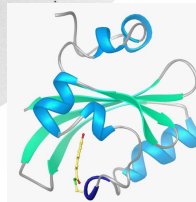
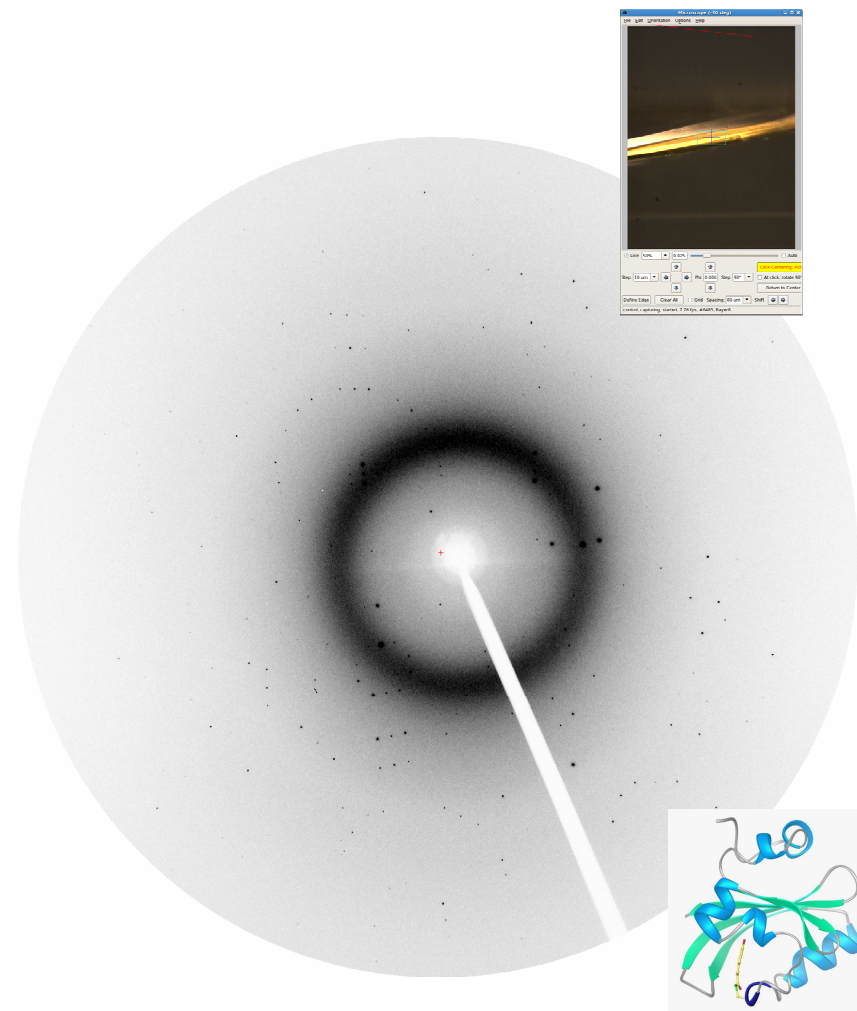
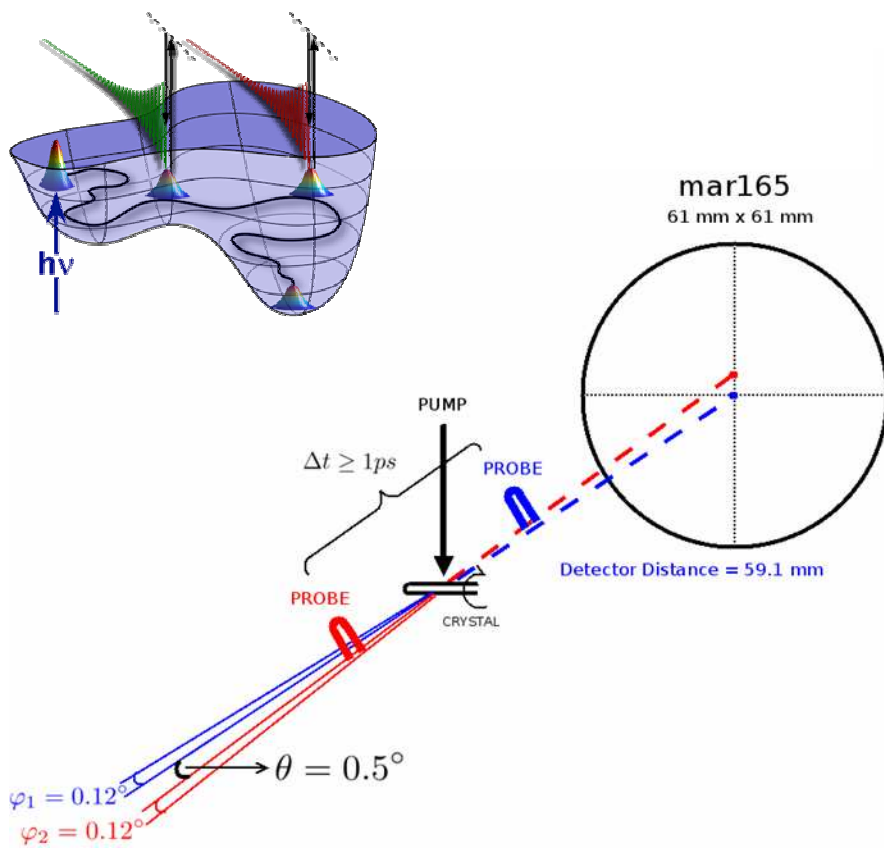


