

BBSRC, MRC, Wellcome (Naismith et al)
2013 – 2019

Funded to join the
SFX Consortium at EuXFEL
and create the Hub

Hub hosted at Diamond from 2013,
since 2019 funded by
Diamond Light Source
and UKRI / STFC



Hub led by A. M. Orville
since Oct 2015

Currently: Wellcome Investigator,
RS Wolfson Fellowship,
& UKRI / BBSRC

Research & Development

- XFELs, Diamond, eBIC, RFI, RCaH
- Time-resolved serial MX, SFX & ED
- **AntiMicrobial Resistance**, especially β -lactam biosynthesis & degradation
- Reactivity in microcrystals
- X-ray emission spectroscopy (XES)
- Microfluidics for microcrystals
- On-demand droplet injectors



Service & Training

- Travel assistance UK scientists
- *Dynamic Structural Biology at XFELs & Diamond BAG*
- Serial MX processing pipelines

Research & Development

- Cryo-EM grid prep methods
- Serial MX at VMXi \pm tr-XES
- Data processing pipeline(s)
- Diamond/CLF PORTO project
- Micro-spectroscopy \pm MX
- Novel sample delivery methods

AMO group	XFEL Hub
Rob Bosman, PhD	Allen M. Orville, PhD
Jos Kamps, PhD	Pierre Aller, PhD
Tiankun Zhou, PhD	Anastasya Shilova, PhD
Anna Bailey, (Jack Stubbs), Emily Freeman, (Johan Glerup), Harold Cannon, Toluwalase Agoro, etc.	




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XFEL Hub supports UK scientist visits to XFELs

Year	UK scientists on expt.	UK scientists XFEL site visits	XFEL Hub scientists site visit
2015*	3	3	3
2016	25	21	19
2017	70	49	22
2018	95	59	34
Total 2015 - 2022	386	206	100

LCLS, SACLA, PAL-XFEL, SwissFEL, & European XFEL

UK grants to the XFEL Hub and/or collaborators

Some key publications with the XFEL Hub

nature

Science

nature methods

nature communications

ScienceAdvances

PNAS

Structure

JACS

Catalysis

Angewandte Chemie

THE JOURNAL OF PHYSICAL CHEMISTRY

Young et al. (2016) *Nature* 540, 453-457

Kern et al. (2018) *Nature* 563, 421-425

Lebrette et al. (2023) *Science* 382, 109

Fuller et al. (2017) *Nature Methods* 14, 443-449

Butryn et al. (2021) *Nature Commun* 12, 4461

Wiedorn et al. (2018) *Nature Commun* 9, 4025

Rabe et al. (2021) *Science Advances* 7, eabh0250

Burgie et al. (2020) *Proc Natl Acad Sci USA* 117, 300-307

Ibrahim et al. (2020) *Proc Natl Acad Sci USA* 117, 12624-12635

Roessler et al. (2016) *Structure* 24, 631-640

Srinivas et al. (2020) *J Am Chem Soc* 142, 14249-14266

Lucic et al. (2022) *ACS Catal* 12, 13349-13359

Lucic et al. (2020) *Angew Chem Int Ed Engl* 59, 21656-21662

Baxter et al. (2022) *J Phys Chem B* 126, 9288-9296

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Most structural biology data are measured from
a crystalline sample held at 100 K
(often at synchrotrons, including Diamond Light Source)

209,159 atomic models
released by the PDB
(03 Sep 2023)

Atomic Models in PDB (03 Sep 2023)

X-ray crystallography	177,905
Cryo-EM (soln.)	16,845
NMR spectroscopy (soln.)	14,070
XFEL data	777
Micro-ED (cryo.)	230
Neutron diffraction	219
"Pharma vaults"	big #



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100 K is

... a bit warmer than the
surface of **Pluto**

33 – 55 K; average 44 K

... *similar to*

The dark side of the **Moon**

~ 90 K

... the temperature of most
crystal structures in the PDB



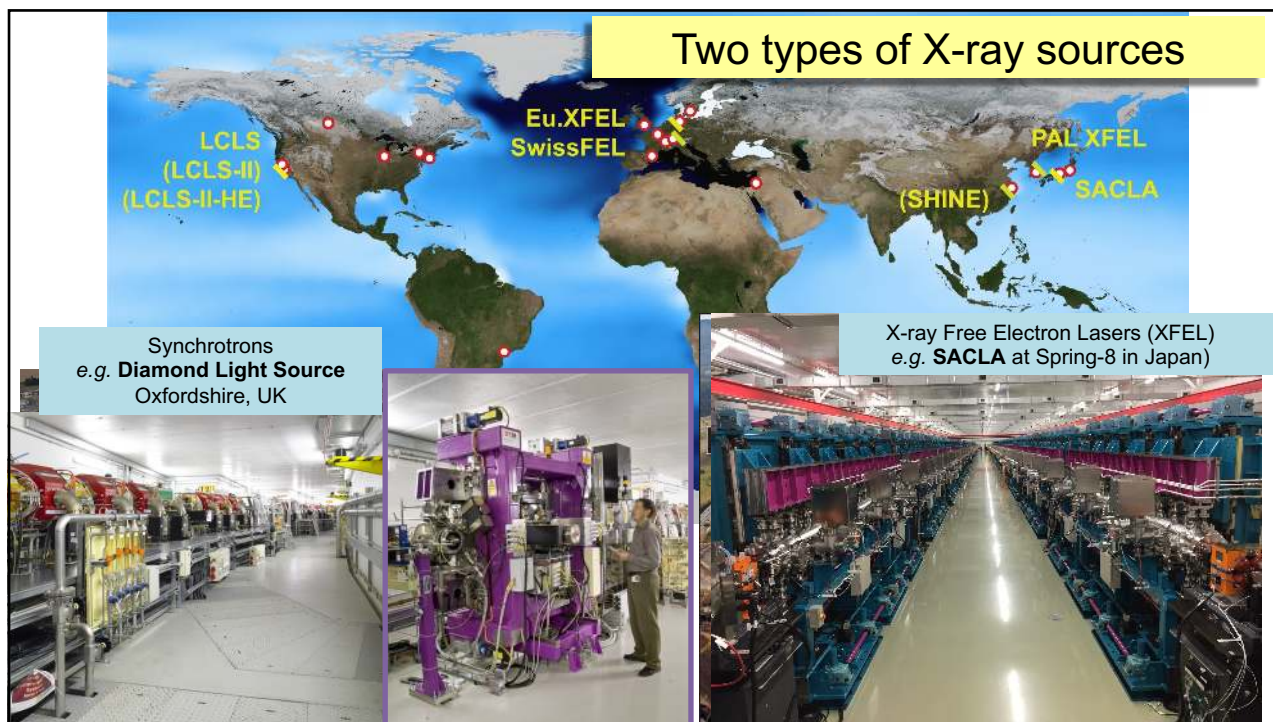
... and so, **remaining frontier challenges**
in structural biology are to determine

