

Crystallography on a chip:

In the quest to improve sampling efficiencies for
FEL sources



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and

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DESY/Center for Free Electron Laser Science (CFEL) and

Department of Physics

University of Hamburg, Germany

Revised Title(s)

One (good?) idea and way more
challenges...Lessons learned...we now
know what to do next...

VERY MUCH WORK IN
PROGRESS

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Part 3

March 2012

Cytoplasmic domain of
Yersinia pestis YscD

Epithelial adhesion 1 from
human pathogen *C. glabrata*

Phc1 5-adenosyl-5'-
cytosine hydrolase complex

DNA (6-4) photoproduct
dT(6-4)T in complex
with Fds fragment

E. cereus adenosine
phosphorylase

S. rubellus 5'-deoxy-3'-
methylthioadenosine
phosphorylase II

Ca²⁺-bound O-methyl-
isourea inhibitor complex

Grid-attached web service
for low-molecular-weight

Effects of cryoprotectants
on human blood group A
and B glycosyl transferases

CYP104D1 from
N. aromaticorans
DSM12444

Stability of Clostridium
thermocellum enzymes

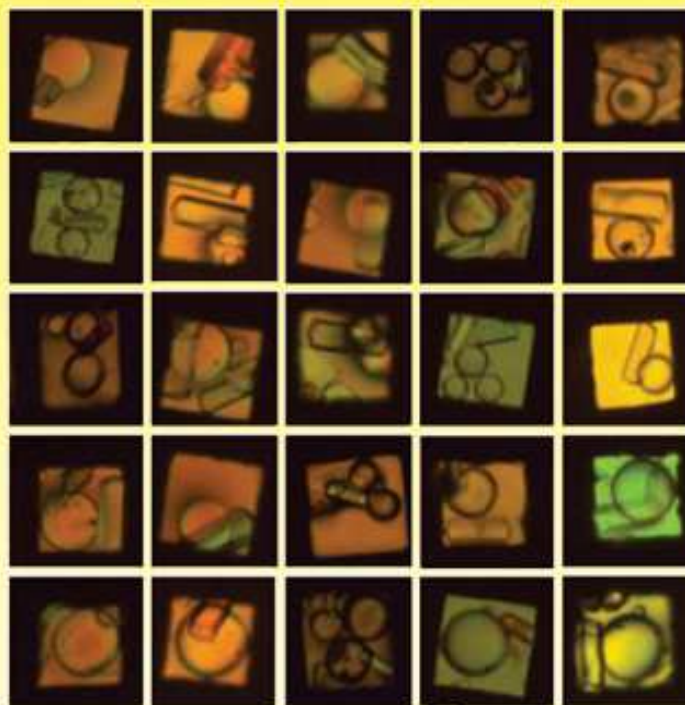
3-hydroxyphosphate
dehydrogenase under
high pressure



Acta Crystallographica Section D

Biological Crystallography

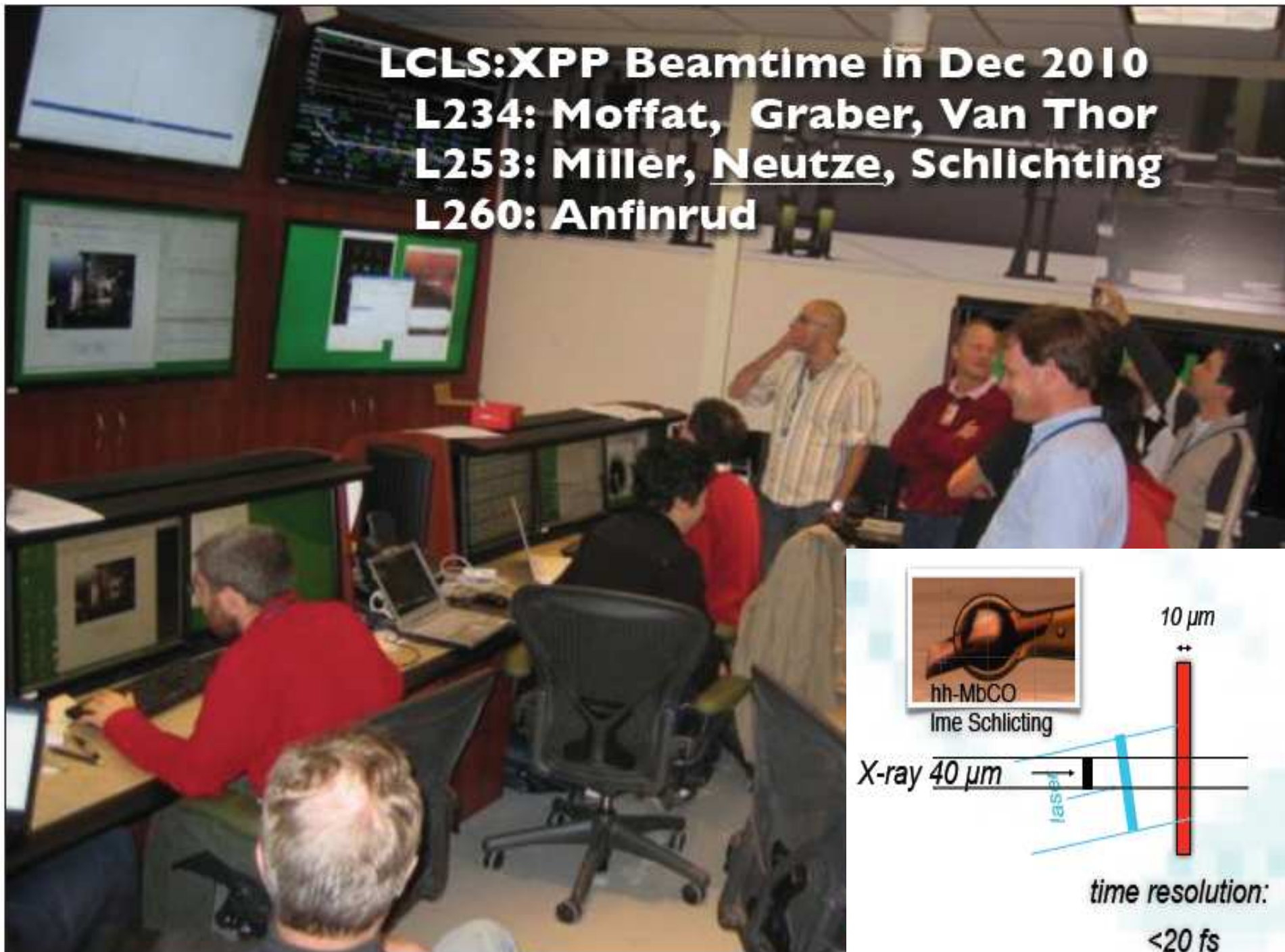
Editors: E. N. Baker and Z. Dauter



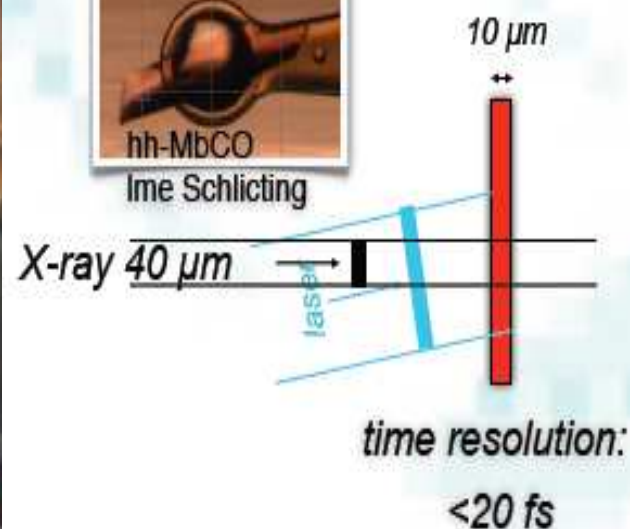
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International Union of Crystallography
Wiley-Blackwell

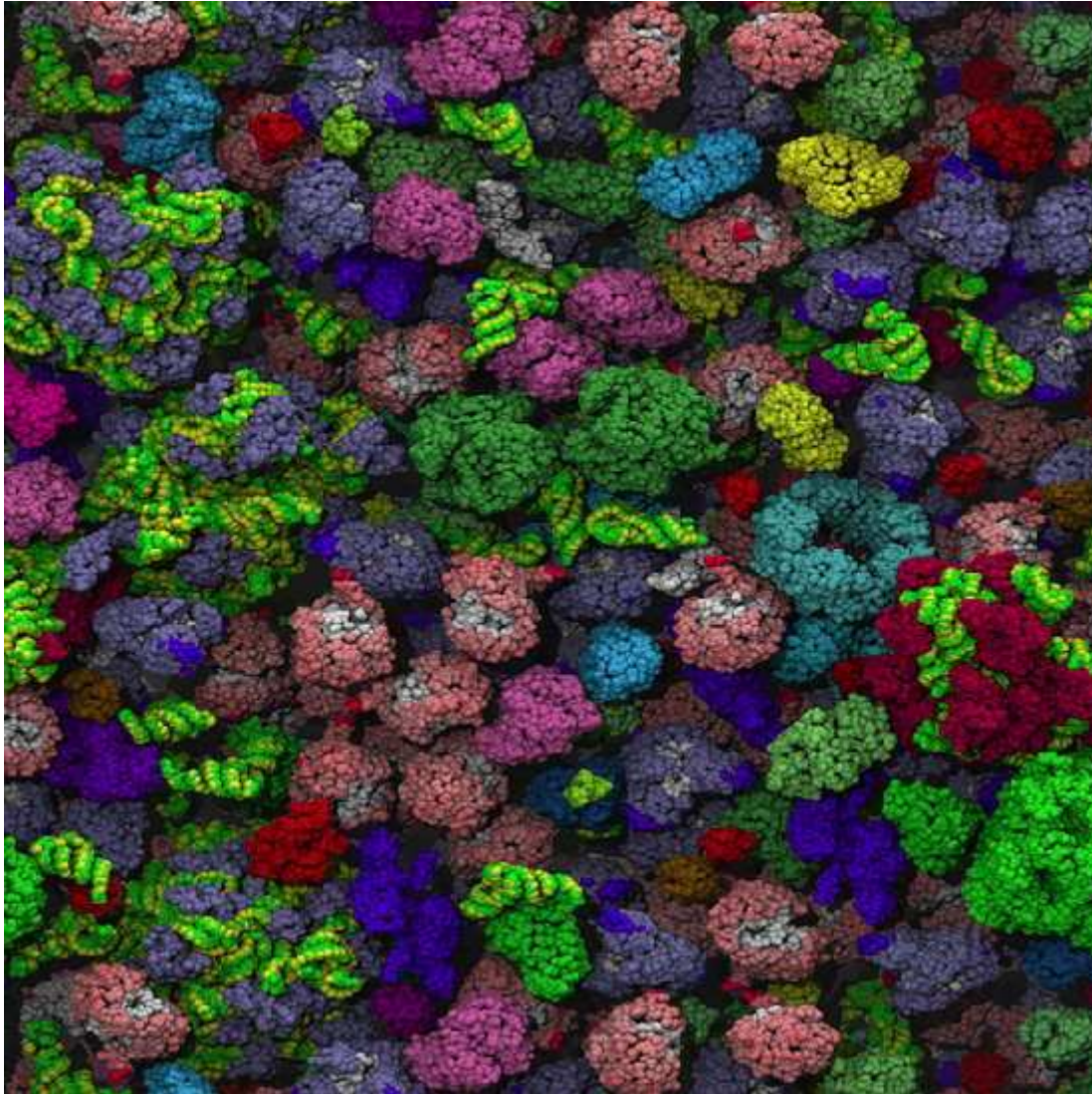
LCLS:XPP Beamtime in Dec 2010
L234: Moffat, Graber, Van Thor
L253: Miller, Neutze, Schlichting
L260: Anfinrud



hh-MbCO
Ime Schlichting



Dynamics in biological systems



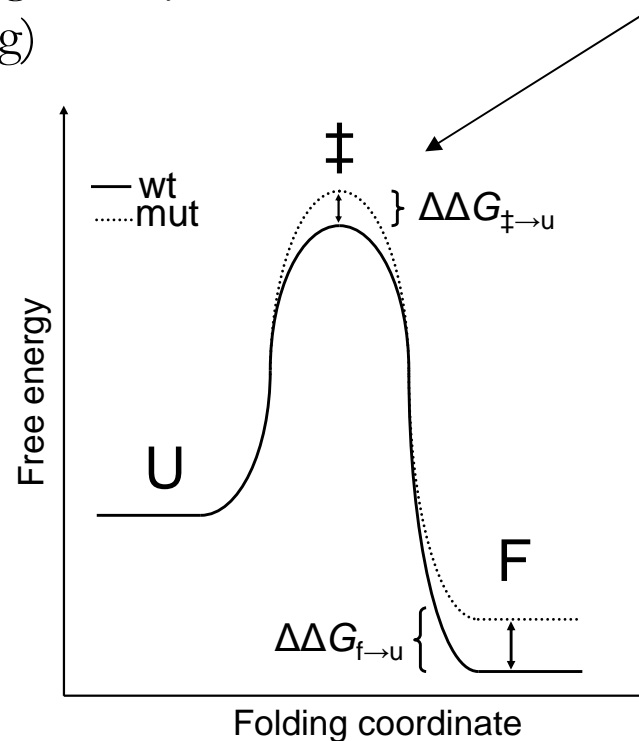
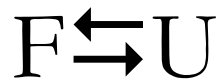
Protein dynamics
(folding/unfolding)

Binding dynamics
(interaction proteomics)

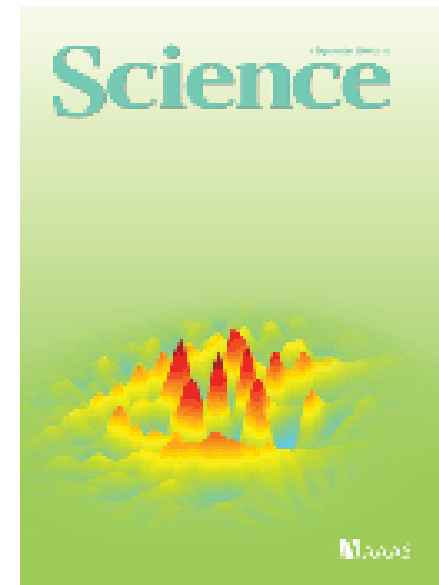
Proteome dynamics
(changes in disease state)
(changes with age!)

