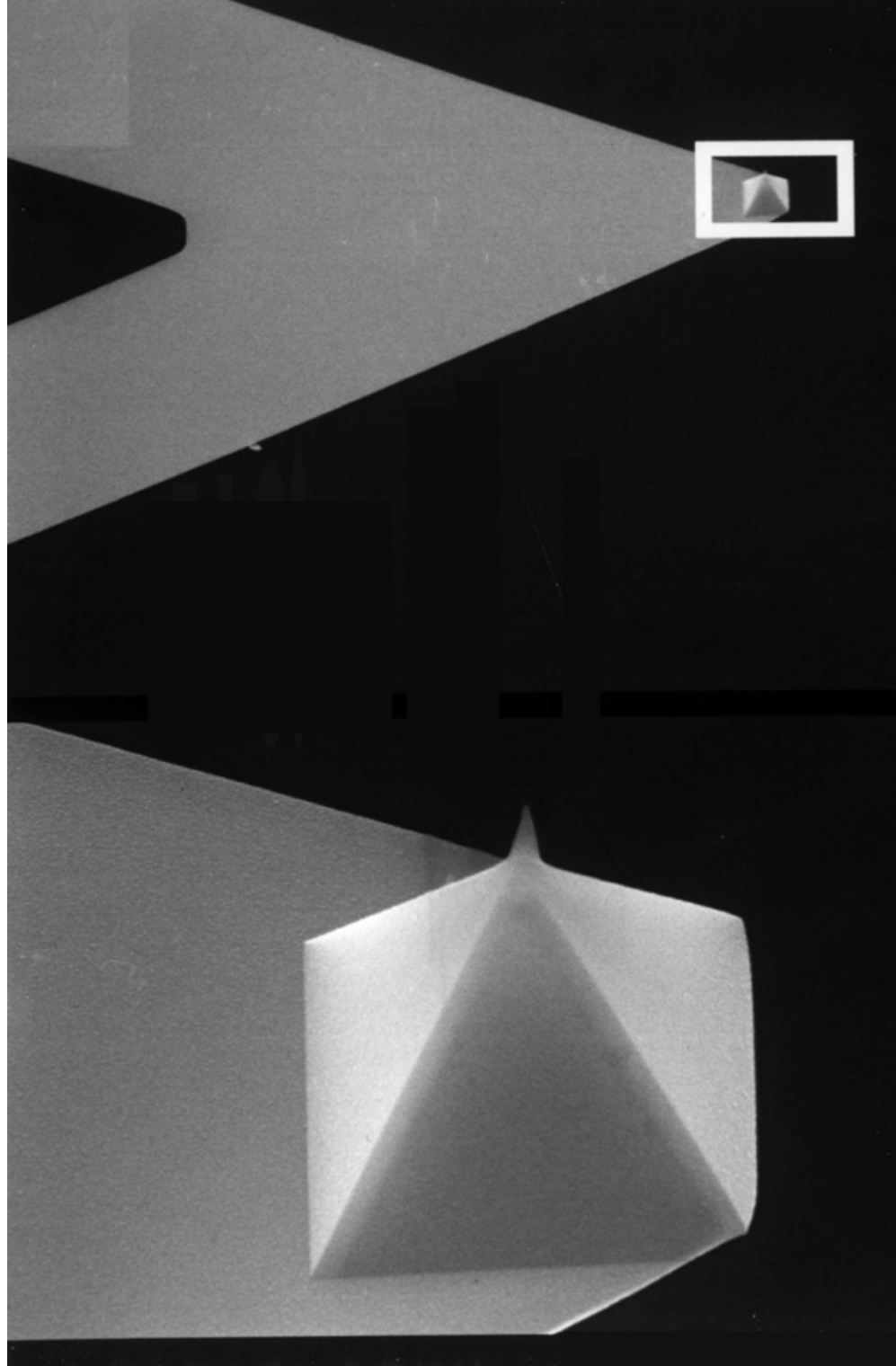


Atomic force microscopy (AFM)

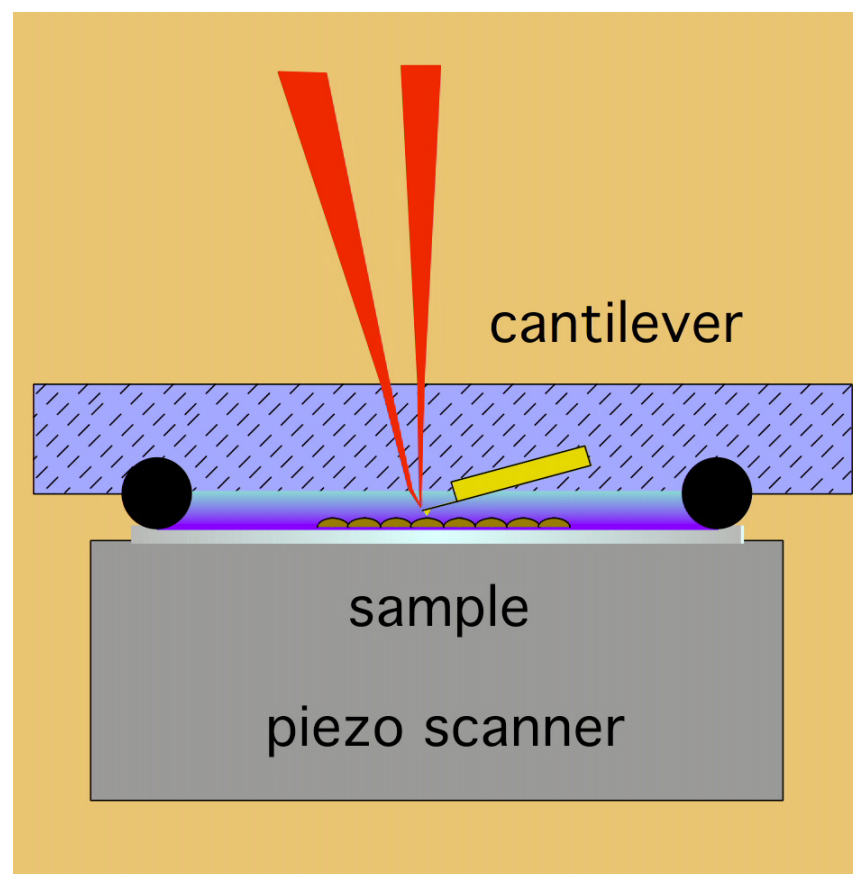
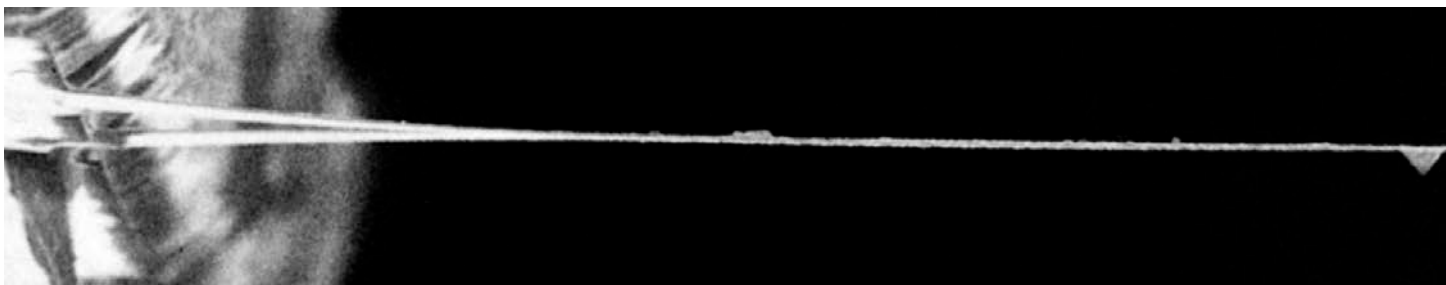


Atomic Force Microscopy

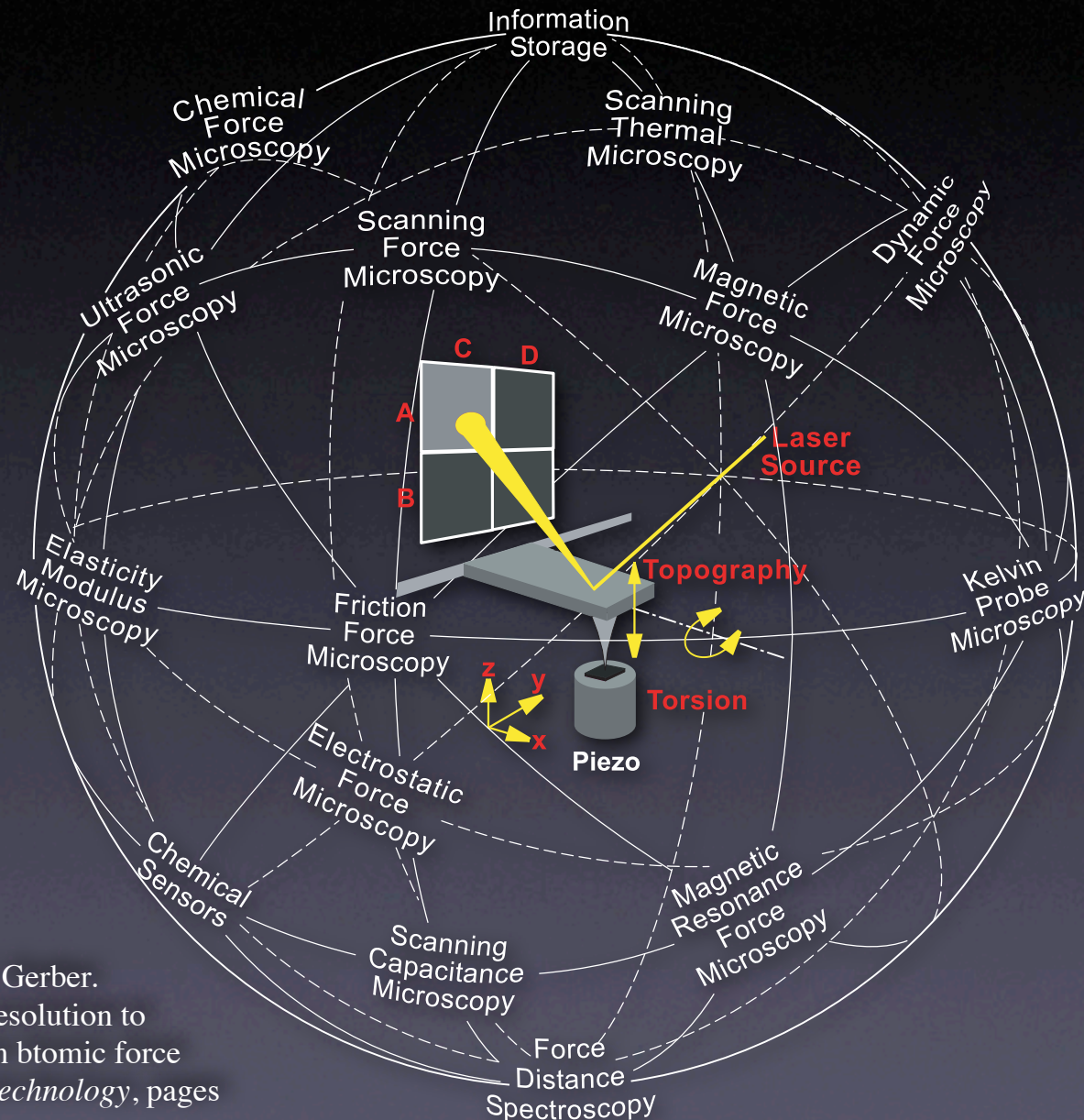




Atomic force microscopy (AFM)

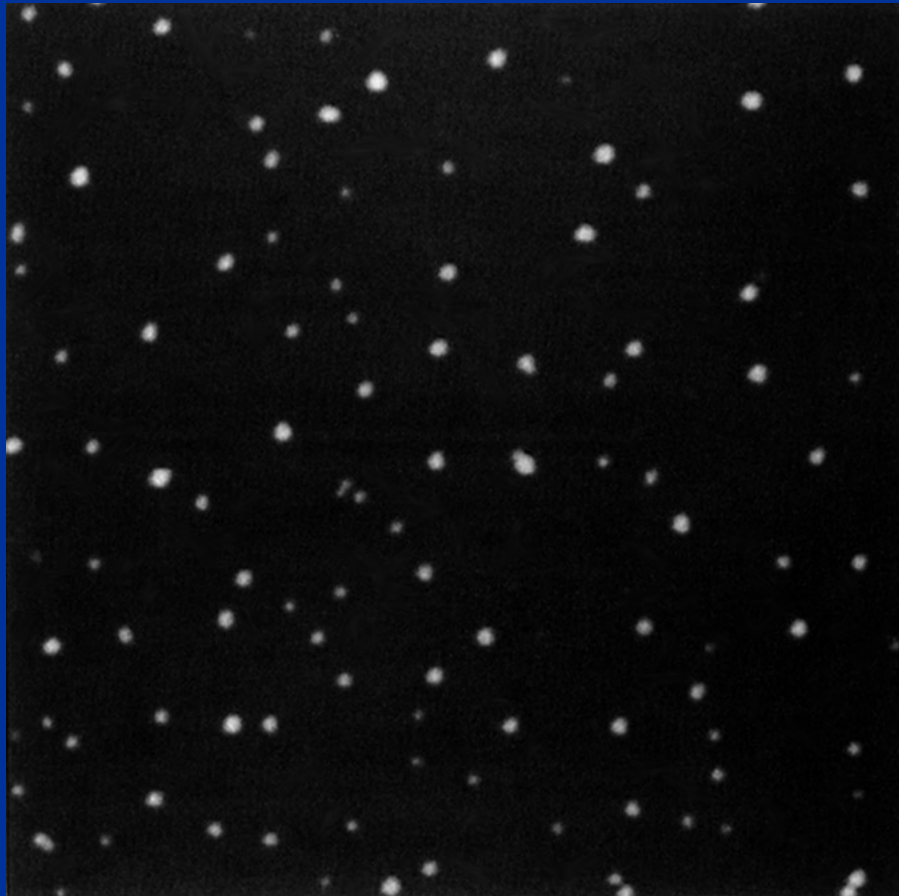


World of Cantilevers

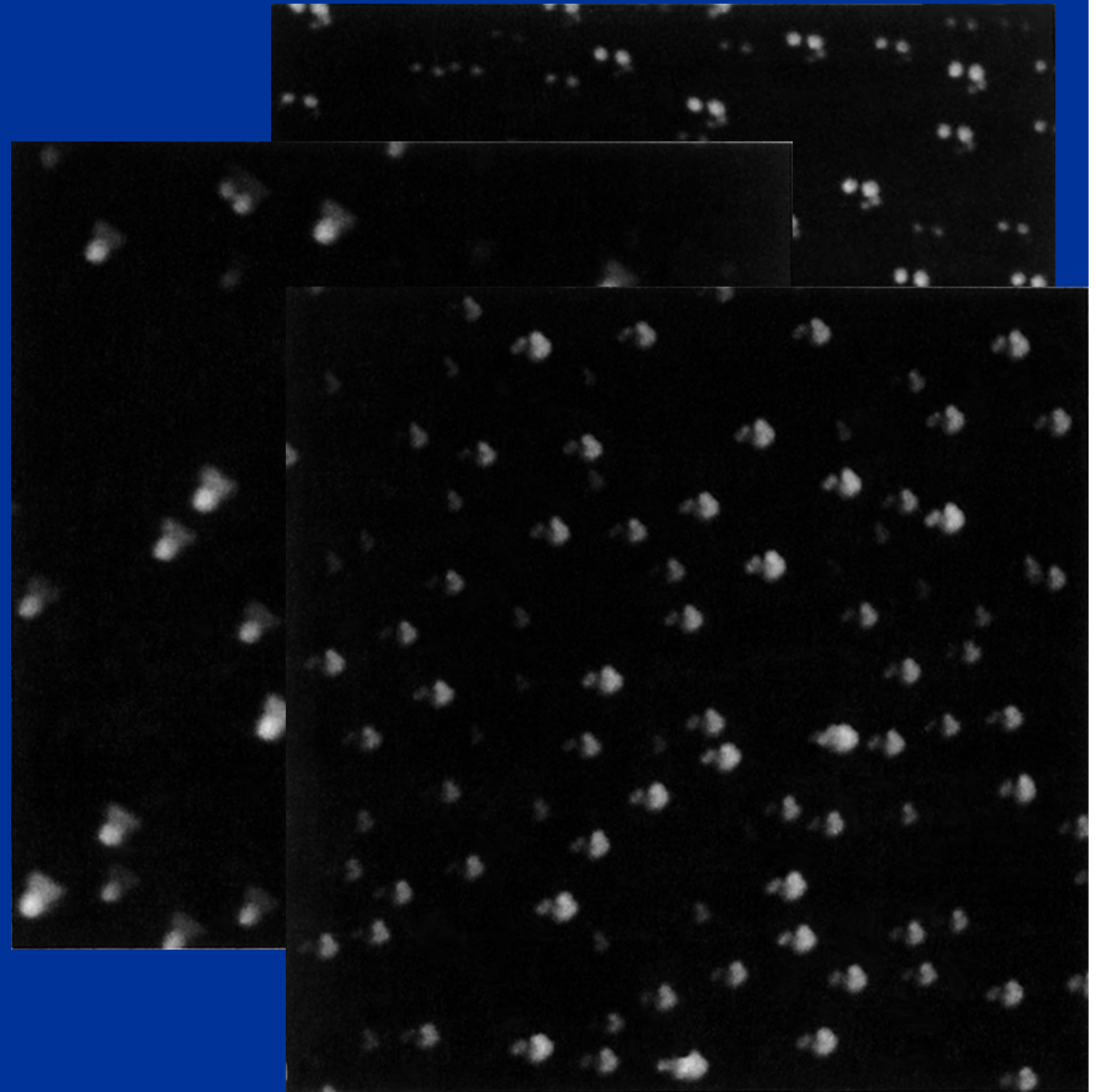


H. P. Lang, M. Hegner, and C. Gerber.
 Nanomechanics from atomic resolution to
 molecular recognition based on atomic force
 microscopy technology. *Nanotechnology*, pages
 R29–R36, 2002.

Atomic force microscopy (AFM)



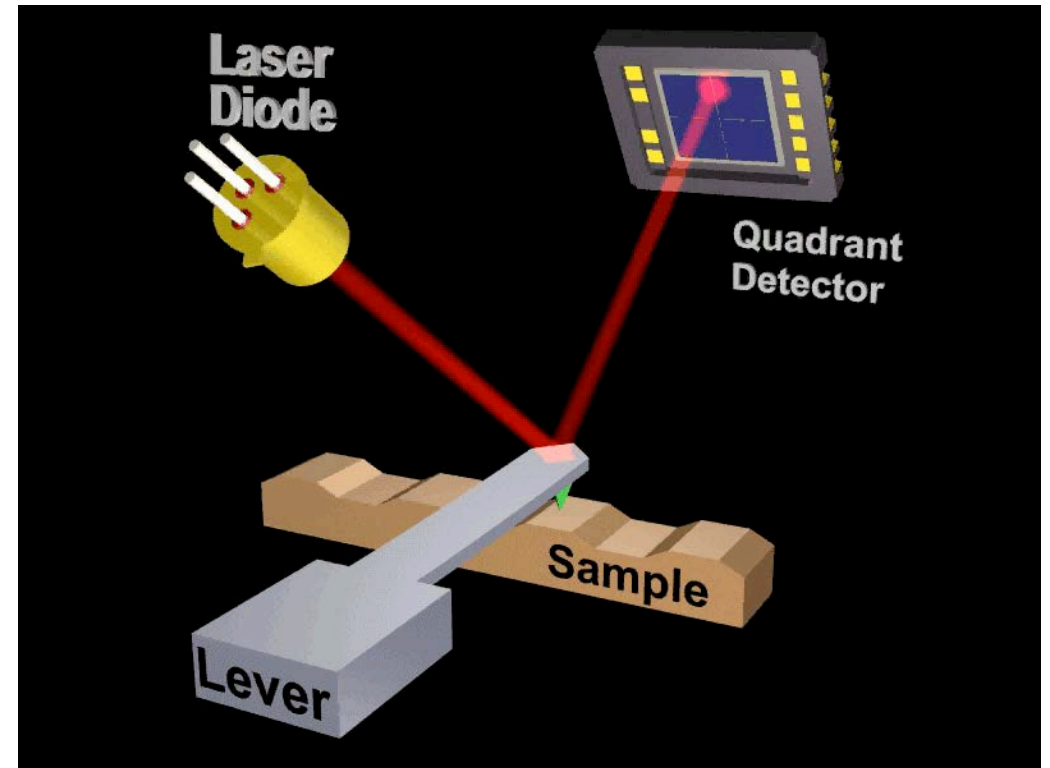
Sharp Tip



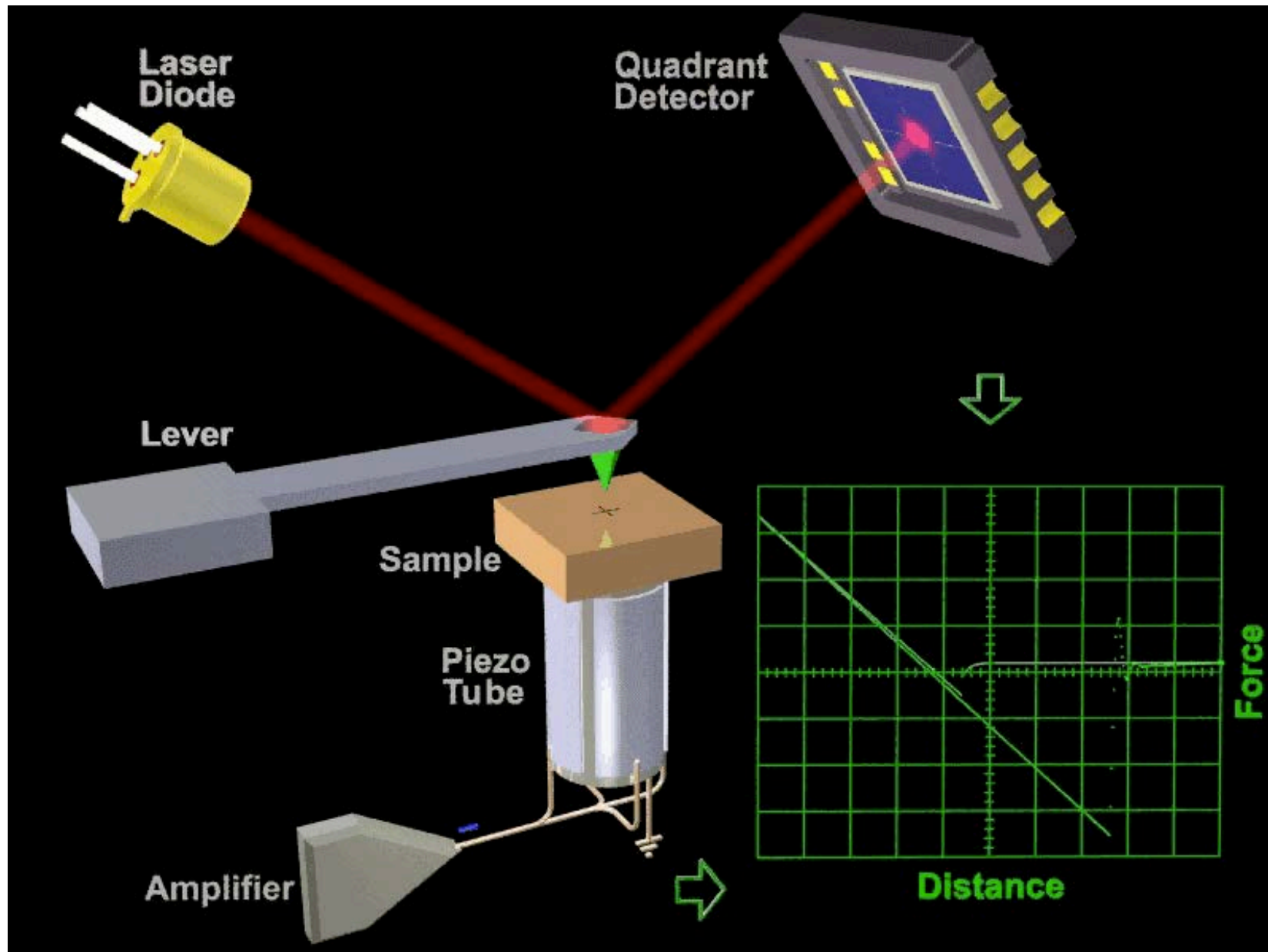
Double Tip

AFM Modes

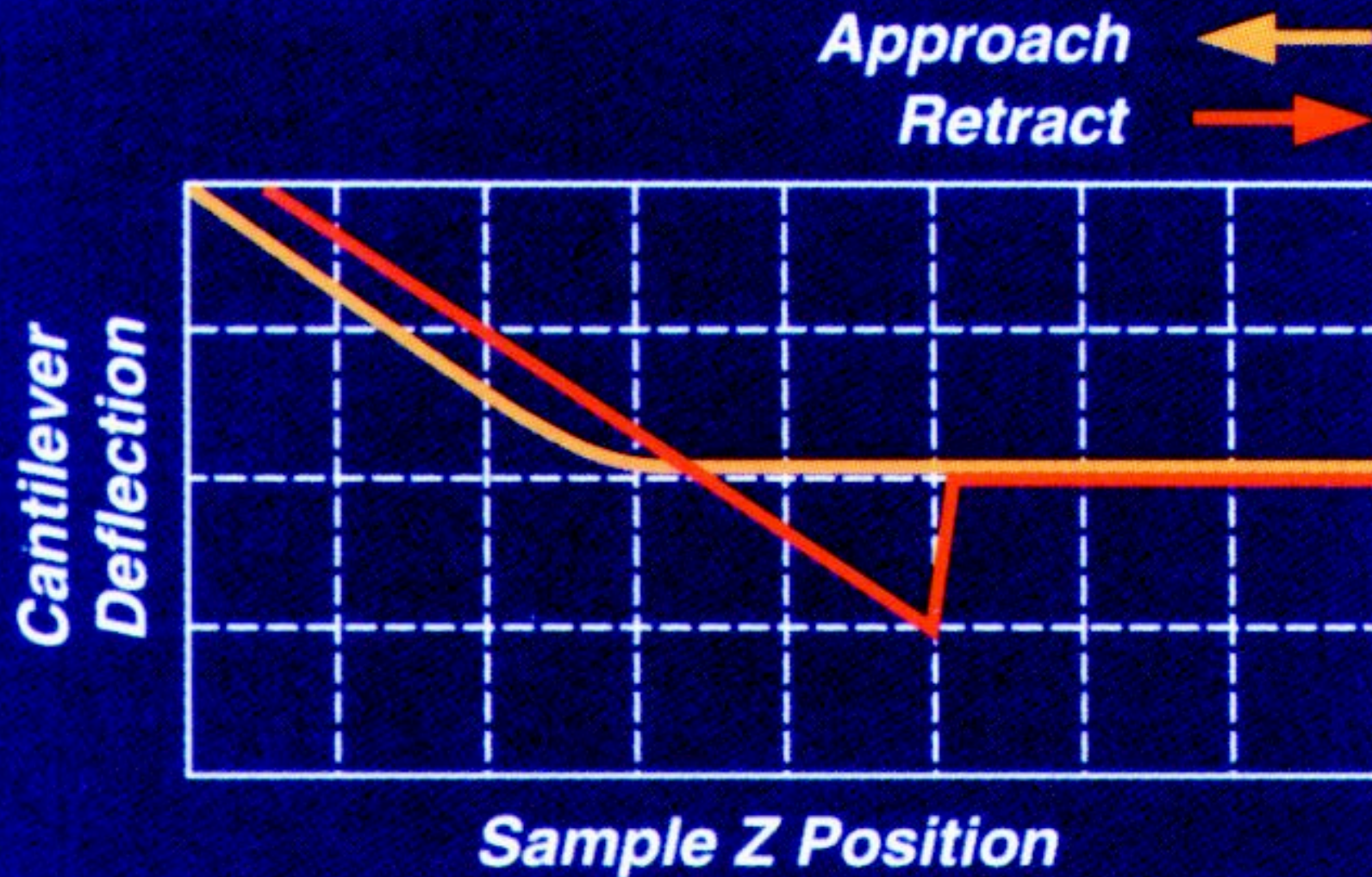
- Constant Height Mode
- Constant Force Mode
- Friction mode
- Tapping Mode, vibrating mode