time-resolved, atomic resolution structures
directly from systems engaged in catalysis,
perhaps even in native context / environment,
and certainly, at physiological temperature and pressure

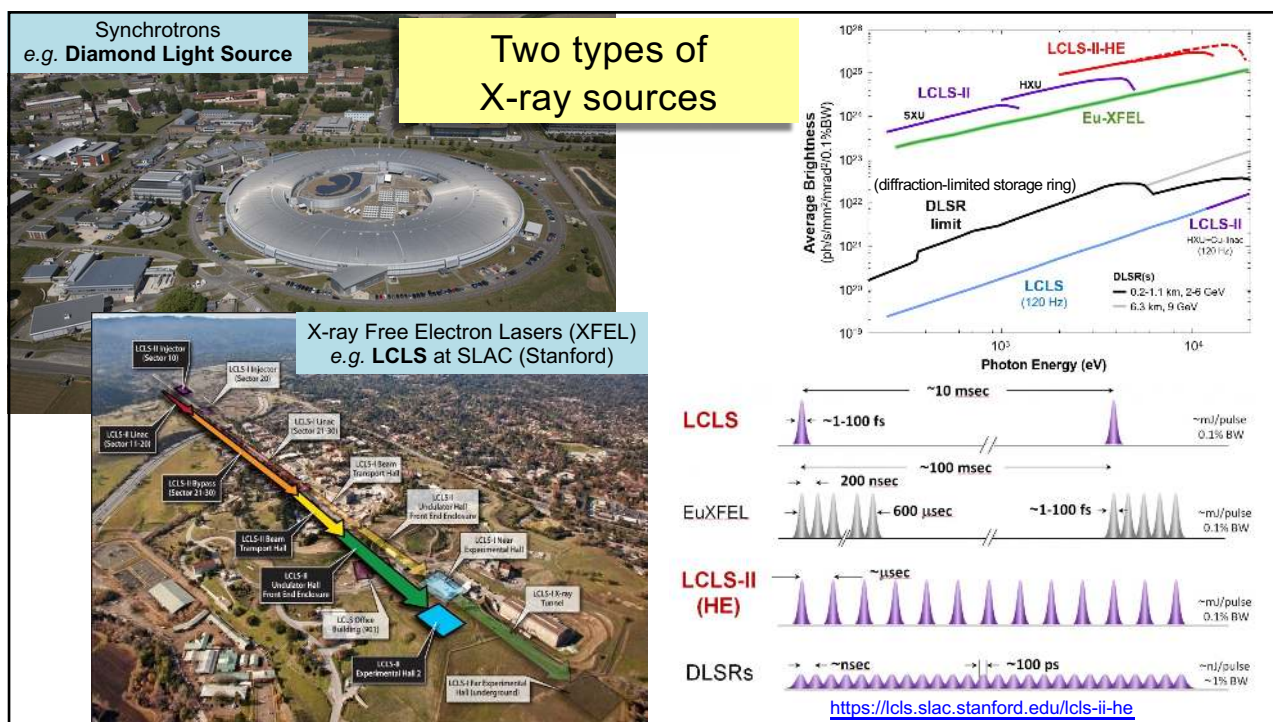
..... **on earth**

24 Dec 1968
NASA / Apollo 8
AS08-14-2383

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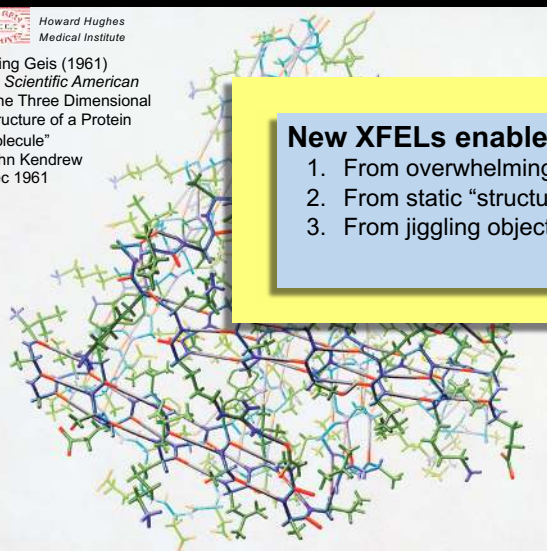
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"... all things are made of atoms; everything that living things do, can be understood in terms of the jiggings and wiggings of atoms."