Time scales in protein and proteome dynamics

Protein dynamics generally ms
(folding/unfolding)



Barrier crossing where
ultra fast motions
ps-fs might be important
(quantum effects?)

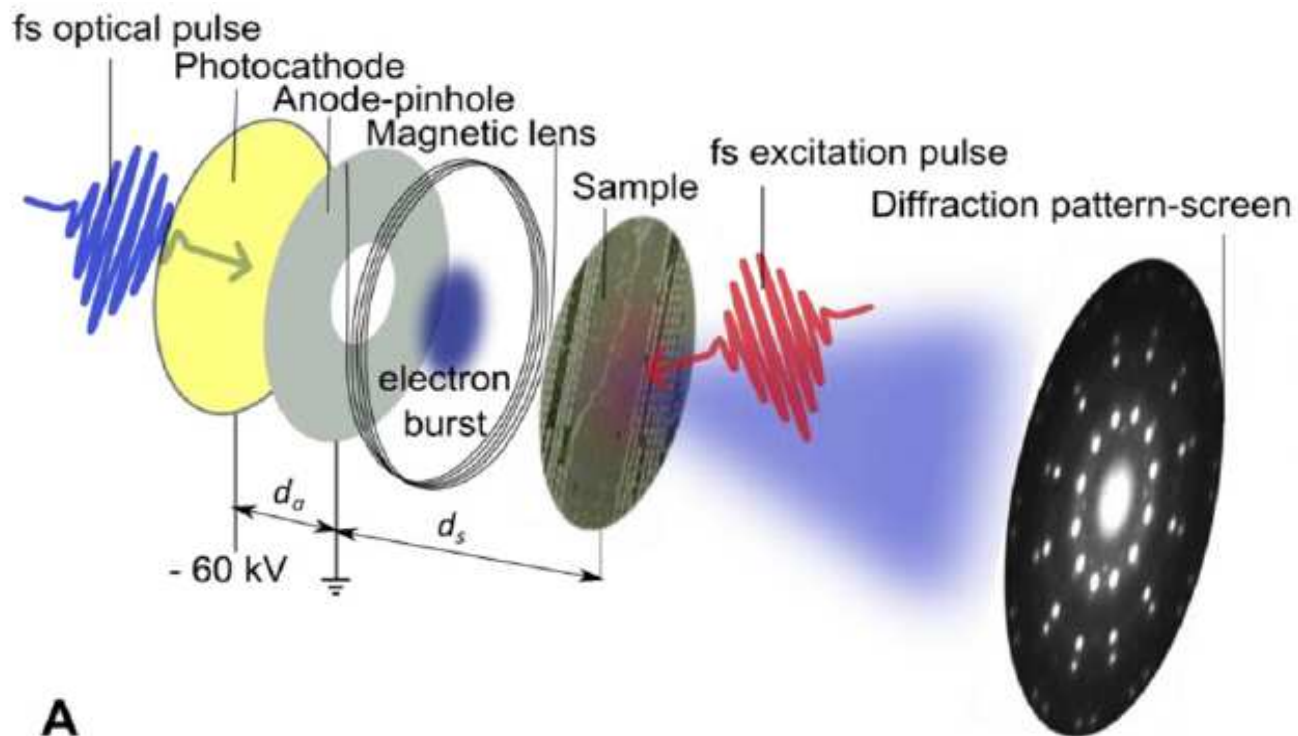
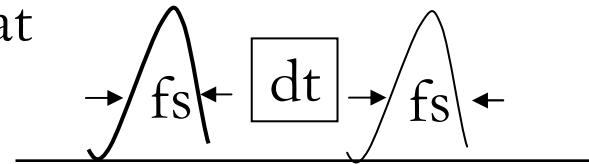


Coherent control of
Rhodopsin isomerization

Proteome dynamics
(hours to months)

Ultrafast dynamics

My introduction to ultrafast science
Complete sampling of structure state at
time point



A

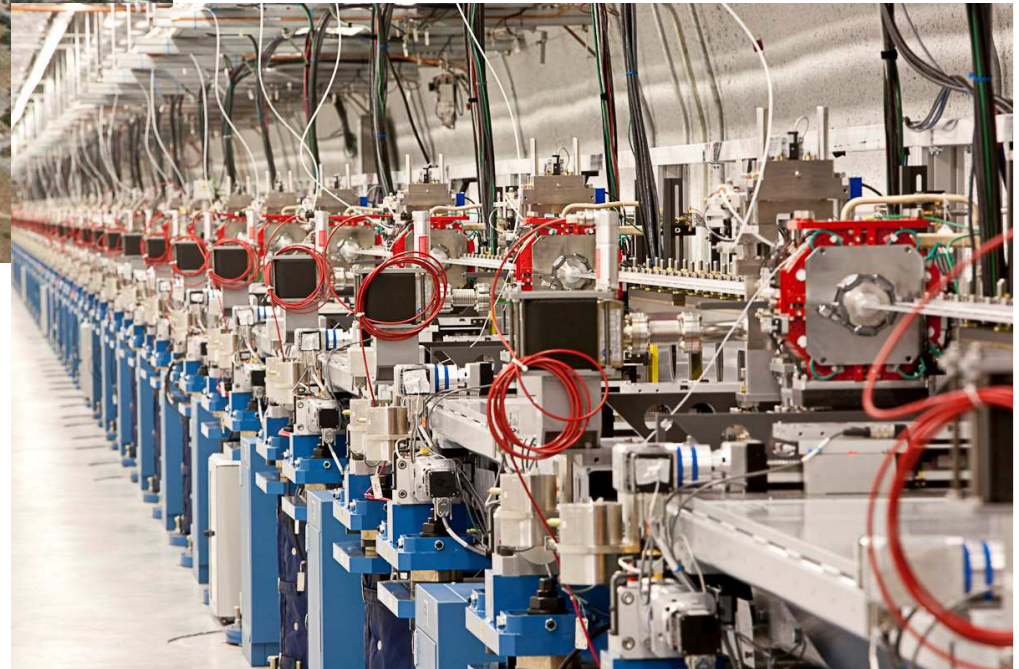
Can do pump probe for time resolved studies

Free Electron Lasers (FELs) produce fs pulses of coherent x-rays



LCLS-SLAC Stanford

Undulator hall

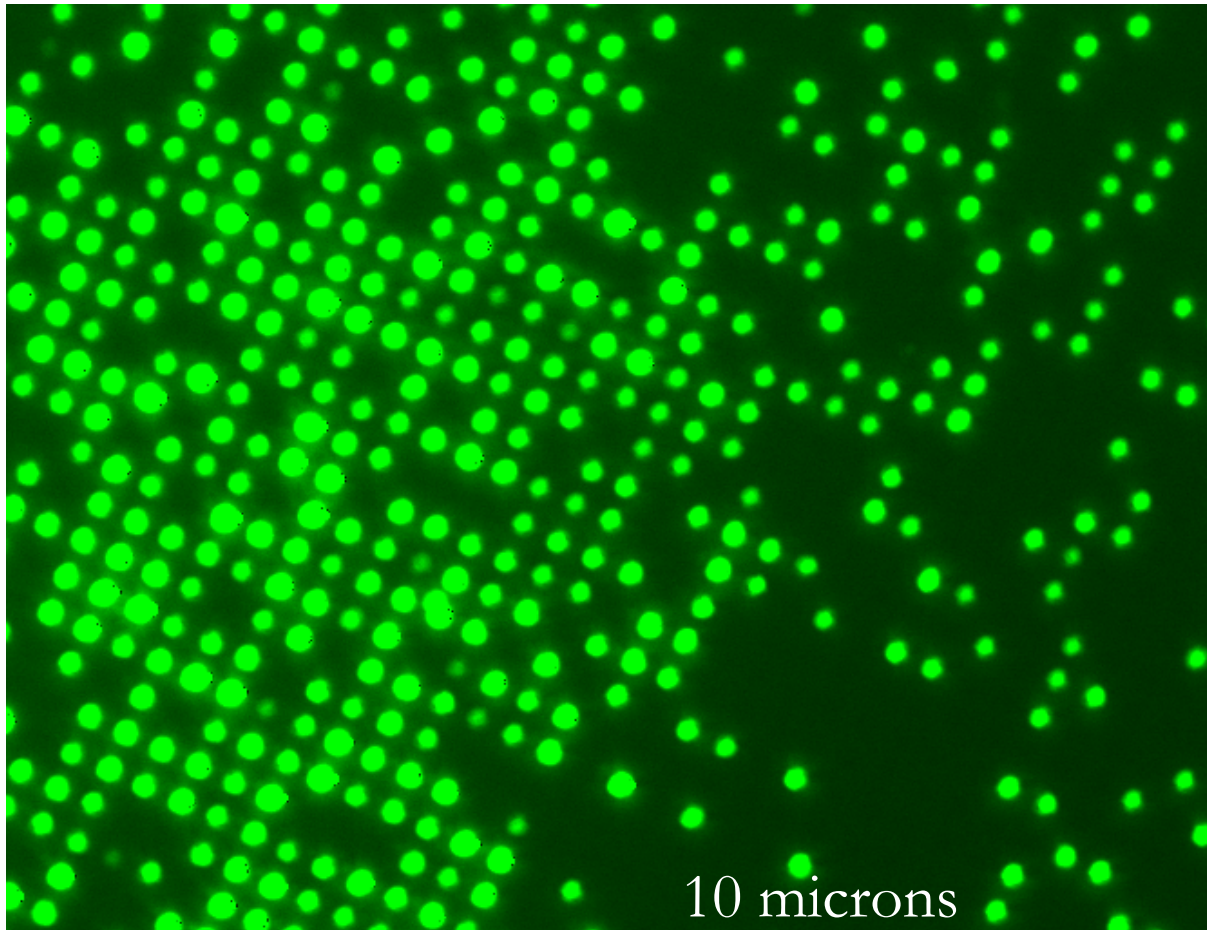


The problem

Ultrafast science generally requires irreversible sampling of the system dynamics

Develop skills for high throughput sampling of analytes (crystals) under study

Dynamics studies invoke another level of complexity;
 t_0 background



Crystals in prescribed positions

Crystals are happy

Translation stage, detector read out are fast

Sampling efficiency is improved

This idea is suitable for dynamics because it allows t_0 diffraction orders to be recorded.

How to assemble this array?-what support material if recording in transmission

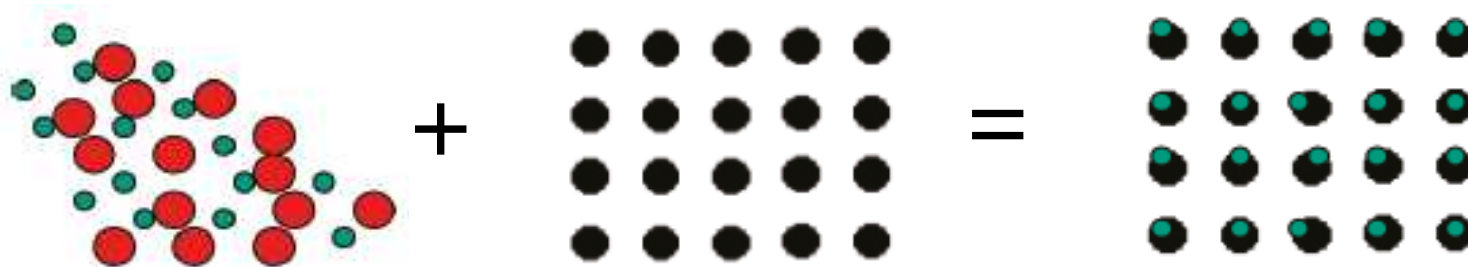
Assembly of the array

Thought experiments:

Grow crystals *in situ* and diffract

Position crystals in prescribed positions using robotics

Design a `smart` surface to fish out desired crystals from a suspension

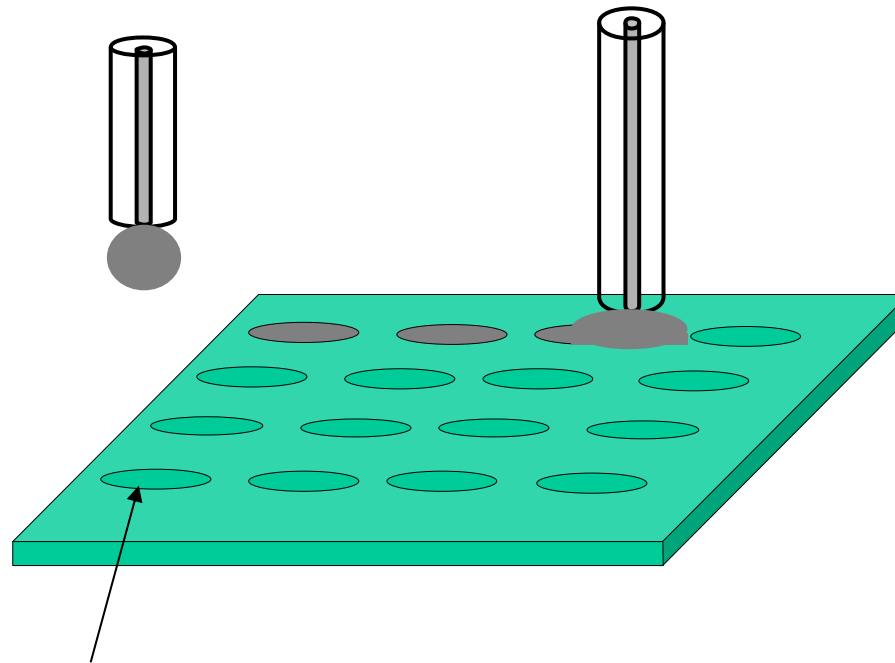


hydrophilic



hydrophobic

Enhancing the liquid pinning potential

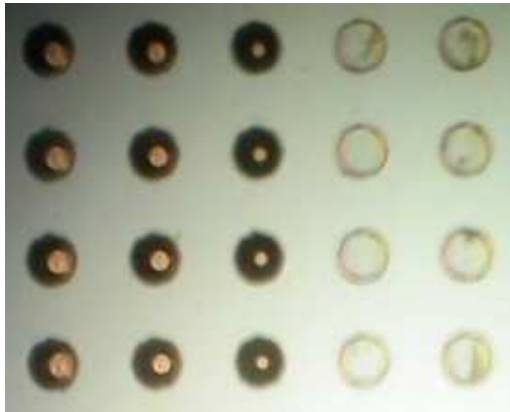


Stabilized contacts for analyte

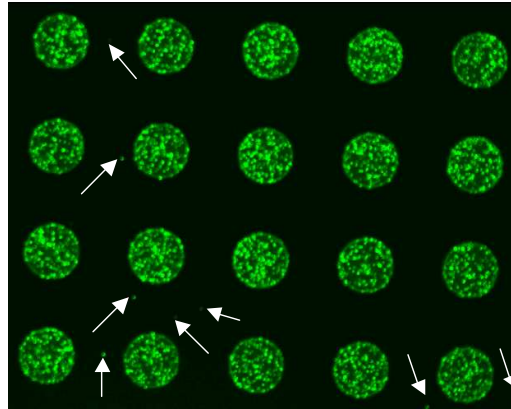


Wetting is very specific

A

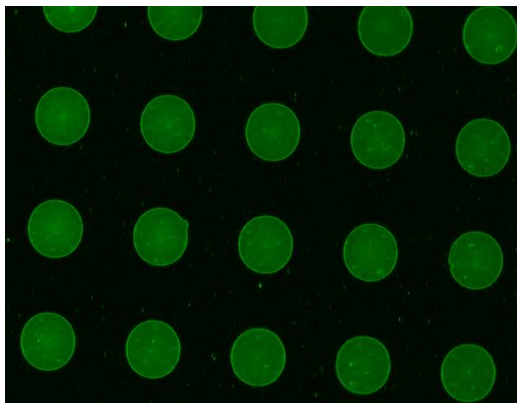


C



B

↑
↑
Empty wells



A: water

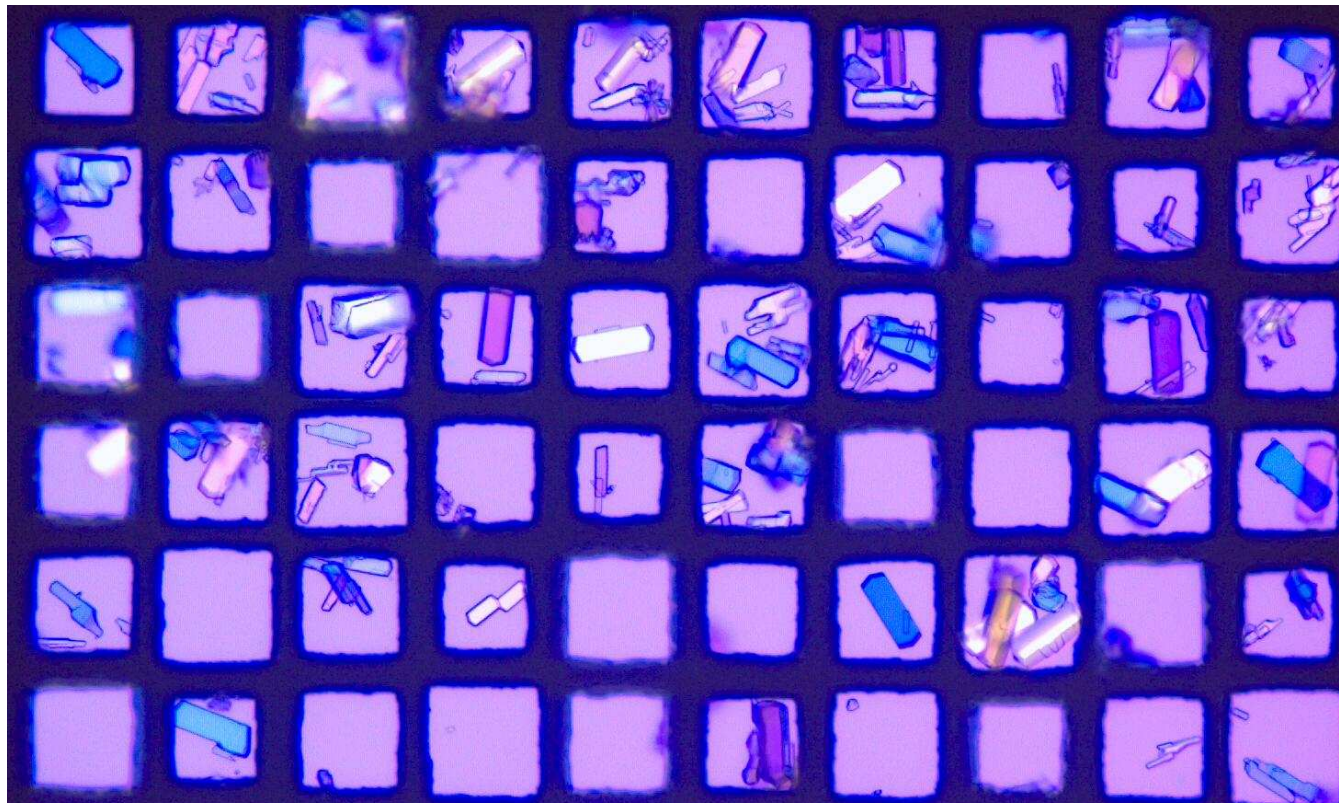
B: Qdot solution. Intensities are identical

C: $\sim 3 \mu\text{m}$ beads suspension. 0.1% nonspecific wetting.

Aspect ratio of 20

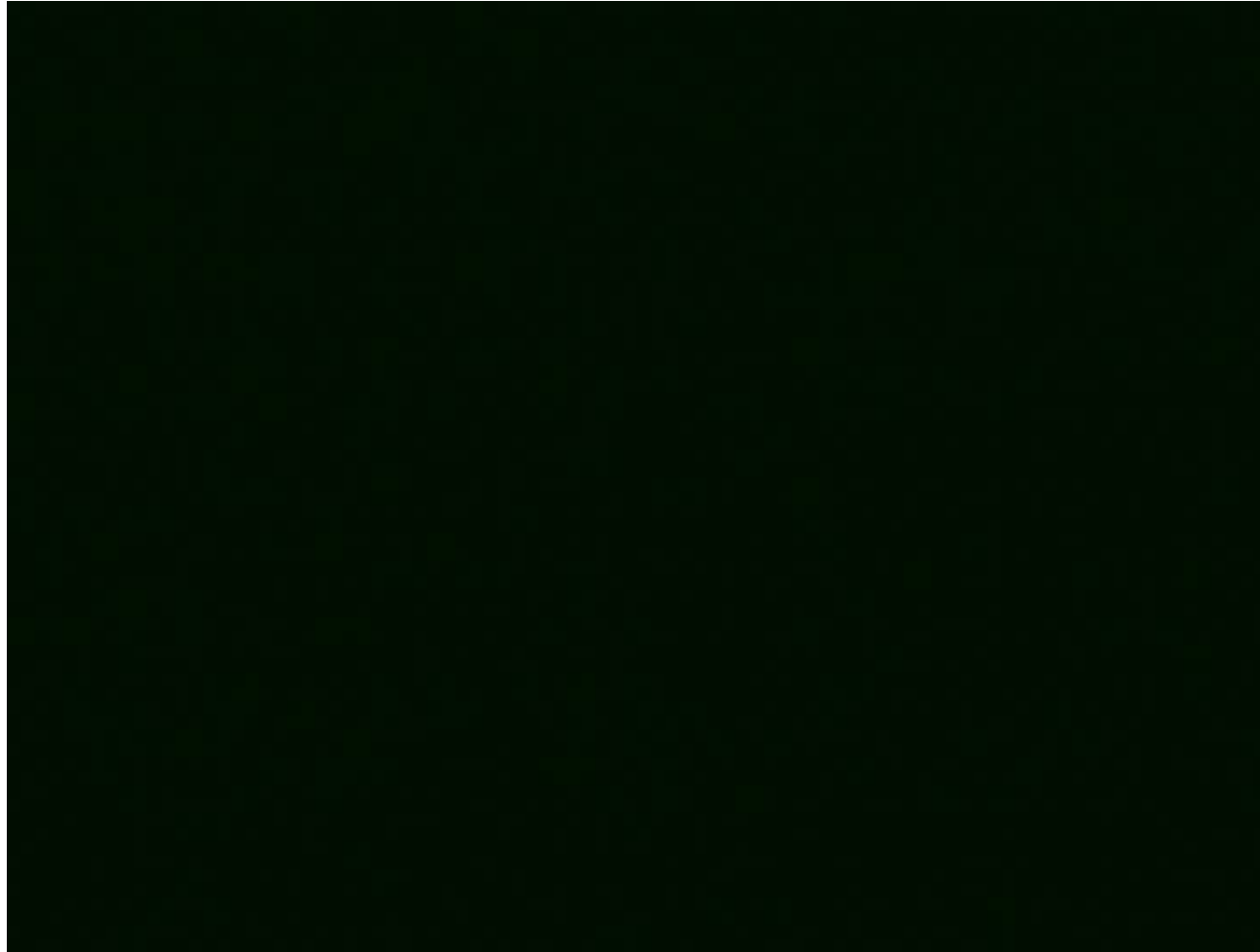
Substrate is silicon (etched by Reactive Ion Etching; F^- plasma)

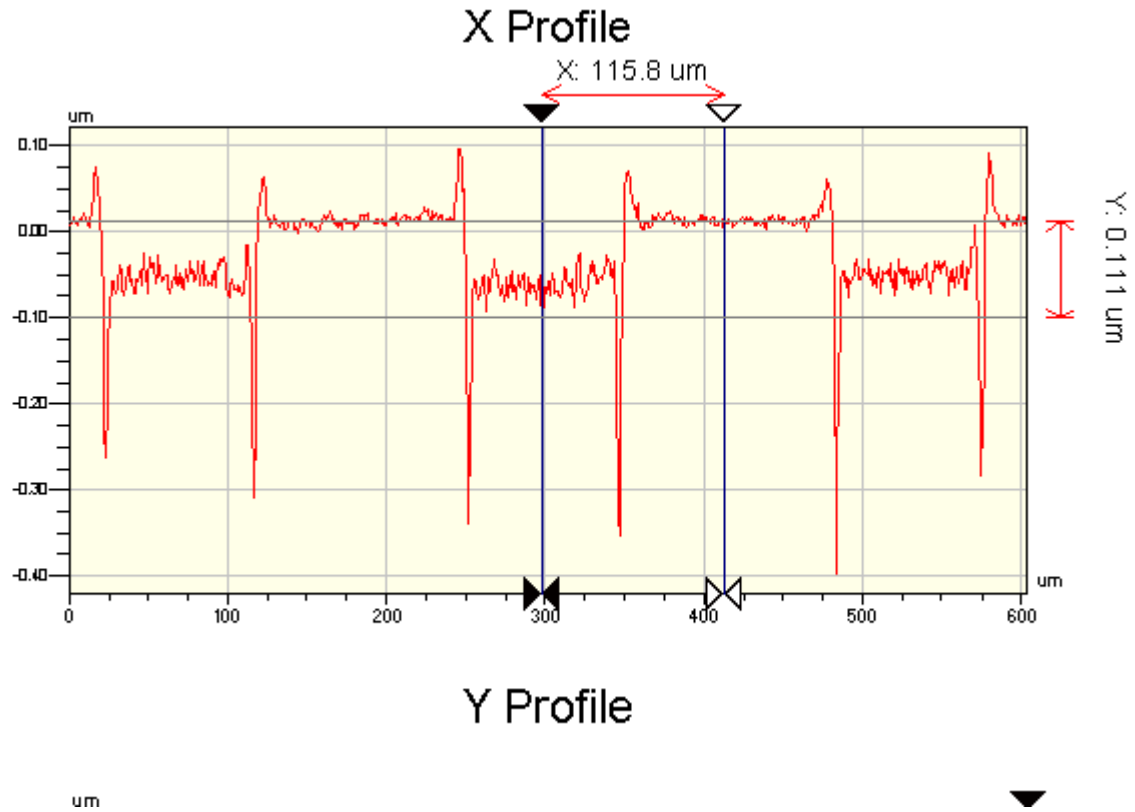
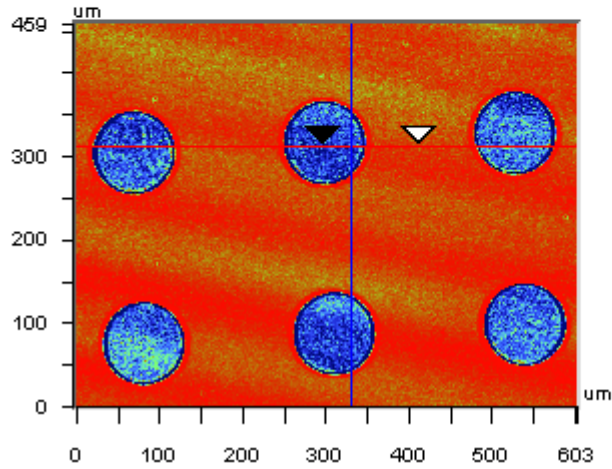
The idea is to have the liquid
localization self assemble the crystal
array