Tip-Sample Interaction in Air

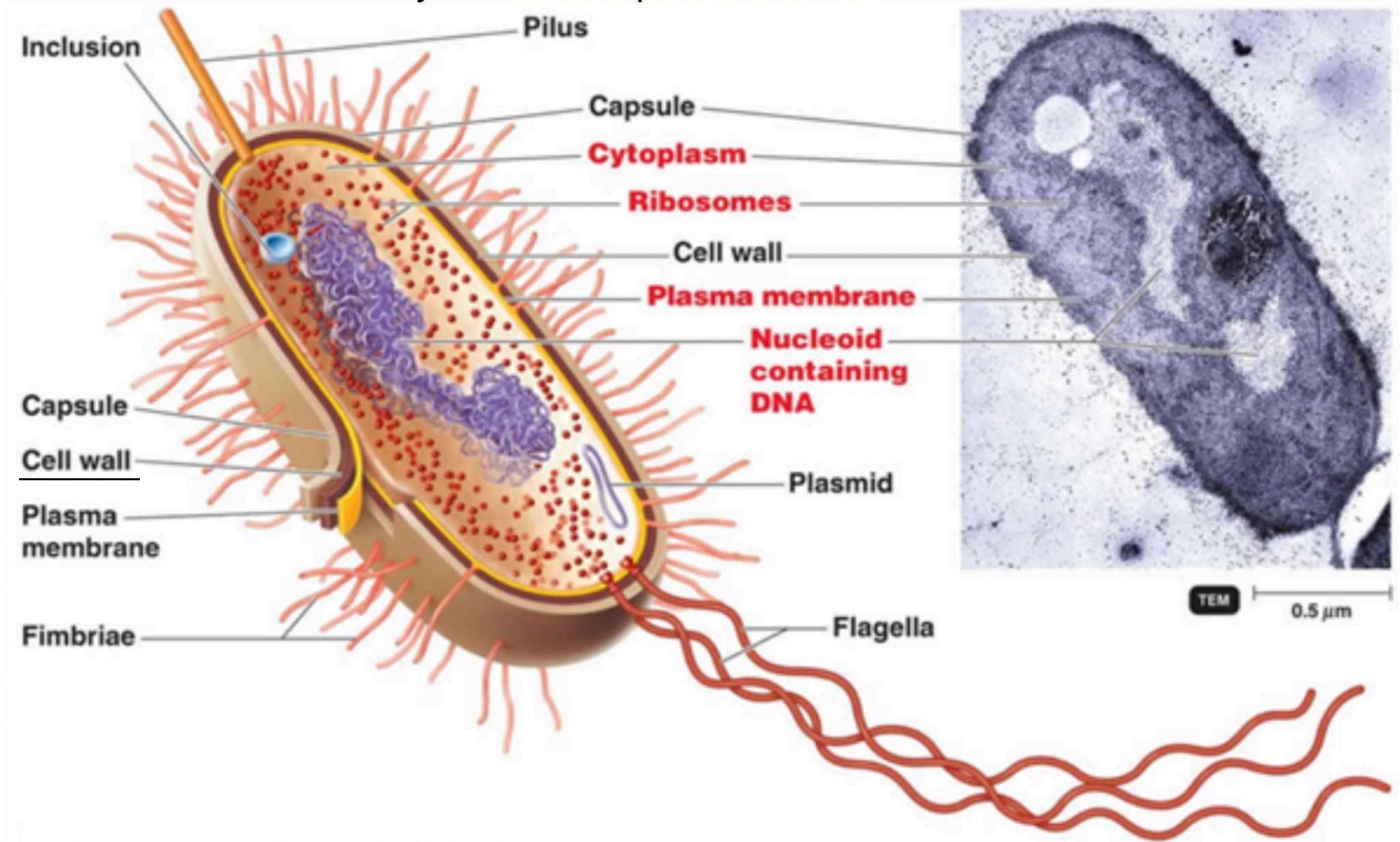


Tip-Sample Interaction in Water



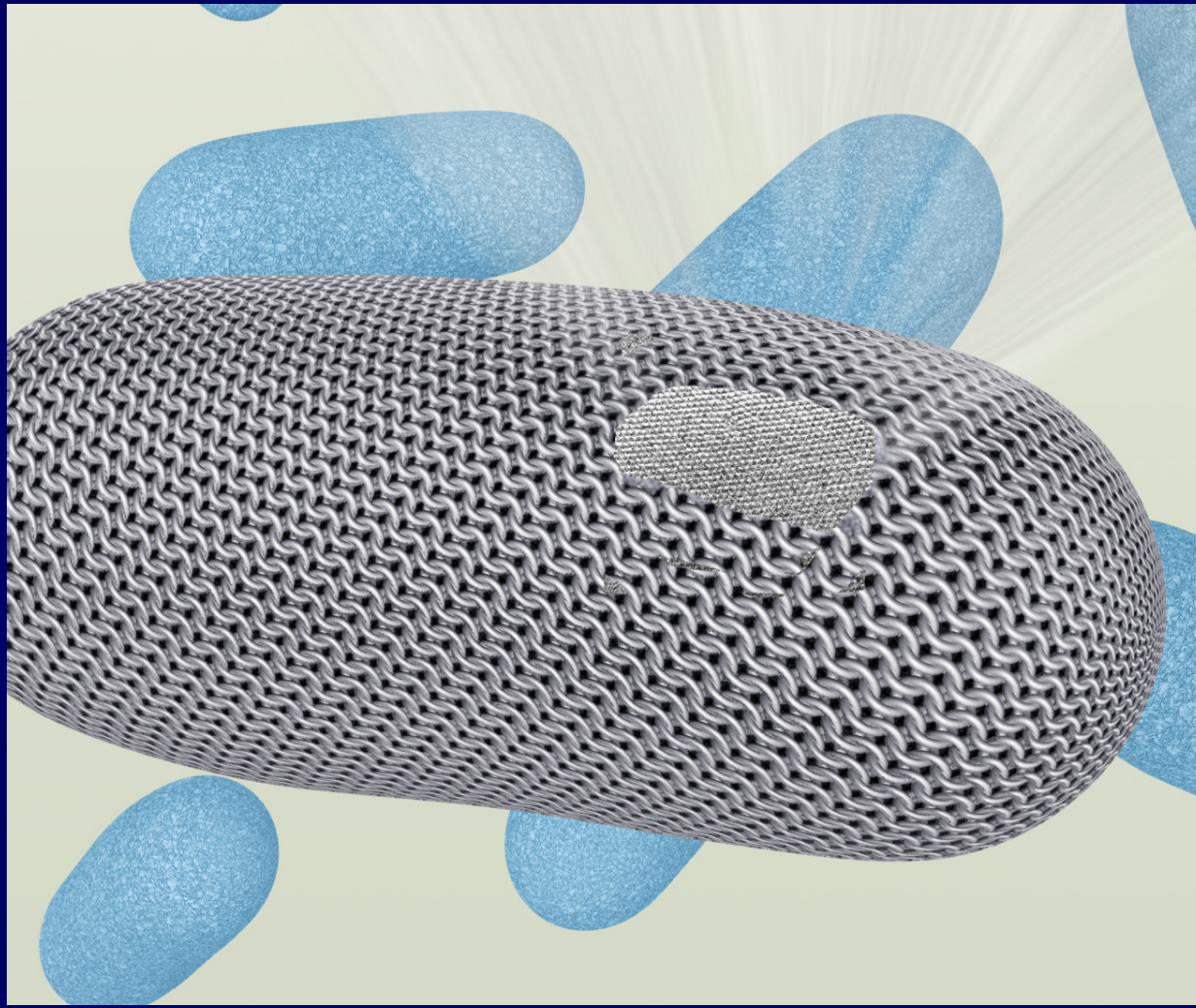
Charting and unzipping the S-layer of *Corynebacterium glutamicum*

The S-layer forms the protective cell wall of bacteria

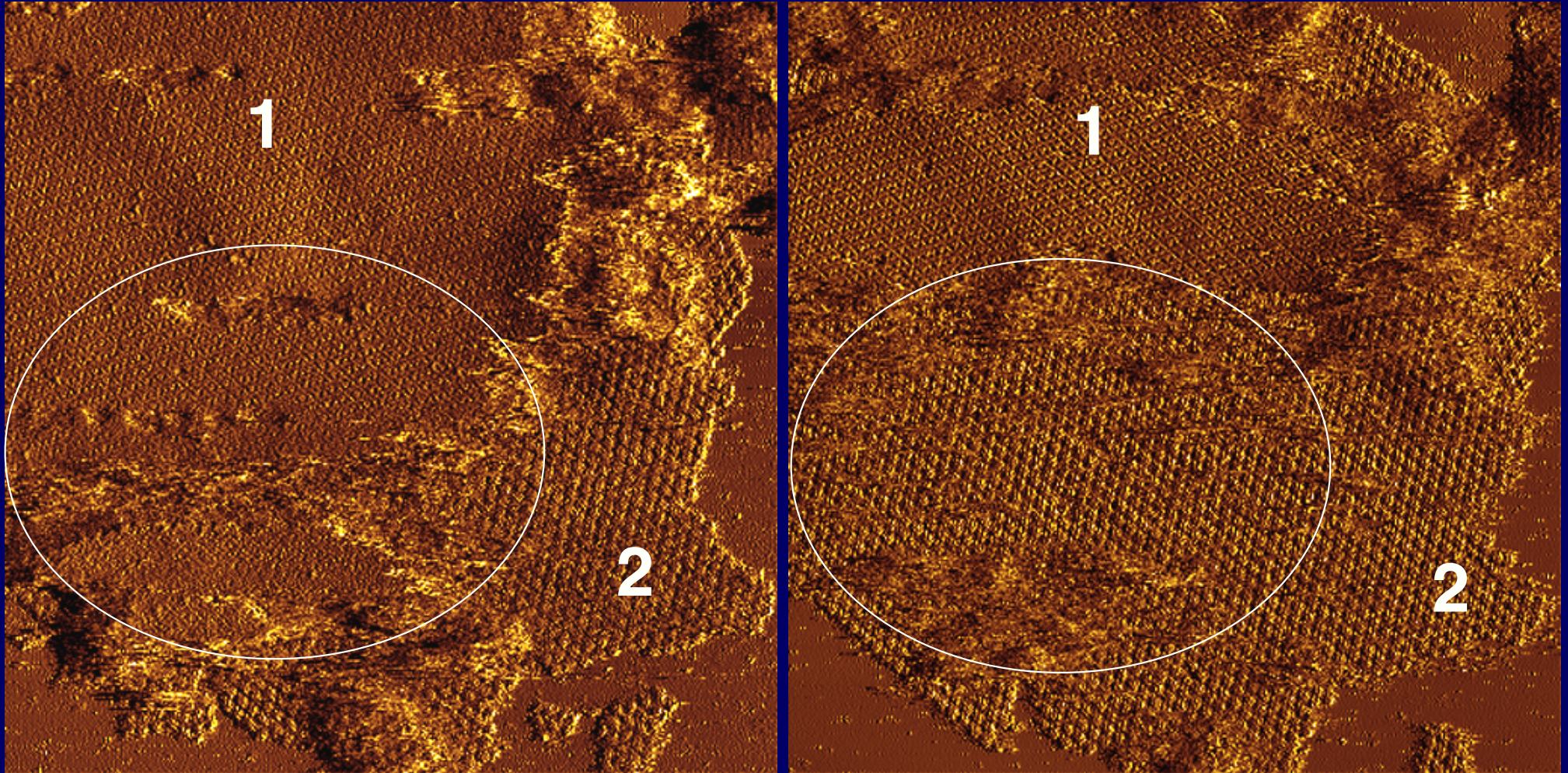


Charting and unzipping the S-layer of *Corynebacterium glutamicum* with the AFM

The S-layer is the protective “armor” of bacterial



**Native S-layer adsorbs double layered
And can be dissected with the AFM tip**

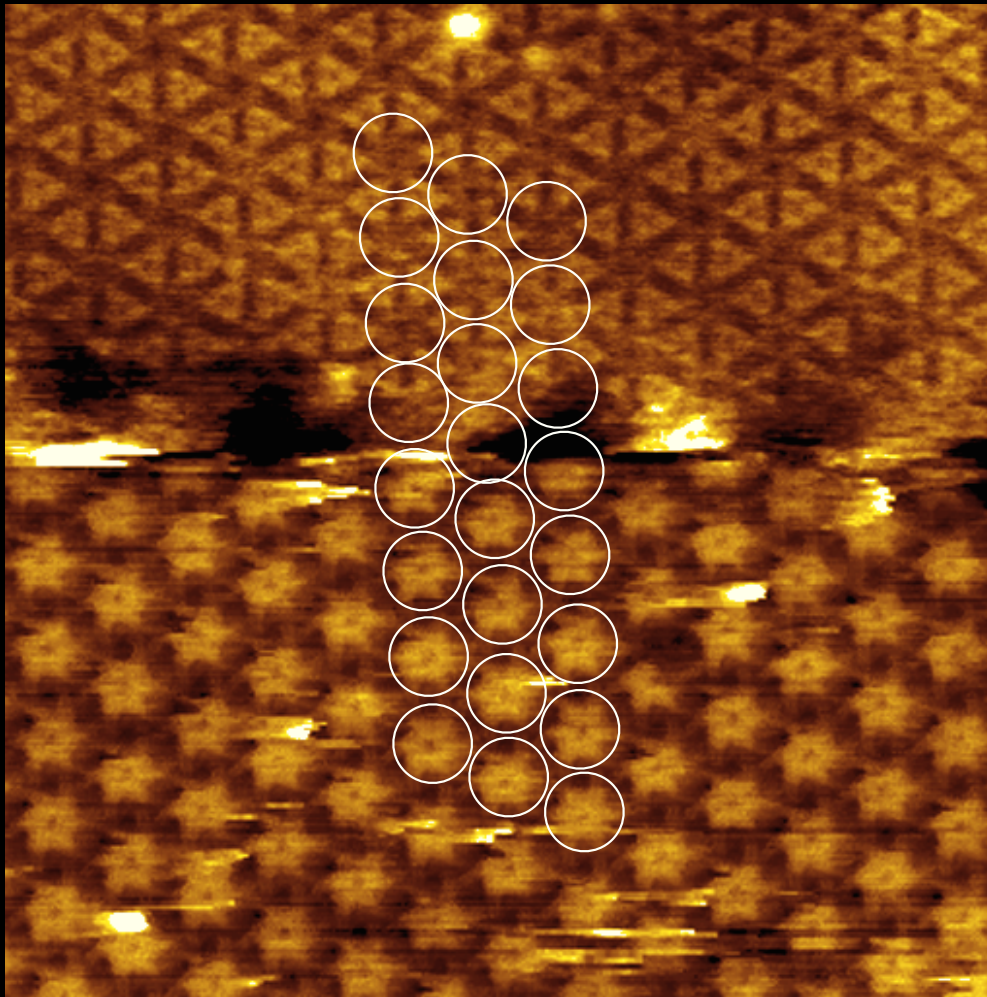


1: triangular surface

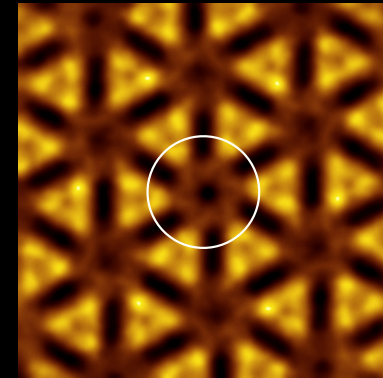
2: flower-shaped surface

Native S-layer adsorbs double layered and can be dissected with the AFM tip

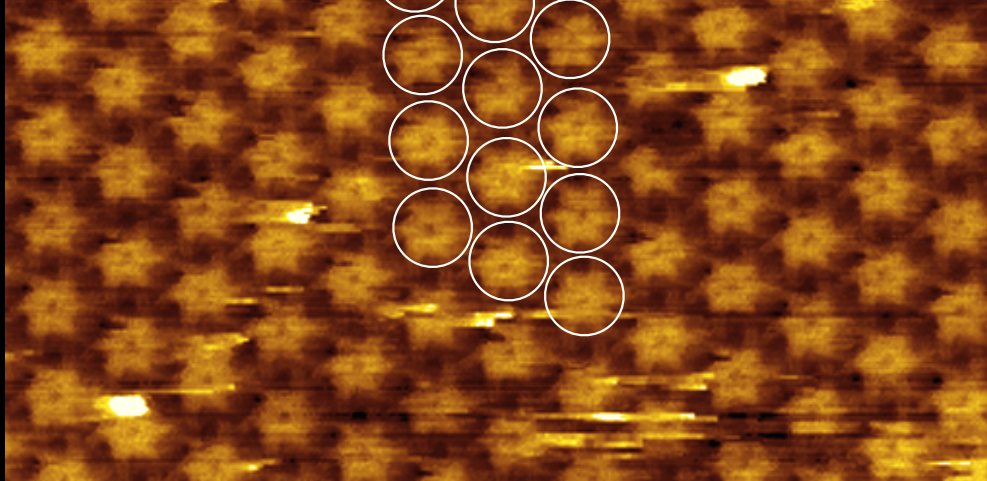
1



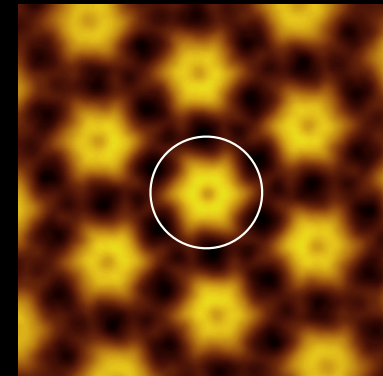
minimal force ($\sim 100\text{pN}$)



2



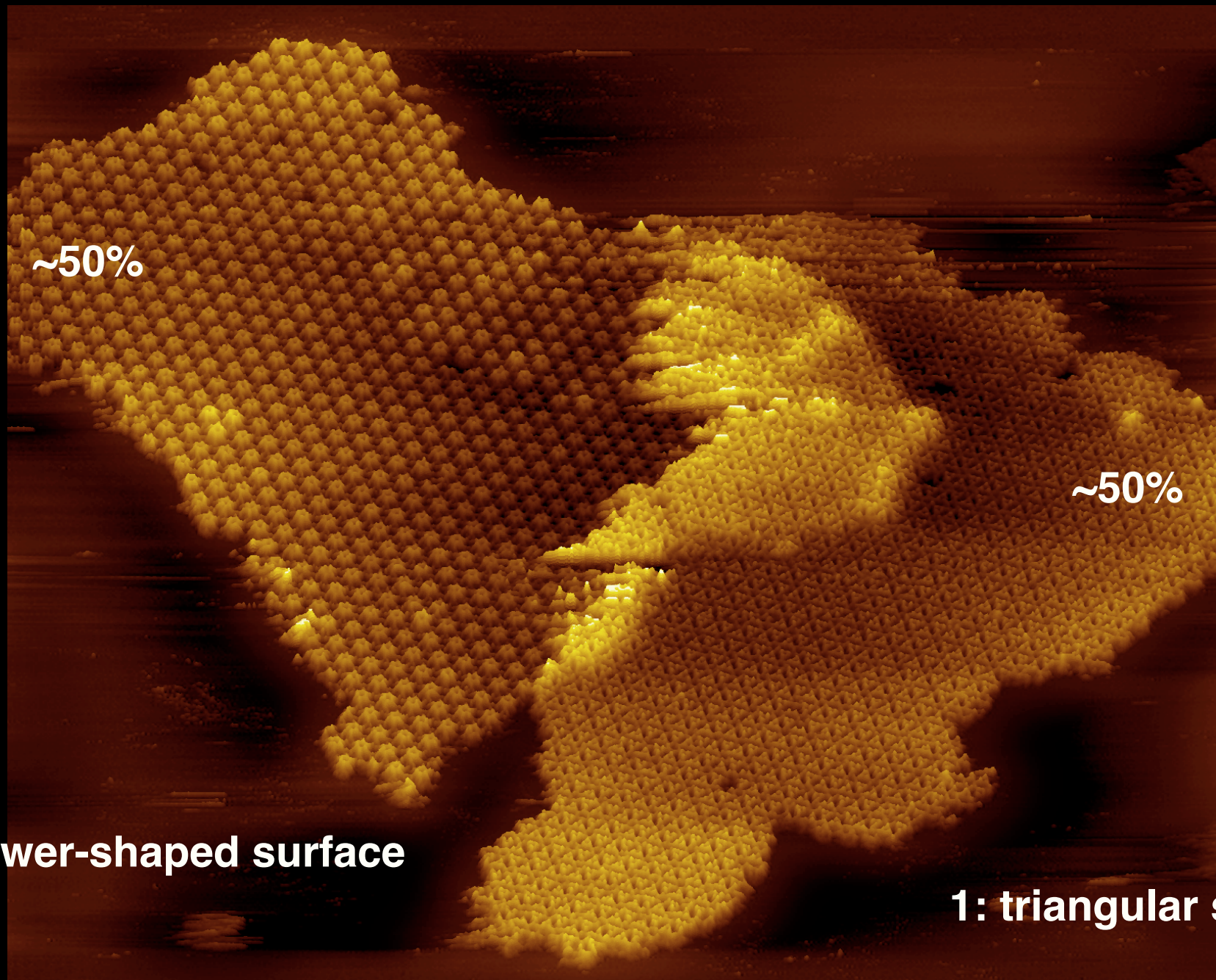
+600pN



1: triangular surface
2: flower-shaped surface

force applied to the AFM tip

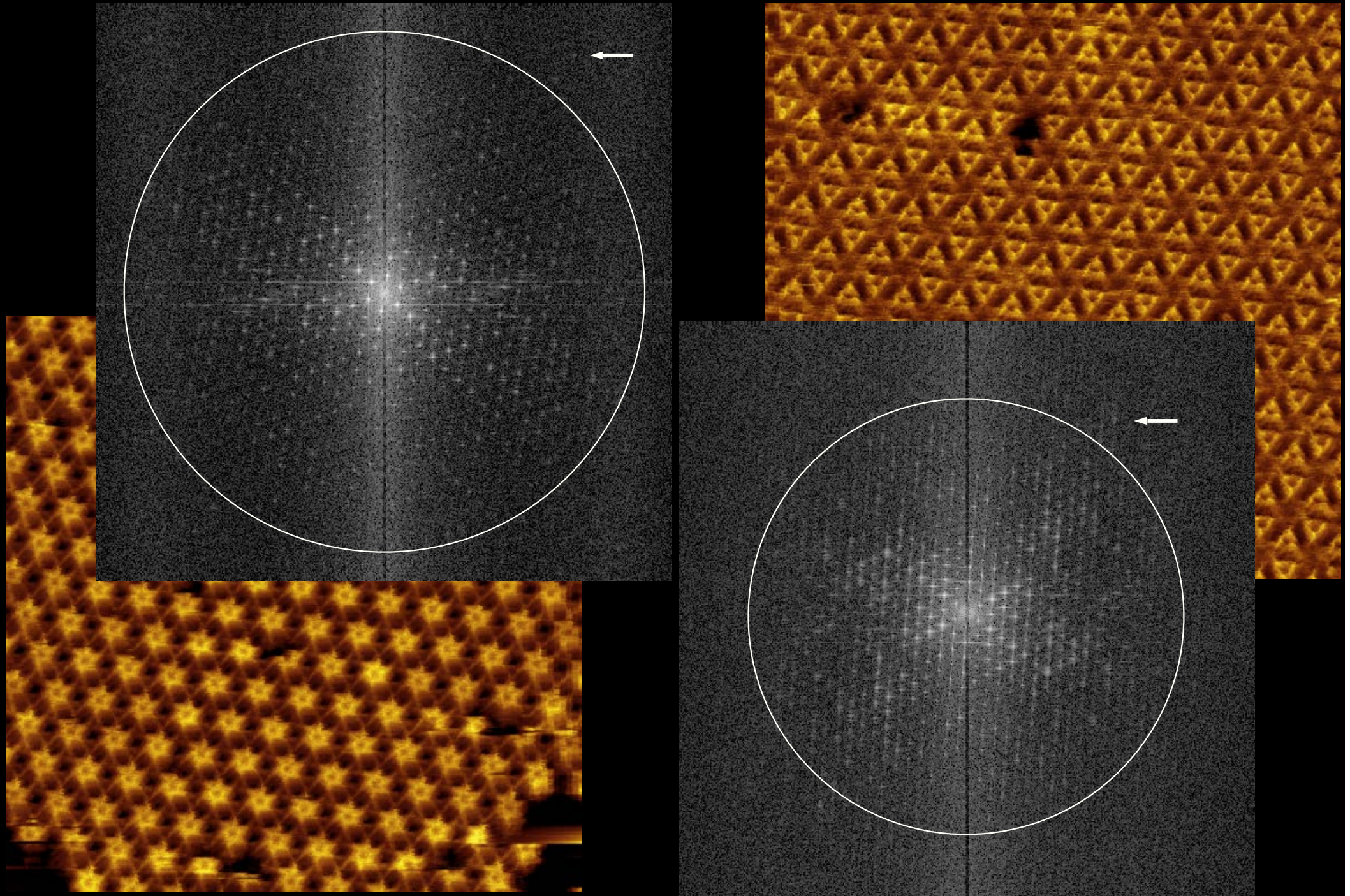
AFM overview topograph of the proteolyzed sample



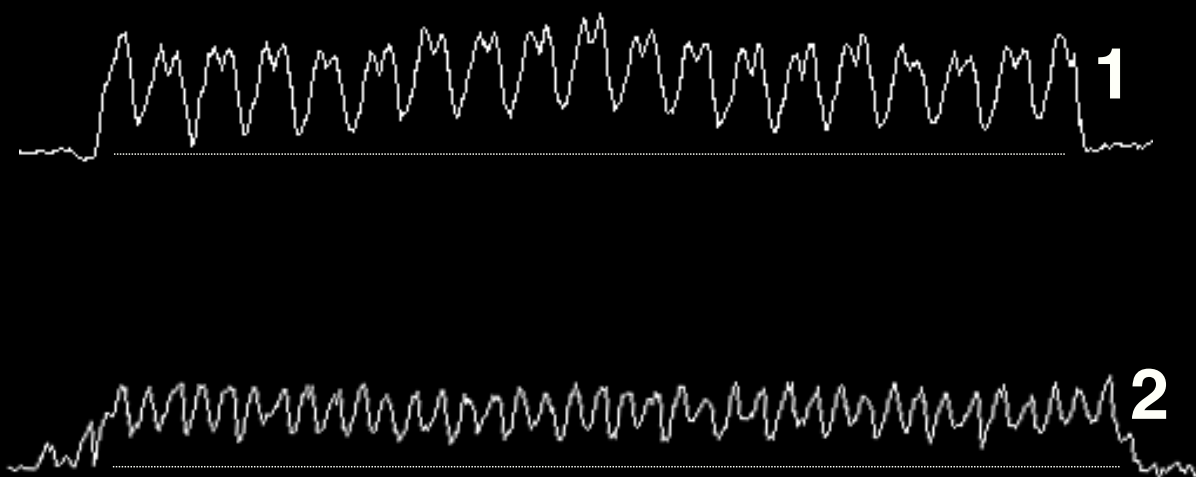
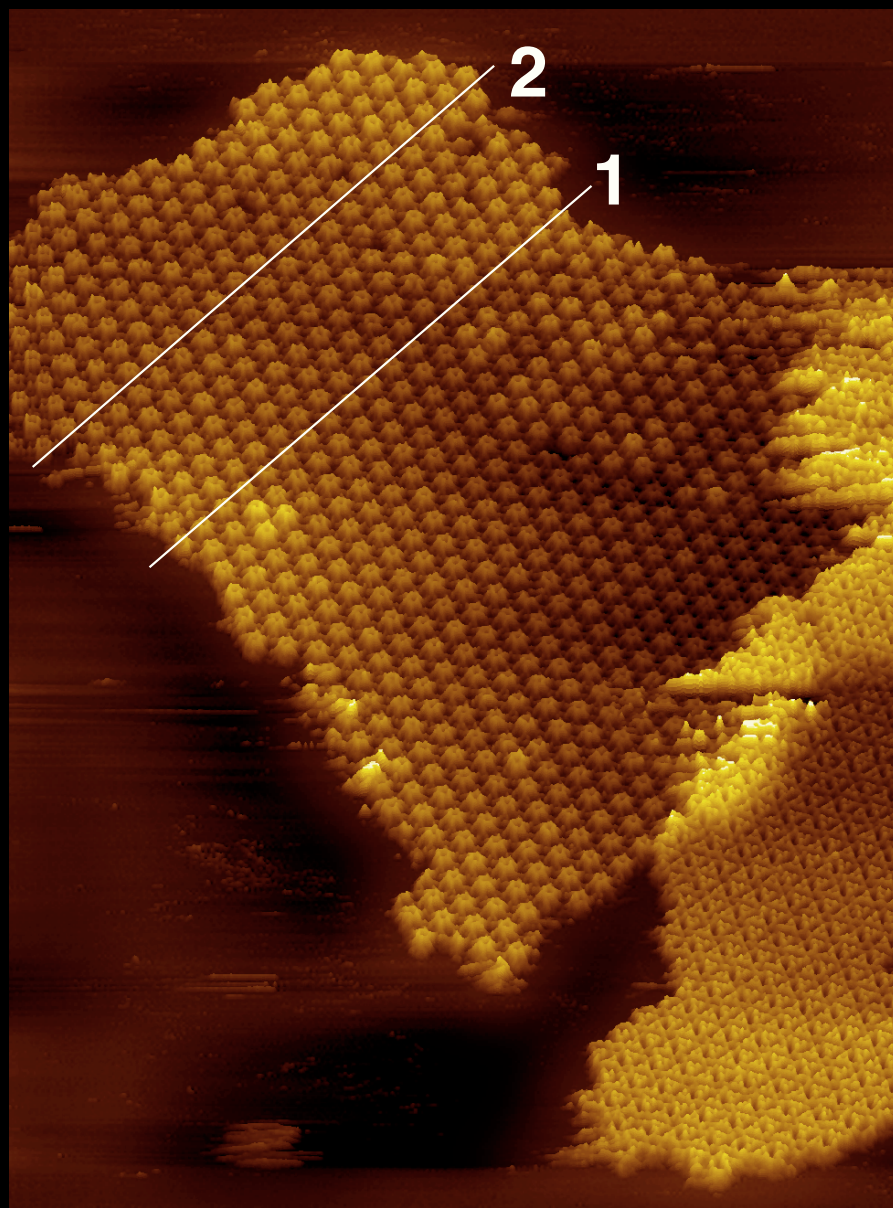
2: flower-shaped surface

1: triangular surface

Raw data topographs diffract to 1nm resolution



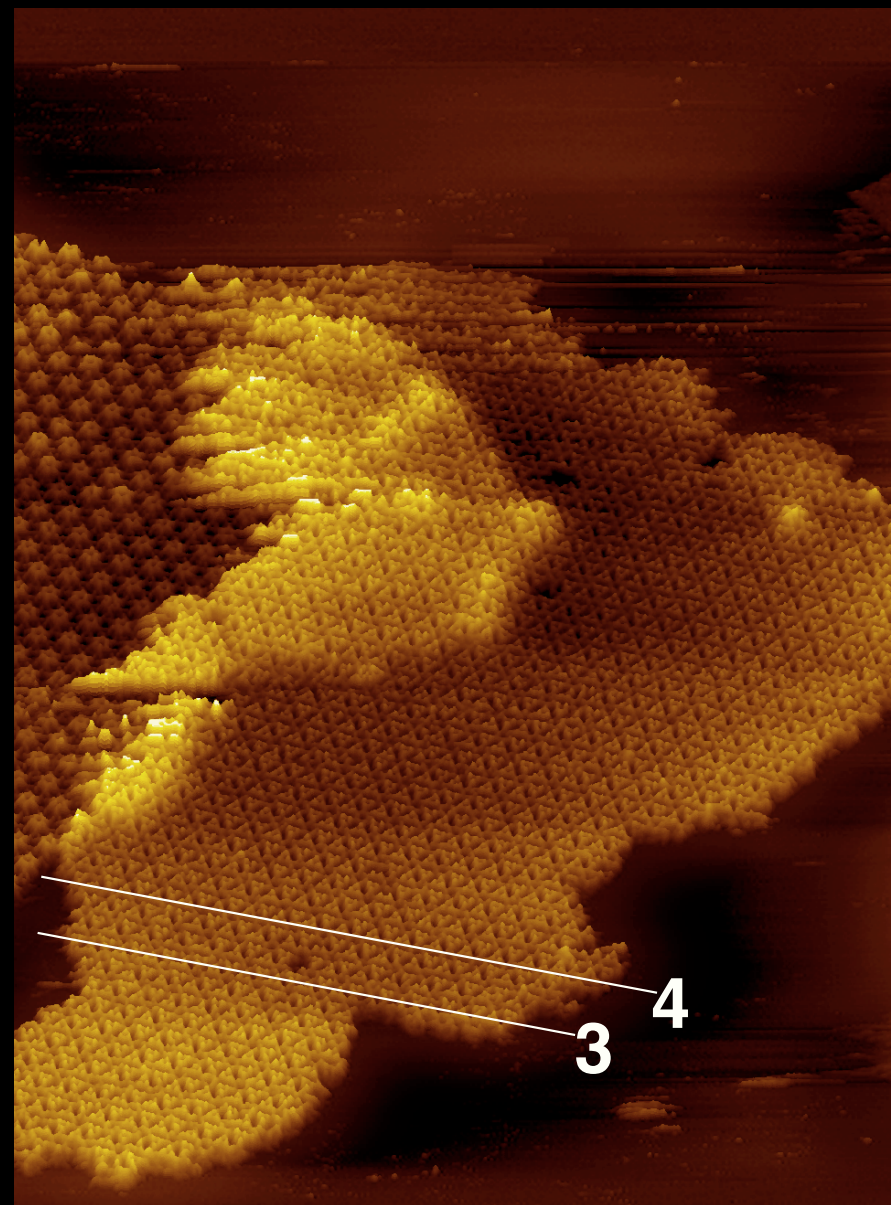
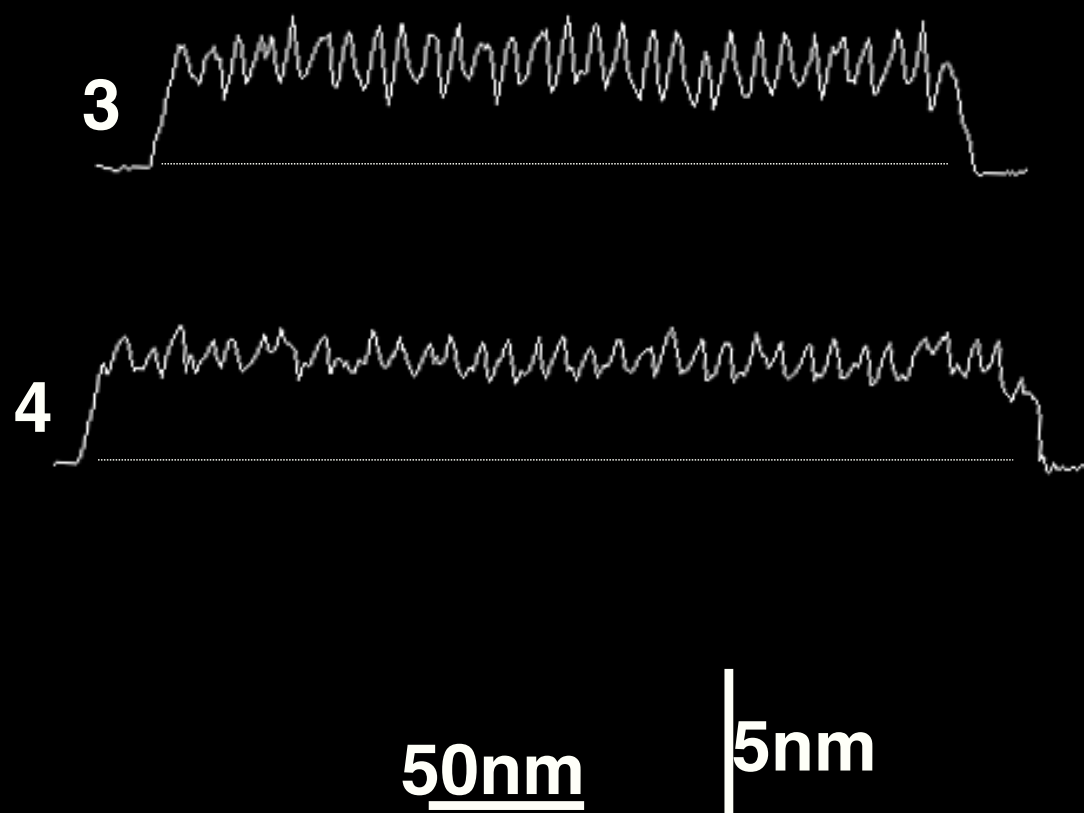
Section analysis