Richard P. Feynman
Lectures on Physics Vol 1, Chapter 3, © 1963

Howard Hughes
Medical Institute

Irving Geis (1961)
for *Scientific American*
"The Three Dimensional
Structure of a Protein
Molecule"
John Kendrew
Dec 1961

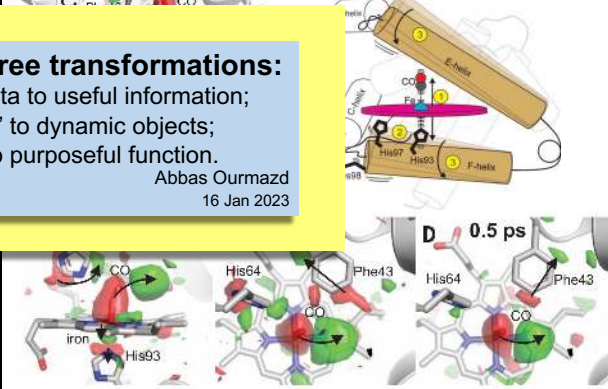
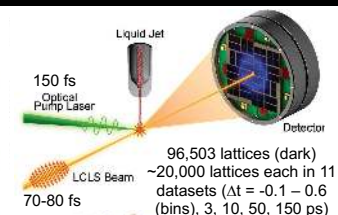


New XFELs enable three transformations:

1. From overwhelming data to useful information;
2. From static "structures" to dynamic objects;
3. From jiggling objects to purposeful function.

Abbas Ourmazd
16 Jan 2023

$\Delta t = 0.5$ ps
 $F_{\text{(light)}} - F_{\text{(dark)}}$
 $+3\sigma$ (green) & -3σ (red)



Mb-CO photodissociation: time-resolved SFX
Barends et al (2015) *Science* 350, 445-450

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Current 3rd generation synchrotrons and XFELs



Parameter / XFEL	LCLS (USA)	SACLA (Japan)	PAL XFEL (Korea)	SwissFEL (Switzerland)	EuXFEL (Germany)	LCLS-II-HE (USA)	SHINE (China)
first beam	2009	2011	2017	2017	2017	~2025	~2026
photons / pulse	$\sim 10^{12}$	2×10^{11}	$>1 \times 10^{11}$	7×10^{11}	$\sim 10^{12}$	$\geq 10^{12}$	$\geq 10^{12}$
max. pulses / s	120	60	60 - 120	100	27,000* (4.5 MHz)*	1,000,000 (1 MHz)	1,000,000 (1 MHz)
Detector(s) (image rate, Hz)	CSPAD / Rayonix (120 / 10 - 30)	MPCCD (60)	MPCCD (60)	Jungfrau (100 +)	AGIPD (3520) Jungfrau* (160)	ePIX (R&D) (10,000)	tbd (R&D) (17,000)
typical X-ray beam size (μm^2)	3 x 3	3 x 3	5 x 5	5 x 5	3 x 3	tbd	tbd
SFX stations	3	1	1	1	2	3	tbd

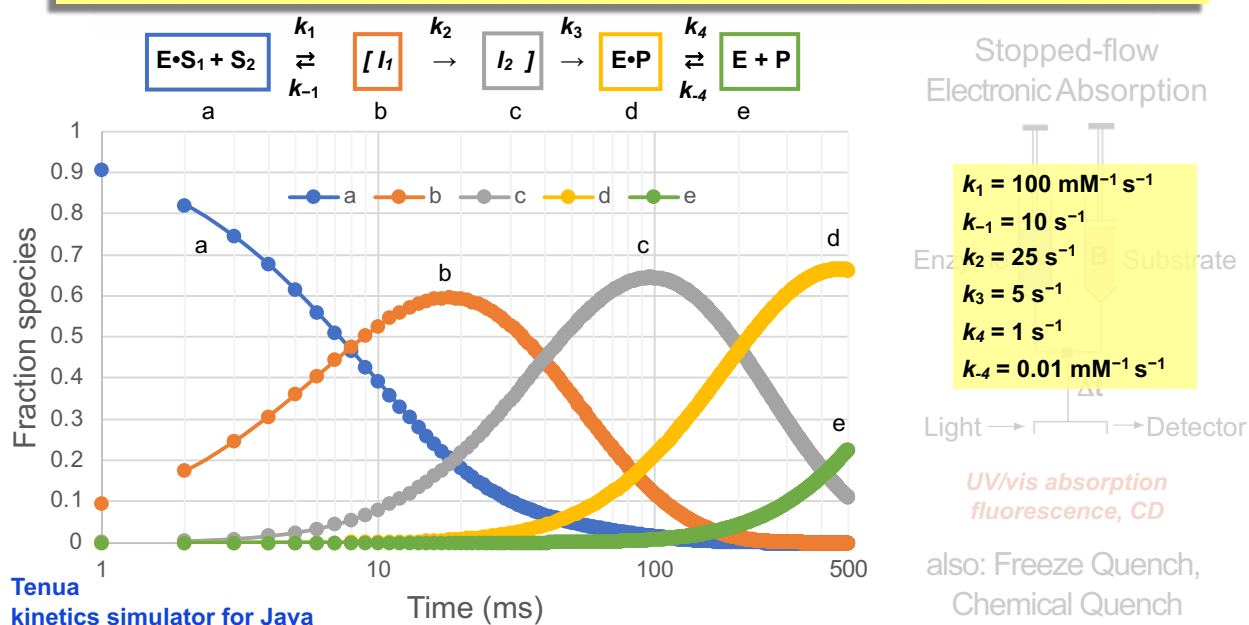
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Emerging capabilities for tr-SSX at synchrotrons

Beamline	Focus μm^2	Flux $\times 10^{13} \text{ ph s}^{-1}$	Energy keV	Detector(s)	Sample delivery	Other key features
I24 / KMX Diamond, Diamond II	4×4 to 30×30	~0.2 (DCM) ~8 (DMM) ~100 (D-II)	7 – 30	CdTe Eiger2 9M, Integrating tbc, Time-resolved px (Tristan 10Mpx)	Cryo pin, fixed target, viscous extruder, drop on demand	XES + optical spec., Dual DCM DMM, PORTO, Chopper shuttering
MicroMAX, Max IV	1×1 to 10×10	0.8 (DCM) ~100+ (DMM)	5 – 25	CdTe Eiger2 9M, Integrating tbc	Cryo pin Fixed target. Other SSX tbc	Dual DCM DMM, Chopper shuttering
ID29, ESRF-EBS	0.5×0.5 to 5×6	~100+ (DMM)	10 – 25 and 35	Jungfrau 4M	Fixed target, tape drive extruder	Chopper shuttering, Flexible sample environment
FMX, NSLS-II	1×1.5 to 10×10	0.4 (12.4 keV)	5 – 30	Eiger2 16M	Cryo pin. Serial (fixed target) in development	Two goniometers
P14-EH2, PETRA-III "T-REXX"	15×10	0.2 (12.7 keV)	12.7	CdTe Eiger 16M (EH1) Eiger 4M (EH2)	Cryo pin (EH1) Fixed targets (EH2)	Parameters are for EH2, Δtemp , Laser excitation available