50 micron lysozyme crystals

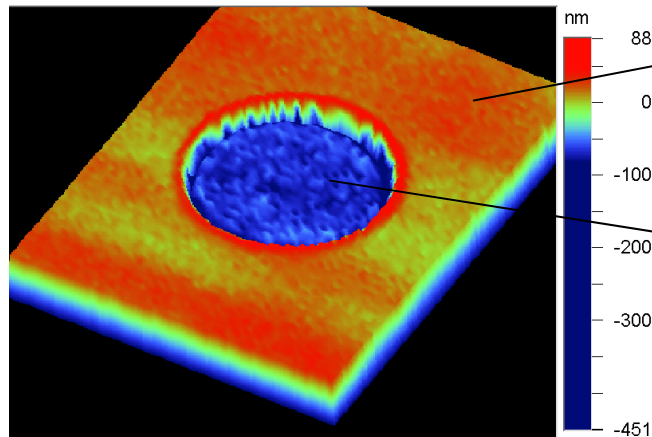
Enhancing liquid pinning potential
results in self assembly





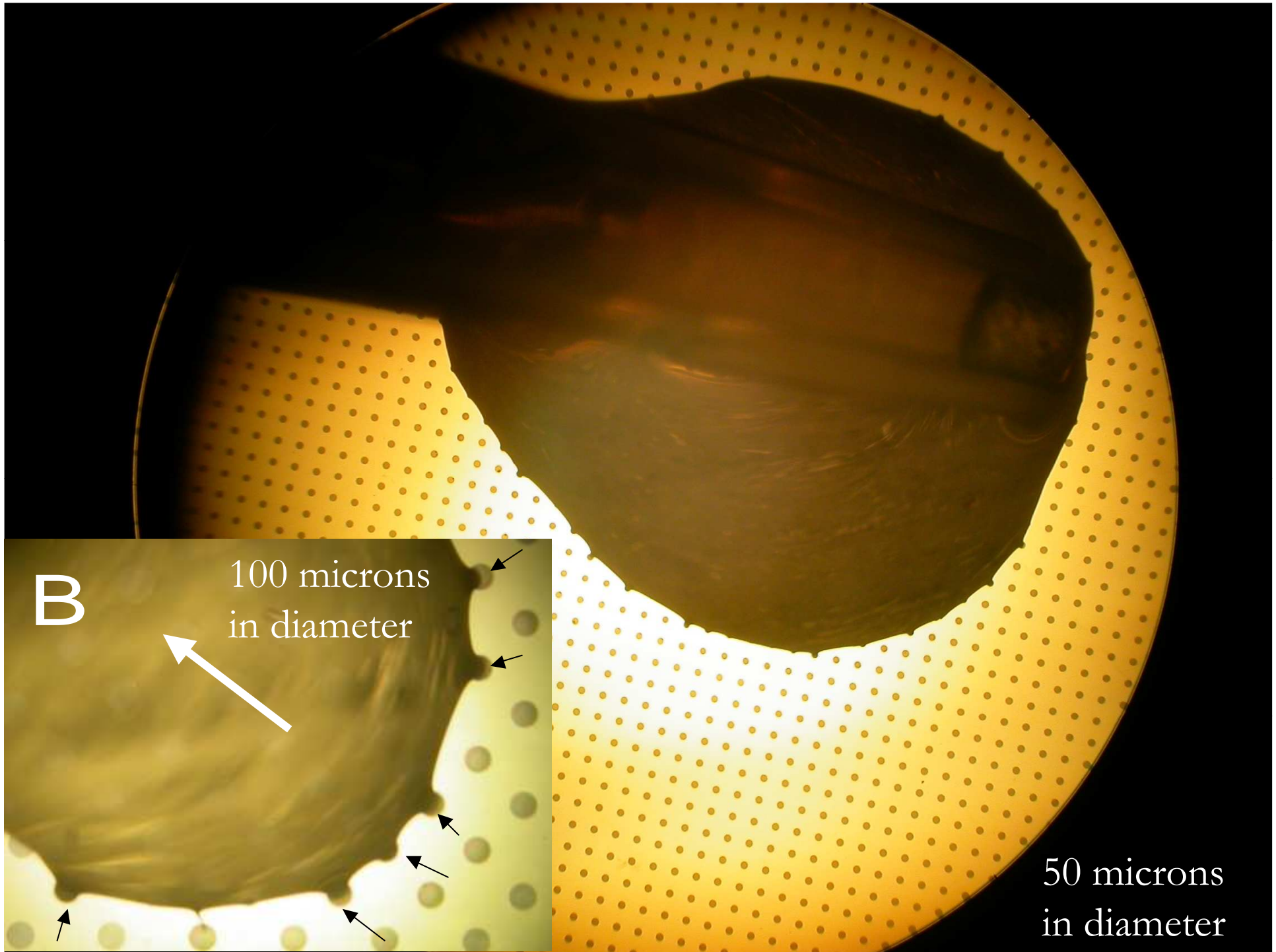
Silicon surface (native oxide) with 80nm silicon nitride

Plasma etched



hydrophobic
(nitride)

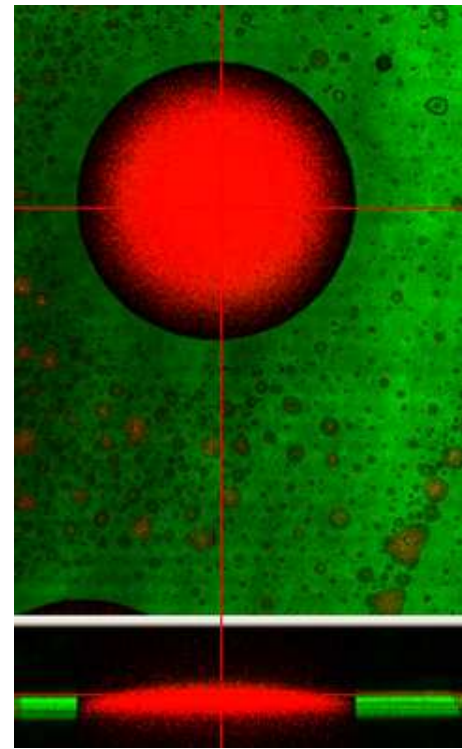
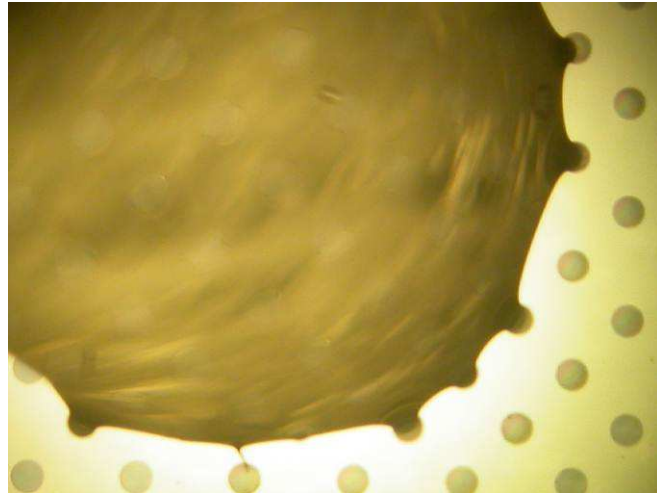
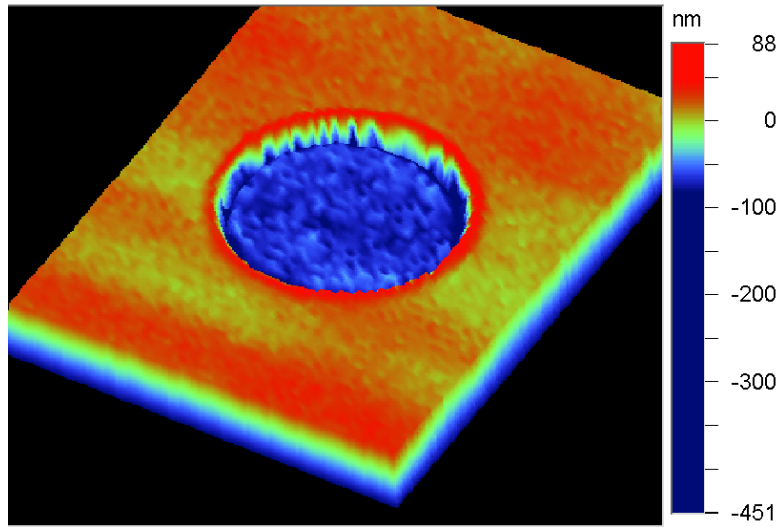
hydrophilic
(oxide)



50 microns
in diameter

B

100 microns
in diameter

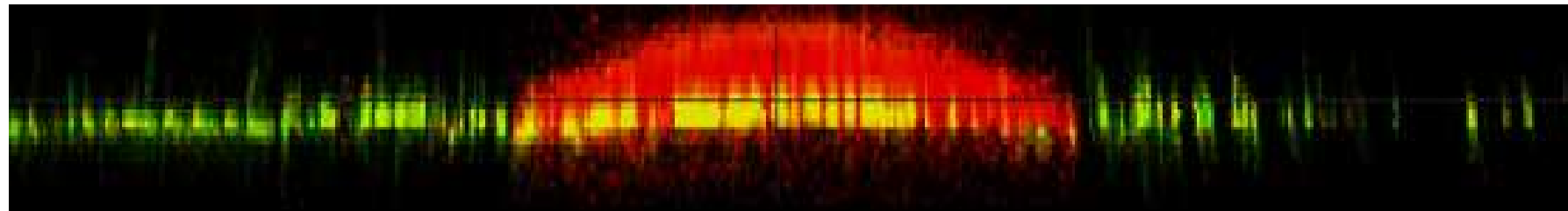


Laser scatter, 543

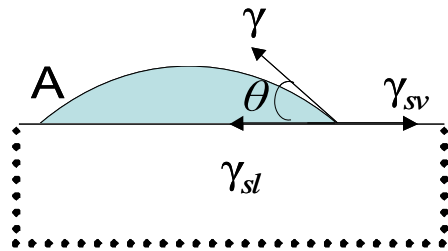
Rhodamine fluorescence, filter cube

Film thickness = 3 microns

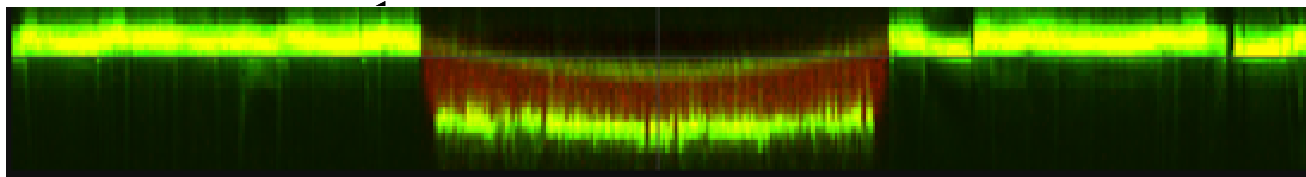
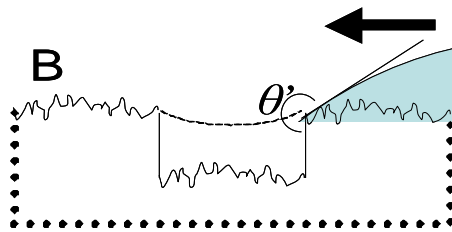
Well diameter = 100 microns



Can make the wells deeper (carrying larger crystals)



Contact line instability and wells with sharp walls allow consistent volumes to be captured