50nm

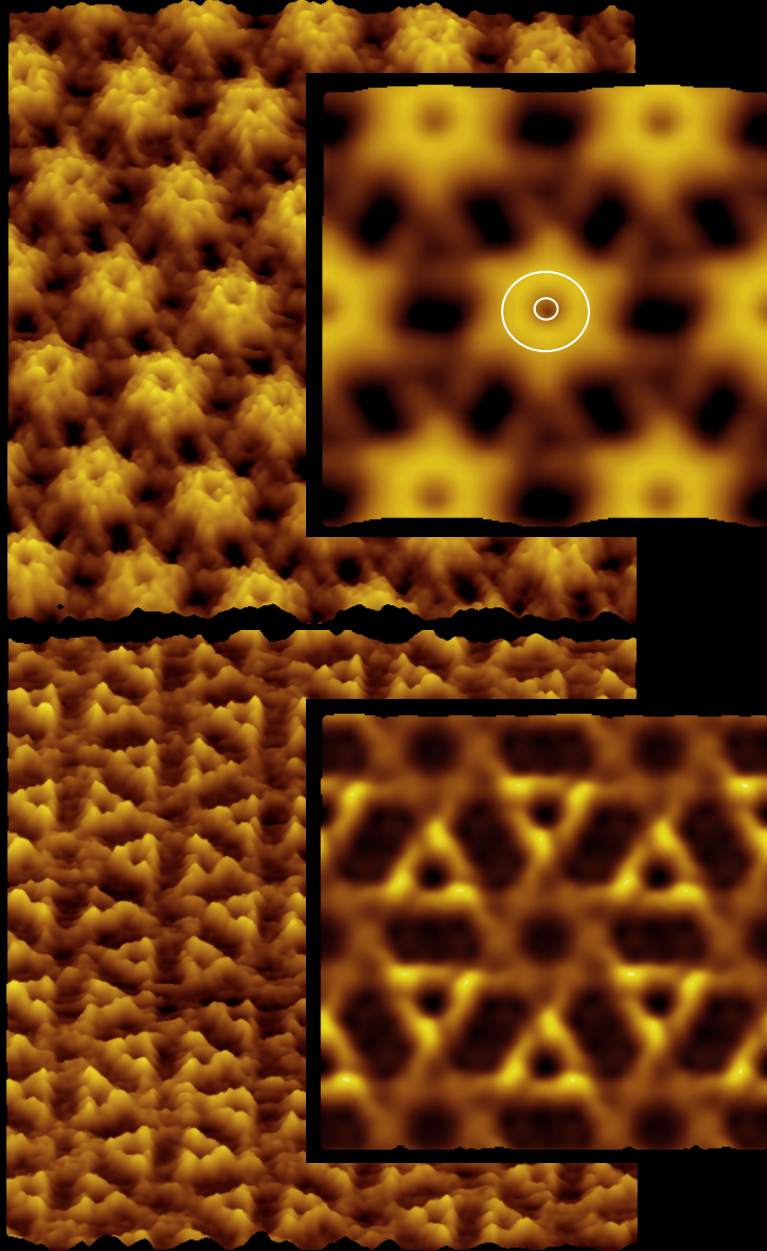
5nm

Section analysis

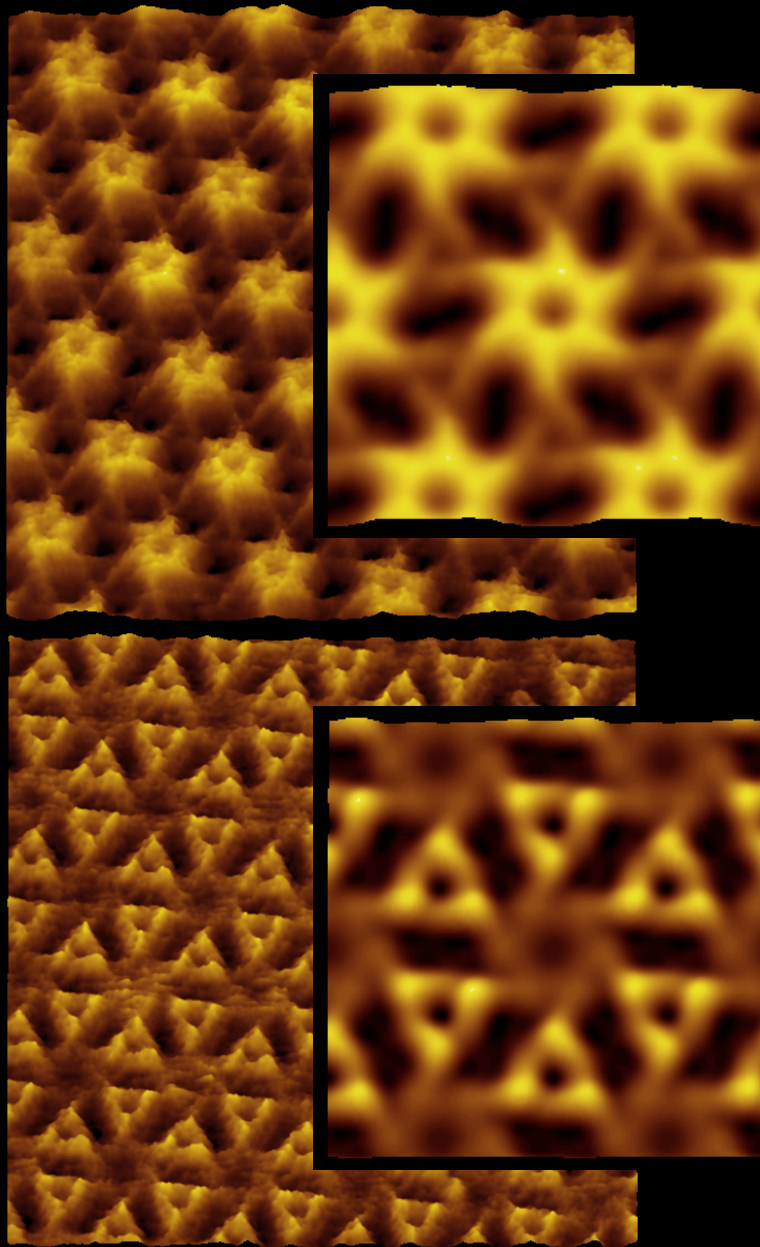


Localization of the C-terminus and sidedness assignment

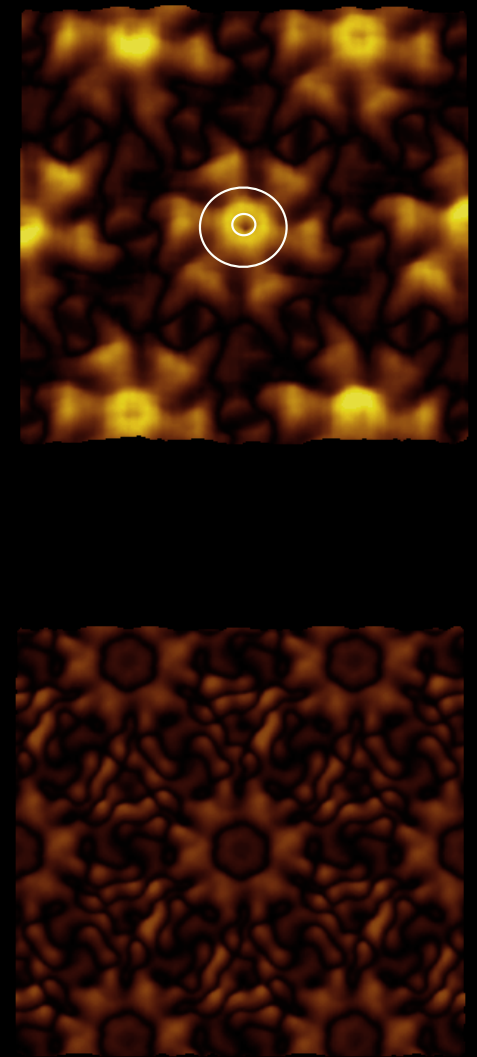
Native sample



Proteolysed sample (Trypsin)



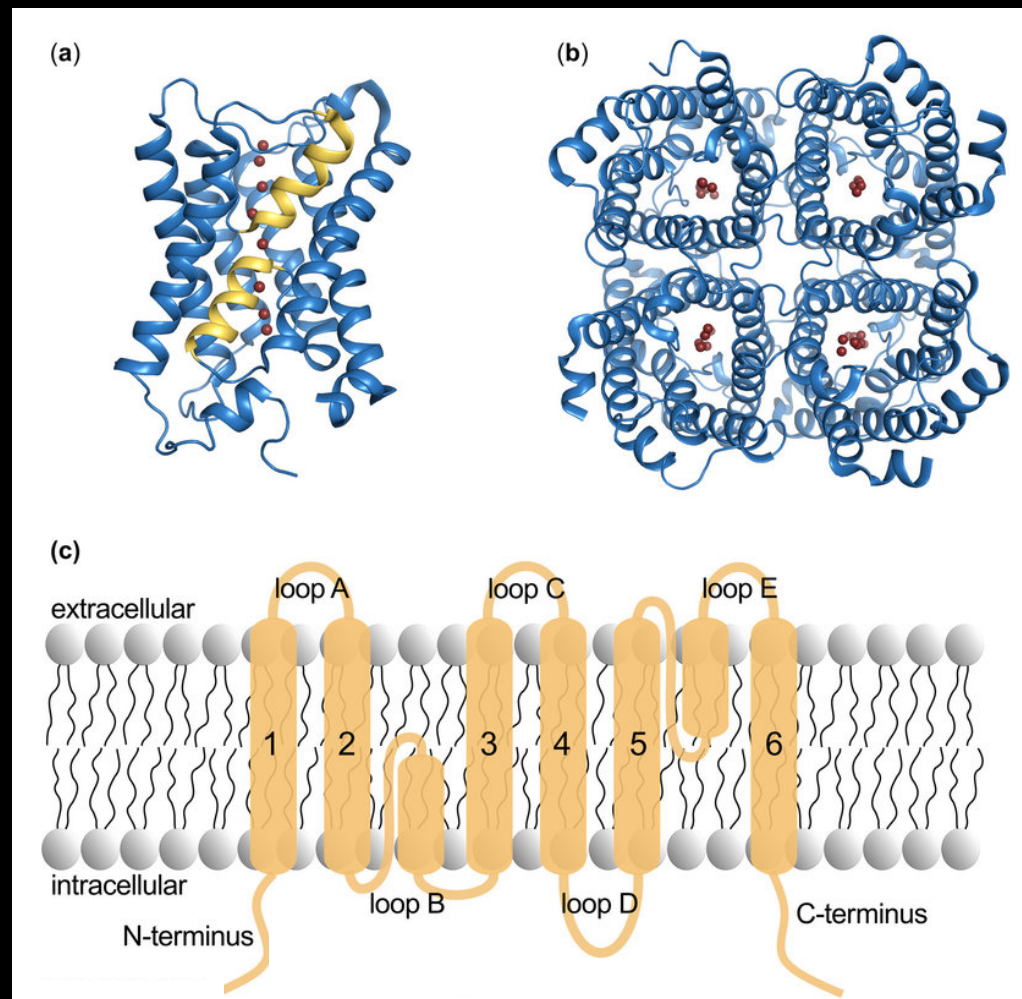
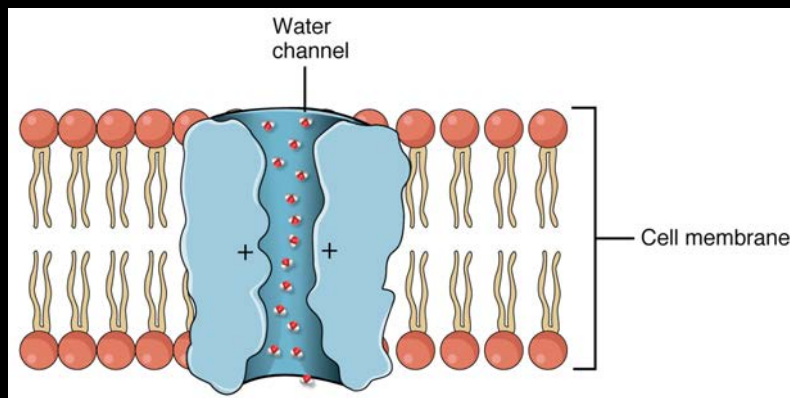
difference



The Conformational Energy Landscape of Aquaporins

The tetrameric aquaporin has four channels through which water can very easily traverse the cellular membrane.

No other molecules or ions can traverse, not even hydrogens!

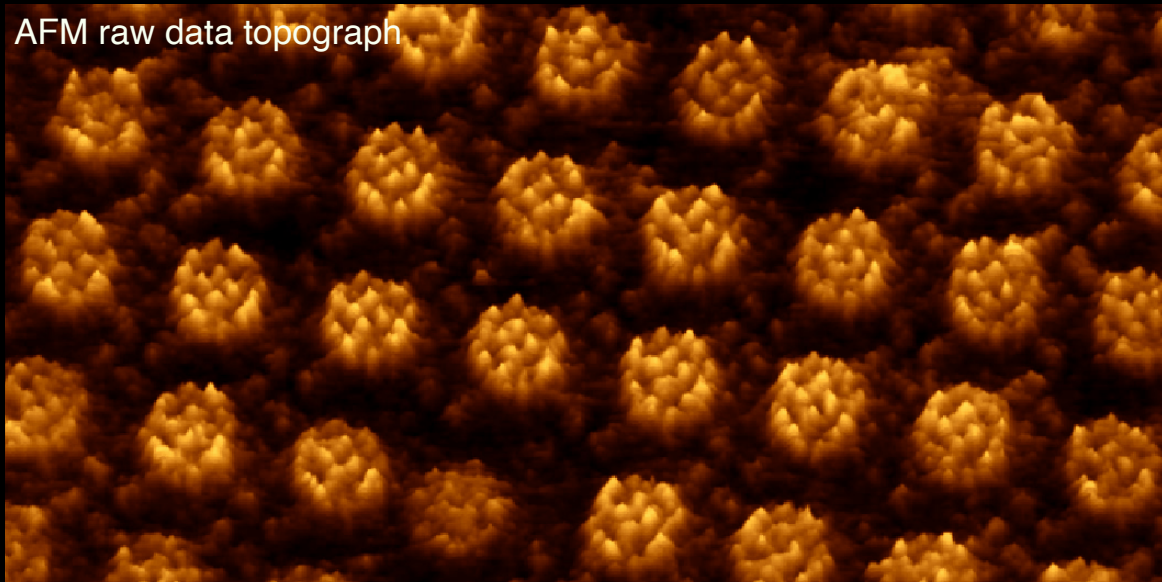


E. Coli Waterchannel AQPZ

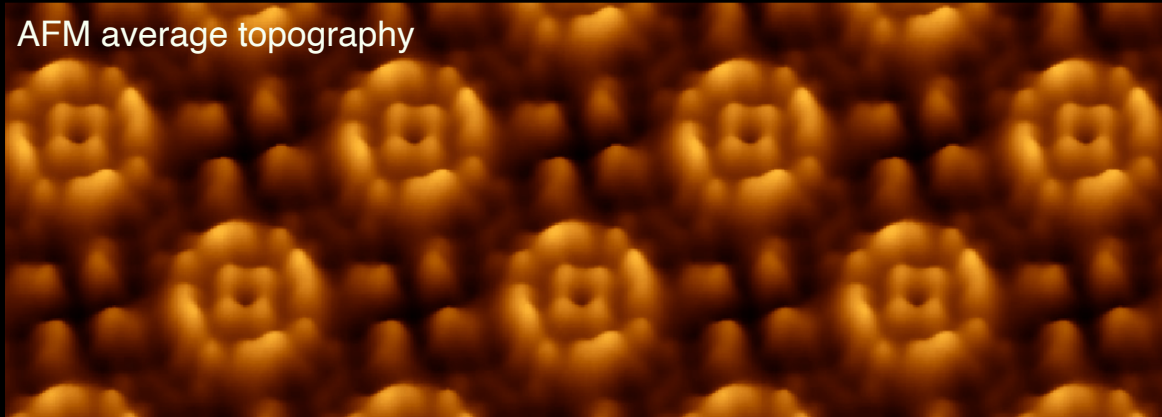
The bacterial aquaporin AQPZ is here in an artificial membrane, where it is arranged in a 2D crystalline formation.

Topography and molecular surface

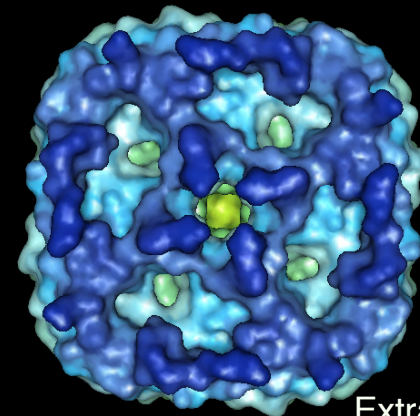
AFM raw data topograph



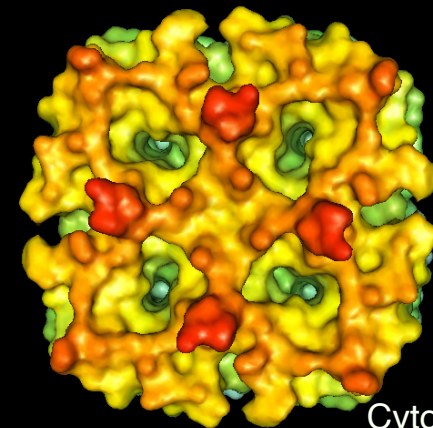
AFM average topography



Molecular surface
X-ray structure (2.8Å)

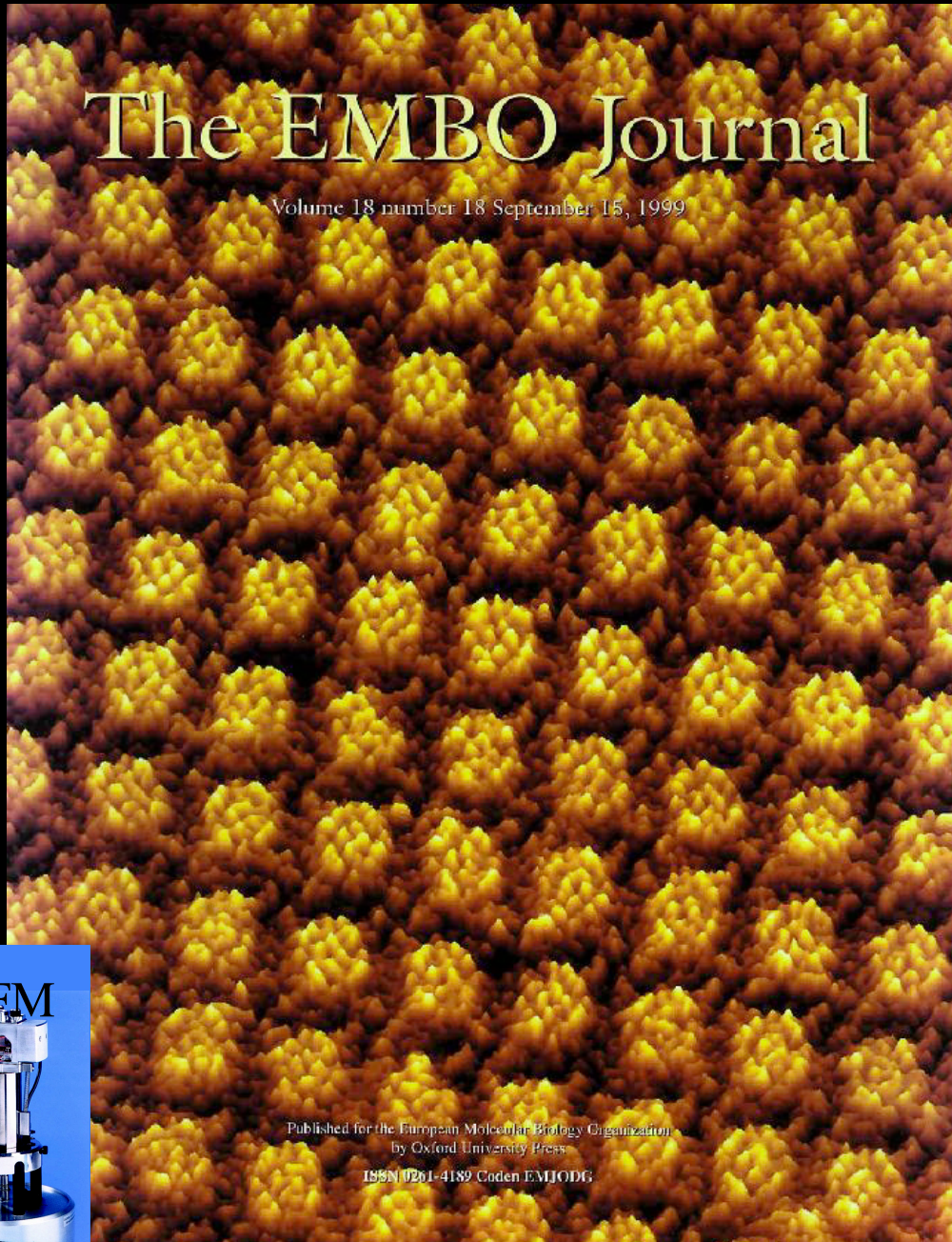


Extracellular surface



Cytoplasmic surface

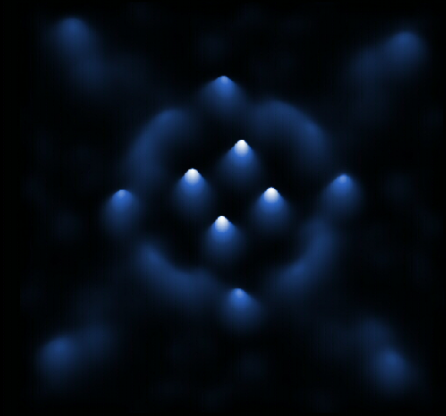
Conformational space of the AqpZ surface



Similarity ranked images
are assembled into a movie



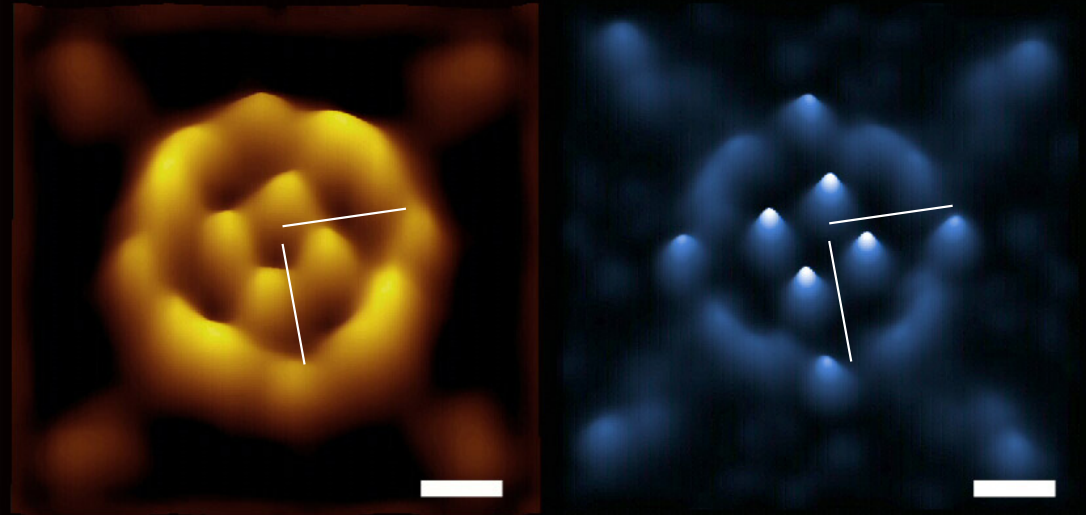
position probability



AqpZ: energy landscape

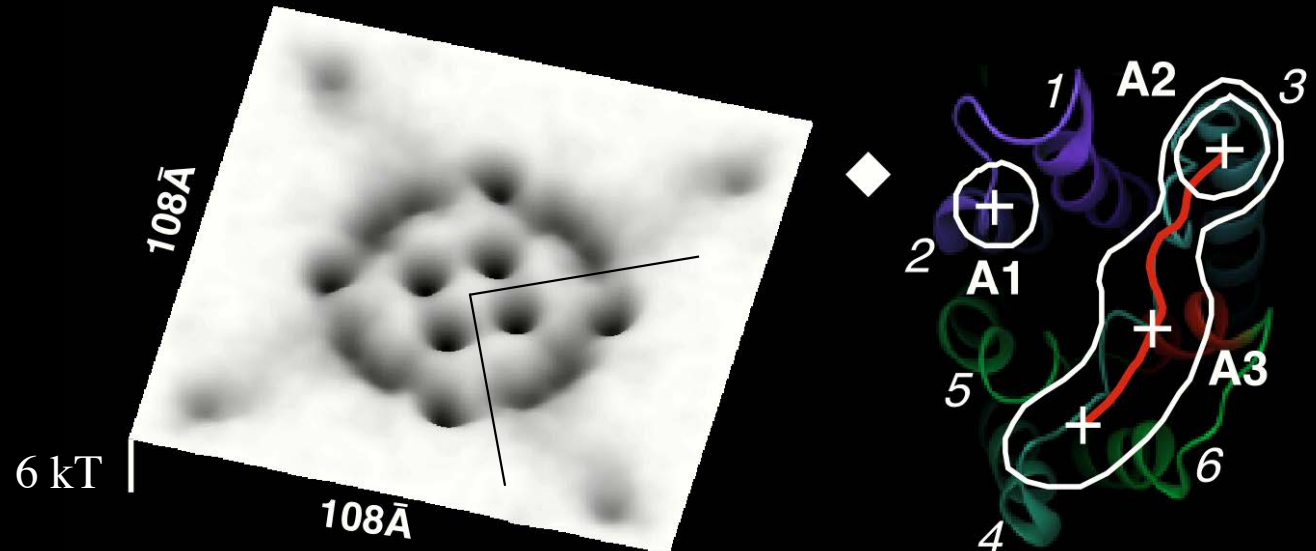
$$p_d(r)$$

peak position probability
of domain d



$$F_d = -kT \ln p_d(r)$$

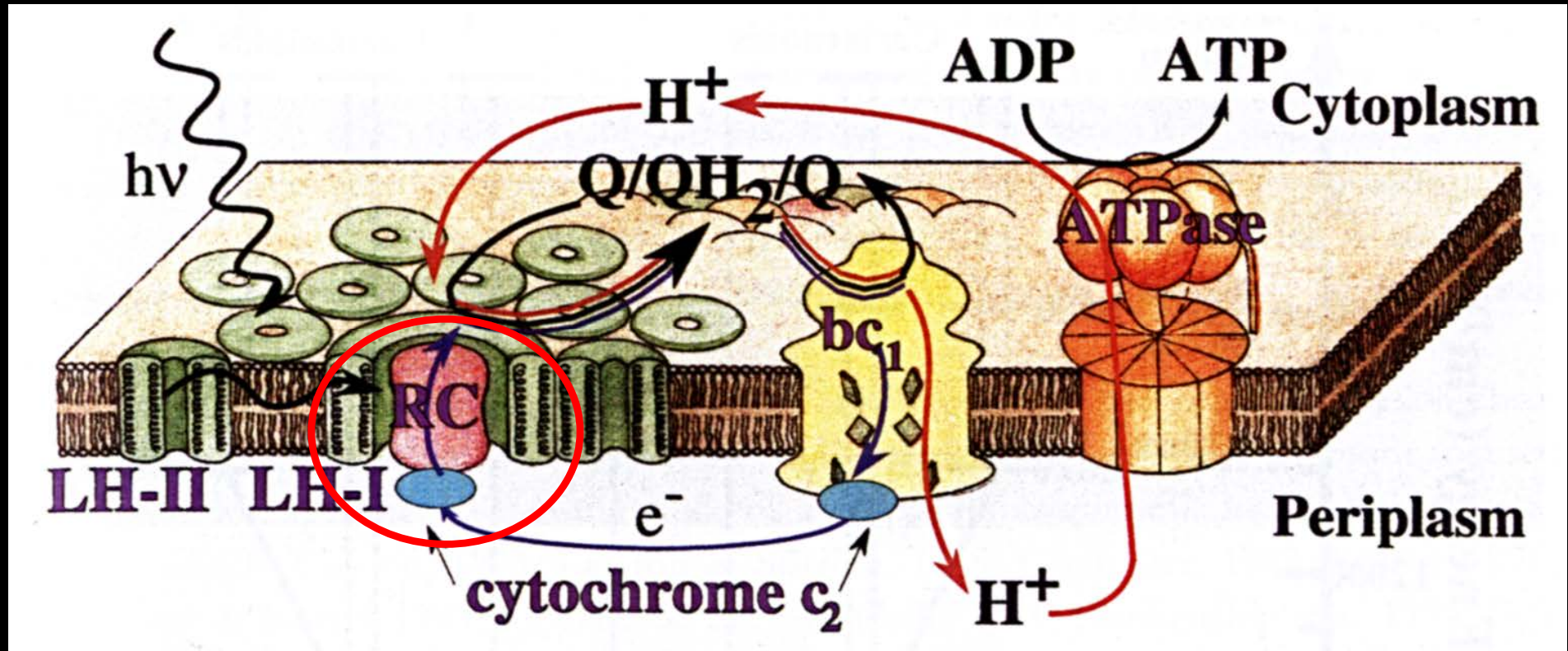
Relative free energy



Imaging Native Membranes

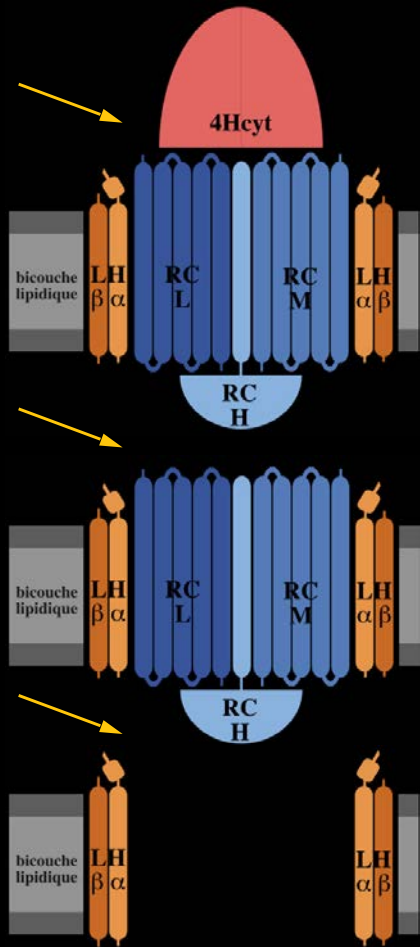
The Bacterial Photosynthetic Apparatus

The core-complex : reaction center (RC) & light harvesting complex 1 (LH1)