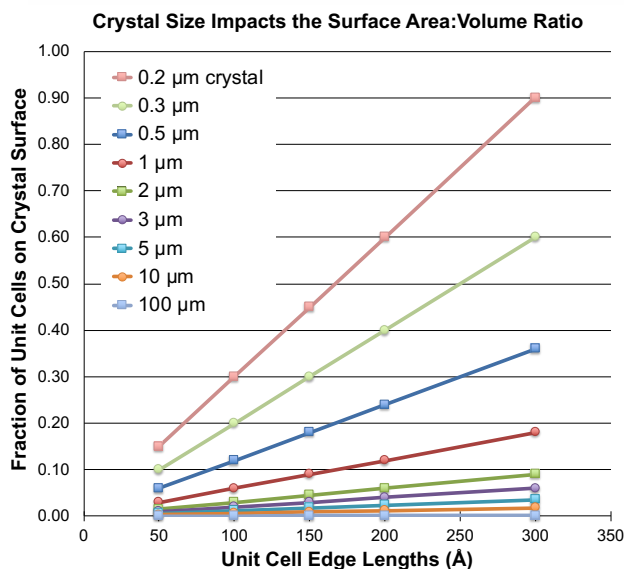
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Transient kinetics measures individual rate constants



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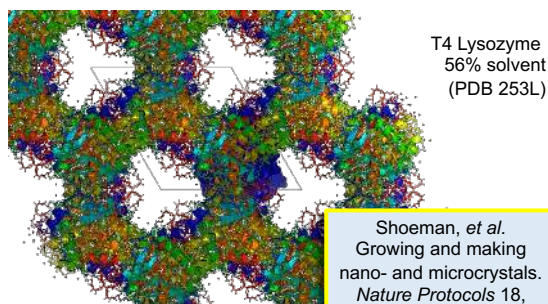
The driving hypothesis to **generalize** time-resolved serial micro-MX



Orville, A. M. (2020) *Current Opinion in Structural Biology* 65, 193-208

Davidi D. et al. (2018) *Chem Rev* 118, 8786-8797
Schmidt, M. (2017) *Methods Mol Biol* 1607, 273-294

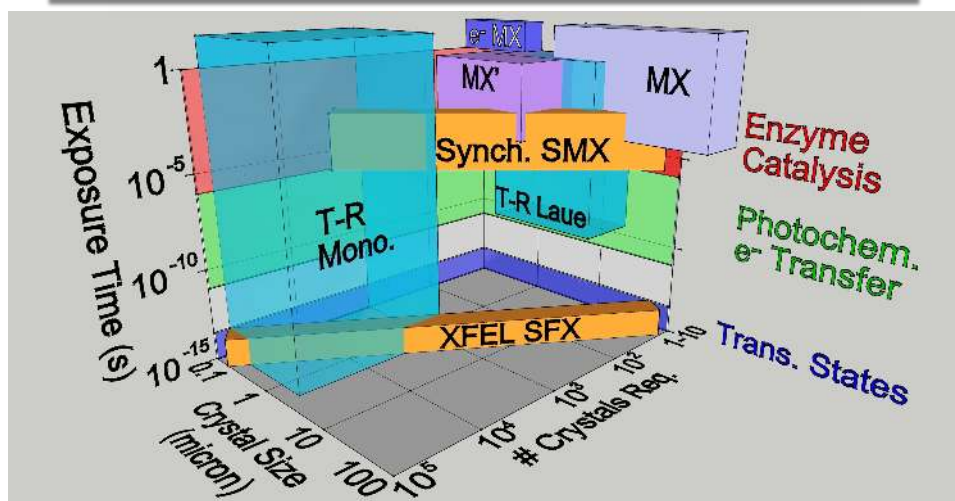
- use **enzyme microcrystals**, $\sim 2 \times 2 \times 2 \mu\text{m}^3$ and smaller, homogeneous size distribution
- substrate(s) diffusion is "fast," **E•S complex will form in $\sim 100 \mu\text{s} - \text{ms}$**
- average enzyme reaction in solution is $\sim 70 \text{ ms}$; 60% with k_{cat} between $1 - 100 \text{ s}^{-1}$
- Thus, **ligand diffusion is many times faster than typical reaction cycle**



Shoeman, et al.
Growing and making
nano- and microcrystals.
Nature Protocols 18,
854-882 (2023)

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Structural biology experimental envelopes

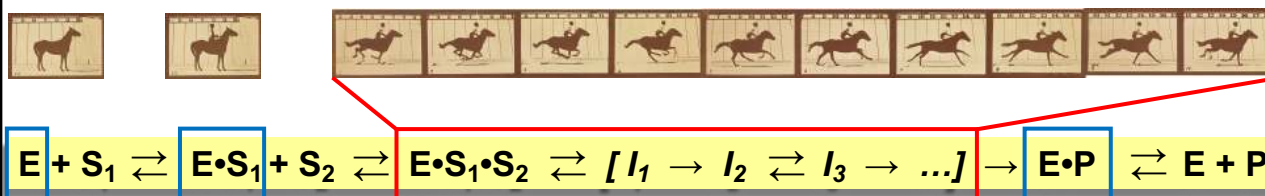


Synchrotron SMX (serial, still (micro)-MX)
XFEL SFX (serial femtosecond MX)
T-R Mono (general, monochromatic, still, time-resolved, micro-MX)

MX (standard, single crystal, rotation MX)
MX' (multicrystal, rotation MX)
e- MX (electron diffraction MX)
T-R Laue (polychromatic, still, time-resolved MX)