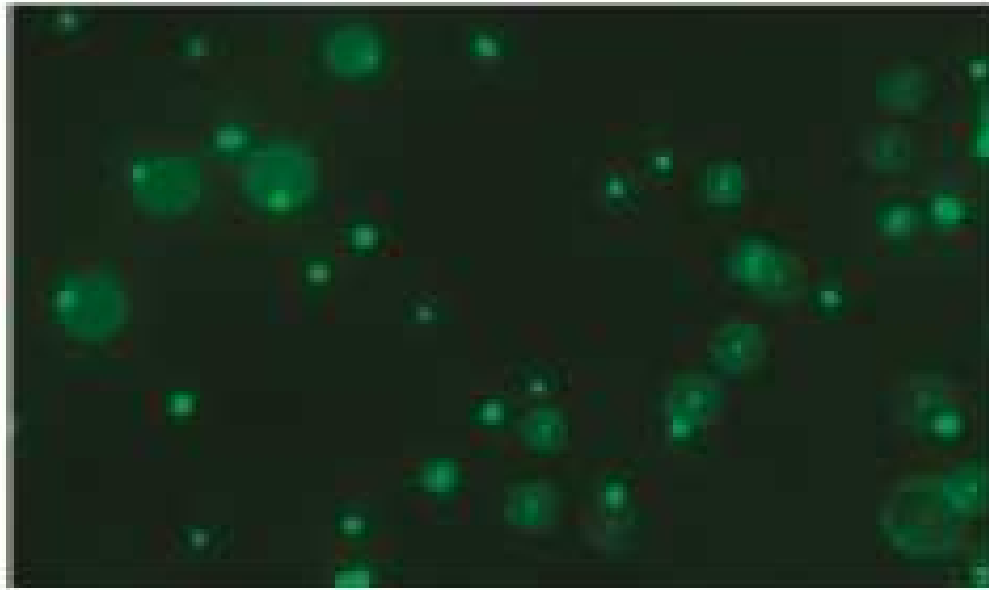


Aspect ratio
10
200 micron
diameter

Laser scatter, 543

Rhodamine fluorescence, filter cube

Characterization of capture by beads carrying FITC label

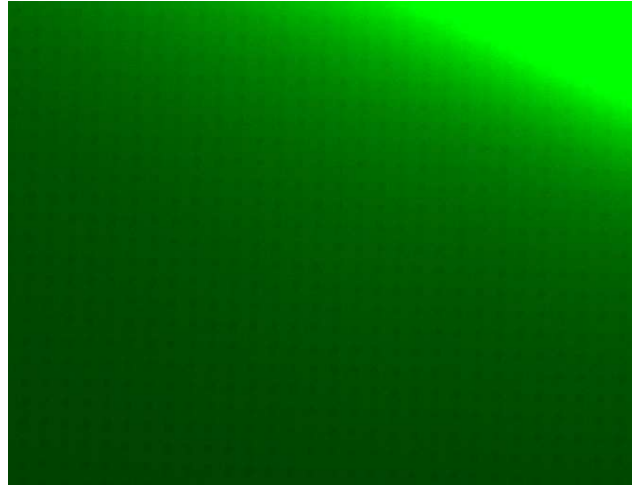


Mixture

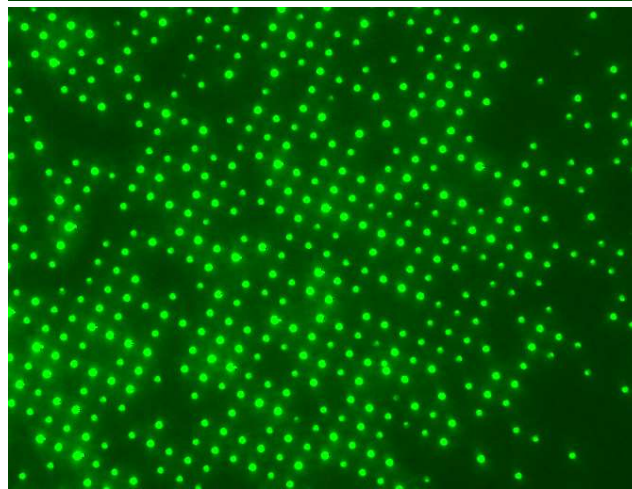
Varying sizes, densities, available

Can make the wells smaller (carrying smaller crystals)

Chip with
microwells

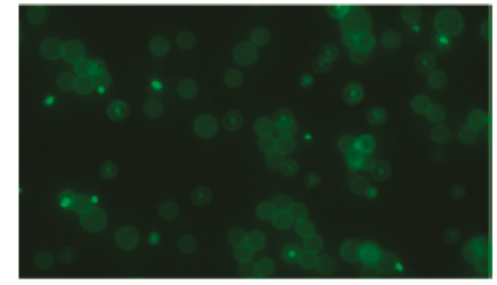
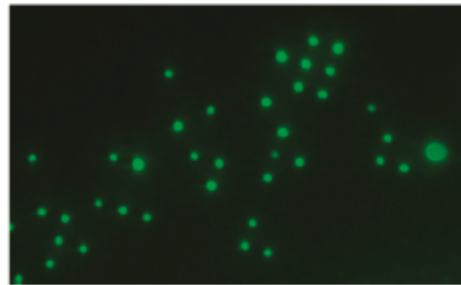
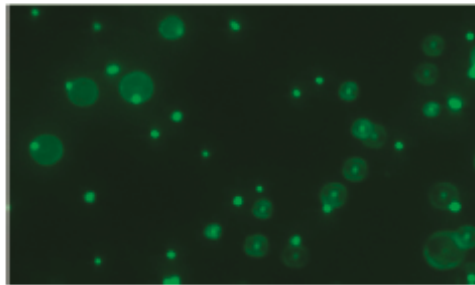
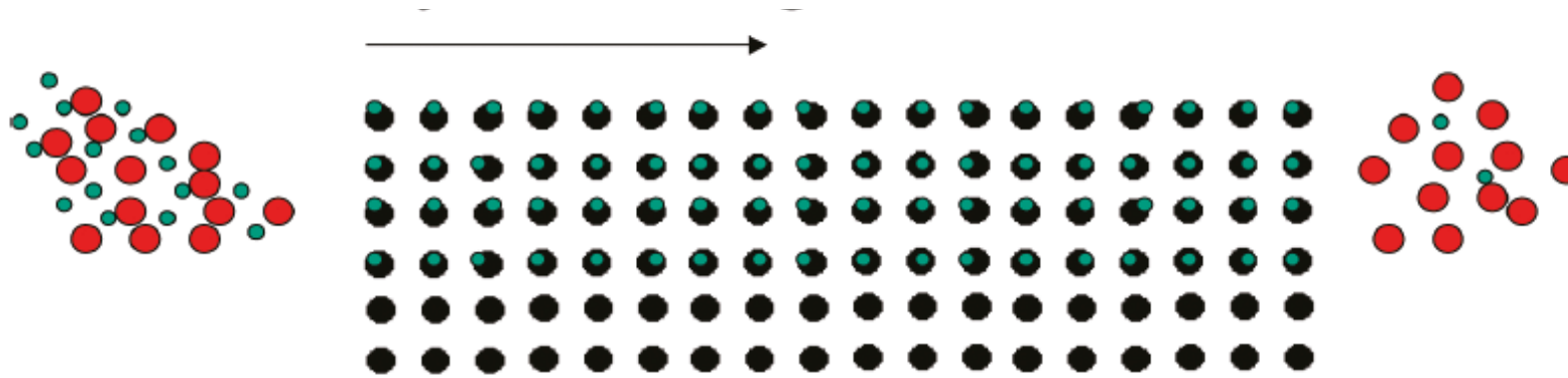


Chip filled
with beads

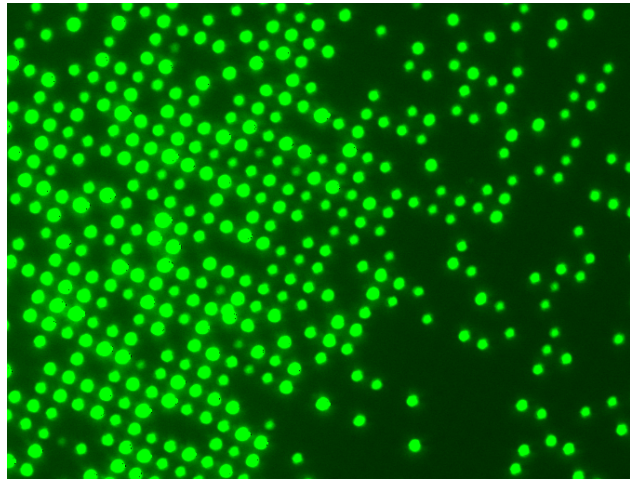


4 micron wells, beads are 2.9 micron

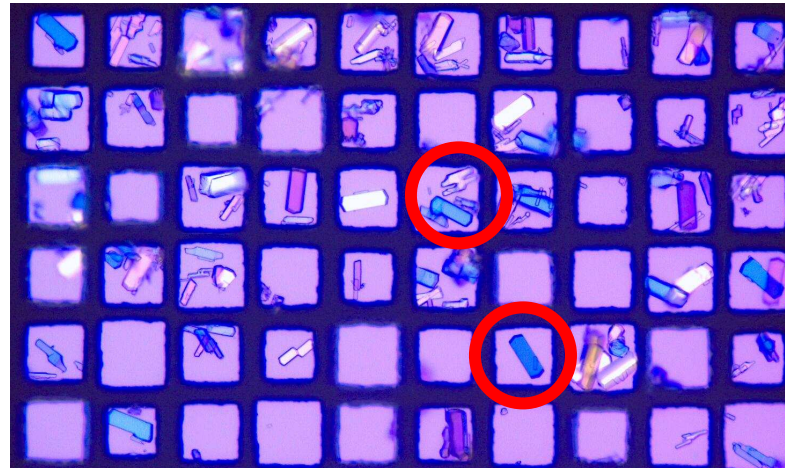
Size exclusion is available



Can this be adapted to crystals?



well size \sim crystal size



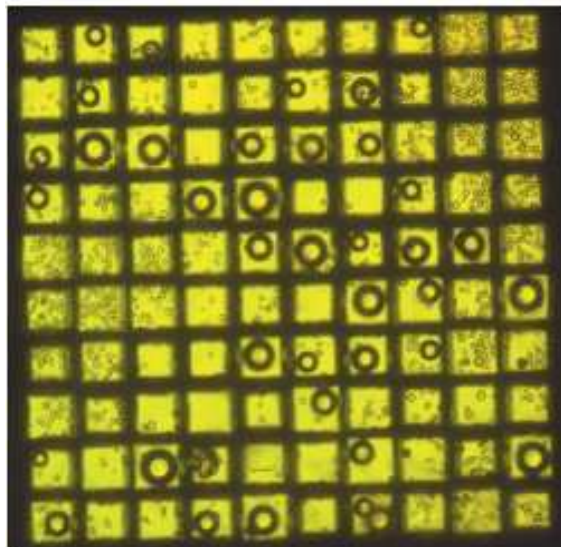
In adapting the scheme to crystals

- (I) Buoyancy is an issue
- (II) Beads are homogeneous in size; crystals may not be
- (III) Beads are suspended in low salt; evaporation forms salt crystals
- (IV) Crystal morphologies could be complicating; do they 'roll' or stick to surface?
- (V) Interactions with the surface may result in preferred orientations that can limit sampling of reciprocal space
- (VI) Solid support should have small background (exposure in transmission)

What is needed

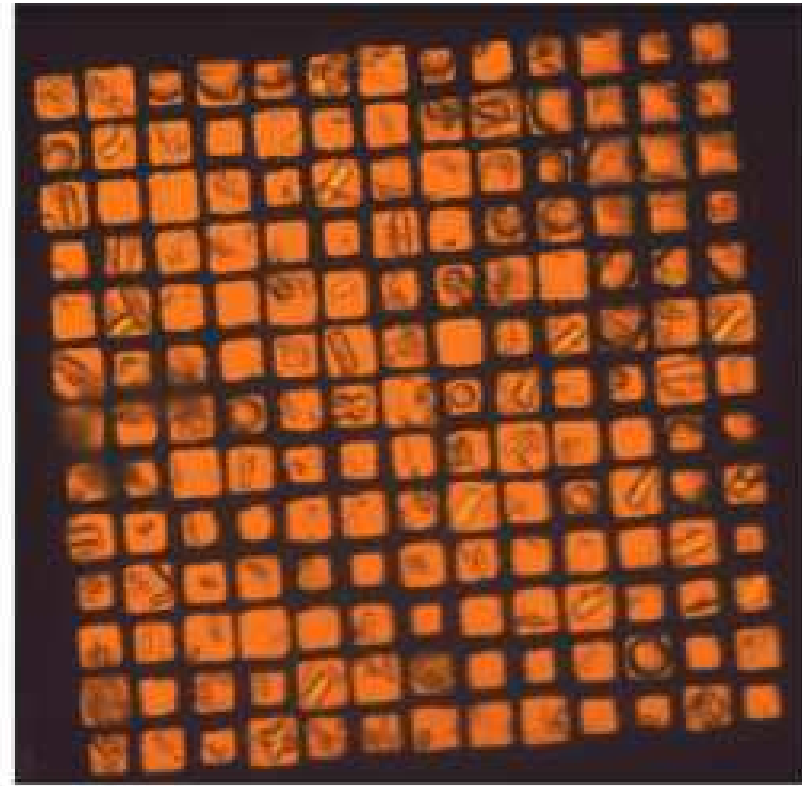
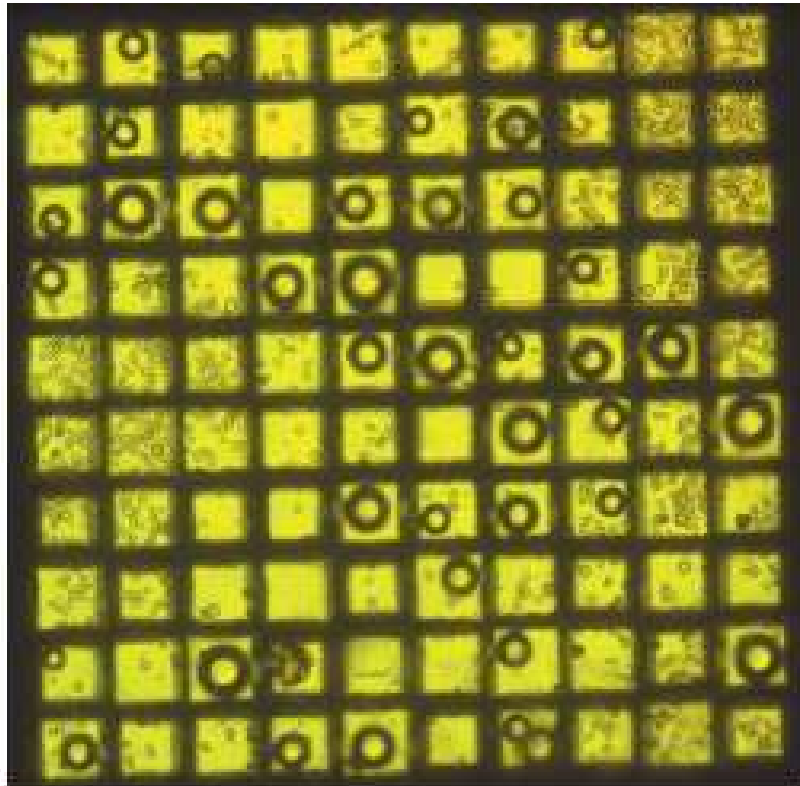
- (I) A support transparent to x-rays (low background)
- (II) A surface that collects little water (reduce absorption)
- (III) A surface that has roughness to induce some randomness to flat crystals