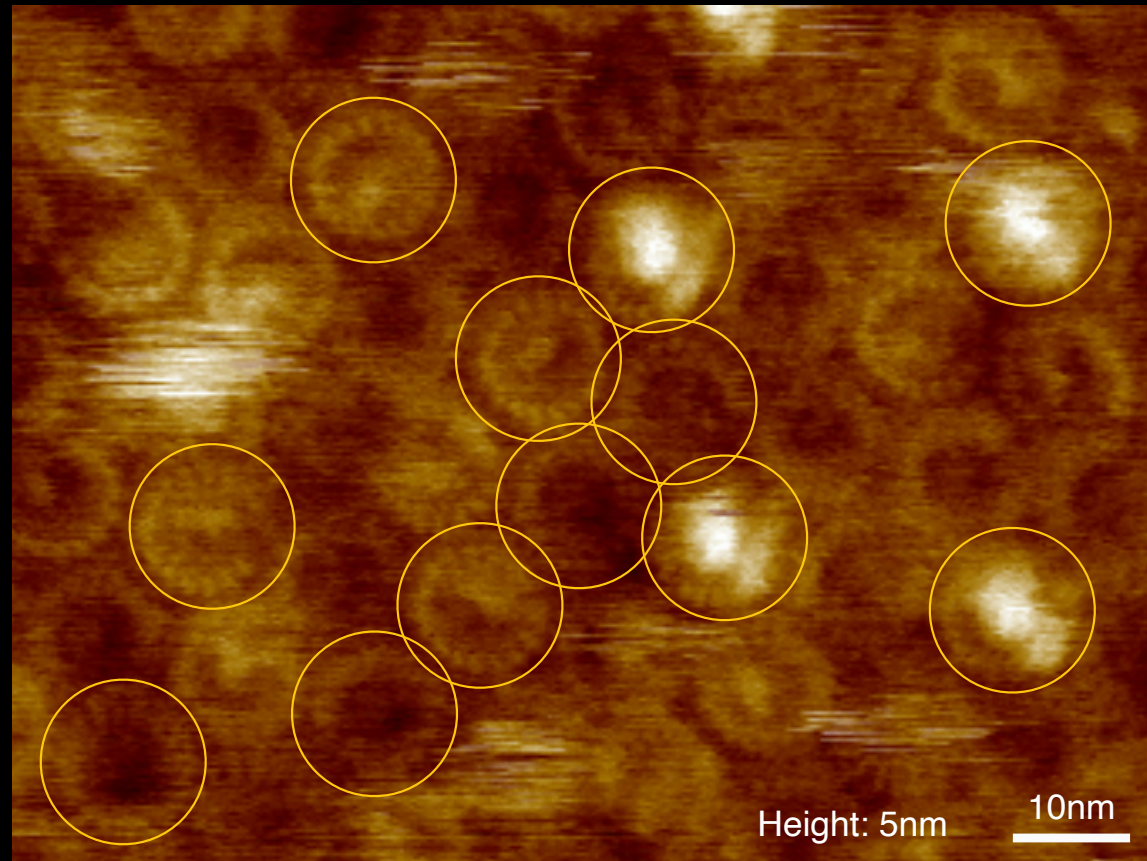


Blastochloris Viridis Core-Complex

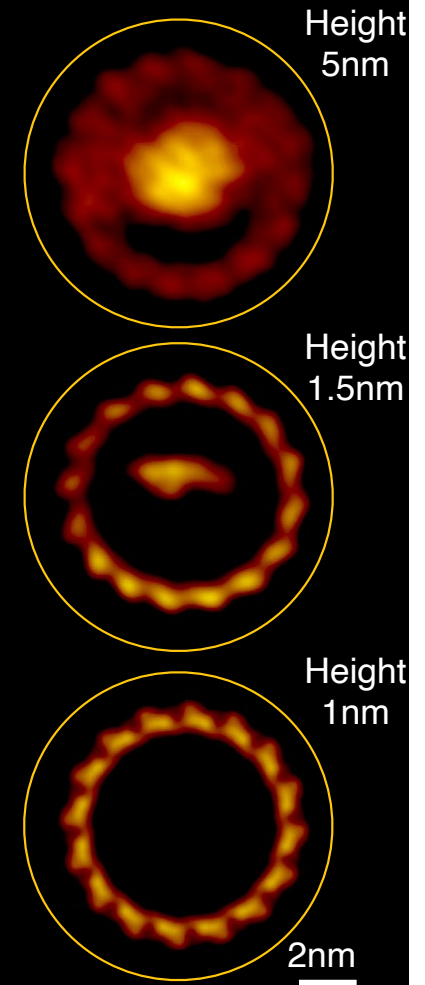
Model



AFM (raw data topograph)



Averages



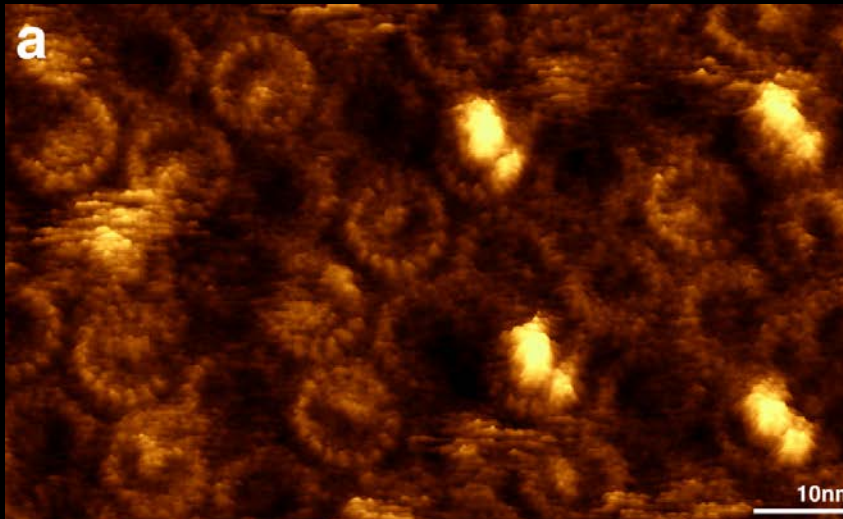
Scheuring, S.*, Seguin, J., Marco, S., Lévy, D., Robert, B. & Rigaud, J.L. (2003)

Nanodissection and high-resolution imaging of the *Rhodospseudomonas viridis* photosynthetic core-complex in native membranes by AFM.

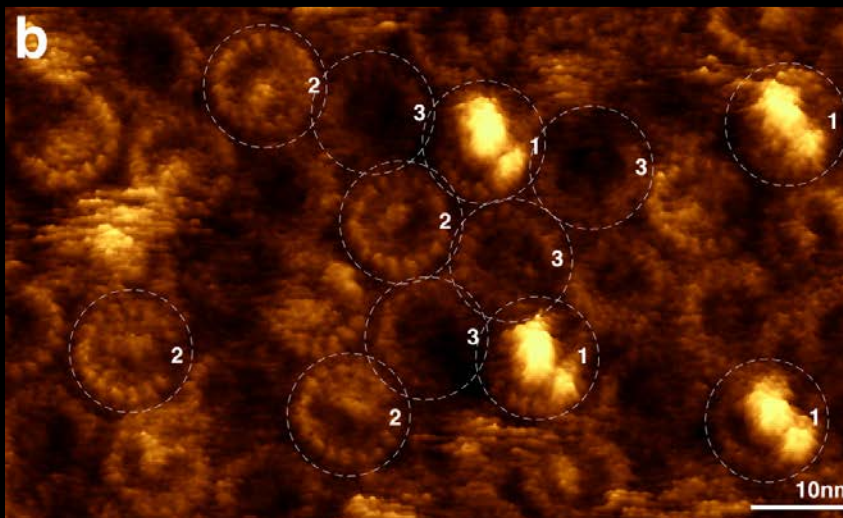
PNAS, 100, 1690-1693.

Blastochloris Viridis Core-Complex

AFM topograph

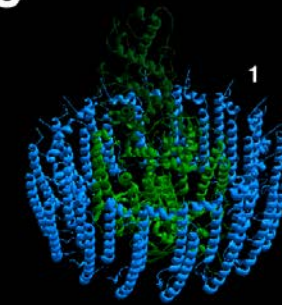


AFM topograph

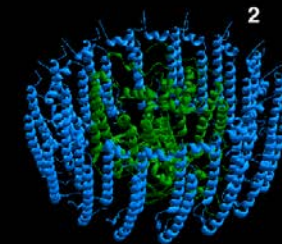


c

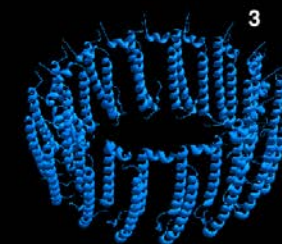
Models



4Hcyt-RC-LH1



RC-LH1



LH1

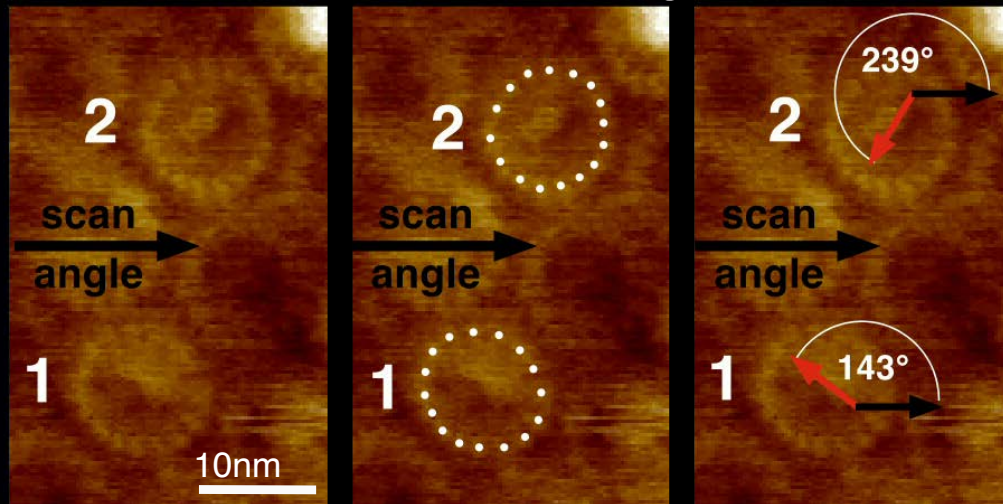
Scheuring, S.*, Seguin, J., Marco, S., Lévy, D., Robert, B. & Rigaud, J.L. (2003)

Nanodissection and high-resolution imaging of the *Rhodospseudomonas viridis* photosynthetic core-complex in native membranes by AFM.
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Blastochloris Viridis Core-Complex

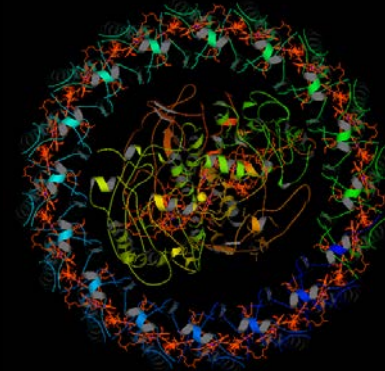
The LH1 subunits around the RC

Raw data AFM topograph



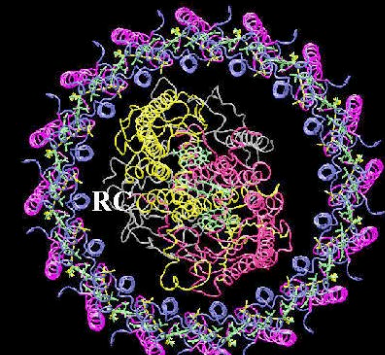
LH1 subunits distribution and RC orientation

Computed models



Isaacs group

<http://www.chem.gla.ac.uk/protein/LH2/core.html>



Schulten group

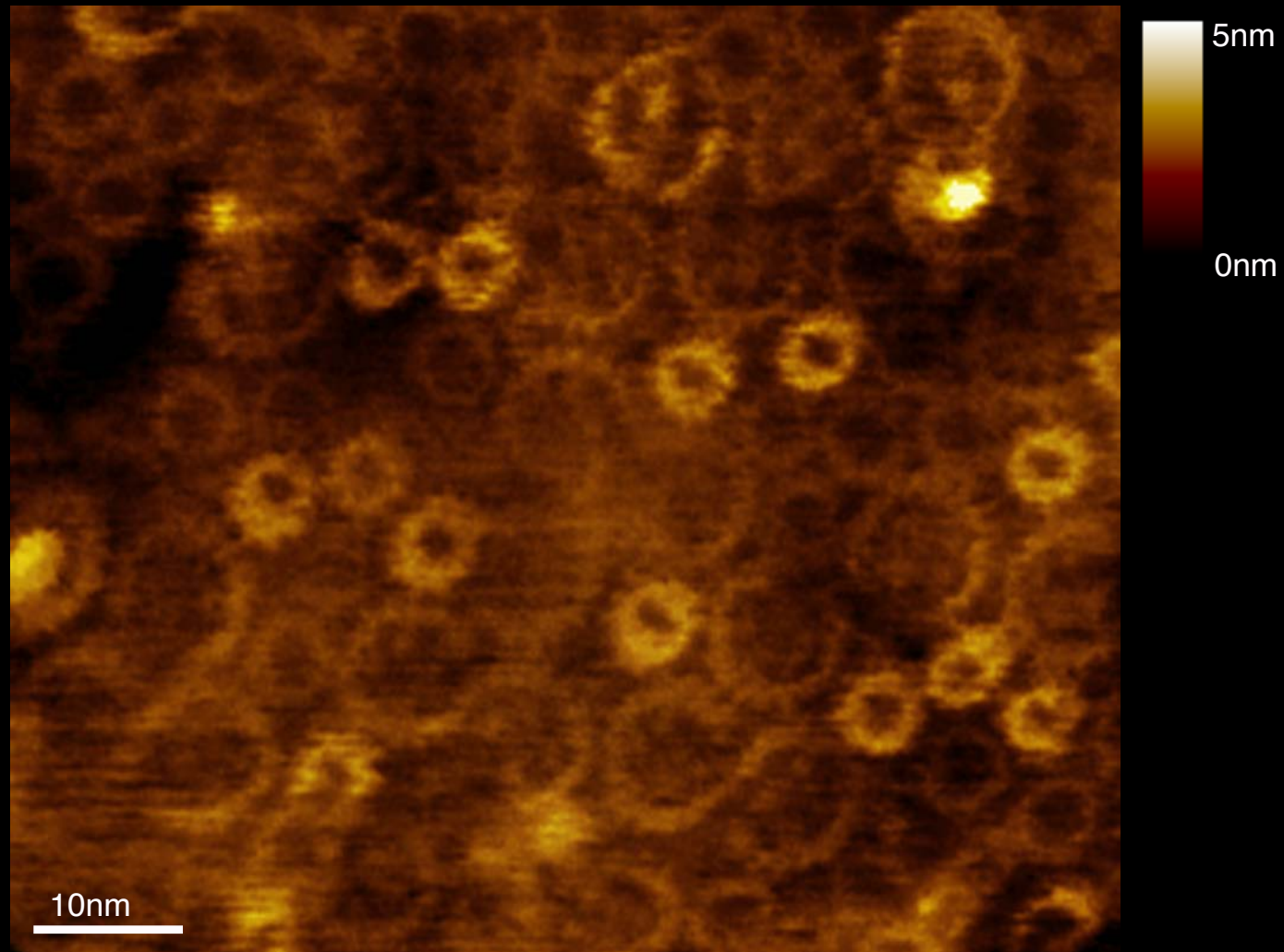
http://www.ks.uiuc.edu/Research/psu/psu_model.html

Scheuring, S.*, Seguin, J., Marco, S., Lévy, D., Robert, B. & Rigaud, J.L. (2003)

Nanodissection and high-resolution imaging of the Rhodospseudomonas viridis photosynthetic core-complex in native membranes by AFM.
PNAS, 100, 1690-1693.

Rhodobacter Blasticus Core-Complex

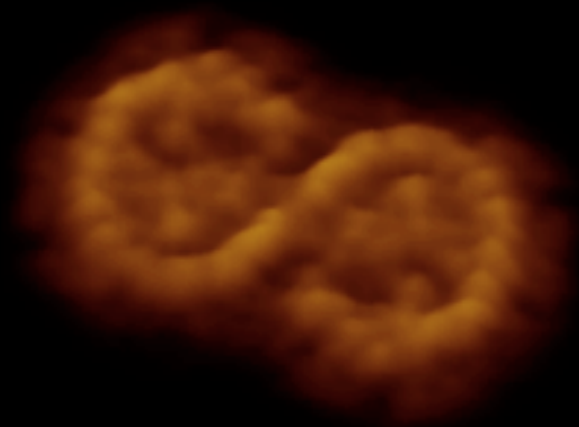
High-resolutionAFM topograph



Scheuring, S.* , Busselez, J., & Lévy, D. (2005)
Structure of the dimeric PufX-containing core complex of *Rhodobacter blasticus* by in situ AFM.
JBC, 2005, 280, 2, 1426-1431.

Rhodobacter Blasticus Core-Complex

S-shaped dimeric core-complexes

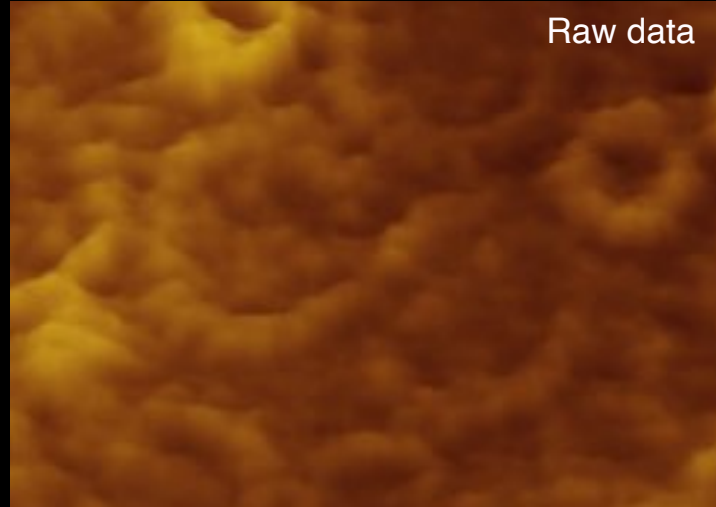


Height: 8Å

10nm

2-fold-symmetrized

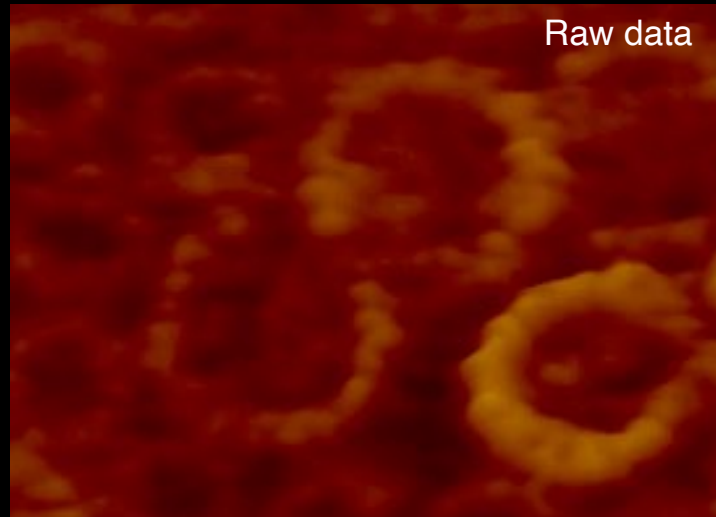
Raw data



Average



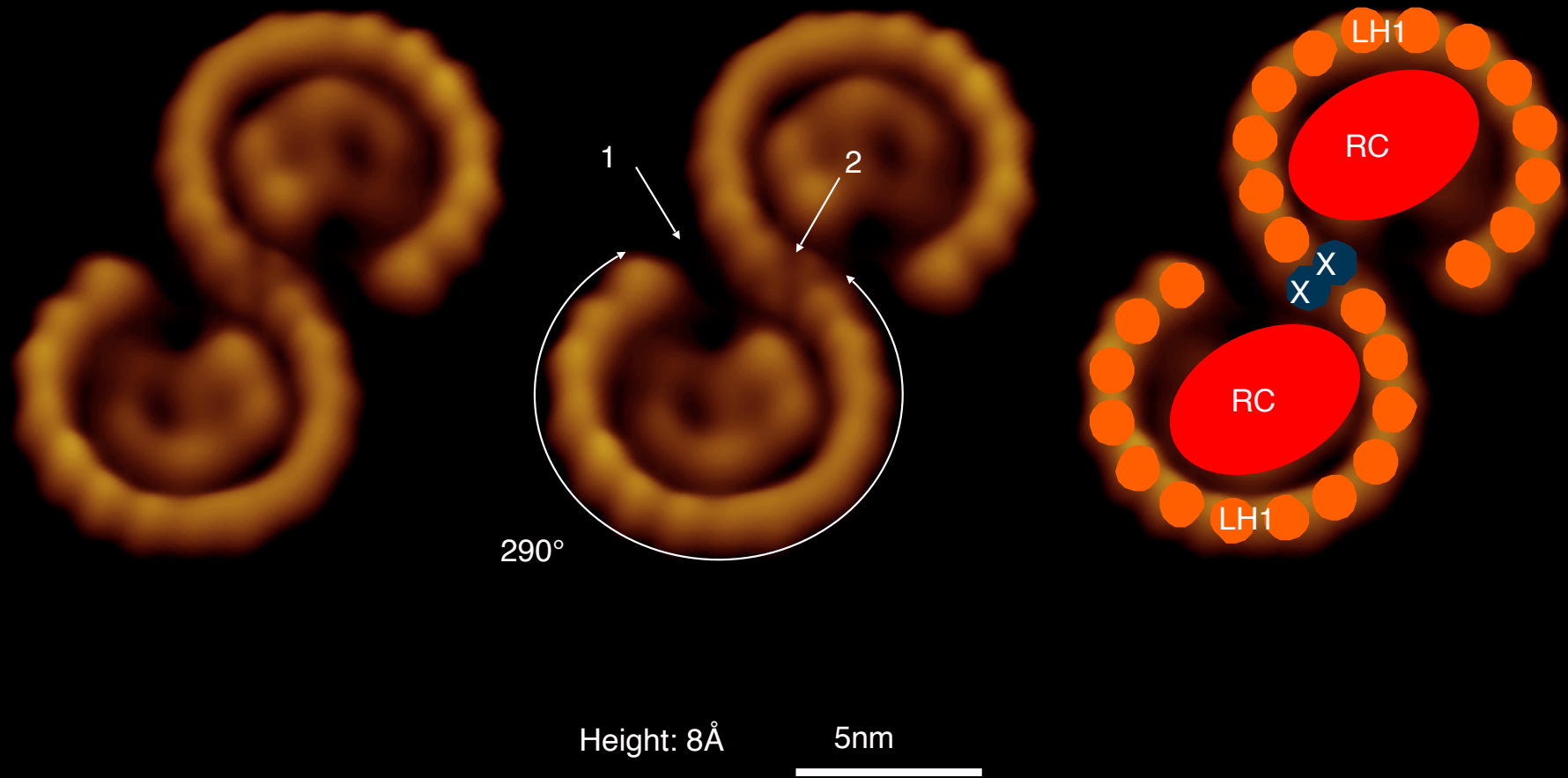
Raw data



Scheuring, S.*, Busselez, J., & Lévy, D. (2005)
Structure of the dimeric PufX-containing core complex of *Rhodobacter blasticus* by in situ AFM.
JBC, 2005, 280, 2, 1426-1431.

Rhodobacter Blasticus Core-Complex

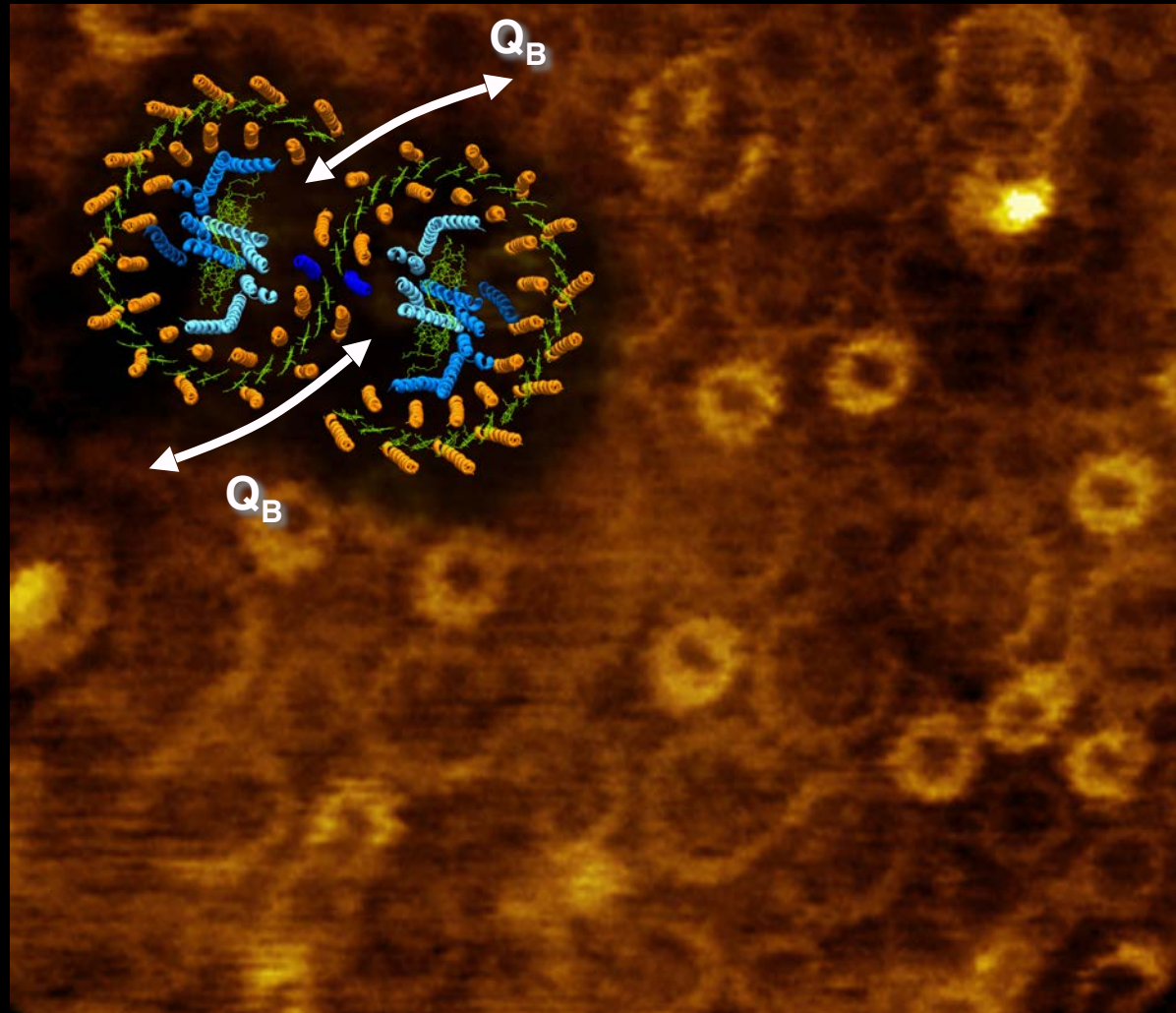
Localization of PufX



Scheuring, S.*, Busselez, J., & Lévy, D. (2005)
Structure of the dimeric PufX-containing core complex of *Rhodobacter blasticus* by in situ AFM.
JBC, 2005, 280, 2, 1426-1431.

Rhodobacter Blasticus Core-Complex

Model & Data

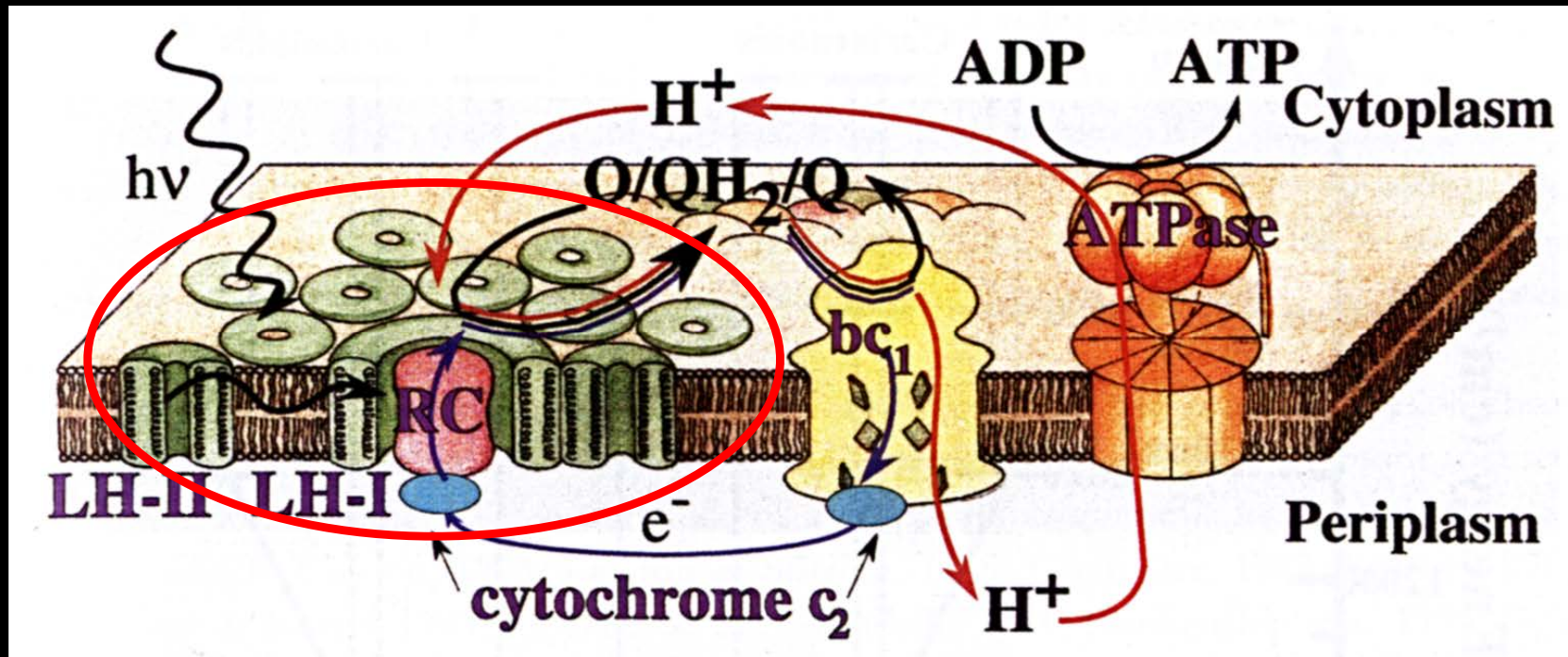


Scheuring, S.*, Busselez, J., & Lévy, D. (2005)
Structure of the dimeric PufX-containing core complex of *Rhodobacter blasticus* by in situ AFM.
JBC, 2005, 280, 2, 1426-1431.