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Concepts of time-resolved *dynamic* structural biology



Traditional MX: synchrotrons, macro-crystals, 100 K, resting state **E**, soaked **E•S₁** or **E•P**; soaking or crystallization lacks function and dynamics: >90% structures PDB / year

Cryo-EM: in solution, low Temp or freeze-quench \approx ms time resolution, complements & benefits from MX, class averages, limited dynamics, no spectroscopic confirmation

Serial MX at XFELs & Diamond (SFX & SMX)

- study entire reaction cycles at room temp & pressure
- XFEL fs pulse \approx bond vibrations, photo-active reactions
- No radiation-induced damage to reactive intermediates
- DLS / VMXi \approx μ s time resolution with mixing strategies
- μ -crystal slurries \approx atomic & electronic structural data

Entering an era of **dynamic structural biology**... a concept, a set of tools, to collect as much data as possible from every sample and X-ray pulse, enables atomic resolution "stop-motion movies" of macromolecules engaged in catalysis

AIM: Within 5 – 10 years, routine molecular movies via serial MX at all XFELs & synchrotrons

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Dynamic structural biology \rightarrow observing structure & function

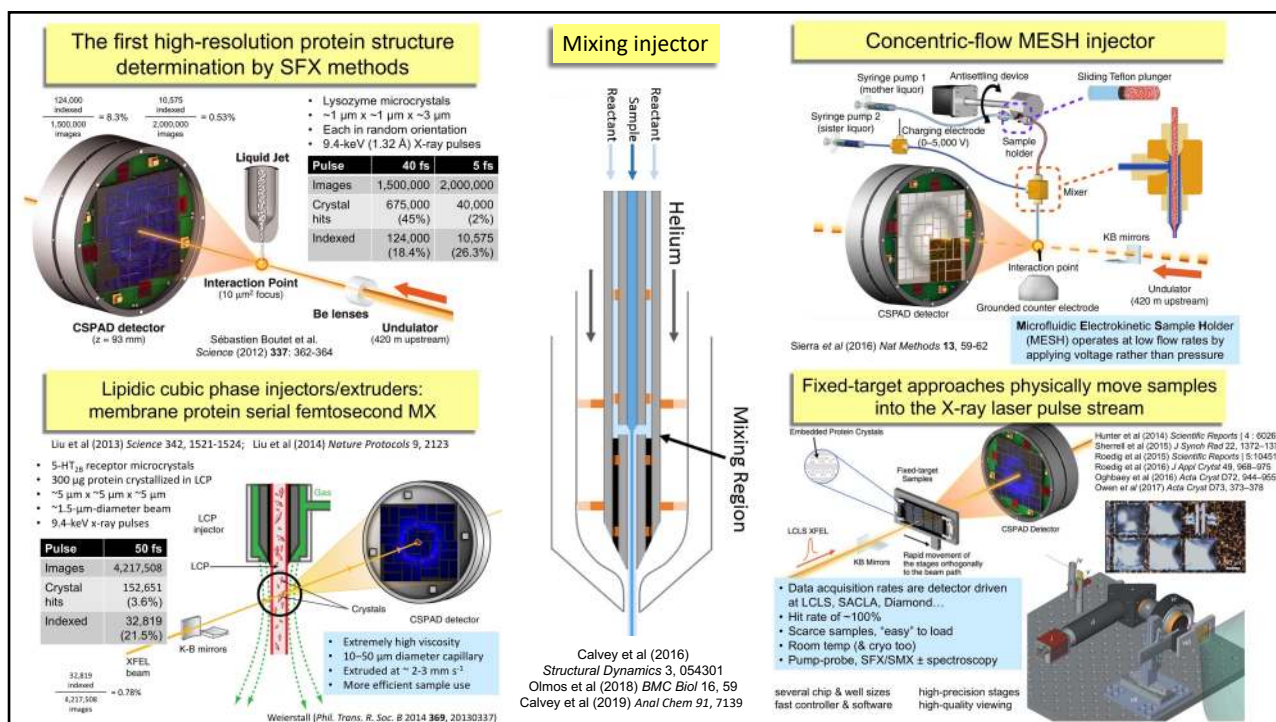
An ideal experiment...	How & Where ?	What do we need ?
One or more correlated methods tr-SMX/SFX \pm tr-XES \pm optical \pm other X-ray spectroscopies	Integrated instrumentation, Synchrotrons, XFELs, (EM &/or MeV-ED facilities)	Data tracking, analysis, feedback, deep datasets (Δt and ground-state); joint refinement strategies
Under physiological conditions Temp, pressure, pH, salt ...	pump-probe, illumination, reagent mixing; equilibration Δt range	Catalytic rates in crystal slurries; efficient sample delivery methods
High spatial resolution e.g. from microcrystal slurries	better than 2 Å; completeness, high redundancy, serial MX / SFX, ED	Made-to-order homogenous slurries, bright micro-focus beams
High temporal resolution Fast and/or slow reactions, homogenous samples, initiation	pump-probe; light; mixing; gas; fs – XFELs; μ s – Synchrotrons; ms – cryo-EM/ED via freeze trapping	Caged compounds; sample handling; triggering methods; appropriate quantum yields
Element-specific reporters help identify / verify critical reaction intermediates (e.g. PEP/PPi)	Native transition states; probe functional mechanisms & multiple pathways online	Integrated / correlated data streams; joint refinement strategies
Barends et al (2022) <i>Nature Reviews Methods Primers</i> 2, 59 Schulz et al (2022) <i>Acta Cryst D</i> 78, 14-29 Gorel et al (2021) <i>IUCrJ</i> 8, 532-543 Hough & Owen (2021) <i>Curr Opin Struct Biol</i> 71, 232-238		Kupitz et al (2020) <i>Crystals</i> 10, 251 Bernstein (2020) <i>Struct Dyn</i> 7, 014302 Pearson & Mehrabi (2020) <i>Curr Opin Struct Biol</i> 65, 168-174 Orville, A. M. (2020) <i>Curr Opin Struct Biol</i> 65, 193-208