Multiple ways to satisfy these conditions with silicon technology yet as a proof-of-principle we followed another approach



Silicon mesh custom to size of crystals with **polyimide** support sprinkled with glass beads of varying sizes to create roughness

Role of hydrophilicity

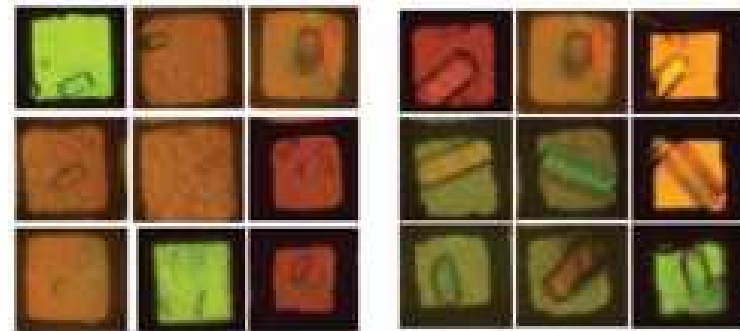
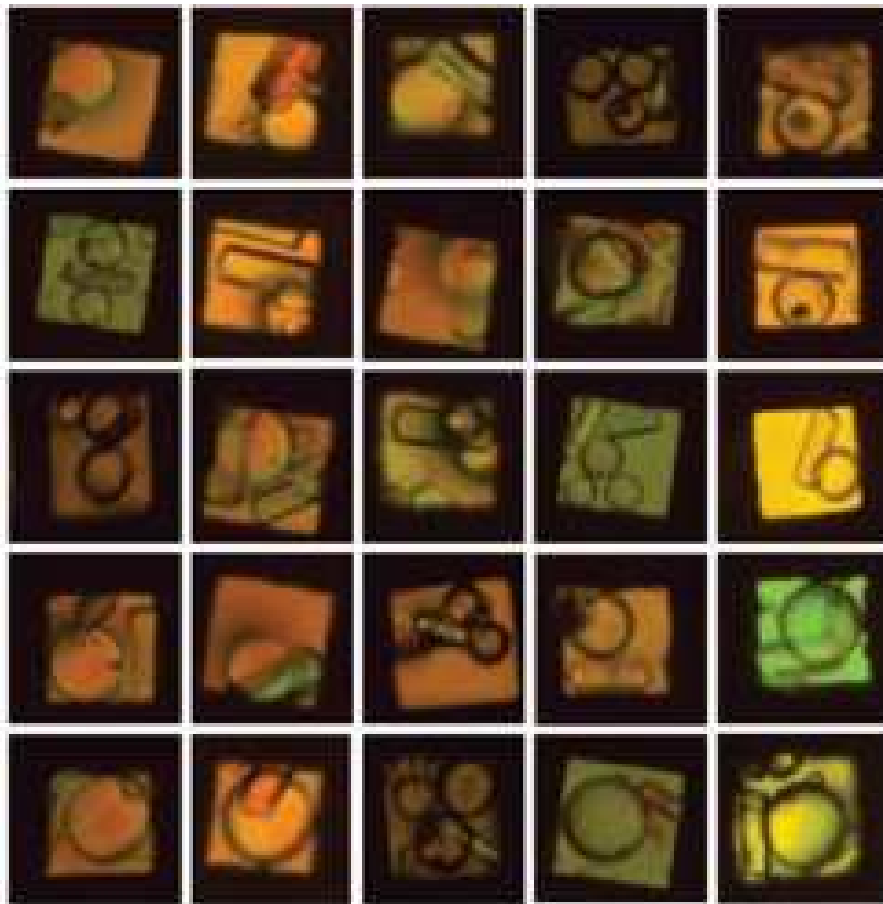


Hydrophilicity of glass on **hydrophobic** polyimide creates pinning for lysozyme storage solution that results in significant single crystals per well

Window size is matched to average crystal size in the batch

Role of surface roughness

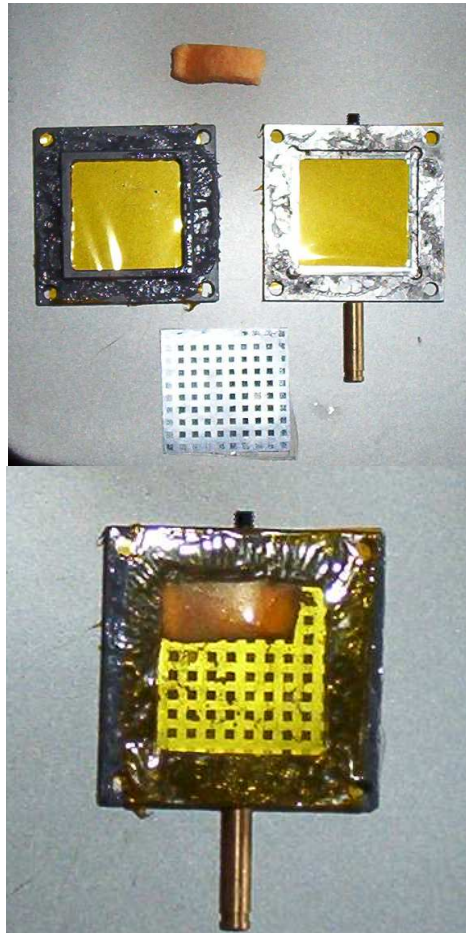
Induces some degree of randomness in crystal orientations



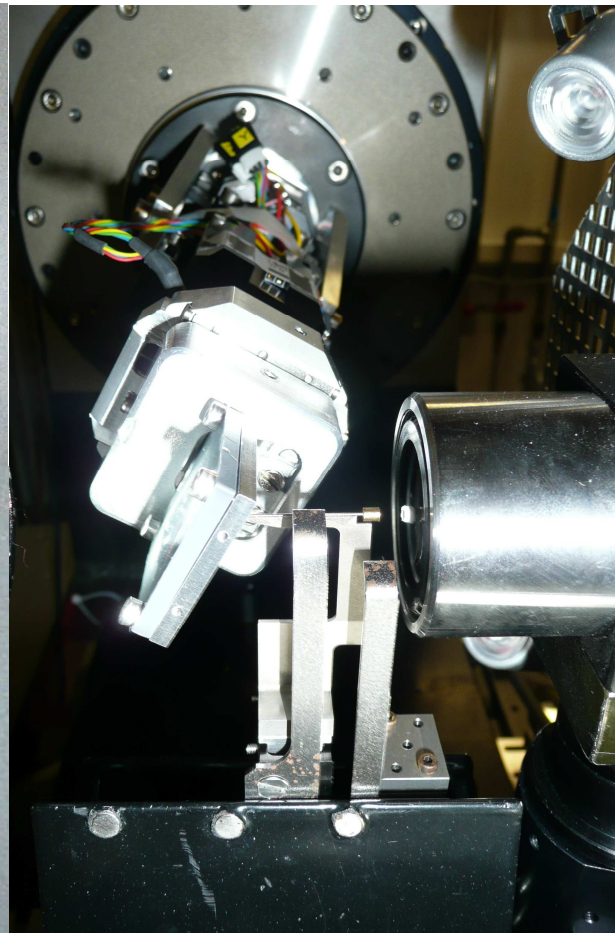
Bead dimensions versus crystal dimensions

Chip holder to satisfy evaporation issues and interfacing

a



b

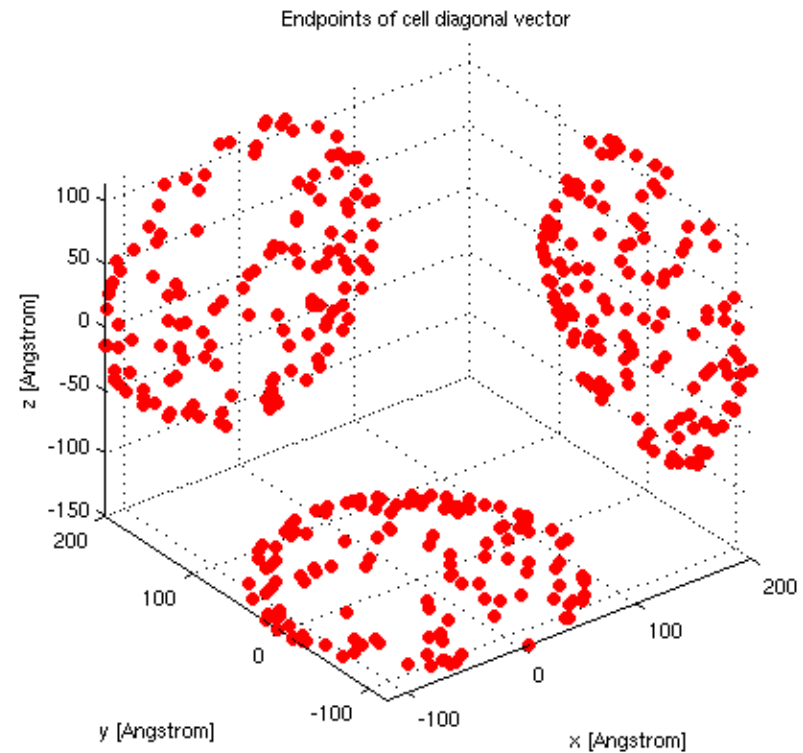
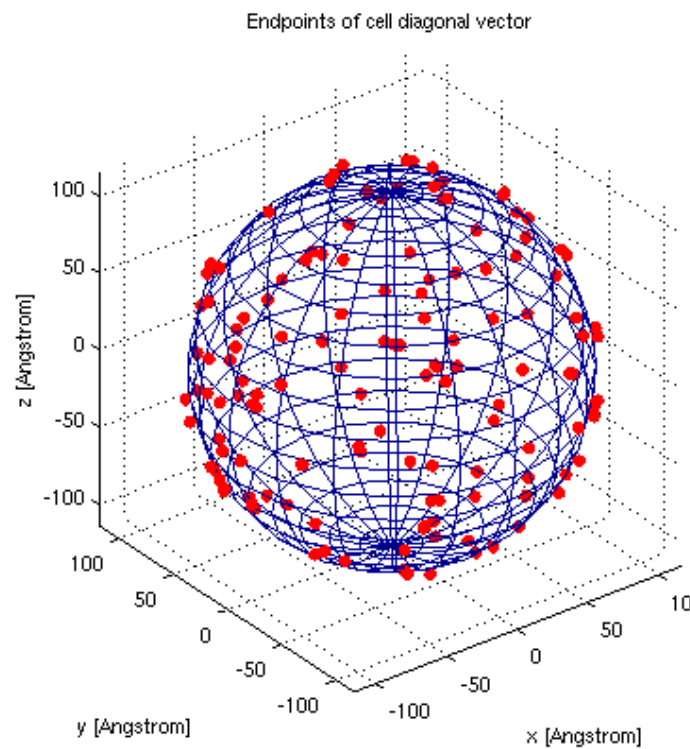


Saturate the environment
With storage solution
vapour pressure

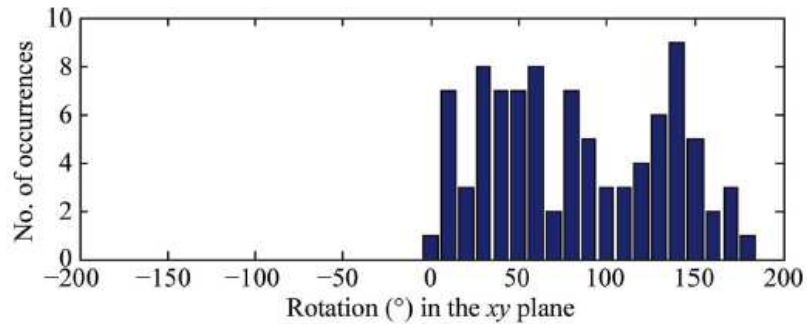
Limited goniometer motion
also underscores the
significance of randomness