Imaging of membrane protein supercomplexes

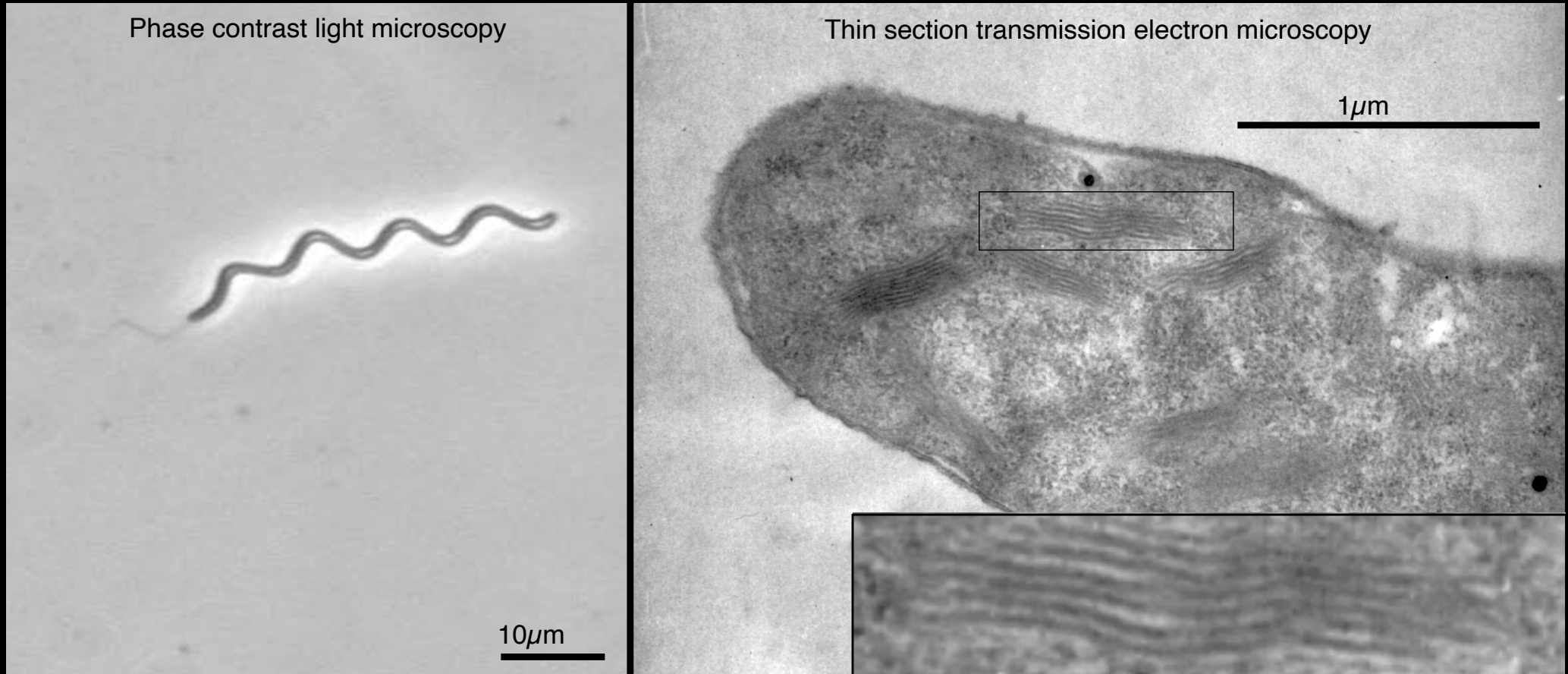
The Bacterial Photosynthetic Apparatus

The apparatus : light harvesting complex 2 (LH2) & light harvesting complex 1 (LH1) & reaction center (RC)



Rps. Photometricum Photosynthetic Apparatus

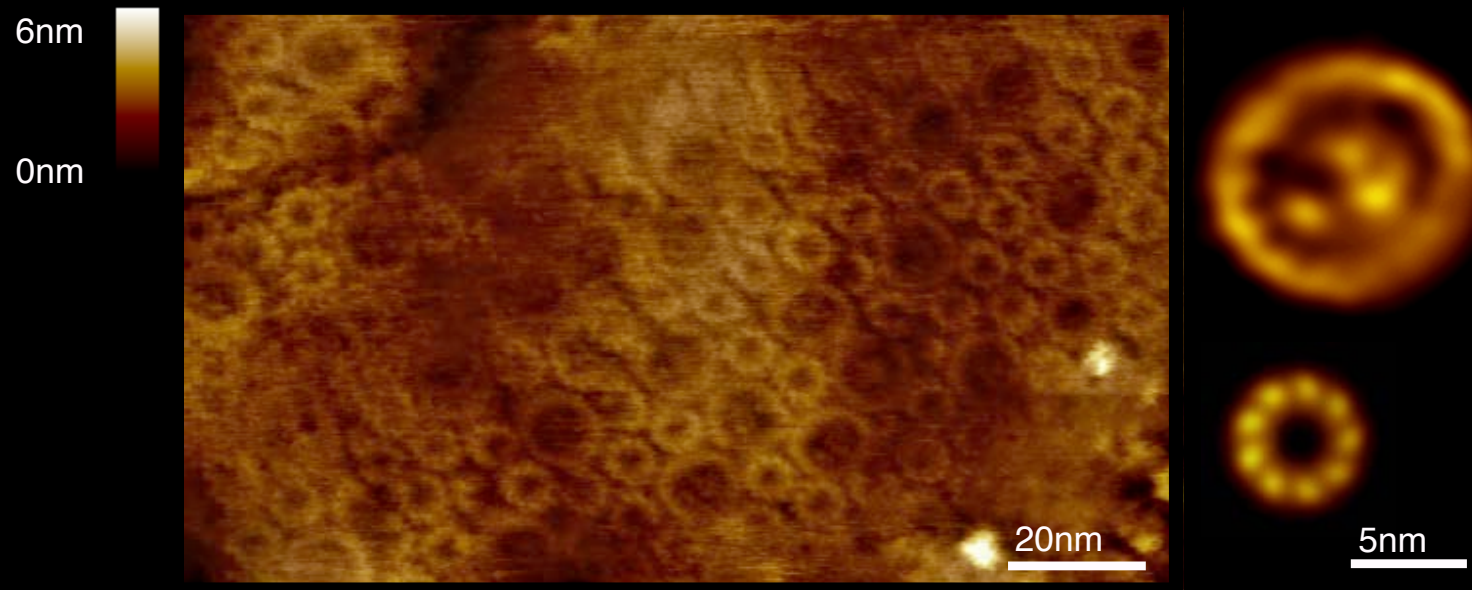
Rhodopseudomonas photometricum cells contain stacked intracytoplasmic membranes



Scheuring, S.* , Sturgis, J., Prima, V., Bernadac, A., Lévy, D. & Rigaud, JL. (2004)
Watching the photosynthetic apparatus in native membranes.
PNAS, 2004, 101, 31, 11293-11297.

Rps. Photometricum Photosynthetic Apparatus

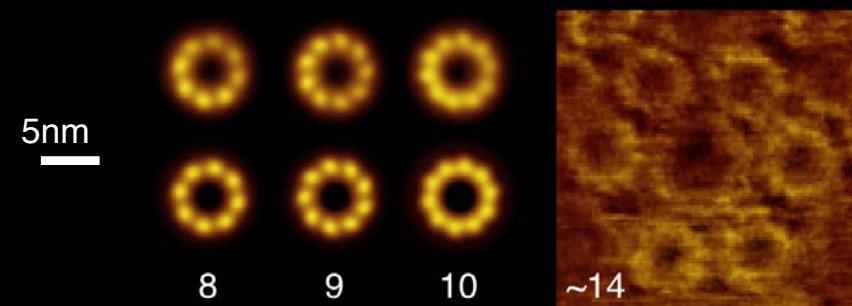
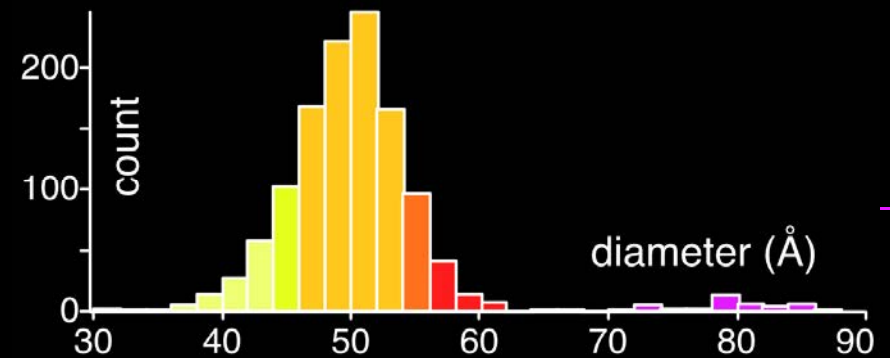
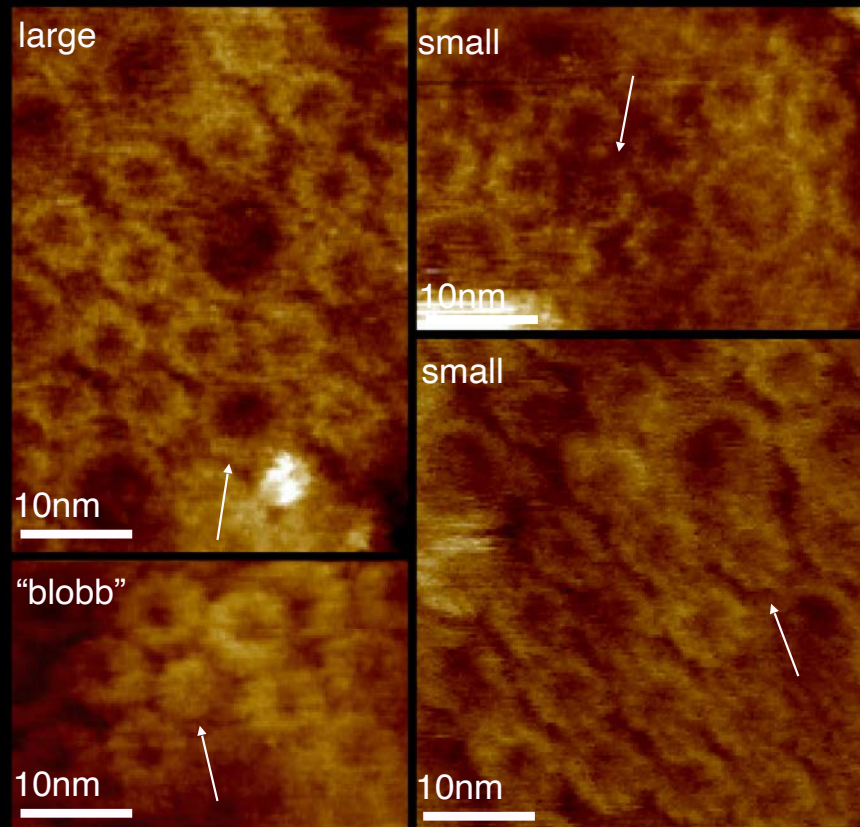
High-resolution topographs



Scheuring, S.*, Rigaud, J.L. & Sturgis, J. (2004)
Variable LH2 stoichiometry and core clustering in native membranes of *Rhodospirillum rubrum*.
EMBO J., 2004, 23, 21, 4127-4133.

Rps. Photometricum Photosynthetic Apparatus

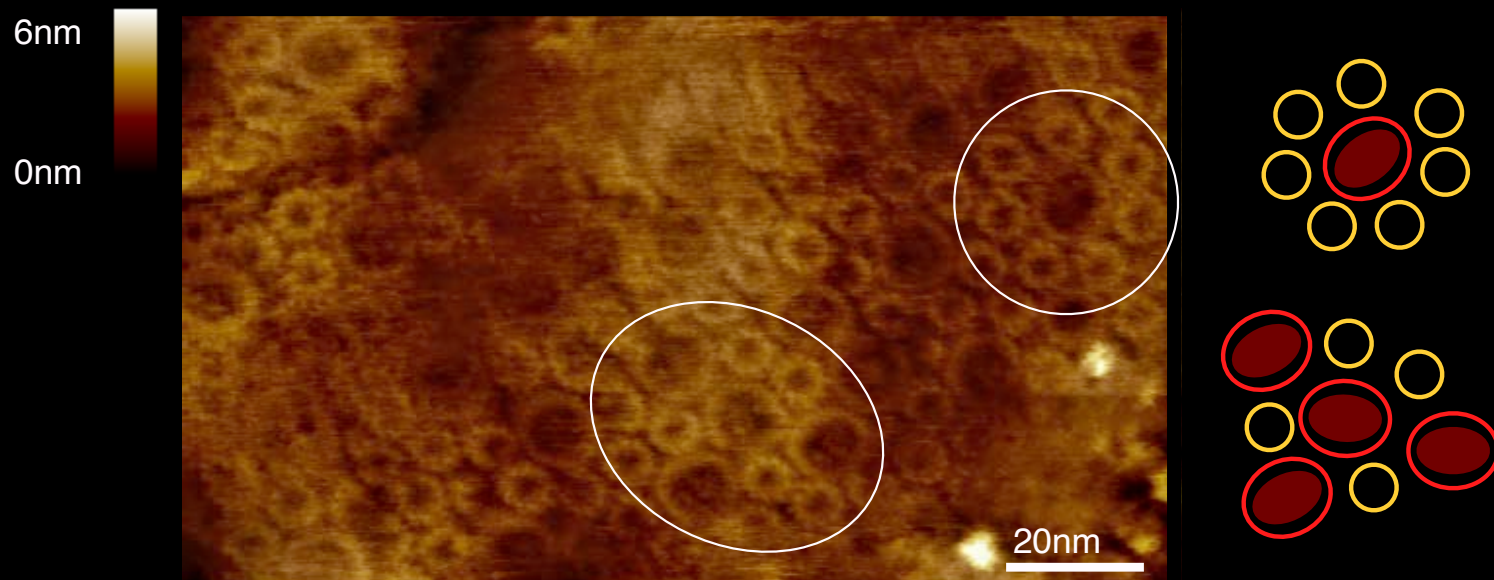
Heterogeneity of LH2 complexes



Scheuring, S.* , Rigaud, JL. & Sturgis, J. (2004)
Variable LH2 stoichiometry and core clustering in native membranes of *Rhodospirillum rubrum*.
EMBO J., 2004, 23, 21, 4127-4133.

Rps. Photometricum Photosynthetic Apparatus

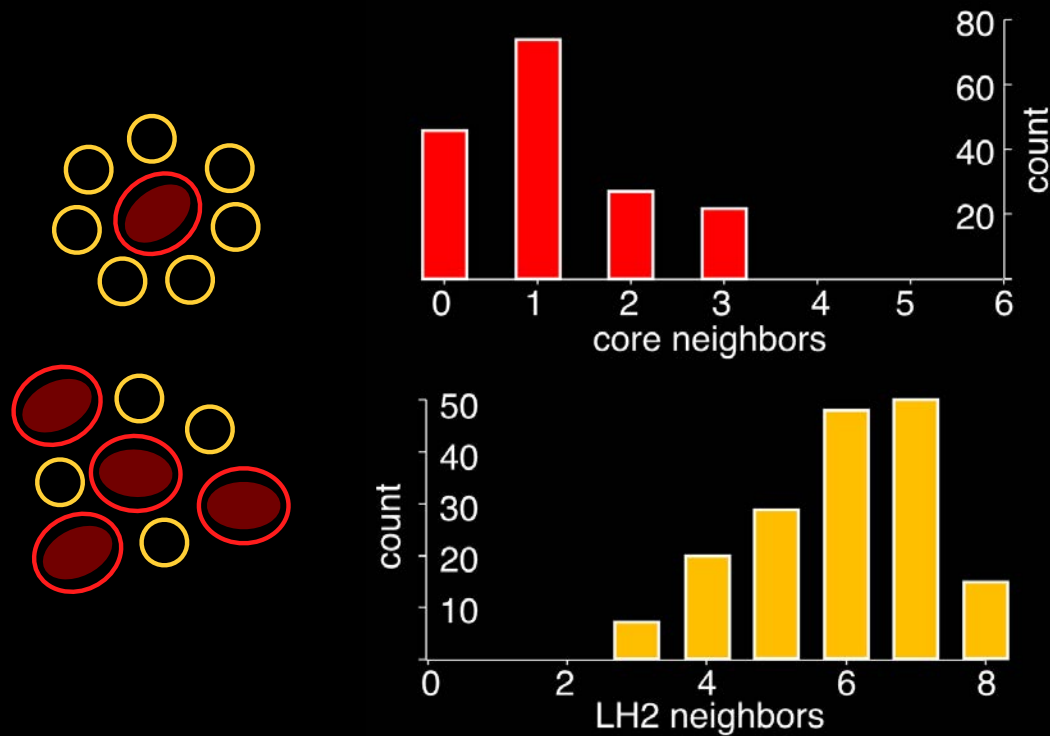
There is no fixed assembly unit



Scheuring, S.*, Rigaud, J.L. & Sturgis, J. (2004)
Variable LH2 stoichiometry and core clustering in native membranes of *Rhodospirillum rubrum*.
EMBO J., 2004, 23, 21, 4127-4133.

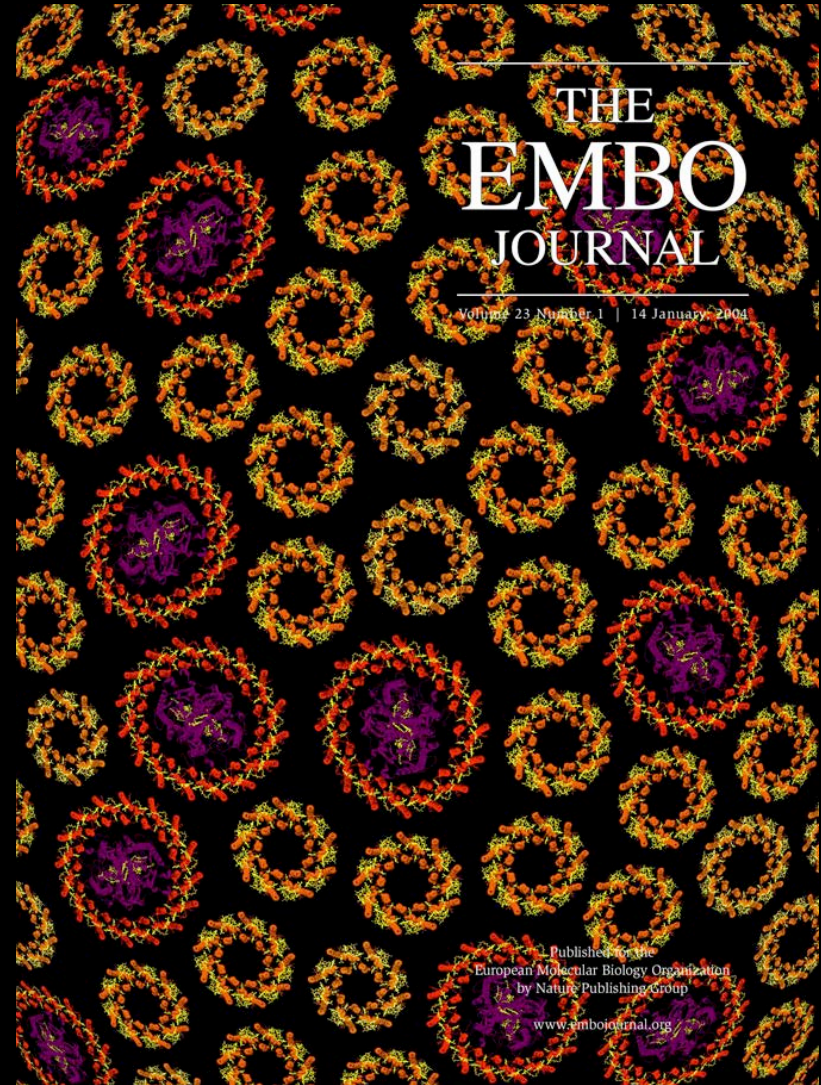
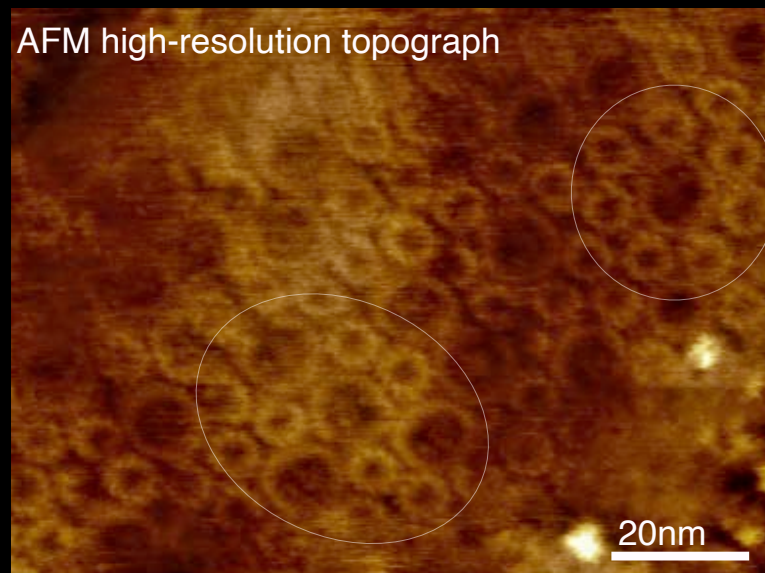
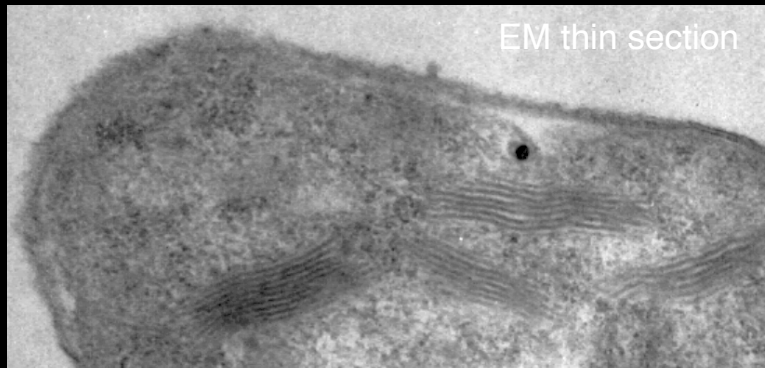
Rps. Photometricum Photosynthetic Apparatus

There is no fixed assembly unit



Rps. Photometricum Photosynthetic Apparatus

There is no fixed assembly unit



Scheuring, S.* , Rigaud, J.L. & Sturgis, J. (2004)
Variable LH2 stoichiometry and core clustering in native membranes of *Rhodospirillum rubrum*.
EMBO J., 2004, 23, 21, 4127-4133.

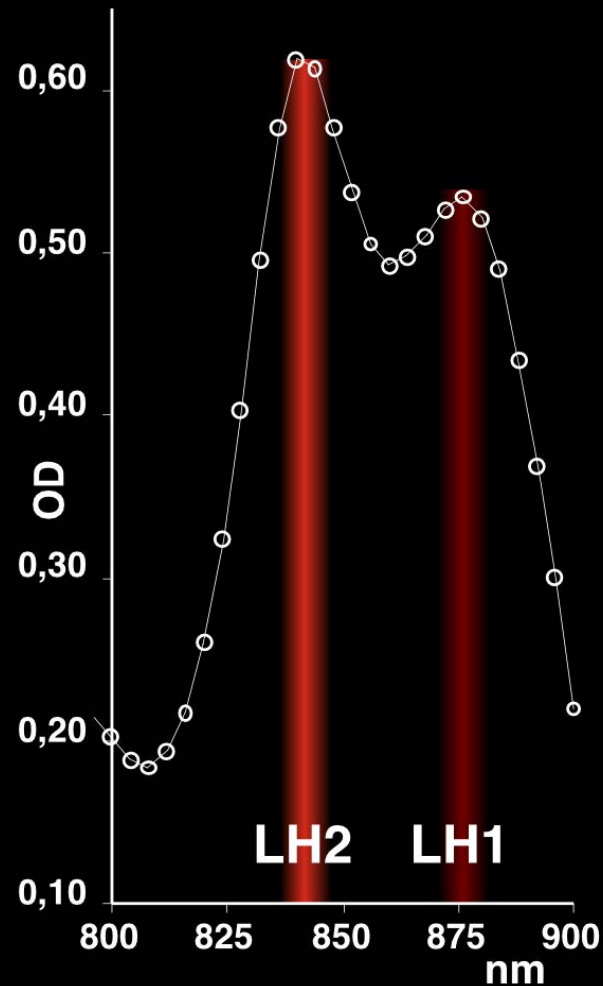
Static assembly?

Or rather:

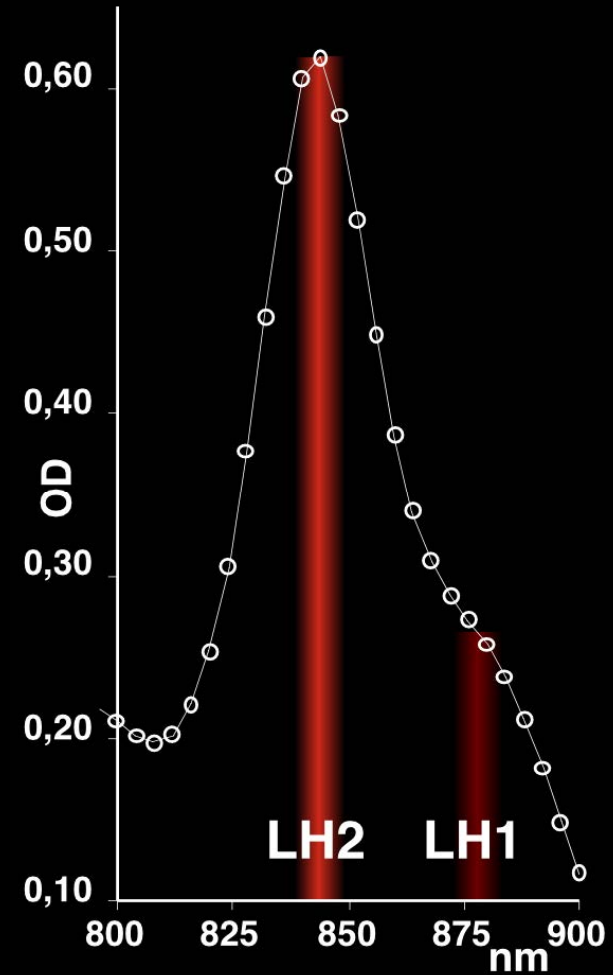
Dynamic Light Adaptation!

Chromatic Adaptation

High-light adapted membranes



Low-light adapted membranes

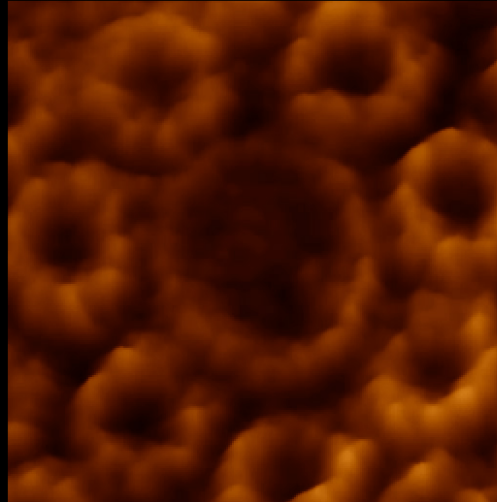


Simon Scheuring*, & James Sturgis (2005).
Chromatic adaptation of photosynthetic membranes.
Science, 2005, 309, 5733, 484-487.

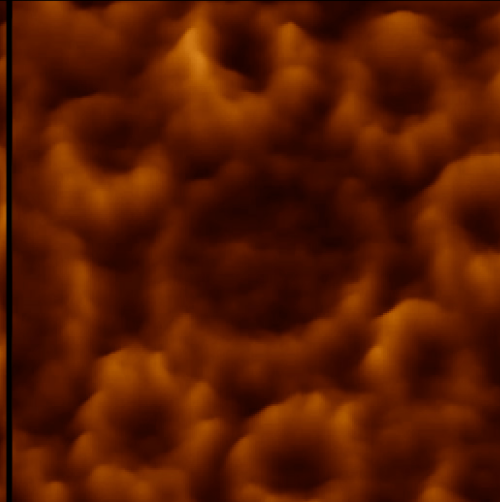
Chromatic Adaptation

The complexes

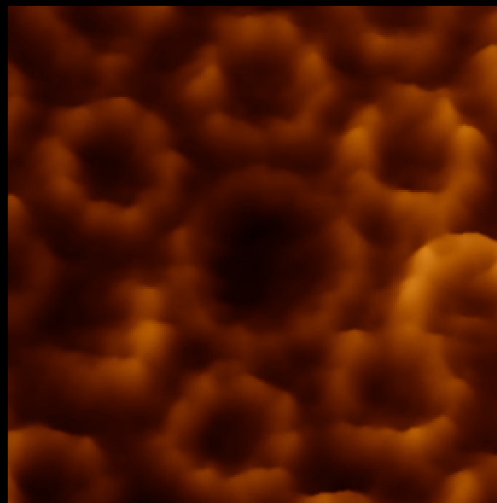
LH1 - RC
core-complex



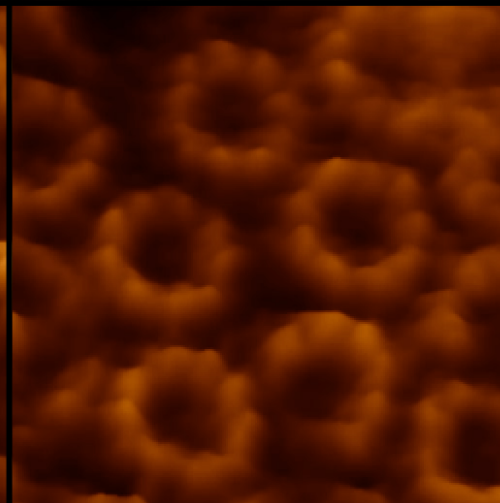
LH1 - RC
core complex



LH?
complex



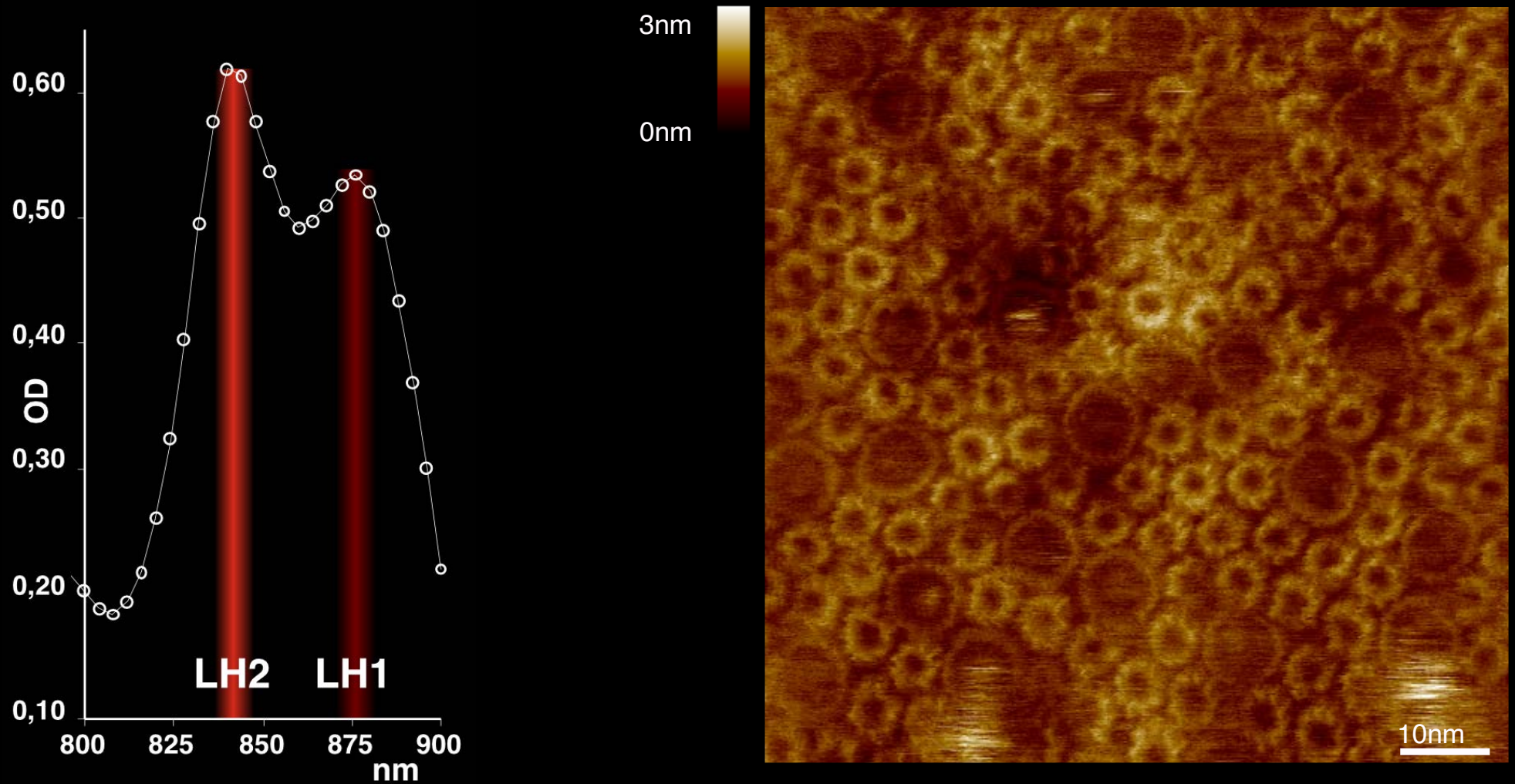
LH2
complex



Simon Scheuring*, & James Sturgis (2005).
Chromatic adaptation of photosynthetic membranes.
Science, 2005, 309, 5733, 484-487.