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Dynamic structural biology → observing structure & function

An ideal experiment...	How & Where ?	What do we need ?
One or more correlated methods tr-SMX/SFX ± tr-XES ± optical ± other X-ray spectroscopies	Integrated instrumentation, Synchrotrons, XFELs, (EM &/or MeV-ED facilities)	Data tracking, analysis, feedback, deep datasets (Δt and ground-state); joint refinement strategies
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Element-specific reporter(s) help identify / verify critical reaction intermediates (e.g. Fe(IV)=O)	Native (transition metals), post-translational modification(s); multiple beamlines / off-line	Integrated / correlated data streams; joint refinement strategies
Easy access ; we must repeat critical observations	Synchrotrons (more plentiful) XFELs (very scarce)	Routine access; similar strategies &/or equipment
All data is curated in database(s) and released upon publication	International standards; metadata from different beamlines / formats	PDB should accept, verify, curate, release correlated datasets

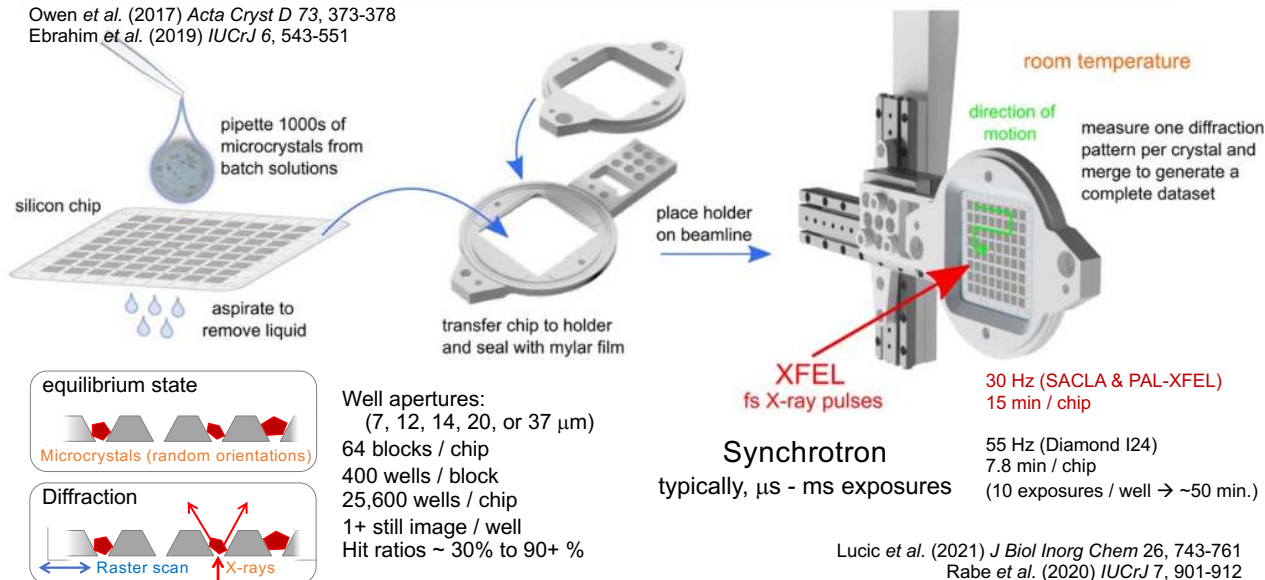
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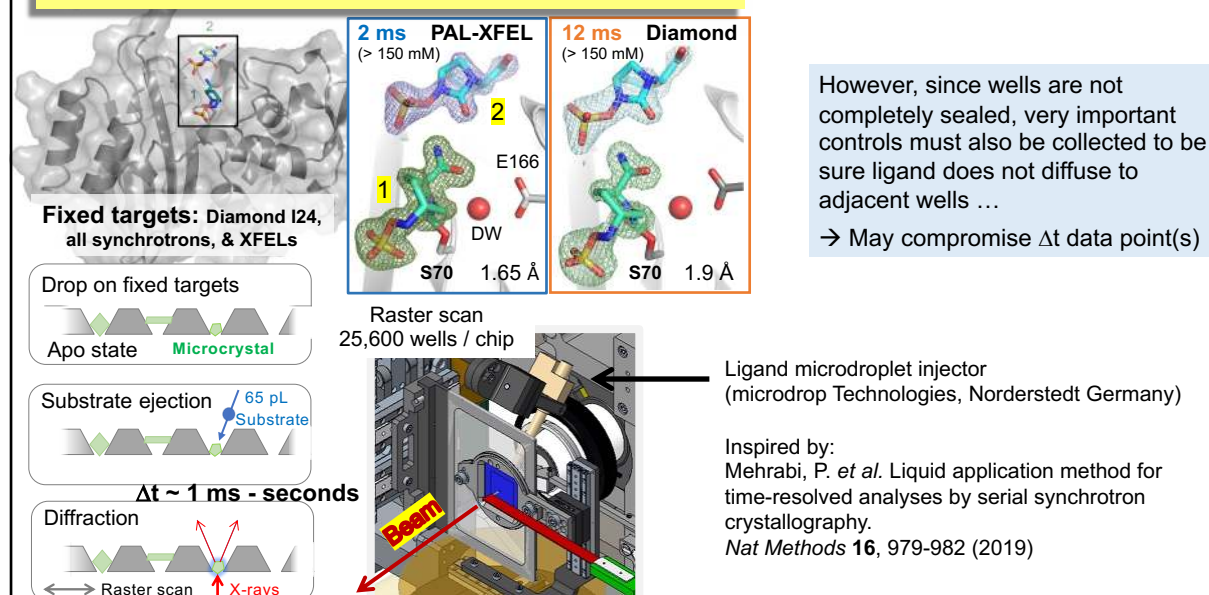
Serial crystallography by raster scanning fixed targets

Owen *et al.* (2017) *Acta Cryst D* 73, 373-378
 Ebrahim *et al.* (2019) *IUCrJ* 6, 543-551