Proof-of-principle assessment of crystal orientations

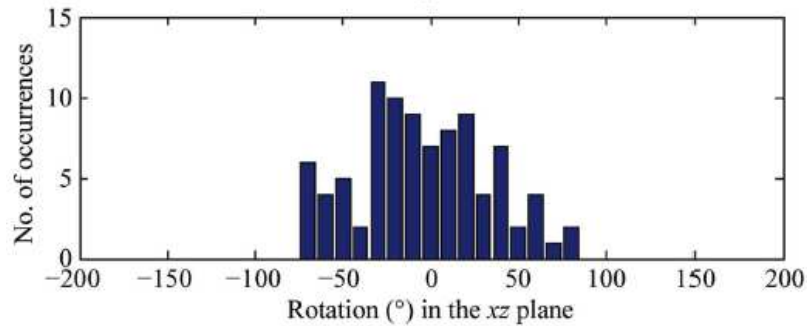
End points of cell diagonal vector



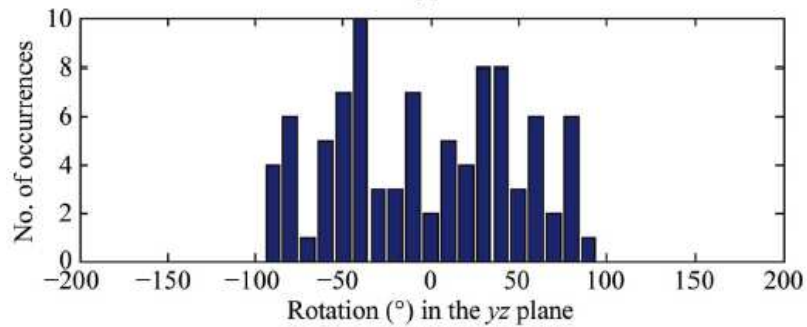
Proof-of-principle assessment of crystal orientations



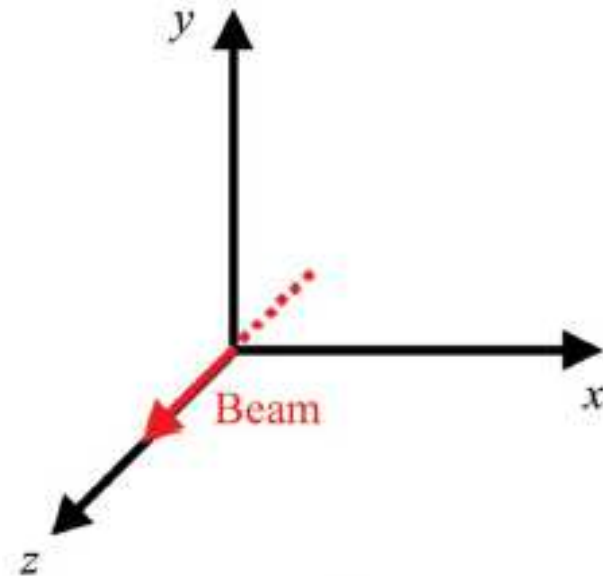
(a)



(b)

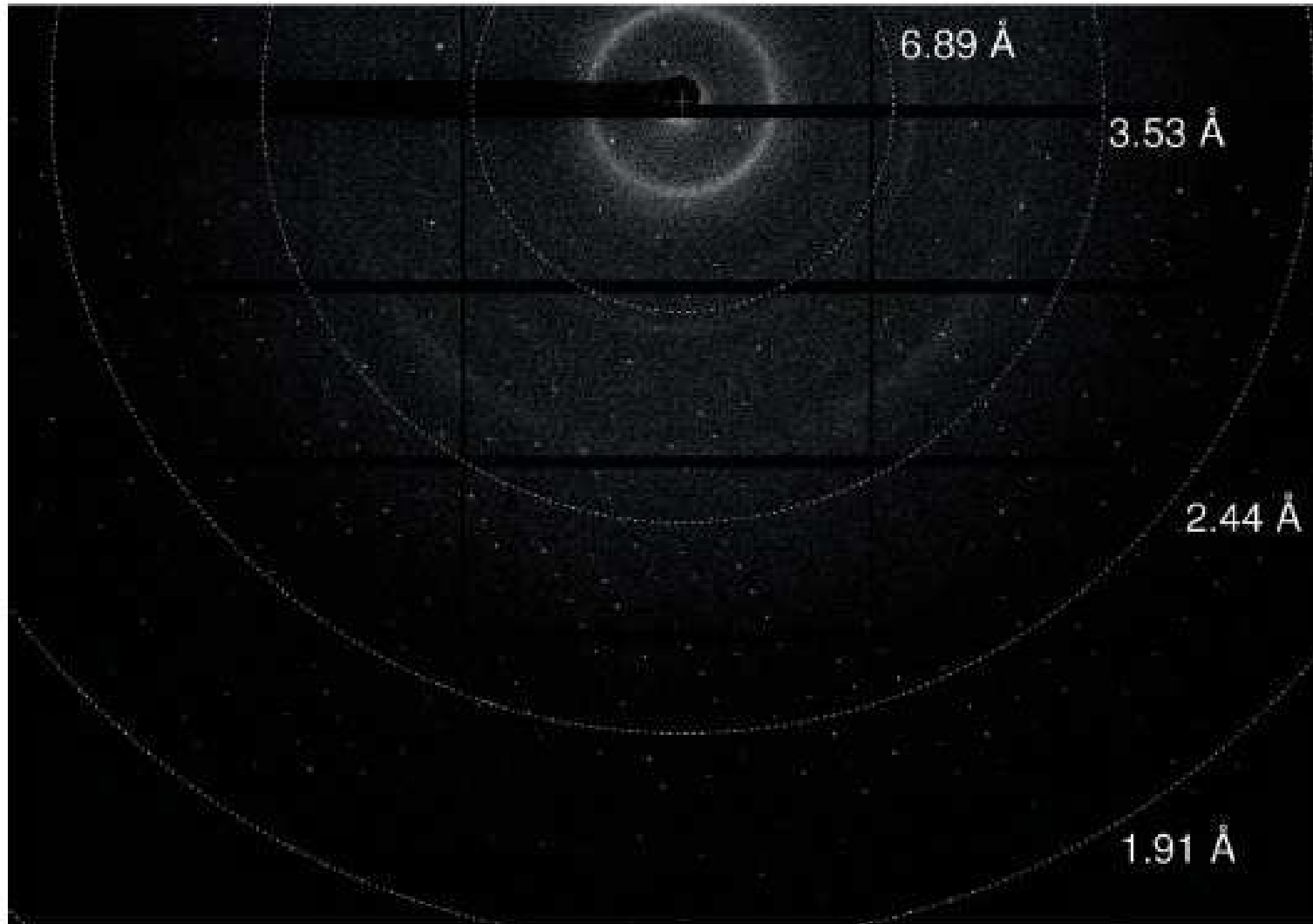


(c)



(d)

Diffraction



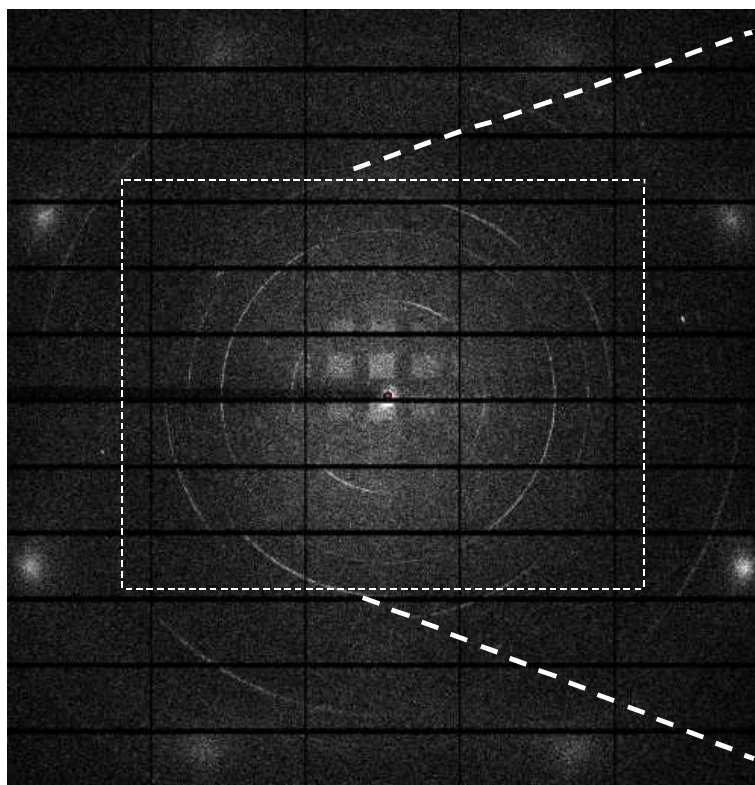
Diffraction statistics

	Ferritin	Lysozyme
Data collection		
Space group	<i>F</i> 432	<i>P</i> 4 ₃ 2 ₁ 2
Unit-cell parameters (Å)	<i>a</i> = <i>b</i> = <i>c</i> = 182.5	<i>a</i> = <i>b</i> = 79.1, <i>c</i> = 38.5
X-ray source	Swiss Light Source, beamline X10SA	Swiss Light Source, beamline X10SA
Wavelength (Å)	1.00	1.00
Resolution (Å)	10–2.5	10–2.3
$R_{\text{merge}}^{\dagger}$	0.13 (0.38)	0.19 (0.31)
$\langle I/\sigma(I) \rangle$	8.0 (3.3)	5.0 (2.8)
Completeness (%)	98.6 (98.8)	92.0 (91.1)
Multiplicity	4.2 (4.4)	3.4 (3.1)
Refinement		
Resolution (Å)	41.88–2.5	69–2.3
$R_{\text{work}}/R_{\text{free}}$	0.19/0.24	0.217/0.256
No. of atoms		
Protein	1377	1001
Ligand/ion	1 [Cd ²⁺]	1 [Cl ⁻]
Water	44	29
<i>B</i> factors (Å ²)		
Protein	23.9	29.2
Ligand/ion	22.4	29.4
Water	25.3	27.7
R.m.s. deviations		
Bond lengths (Å)	0.01	0.01
Bond angles (°)	1.12	0.94

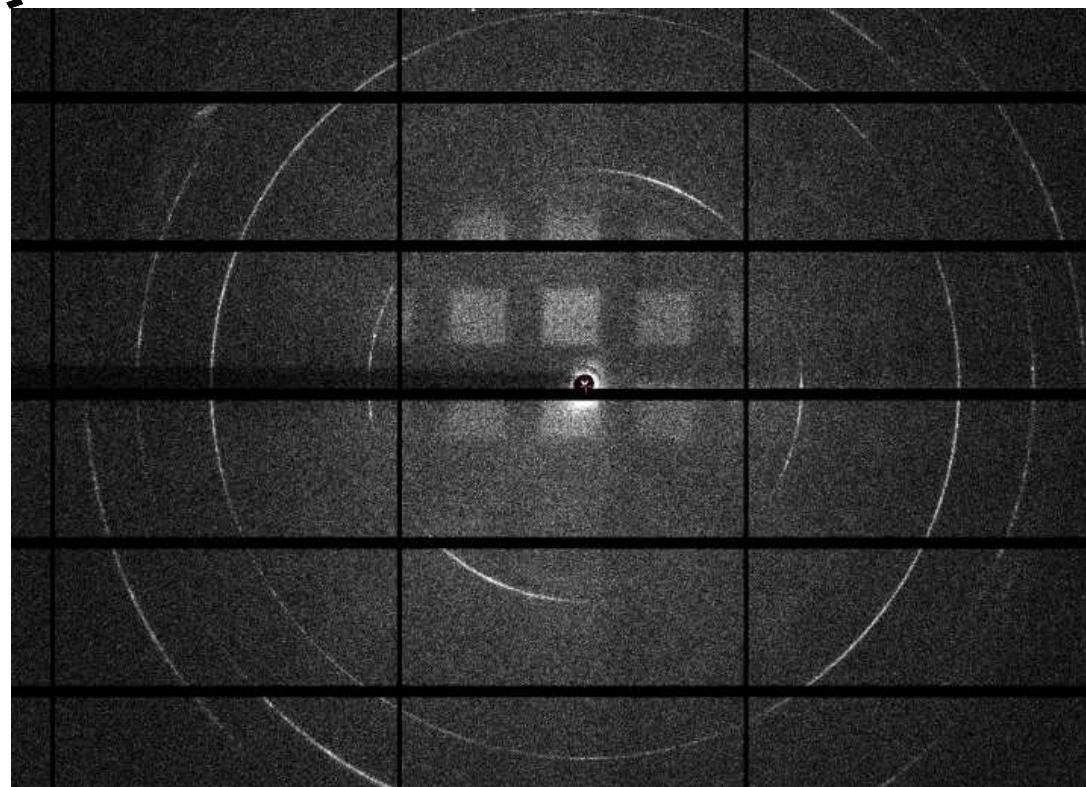
[†] $R_{\text{merge}} = \frac{\sum_{hkl} \sum_i |I_i(hkl) - \langle I(hkl) \rangle|}{\sum_{hkl} \sum_i I_i(hkl)}$.