Chromatic Adaptation

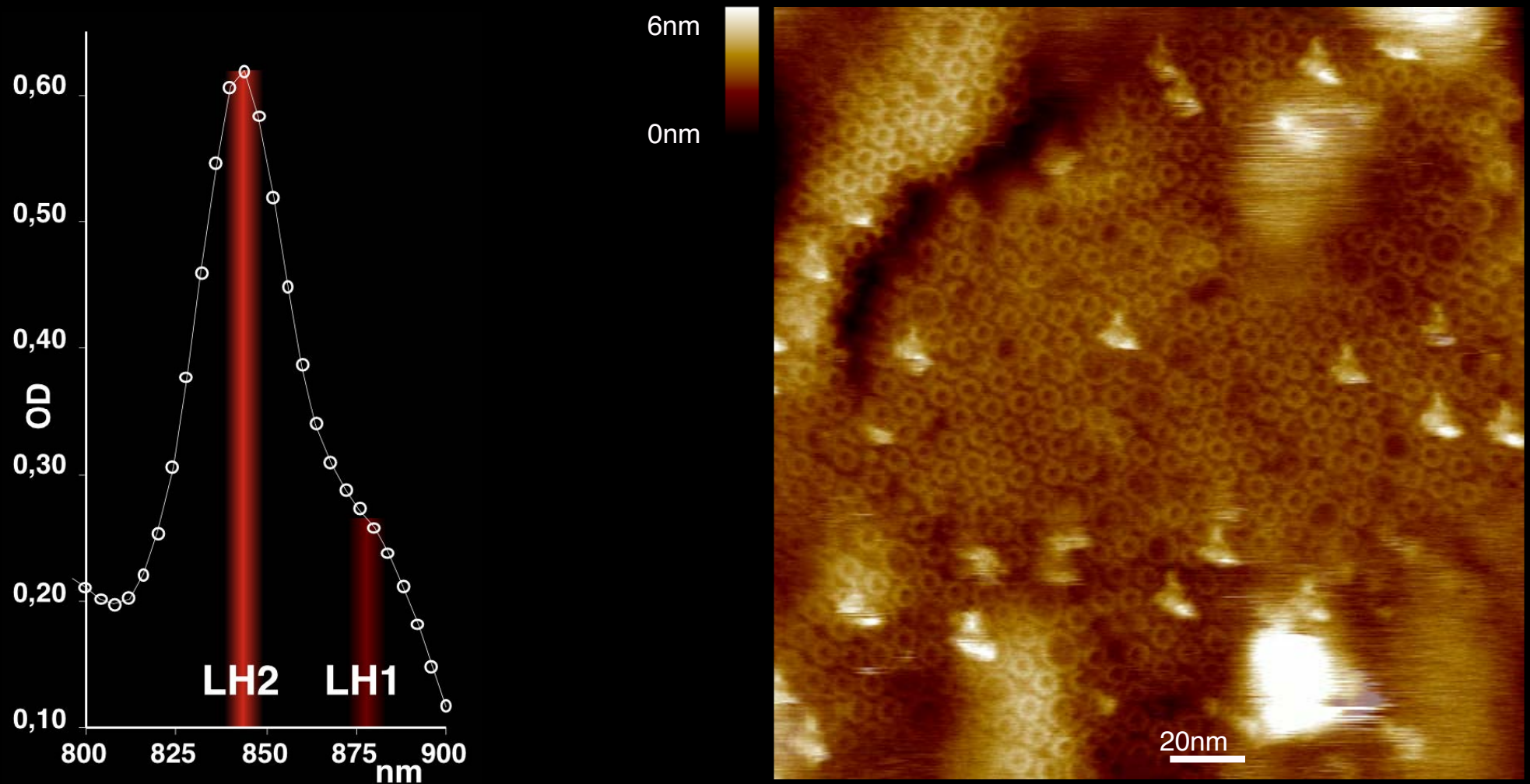
High-light adapted membranes



Simon Scheuring*, & James Sturgis (2005).
Chromatic adaptation of photosynthetic membranes.
Science, 2005, 309, 5733, 484-487.

Chromatic Adaptation

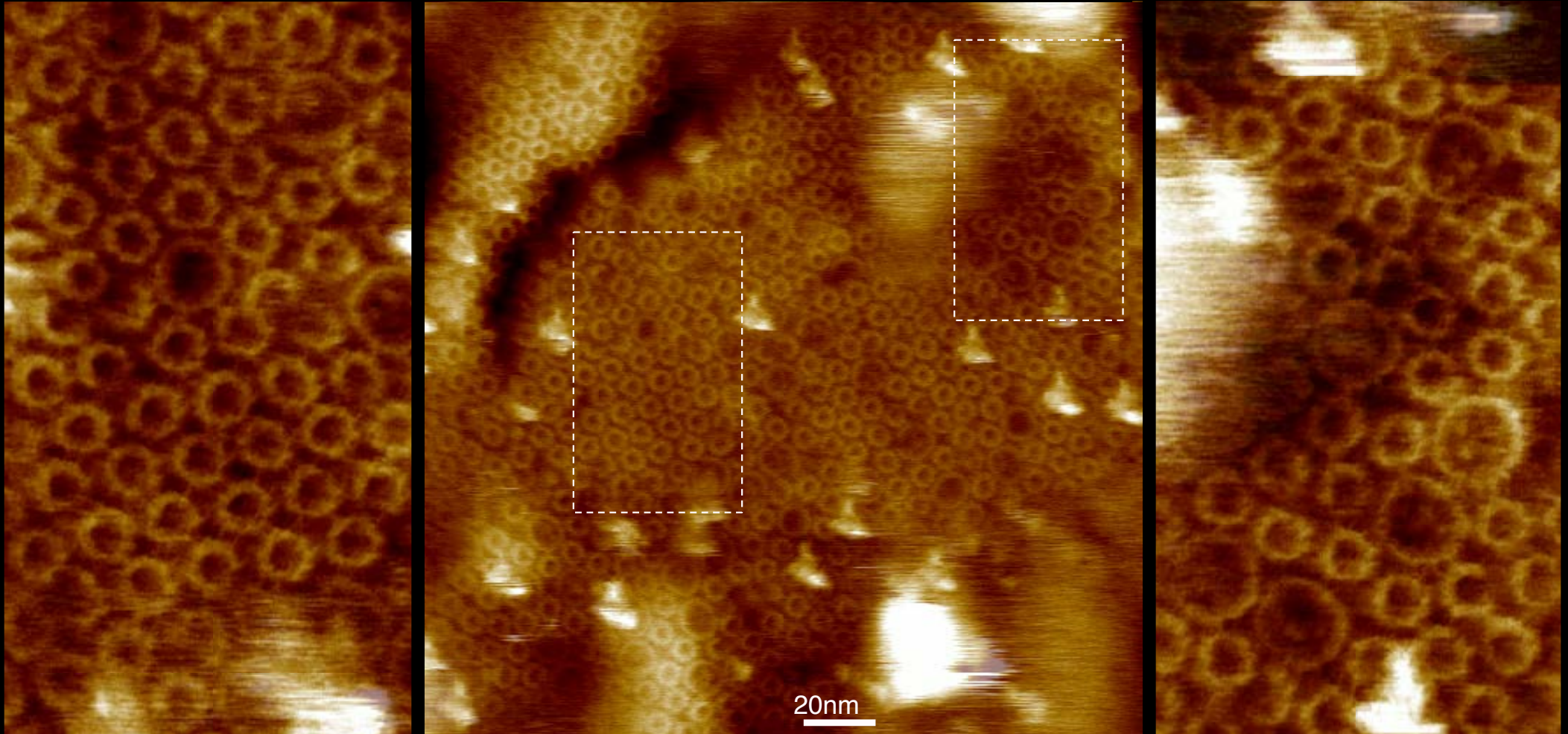
Low-light adapted membranes



Simon Scheuring*, & James Sturgis (2005).
Chromatic adaptation of photosynthetic membranes.
Science, 2005, 309, 5733, 484-487.

Chromatic Adaptation

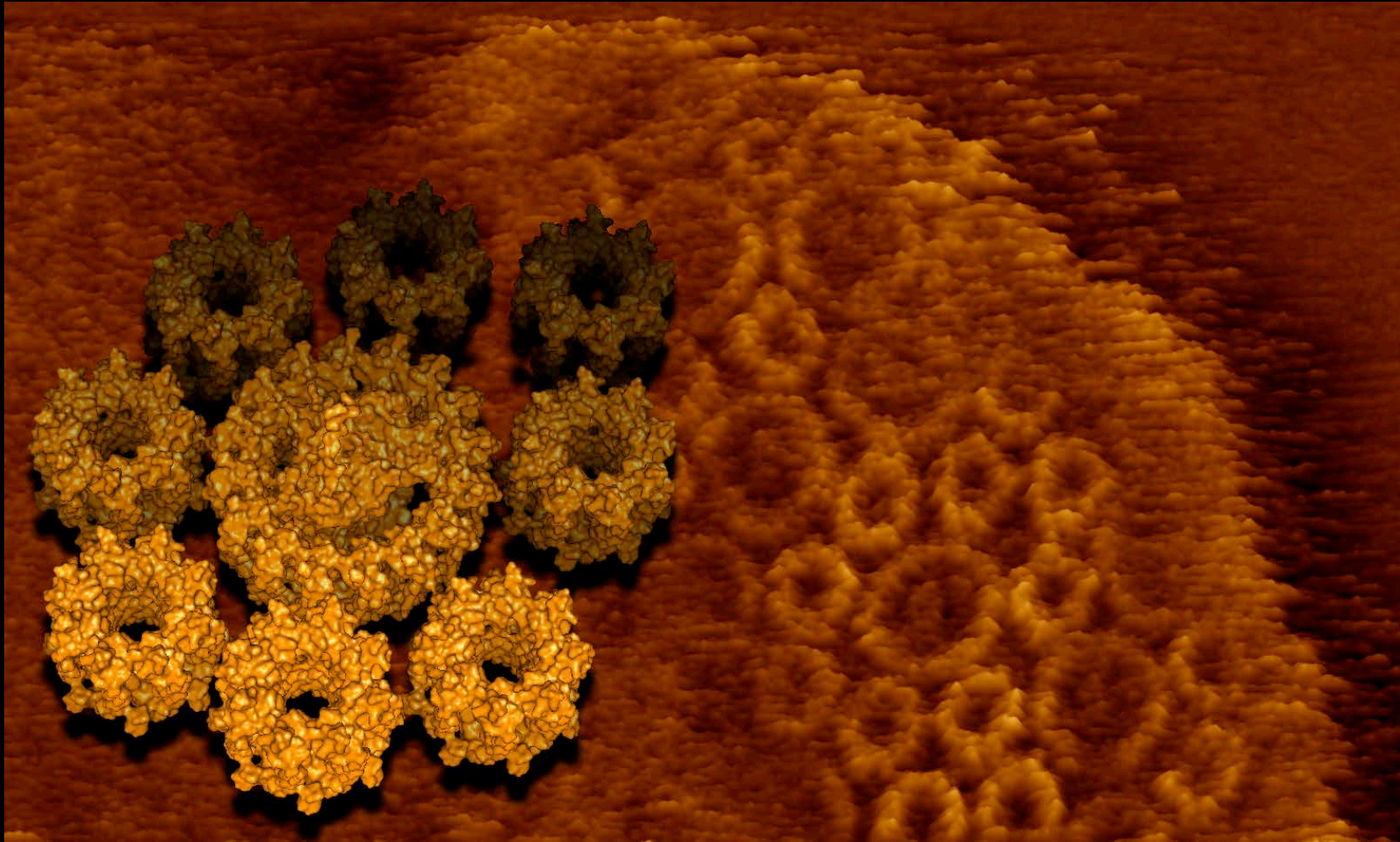
Antenna and “photosynthetically active” domains in low-light adapted membranes



Simon Scheuring*, & James Sturgis (2005).
Chromatic adaptation of photosynthetic membranes.
Science, 2005, 309, 5733, 484-487.

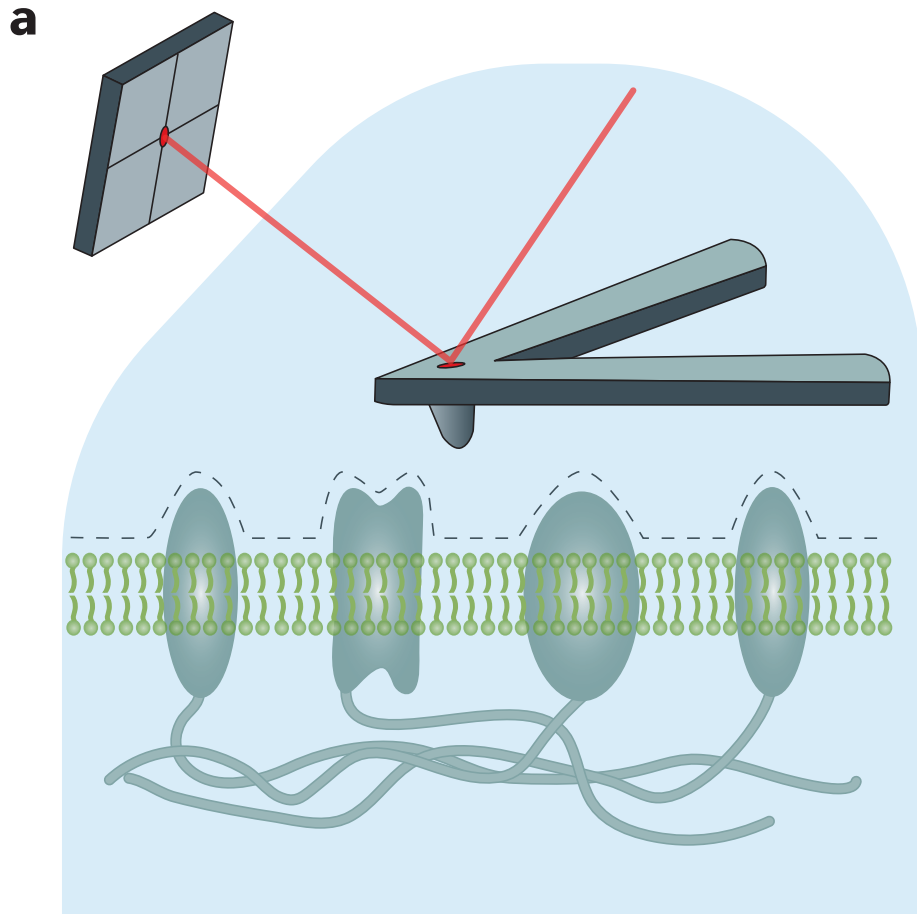
Rsp. Molischianum Photosynthetic Apparatus

Atomic model of the photosynthetic complex assembly, based on AFM topography



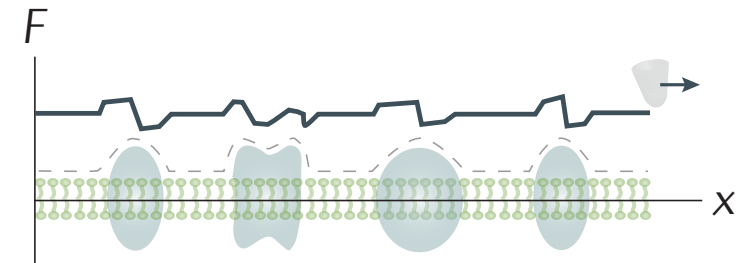
(c) Simon Scheuring

Imaging modes

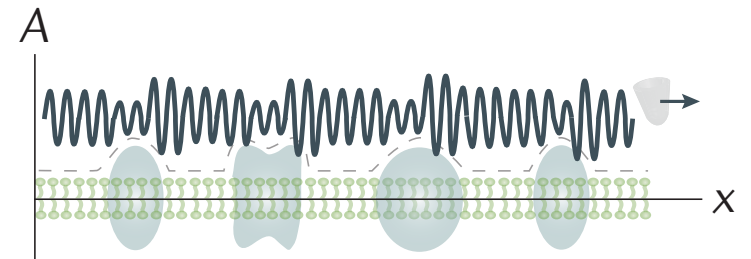


b

Contact mode



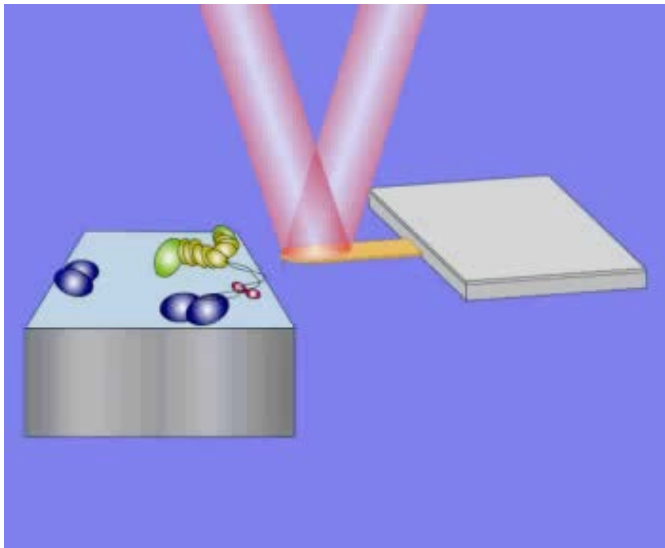
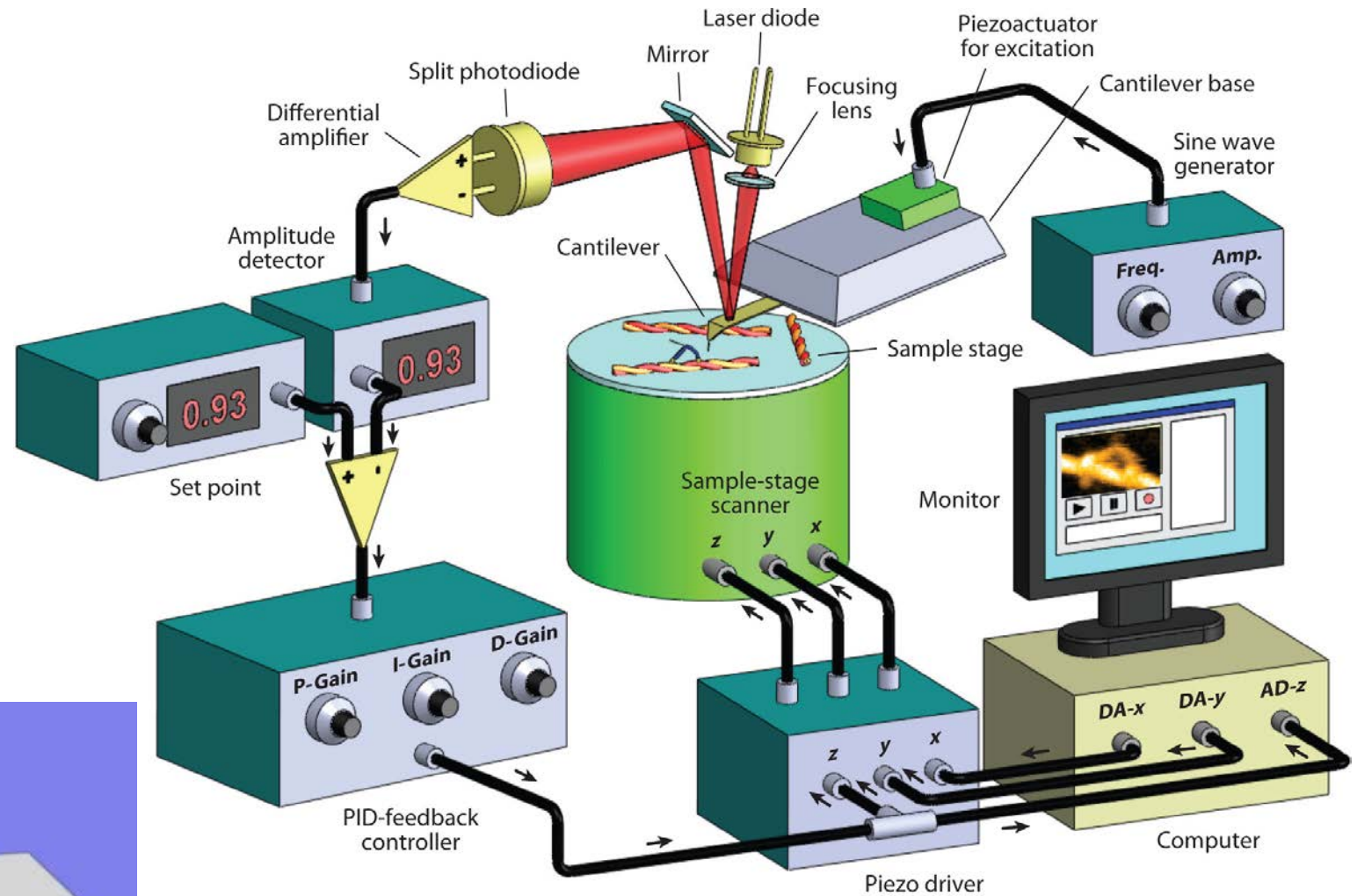
Dynamic mode



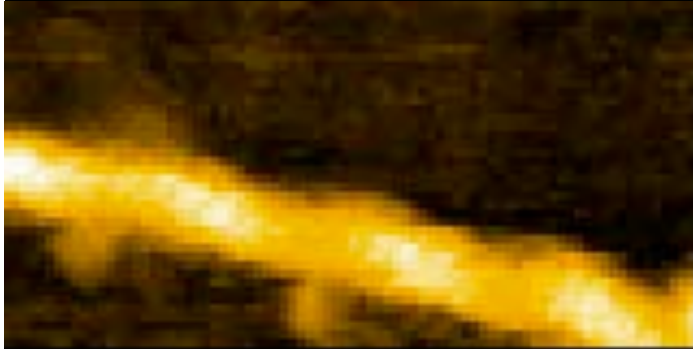
Review:

D. Alsteens, H. E. Gaub, R. Newton, M. Pfreundschuh, C. Gerber, and D. J. Müller, “Atomic force microscopy-based characterization and design of bionterfaces,” Nature Publishing Group, vol. 2, pp. 1–16, Mar. 2017.

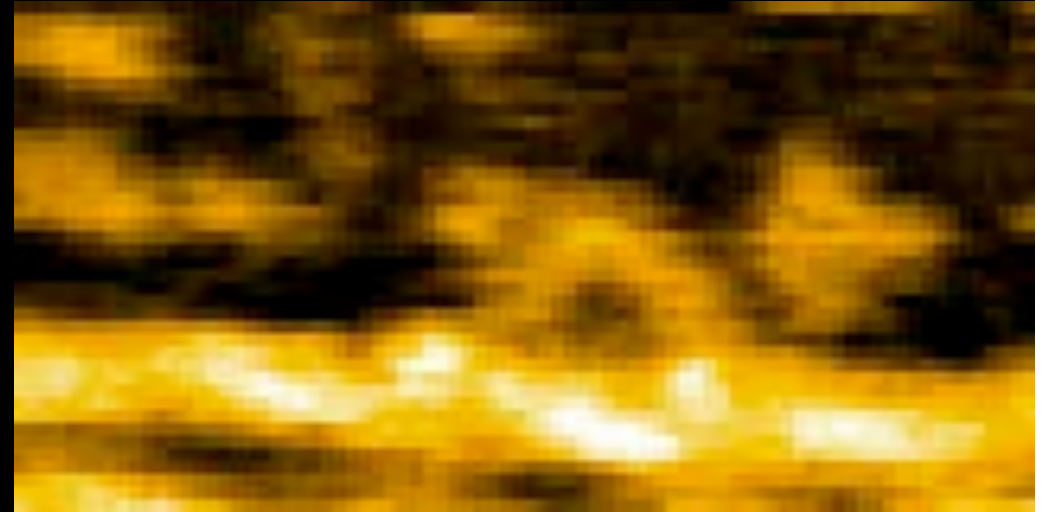
High-Speed AFM



High-Speed AFM shows myosin walking along actin



Processive movement of myosin V (M5-HMM). The dynamic process in 1 μM ATP was captured at 7 fps. Scan range, 130 \times 65 nm² with 80 \times 40 pixel.



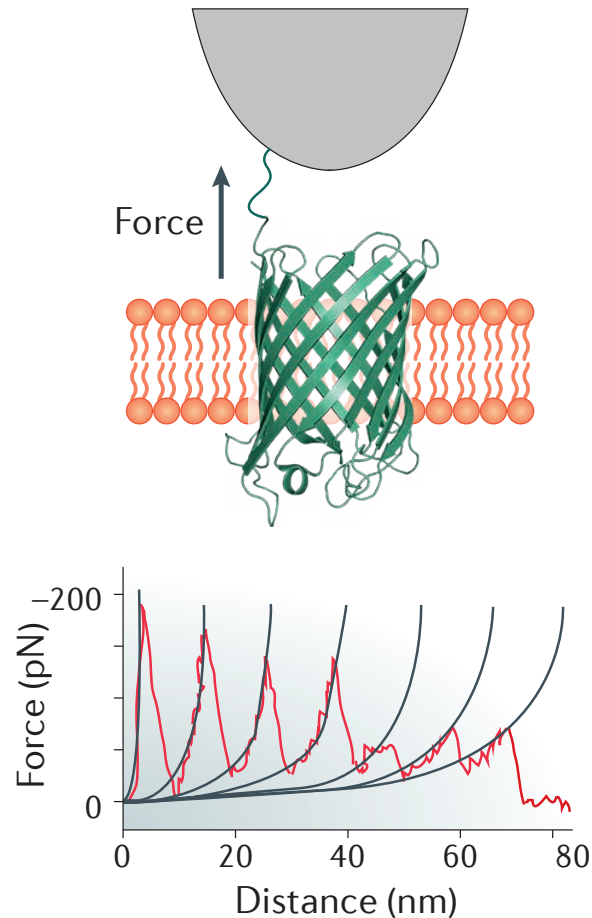
Hand-over-hand movement of myosin V (M5-HMM) including foot stomp of the leading head. The dynamic process in 1 μM ATP was captured at 7 fps. Scan range, 150 \times 75 nm² with 80 \times 40 pixel.



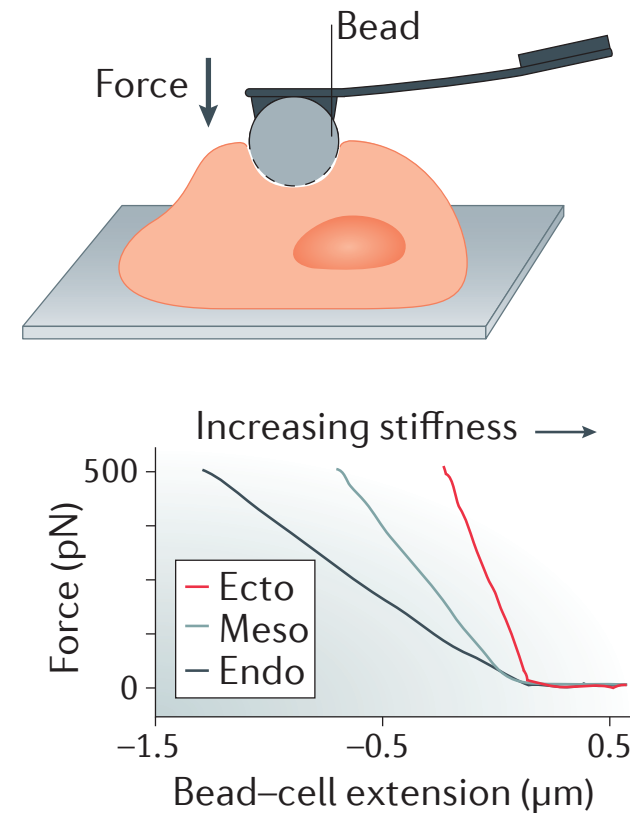
Long tracking of myosin V (M5-HMM) walking along actin filament. This typical movie showing long processive runs in 1 μM ATP was captured at 7 fps. To chase the M5-HMM molecule, the scan area was moved. Scan range, 150 \times 75 nm² with 80 \times 40 pixel; the whole imaging area, 560 \times 120 nm²

Force spectroscopy AFM

Protein unfolding

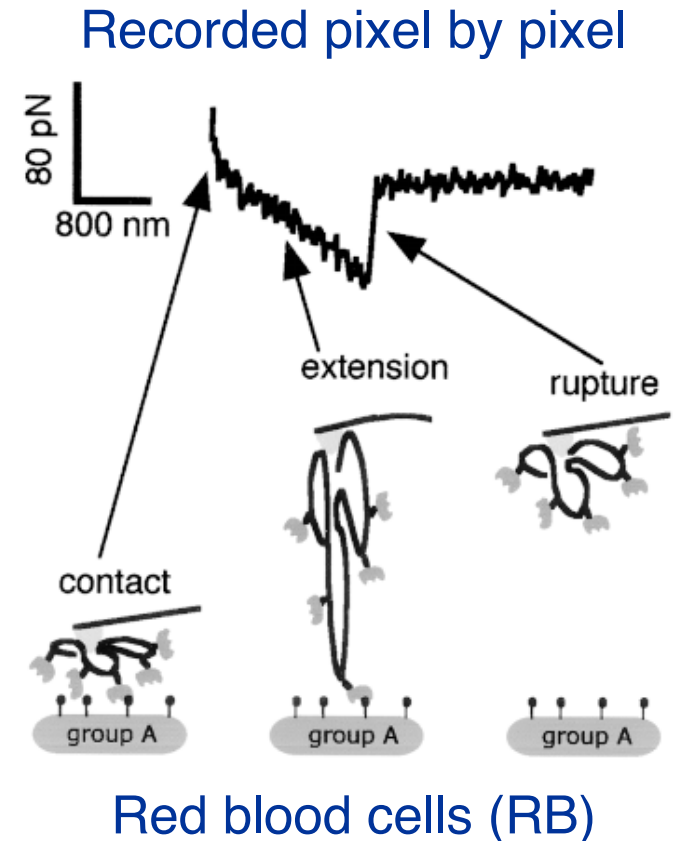
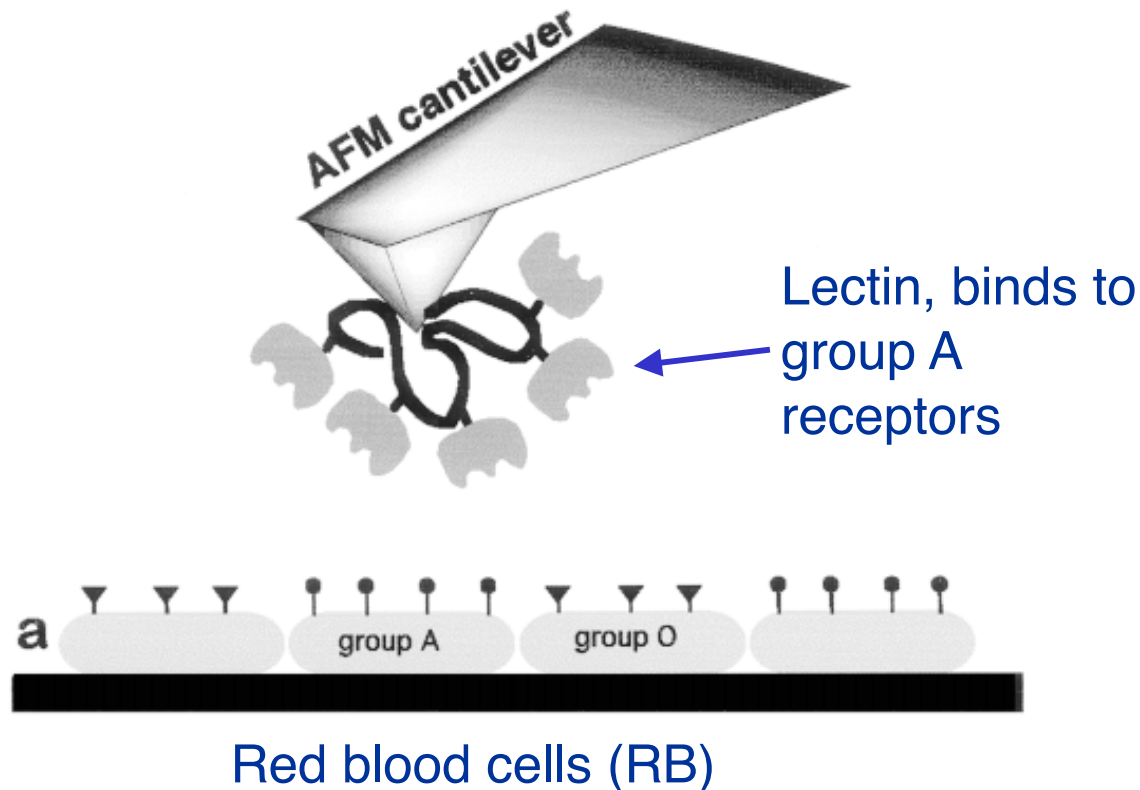