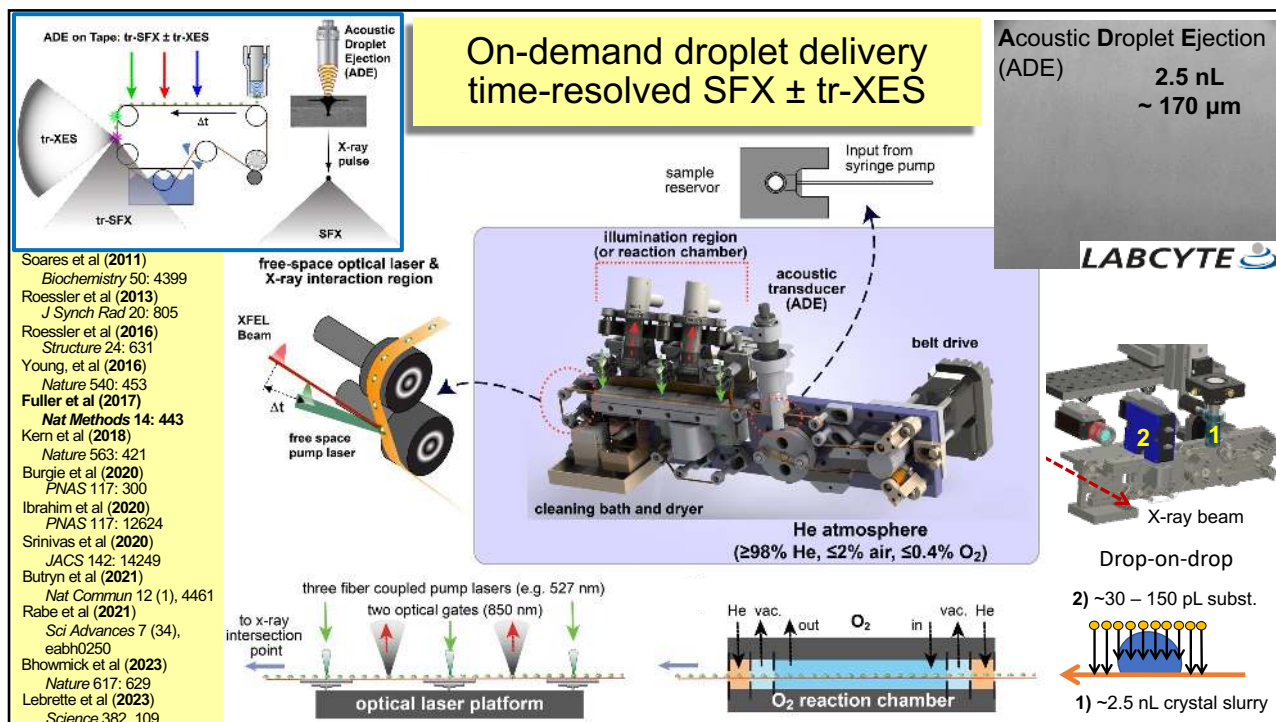


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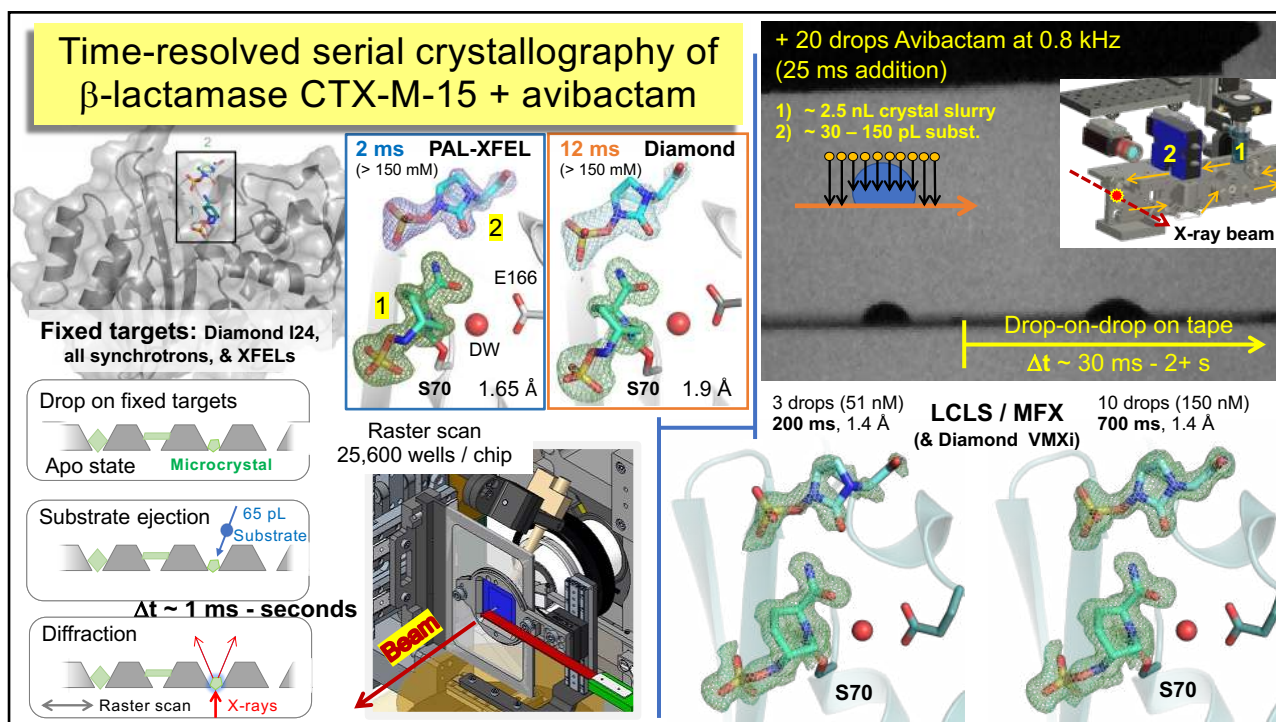
Time-resolved serial crystallography of β -lactamase CTX-M-15 + avibactam