Collimating is necessary

a



b



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Cytoplasmic domain of
Yersinia pestis YscD

Epithelial adhesion 1 from
human pathogen *C. glabrata*

Phc4 5-adenosyl-*homo-*
cysteine hydrolase complex

DNA (6-4) photoproduct
dT(6-4)T in complex
with FtsI fragment

E. cerevisiae adenosine
phosphorylase

S. castellata 5'-deoxy-3'-
methylthioadenosine
phosphorylase II

Ca²⁺-bound O-methyl-
isoureaase inhibitor complex

Grid-attached web service
for low-molecular refinement

Effect of cryoprotectants
on human blood group A
and B glycosyl transferases

CYP110D1 from
N. aromaticolorans
DSM12444

Stability of Clostridium
thermocellum enzymes

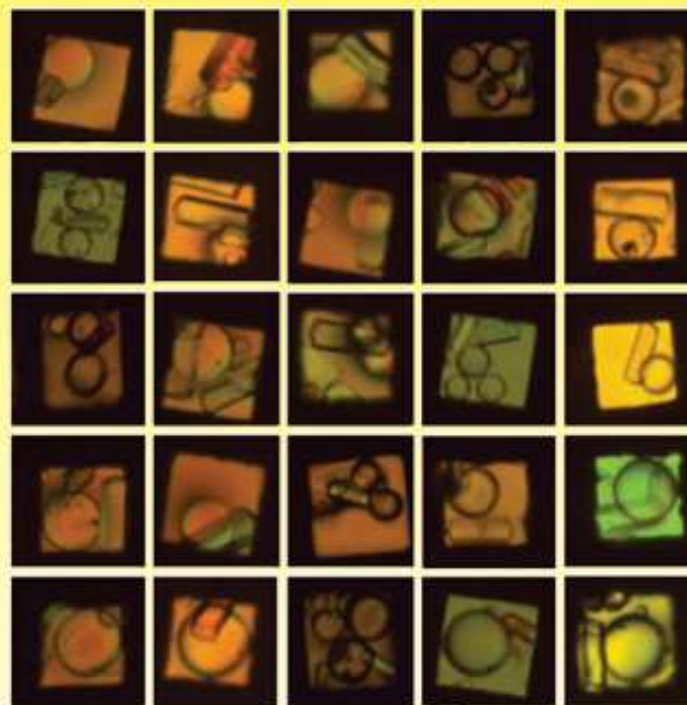
3-hydroxyphosphate
dehydrogenase under
high pressure



Acta Crystallographica Section D

Biological Crystallography

Editors: E. N. Baker and Z. Dauter



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Wiley-Blackwell

Lessons learned

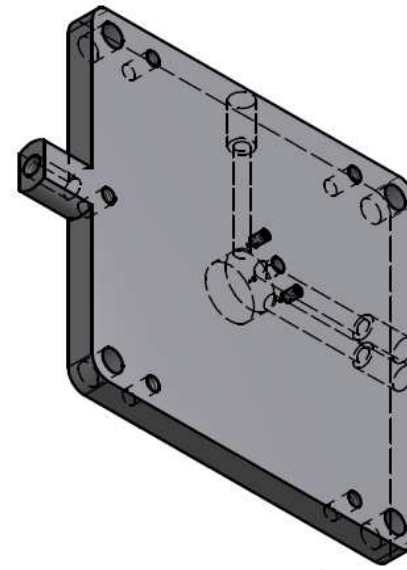
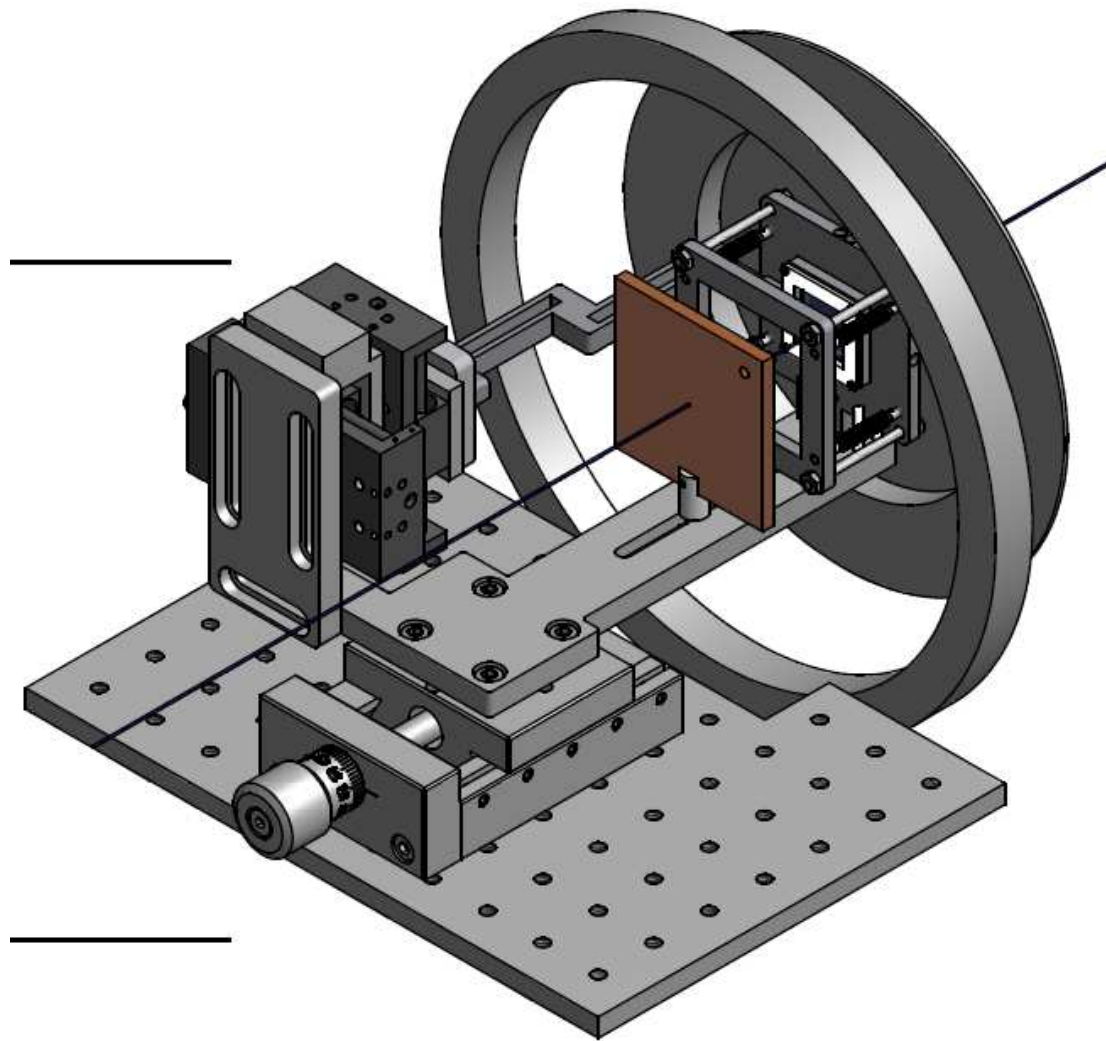
- (I) Chip holder is too bulky
- (II) Beads are strongly absorbing
- (III) There is too much liquid that causes some crystals to swim!

Solutions:

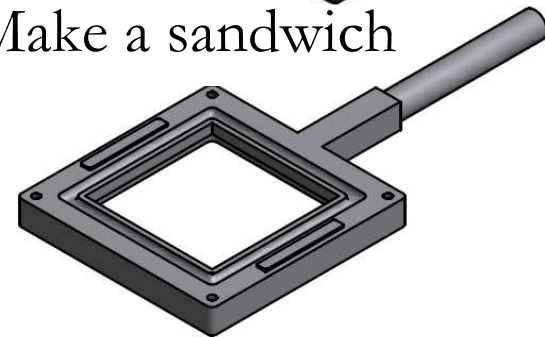
- (I) Go all silicon, make the chip thin (60-80 nm silicon oxide support)
- (II) Include drainage holes, and use centrifugation to get rid of excess liquid
- (III) Pump in He
- (IV) Enclose in He chamber
- (V) Move away from beads; fuse small silicon, carbide chunks to surface

Moving forward

Online sample delivery system



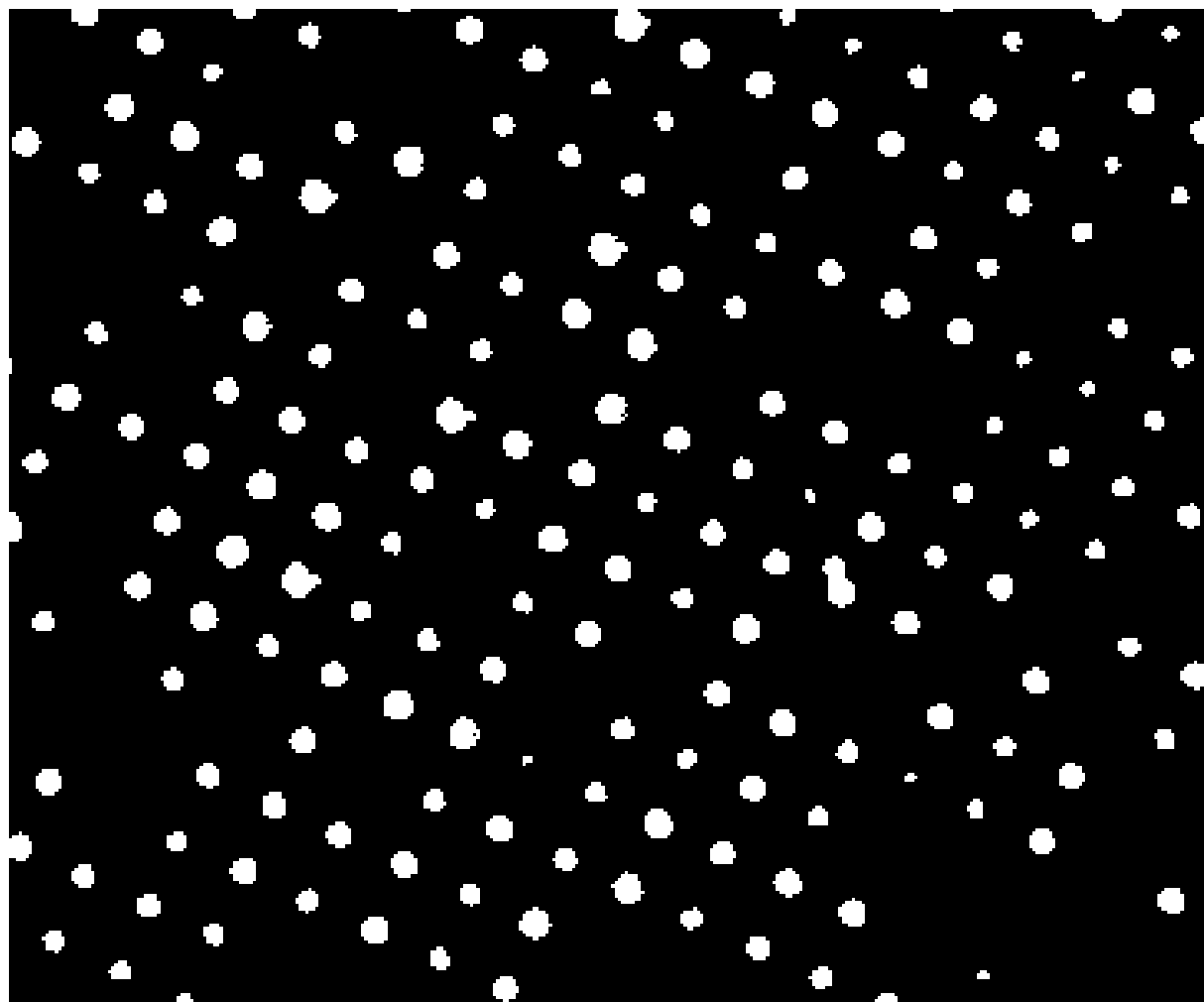
Make a sandwich



Online delivery



“Truly” nanocrystallography



2 micron wells and 900 nm beads

Acknowledgments

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Prof. Jim Rini

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Max Planck Institute for Medical Research, Heidelberg, Germany

Prof. Dr. Ilme Schlichting

Drs. Thomas Barends and Bob Shoeman

Max Planck Group for Structural Dynamics, DESY, Hamburg, Germany

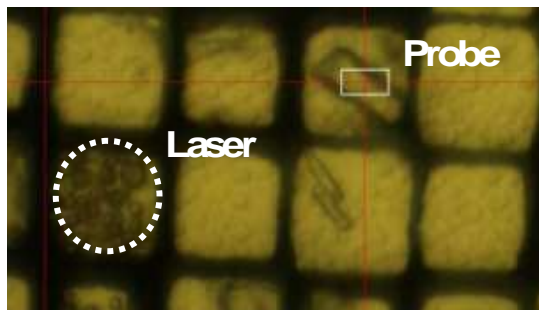
Prof. Dr. RJ Dwayne Miller

The Swiss Light Source

Dr. Martin Fuchs

Chip diffuses the 'shockwaves' expected from FEL pulse

A



B