Cellular intention



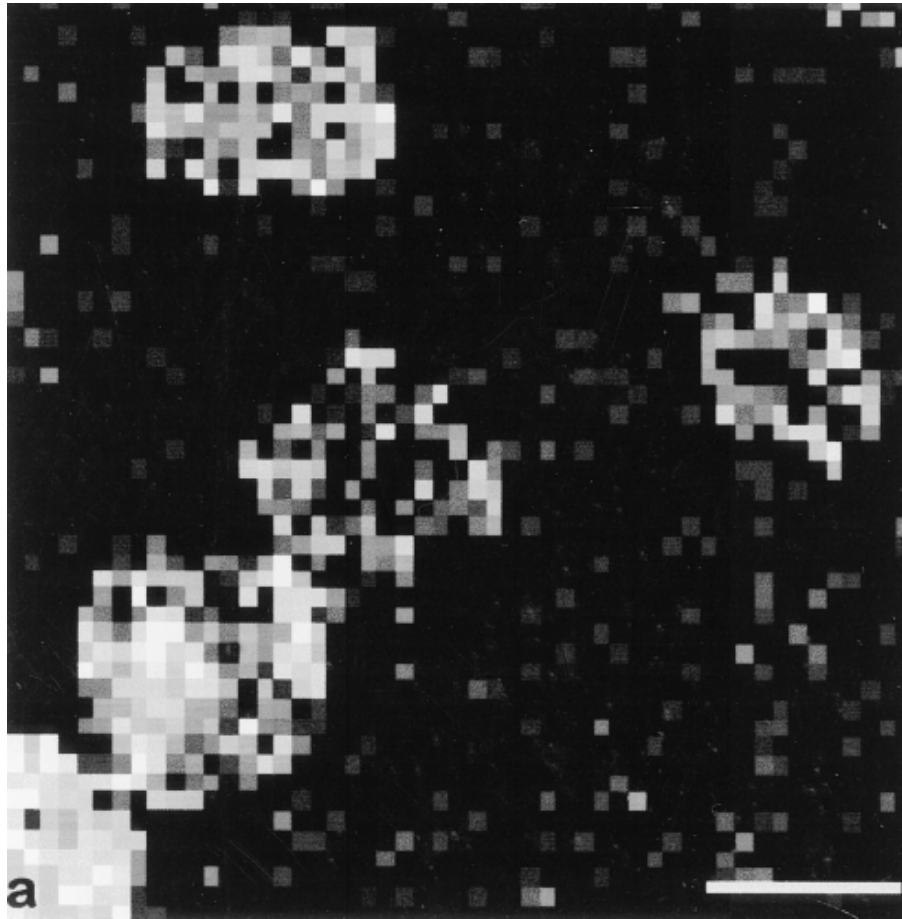
M. Grandbois, W. Dettmann, M. Benoit, and H. E. Gaub, "Affinity imaging of red blood cells using an atomic force microscope," *J. Histochem. Cytochem.*, vol. 48, no. 5, pp. 719–724, 2000.

Affinity imaging by AFM

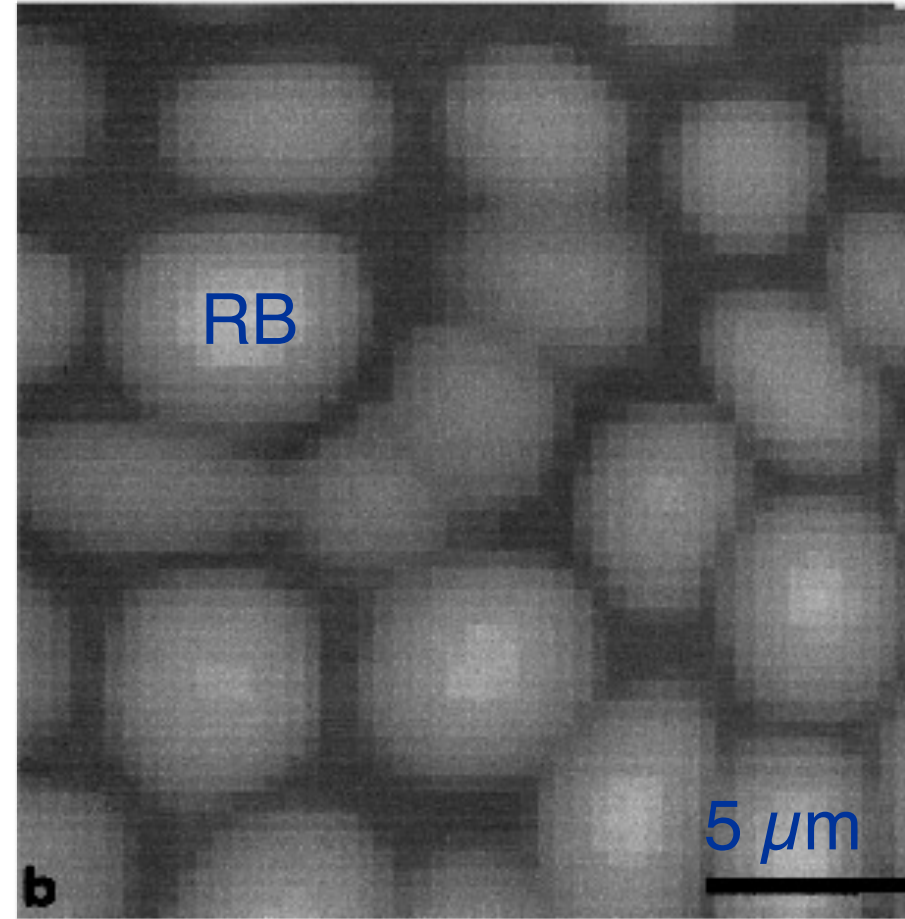


Affinity imaging by AFM

Adhesion image



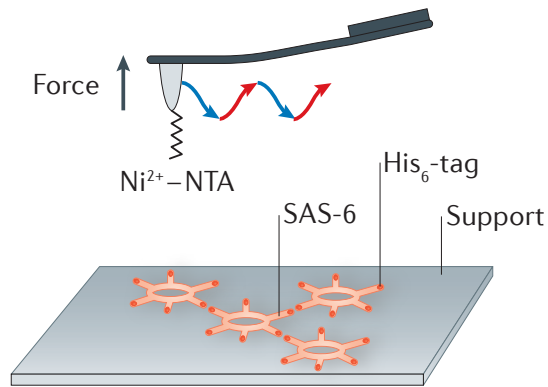
Topography



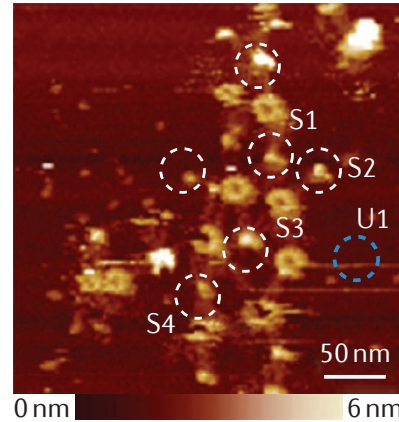
(a) Adhesion image recorded on a layer of mixed group A and O RBCs (1:2) adsorbed on a polylysine-coated glass surface with an AFM tip functionalized with HPL. The bright regions observed in this image correspond to group A RBCs. This image was obtained from the calculation of the rupture force (when observed) for an array of 55 x 55 force curves. Rupture events are responsible for the contrast. (b) Topographic image of the RBC layer scanned in a.

Affinity imaging by AFM

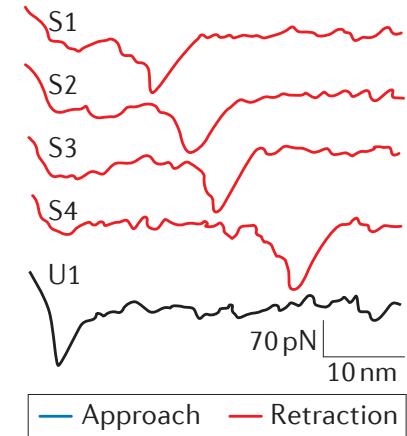
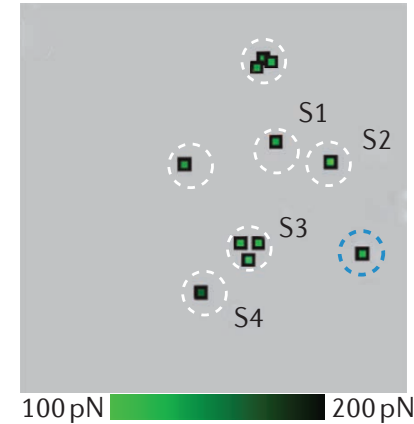
a Affinity imaging



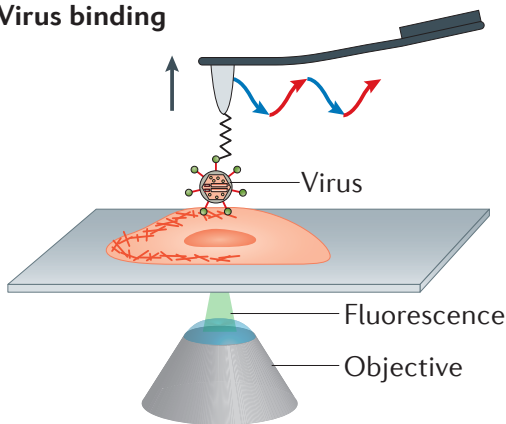
Height image



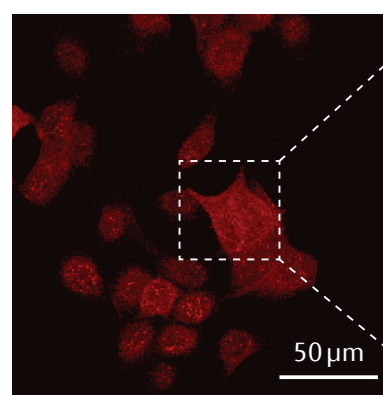
Adhesion map



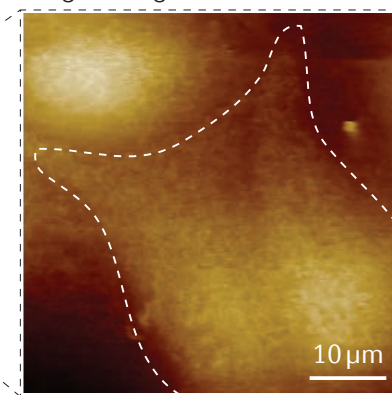
c Virus binding



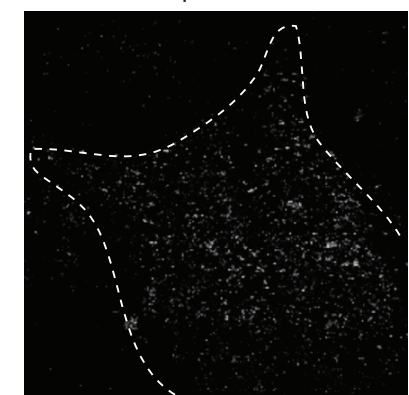
Confocal



Height image



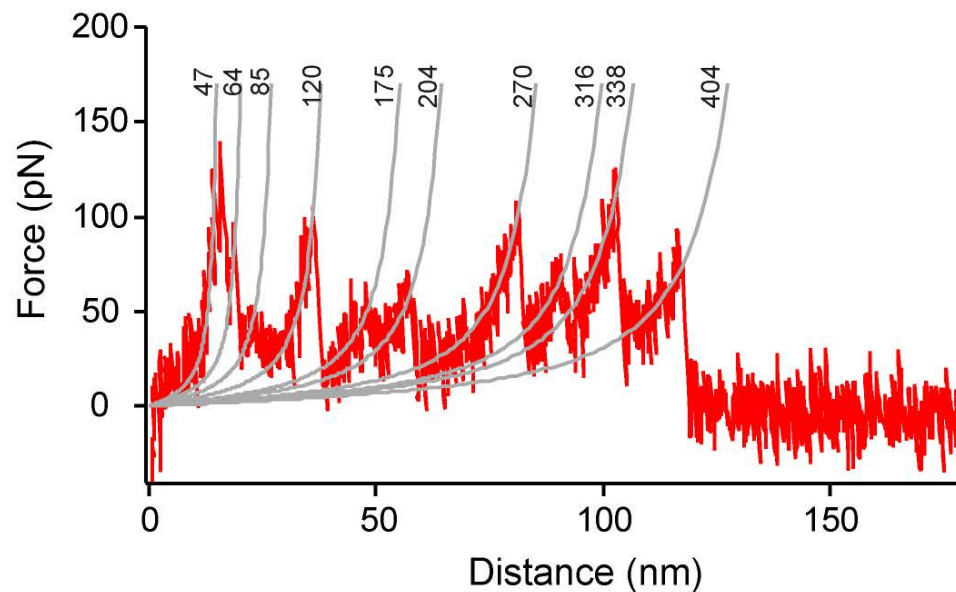
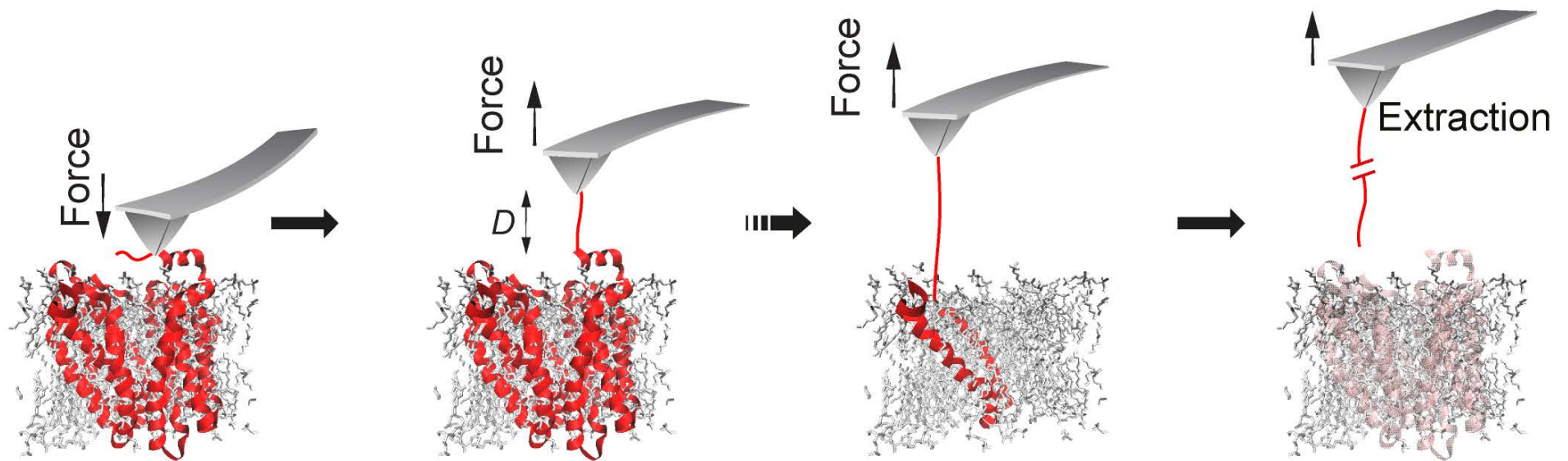
Adhesion map



M. Grandbois, W. Dettmann, M. Benoit, and H. E. Gaub, "Affinity imaging of red blood cells using an atomic force microscope," J. Histochem. Cytochem., vol. 48, no. 5, pp. 719–724, 2000.

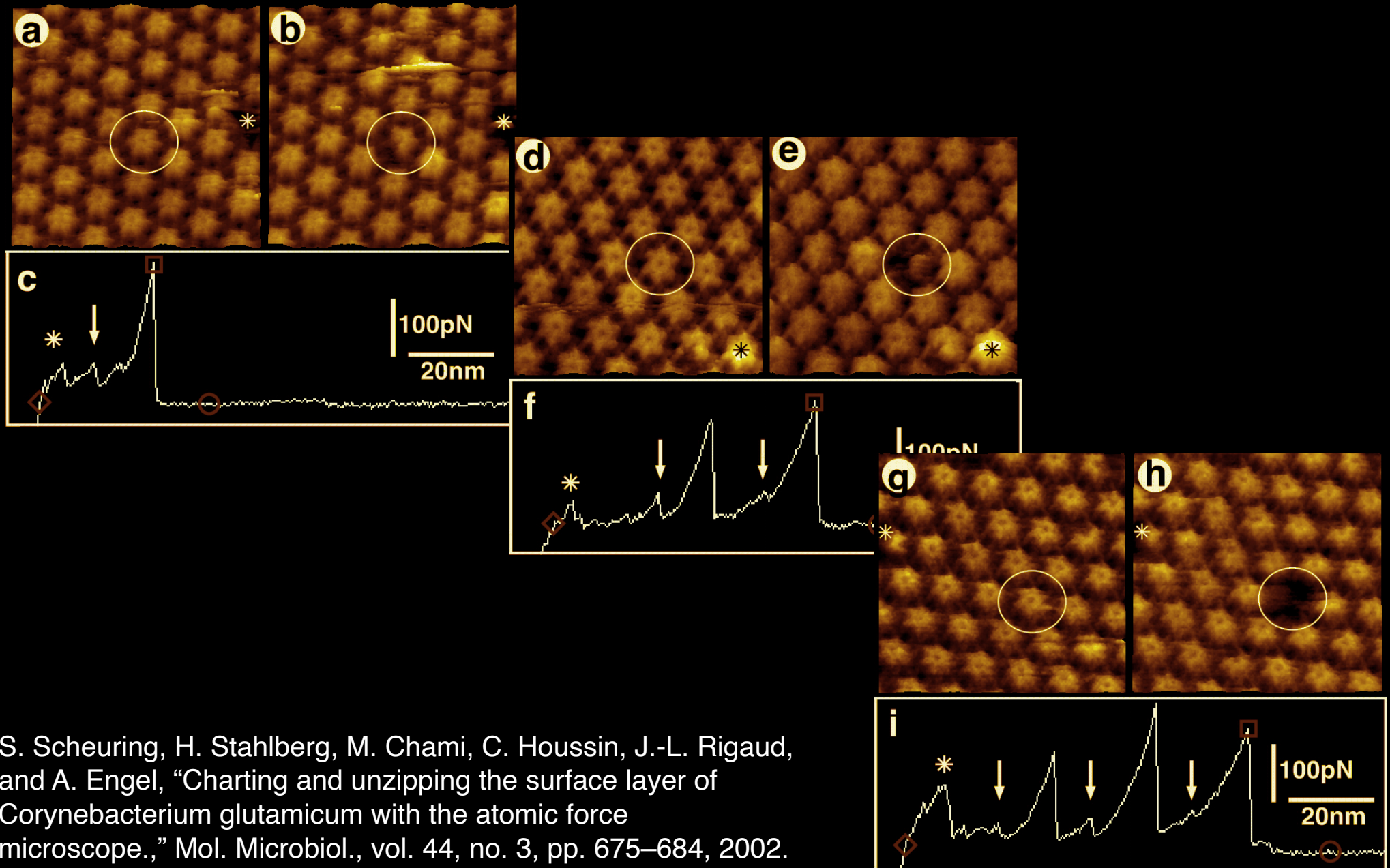
Controlled Unzipping of Proteins

Single molecule force spectroscopy (SMFS)



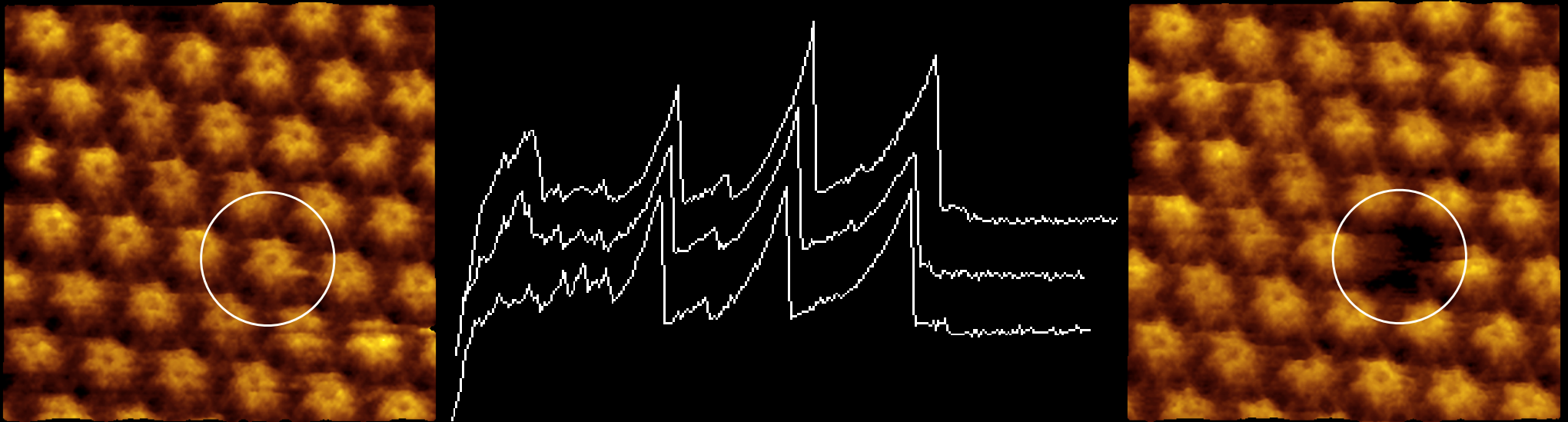
T. Serdiuk, D. Balasubramaniam, J. Sugihara, S. A. Mari, H. R. Kaback, and D. J. Müller, "YidC assists the stepwise and stochastic folding of membrane proteins," *Nat. Chem. Biol.*, vol. 12, no. 11, pp. 911–917, Sep. 2016.

Force spectroscopy of the native S-layer

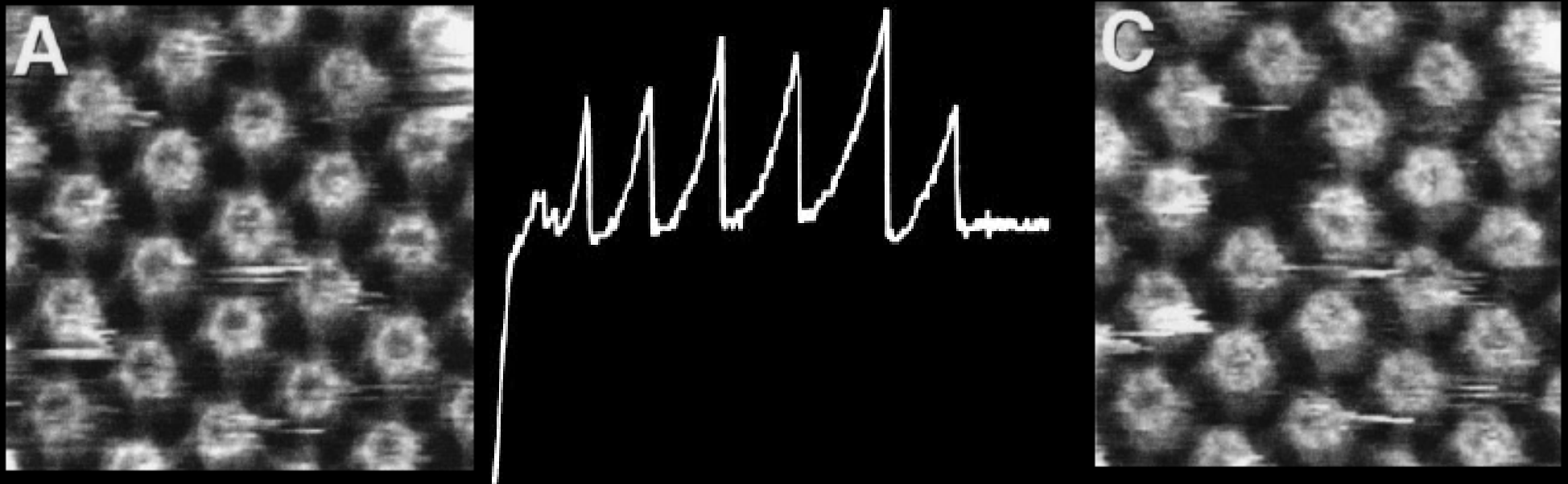


S. Scheuring, H. Stahlberg, M. Chami, C. Houssin, J.-L. Rigaud, and A. Engel, "Charting and unzipping the surface layer of *Corynebacterium glutamicum* with the atomic force microscope.," *Mol. Microbiol.*, vol. 44, no. 3, pp. 675–684, 2002.

Force spectroscopy of the native *Corynebacterium glutamicum* S-layer



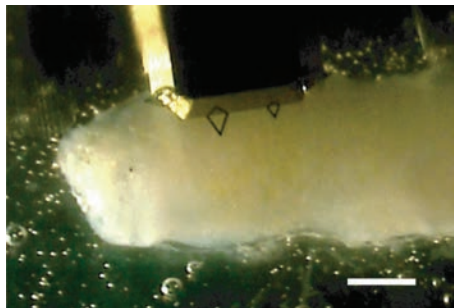
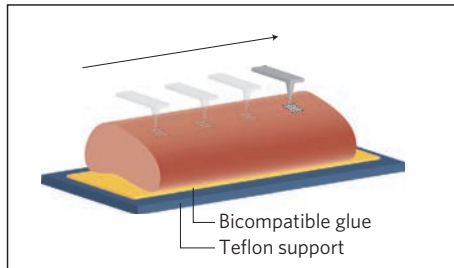
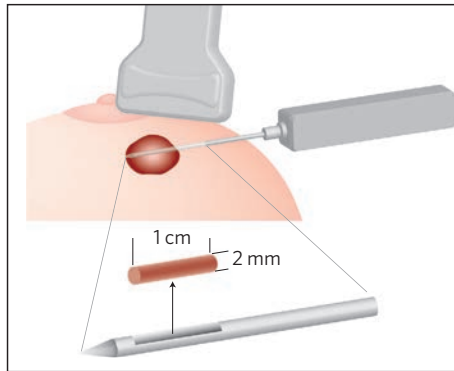
Force spectroscopy of the native *Deinococcus Radiodurans* HPI-layer



Tissue characterisation (I)

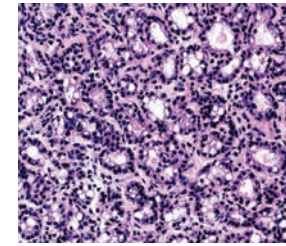
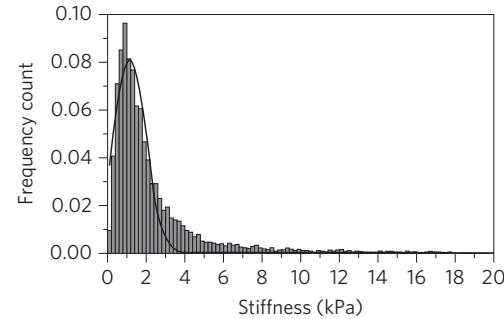
Cancer biopsy and nanmochemical characterisation

a Testing human breast biopsies by IT-AFM

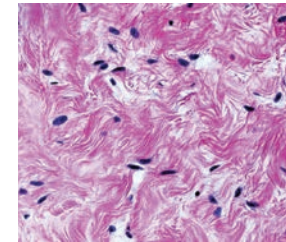
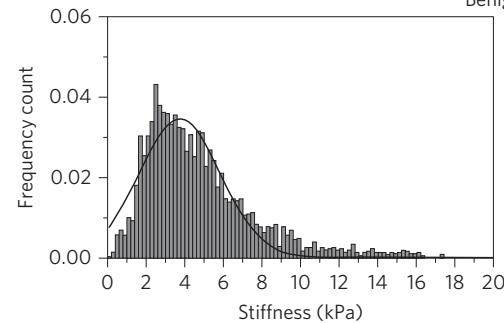


b

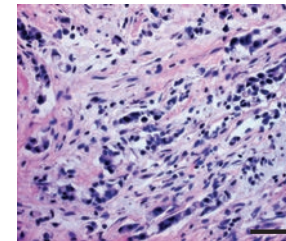
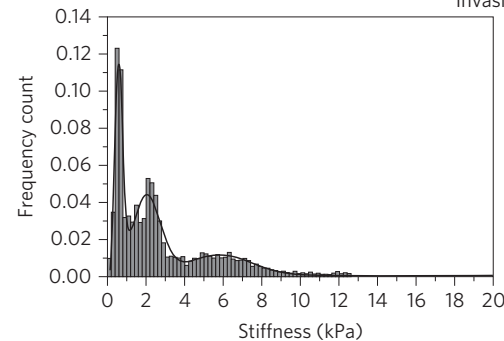
Normal tissue