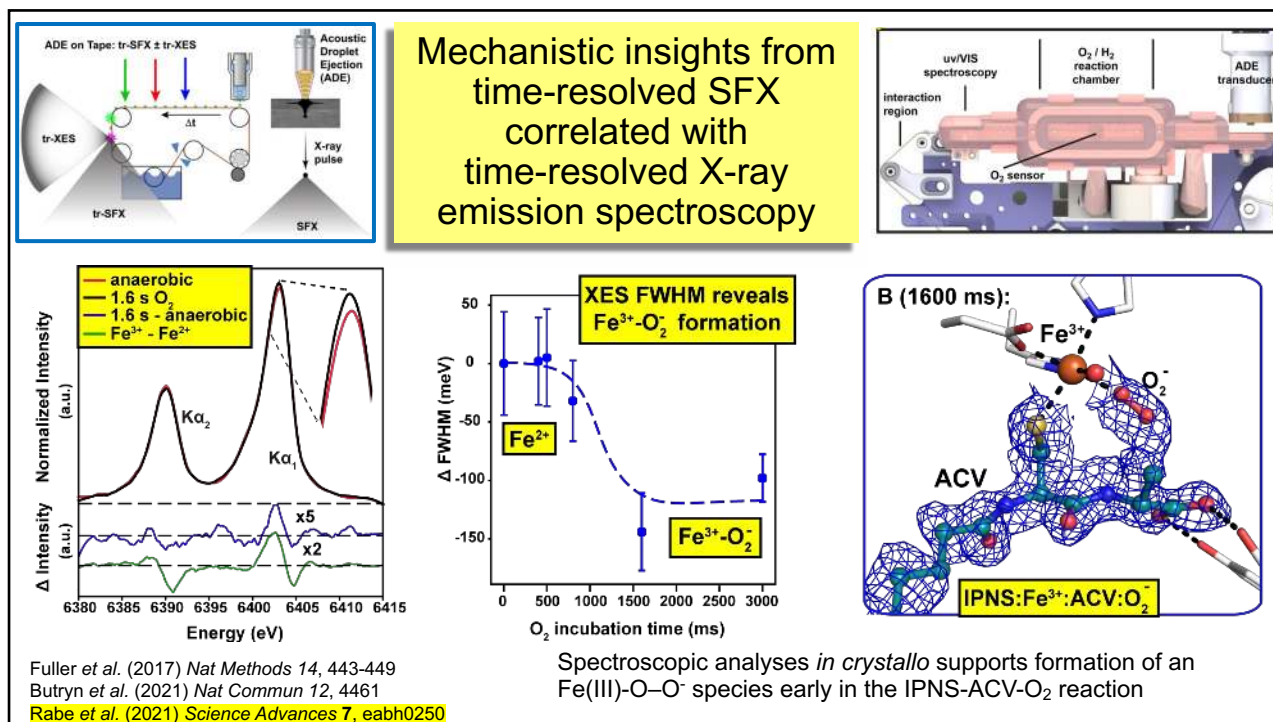
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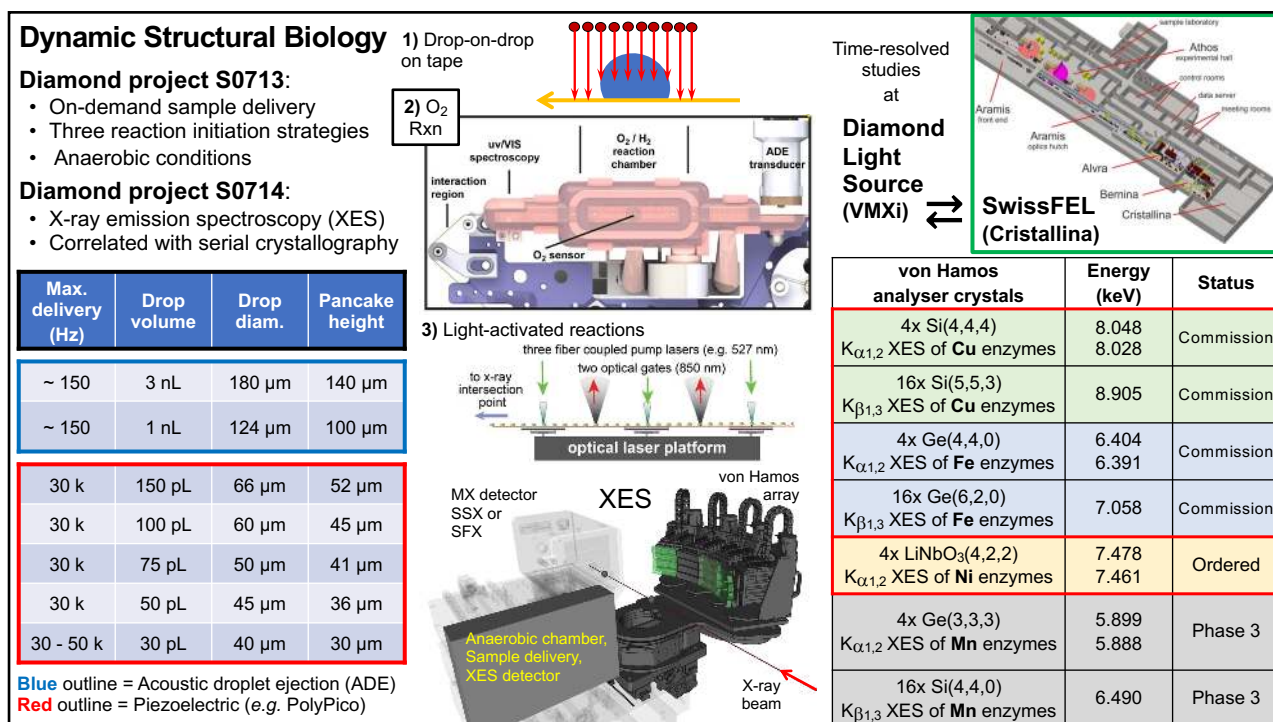
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