Benign lesion

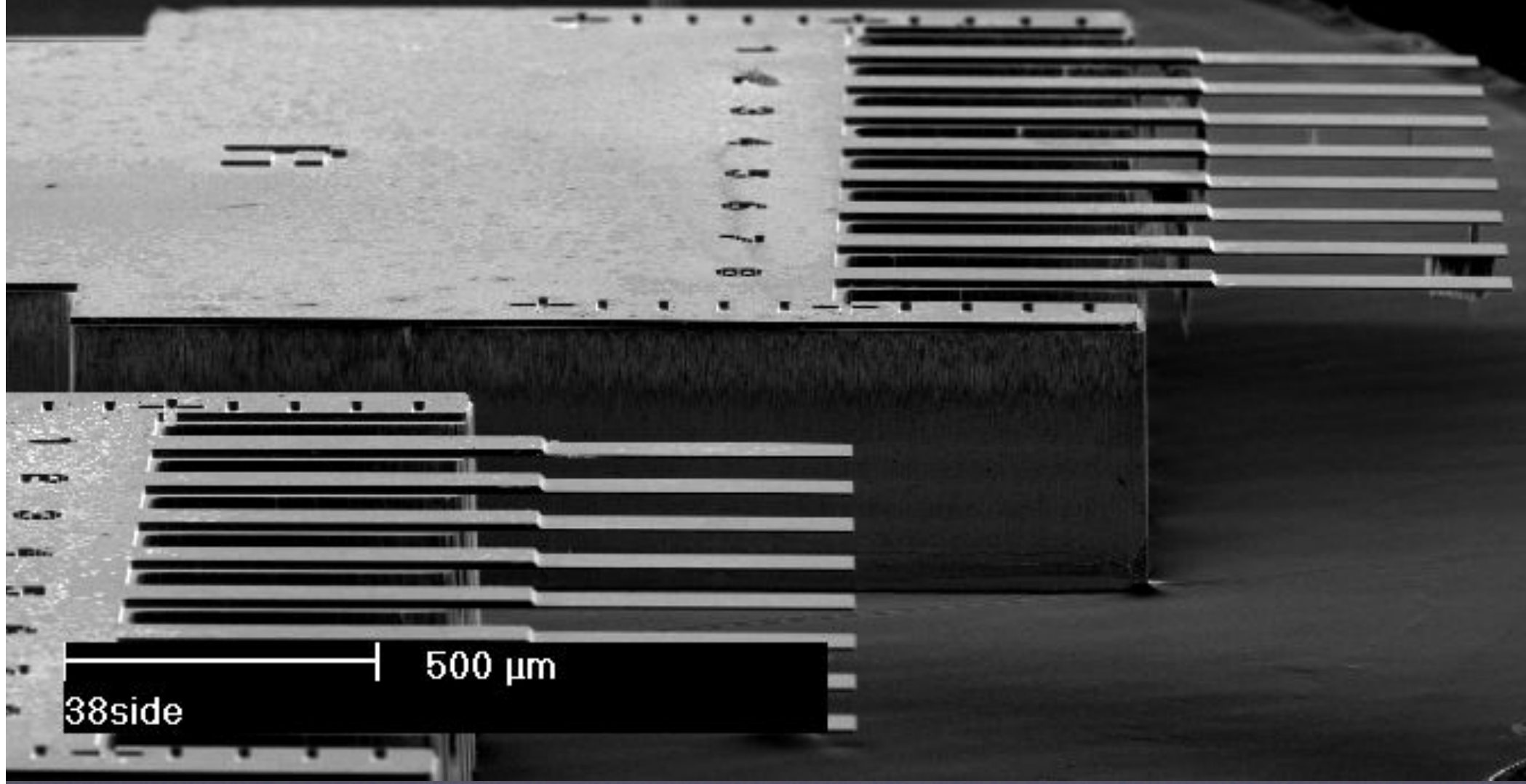


Invasive cancer



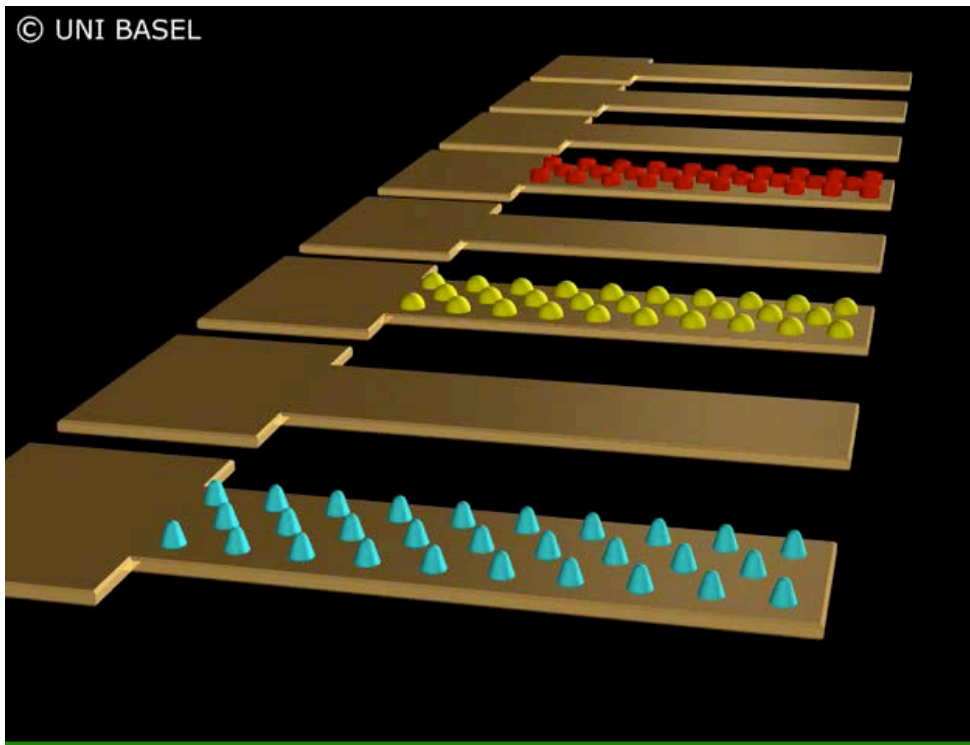
M. Plodinec, M. Loparic, C. A. Monnier, E. C. Obermann, R. Zanetti-Dallenbach, P. Oertle, J. T. Hyotyla, U. Aebi, M. Bentires-Alj, R. Y. H. Lim, and C.-A. Schoenenberger, "The nanomechanical signature of breast cancer," pp. 1–9, 2012.

Nanomechanical sensors



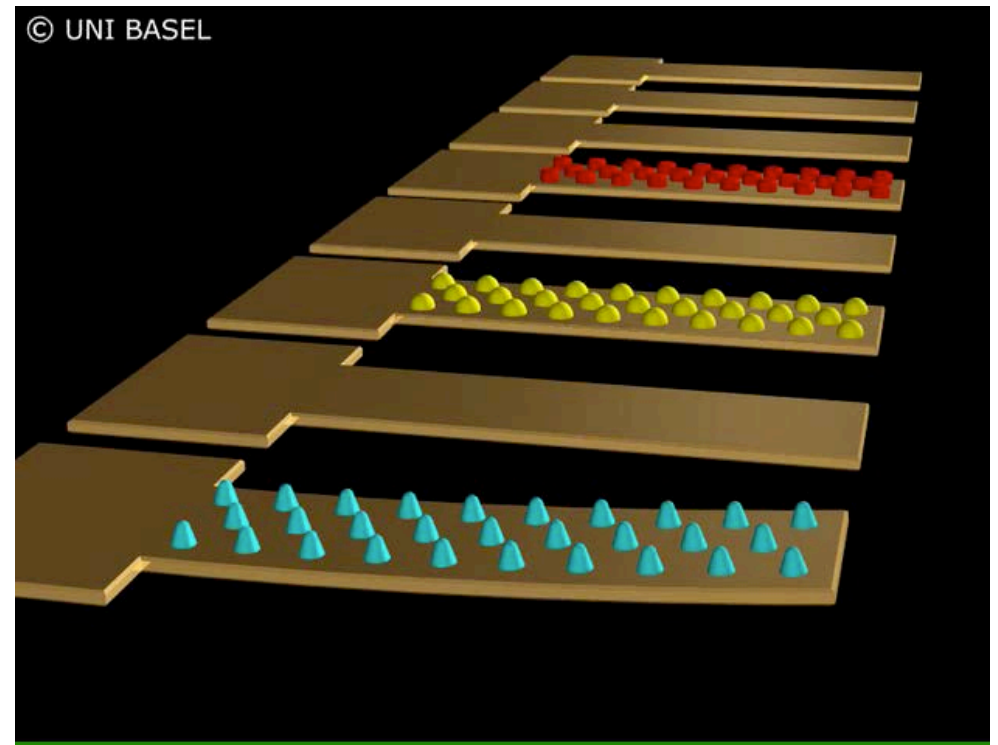
Two modes

Static mode



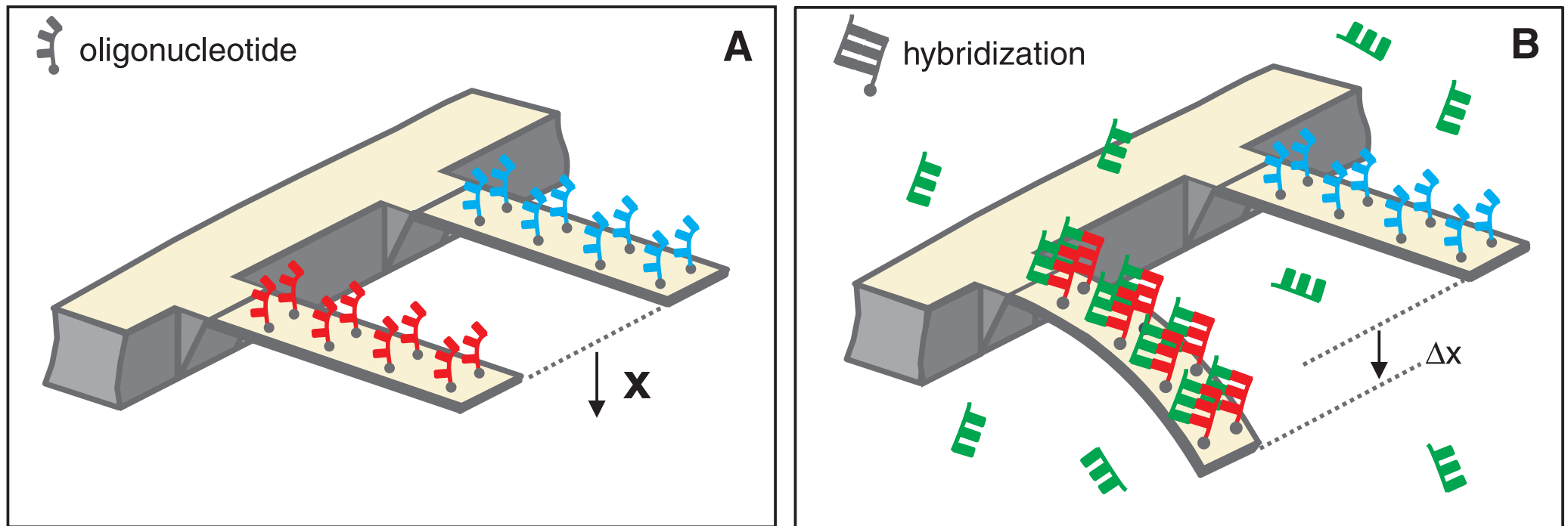
Detects surface stress

Dynamic mode



Detects mass increase

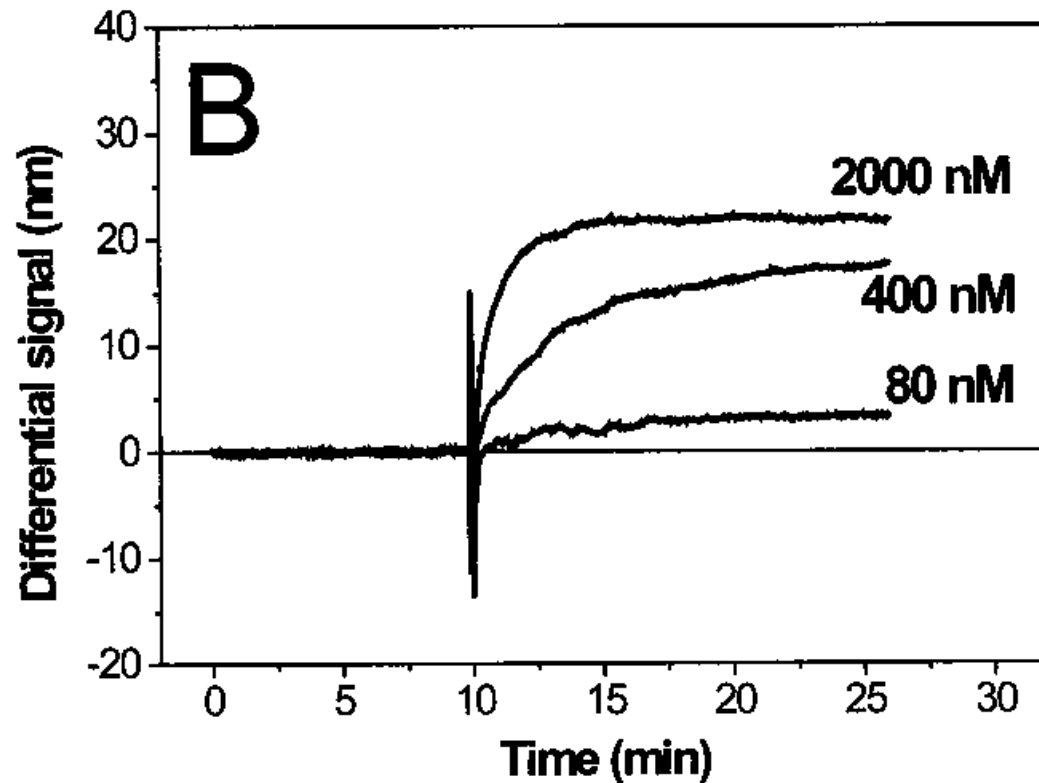
Static mode: DNA hybridisation



Scheme illustrating the hybridization experiment. Each cantilever is functionalized on one side with a different oligonucleotide base sequence (red or blue). **(A)** The differential signal is set to zero. **(B)** After injection of the first complementary oligonucleotide (green), hybridization occurs on the cantilever that provides the matching sequence (red), increasing the differential signal Δx .

J. Fritz, M. K. Baller, H. P. Lang, H. Rothuizen, P. Vettiger, E. Meyer, H. J. Guntherodt, C. Gerber, and J. K. Gimzewski, "Translating biomolecular recognition into nanomechanics," *Science*, vol. 288, no. 5464, pp. 316–318, 2000.

Static mode: DNA hybridisation

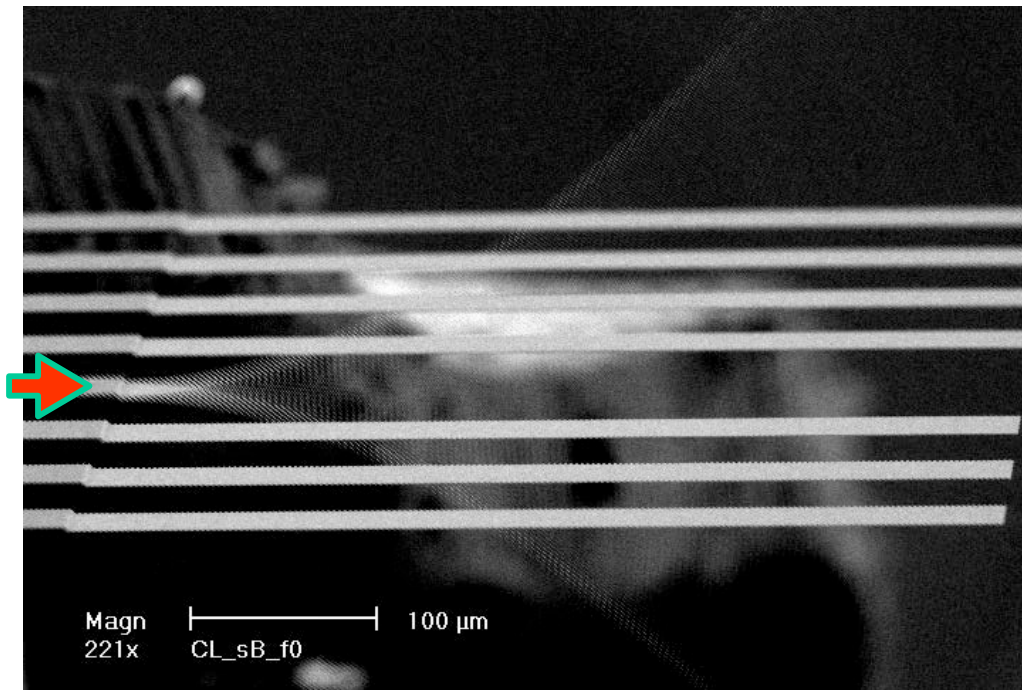


Three successive hybridization experiments with different 12-mer oligonucleotide concentrations using one array.

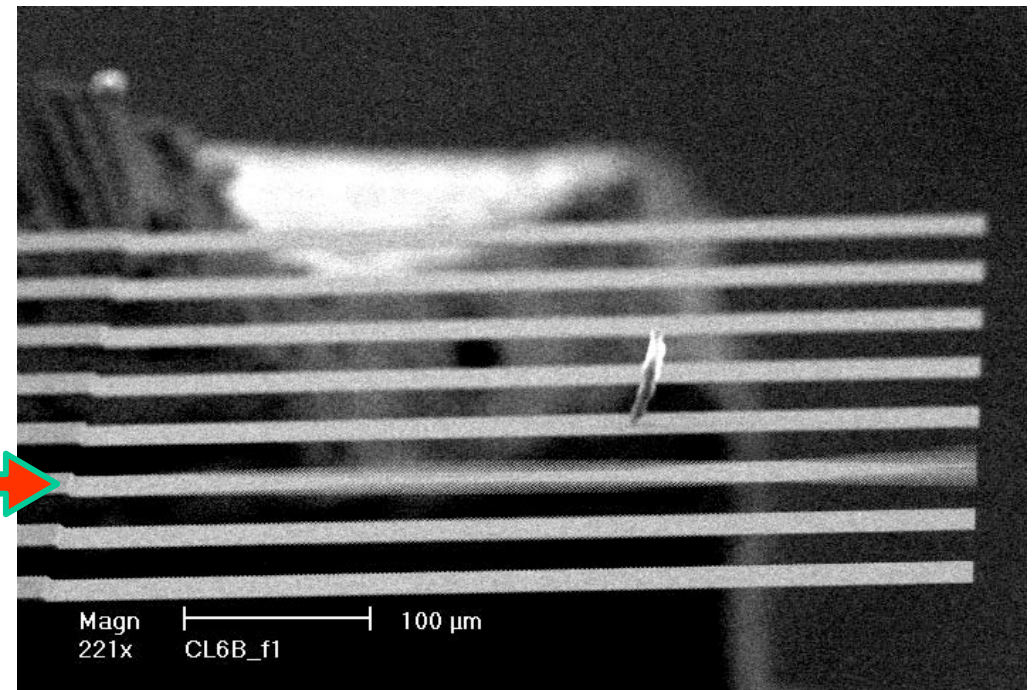
J. Fritz, M. K. Baller, H. P. Lang, H. Rothuizen, P. Vettiger, E. Meyer, H. J. Guntherodt, C. Gerber, and J. K. Gimzewski, "Translating biomolecular recognition into nanomechanics," *Science*, vol. 288, no. 5464, pp. 316–318, 2000.

Dynamic mode

First mode



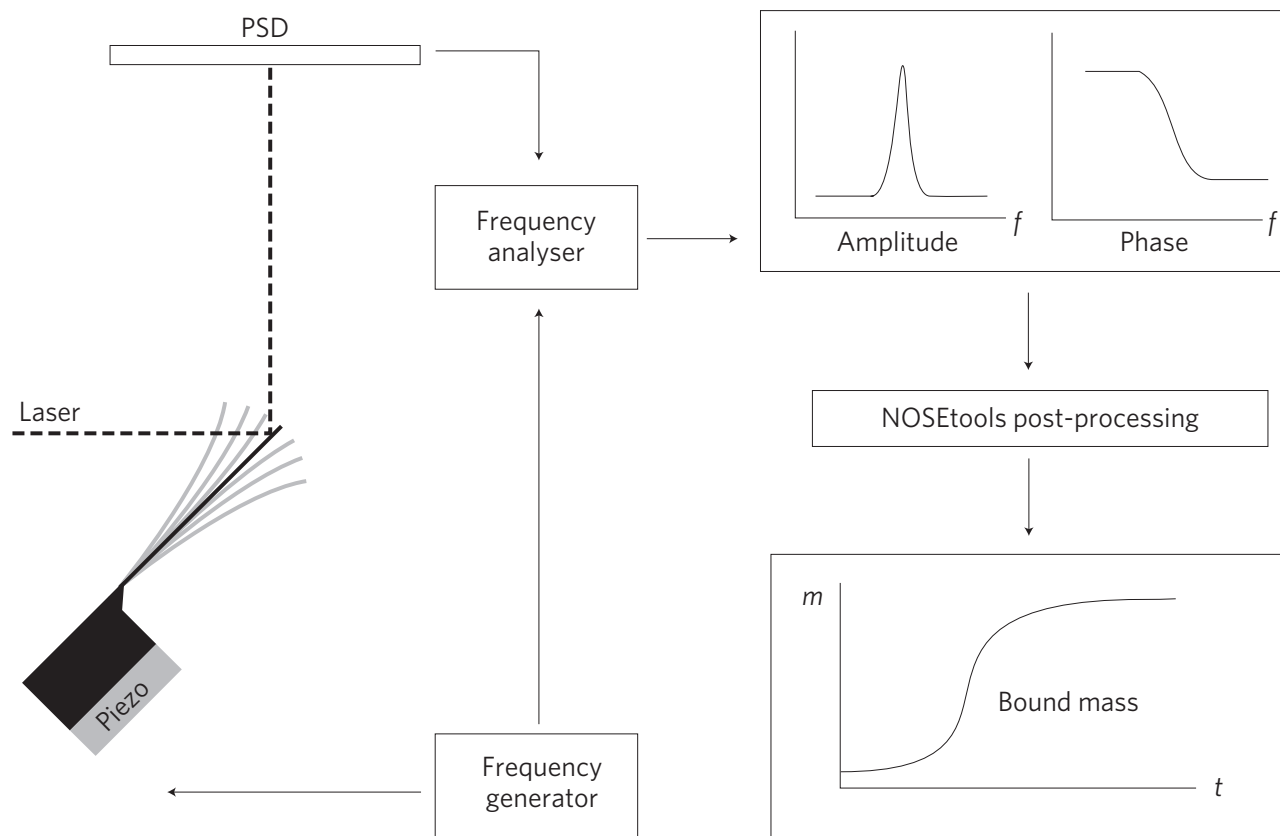
Second mode



In vacuum

M. K. Ghatkesar, V. Barwich, T. Braun, J.-P. Ramseyer, C. Gerber, M. Hegner, H.-P. Lang, U. Drechsler, and M. Despont, "Higher modes of vibration increase mass sensitivity in nanomechanical microcantilevers," *Nanotechnology*, vol. 18, no. 44, pp. 445502–8, 2007.

Dynamic mode

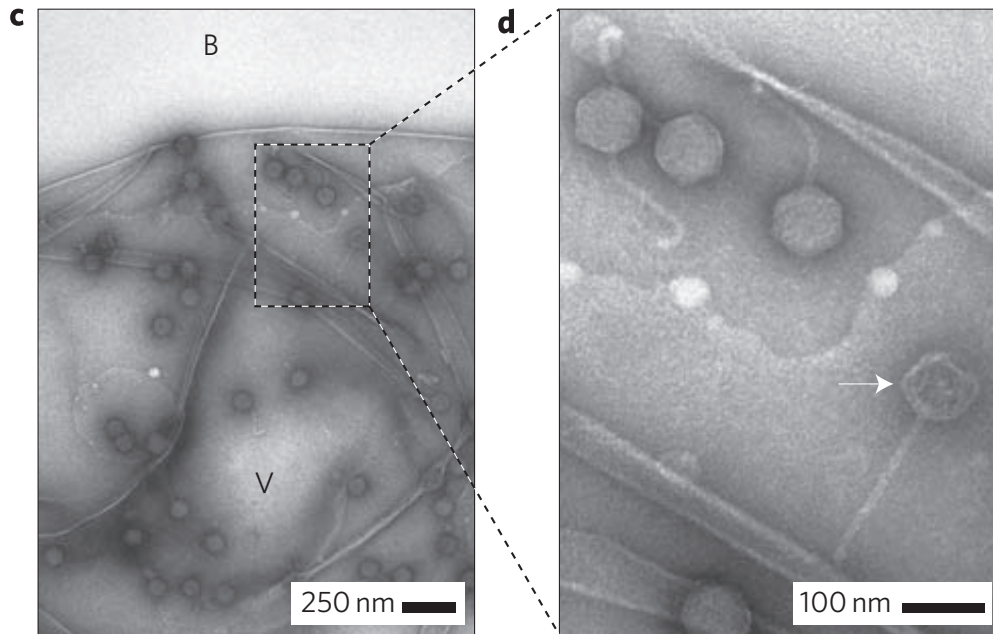


A frequency generator sweeps the frequency by exciting a piezoelectric actuator located beneath the base of the microcantilever array. The response of the cantilever is optically detected with a laser using a position-sensitive detector (PSD). The frequency analyser compares the cantilever response with a reference signal from the frequency generator to determine the phase. The amplitude spectrum is recorded with the corresponding phase values. The raw data are analysed by a post-processing software called NOSEtools, which allows the time evolution of the adsorbed mass to be directly determined from the spectrum.

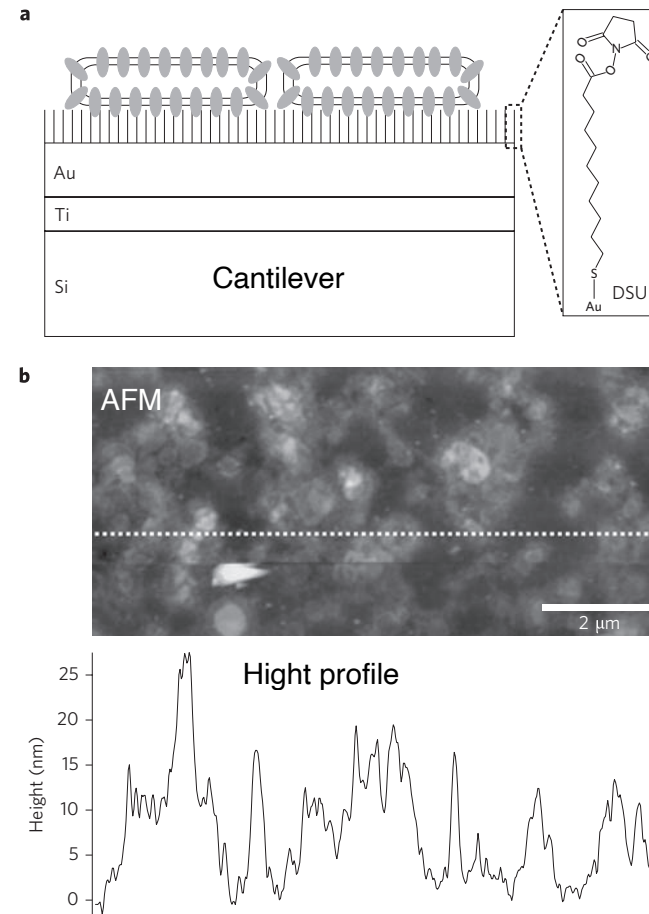
Virtual mass: also liquid is moved, shifting eigenfrequency. Calibration is needed.
High damping, shifts amplitude peak relative to eigenfrequency.

T. Braun, V. Barwich, M. K. Ghatkesar, A. H. Bredekamp, C. Gerber, M. Hegner, and H. P. Lang,
“Micromechanical mass sensors for biomolecular detection in a physiological environment,” Phys.
Rev. E, 72, 3, 2005.

Dynamic mode



Vesicles with T5 virus receptor FhuA in Transmission electron microscope



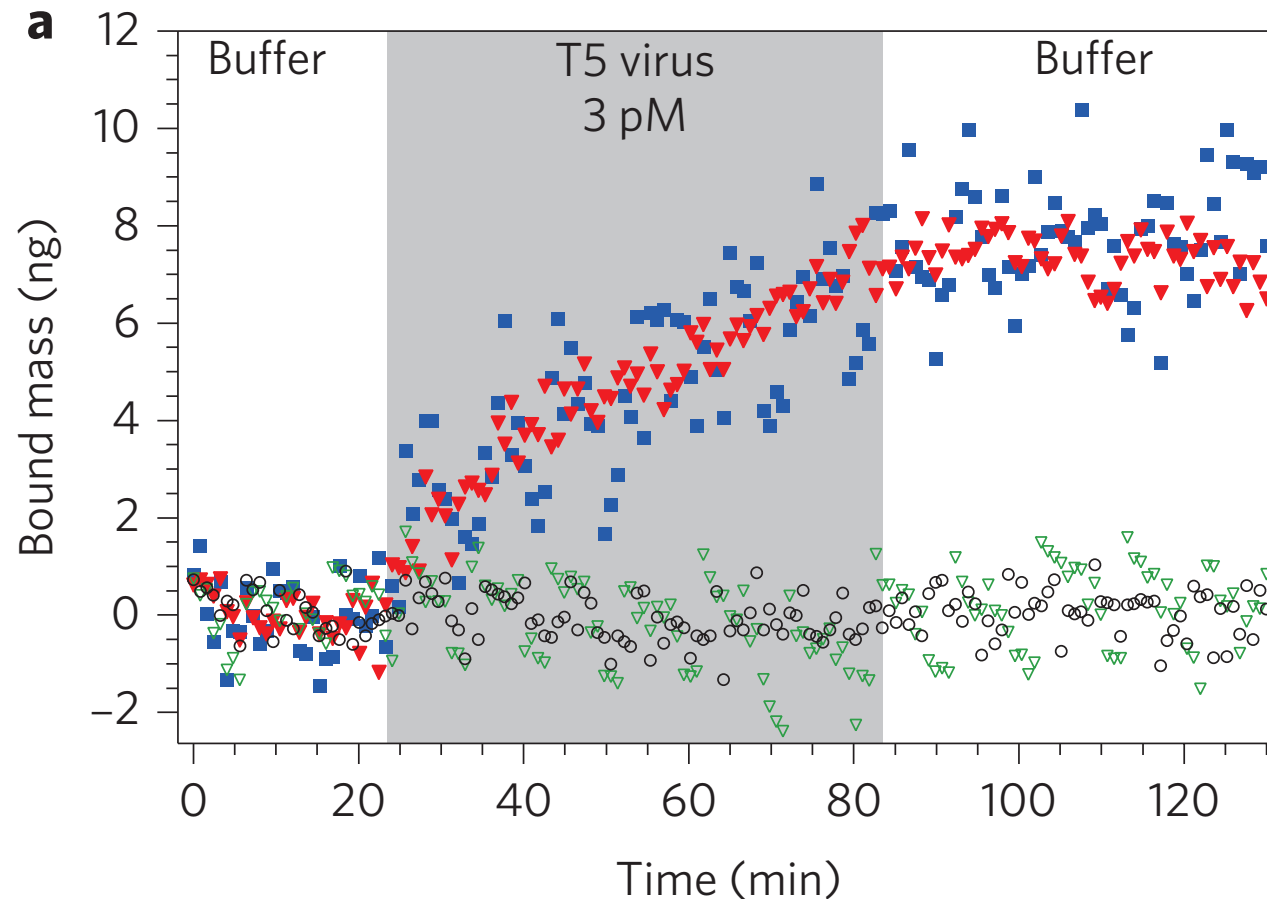
Functionalization of cantilever with FhuA vesicles

a, Schematic of the cantilever functionalization: the gold interface of the cantilever is pre-functionalized with a self-assembling DSU crosslinker, which binds to the gold via a thiol group and reacts by a succinidyl group with primary amines of FhuA–protein reconstituted in lipid vesicles. **b**, Tapping-mode AFM image of the cantilever surface in the middle of the cantilever bar. The line indicates the position of the recorded height profile shown in the lower panel. FhuA-containing proteoliposomes are clearly visible, similar to the one in the image on the left.

T. Braun, M. K. Ghatkesar, N. Backmann, W. Grange, P. Boulanger, L. Letellier, H.-P. Lang, A. Bietsch, C. Gerber, and M. Hegner, “Quantitative time-resolved measurement of membrane protein–ligand interactions using microcantilever array sensors,” *Nature Nanotech*, vol. 4, no. 3, pp. 179–185, 2009.

Dynamic mode

Quantitative realtime virus binding



A T5 phage solution (3 pM) was injected for 1 h at a rate of $10 \mu\text{l min}^{-1}$. The uptake mass was measured simultaneously on four different cantilevers on one array: two positive controls (FhuA-coated cantilevers, blue squares and red triangles), two negative controls (casein-coated cantilevers, black open circles and green open triangles).

T. Braun, M. K. Ghatkesar, N. Backmann, W. Grange, P. Boulanger, L. Letellier, H.-P. Lang, A. Bietsch, C. Gerber, and M. Hegner, "Quantitative time-resolved measurement of membrane protein–ligand interactions using microcantilever array sensors," *Nature Nanotech*, vol. 4, no. 3, pp. 179–185, 2009.