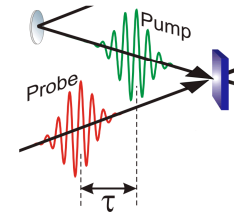
# Femtosecond Protein Dynamics using Split-Delay Line Crystallography

Imperial College  
London

Jasper van Thor



# Pump-Probe instruments



**Synchrotron**



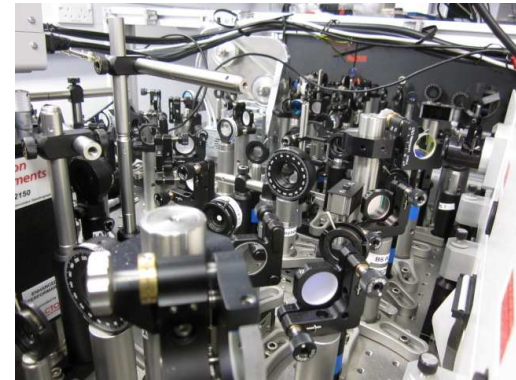
**50 ps**

**XFEL**



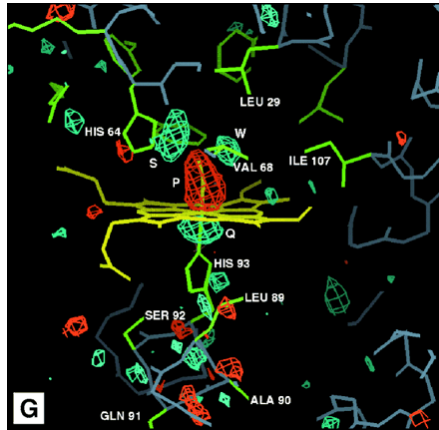
**fs - ps**

**Your lab**



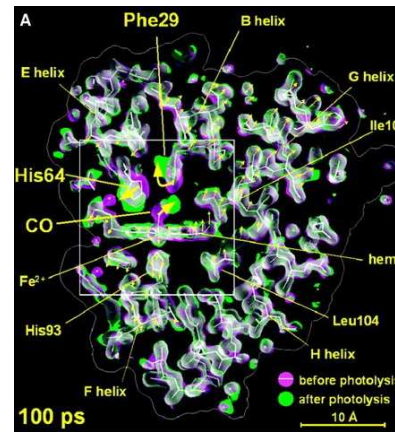
**fs**

## Myoglobin-CO



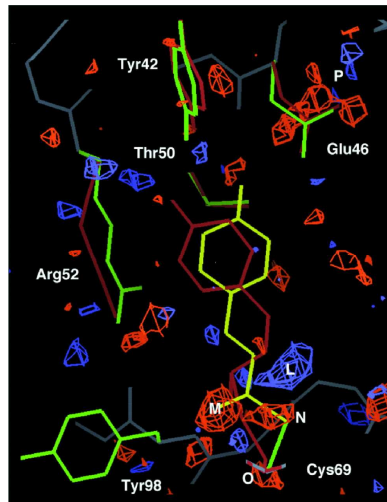
**4 ns**  
Science **1996**:  
274, 1726-1729

## Myoglobin-CO



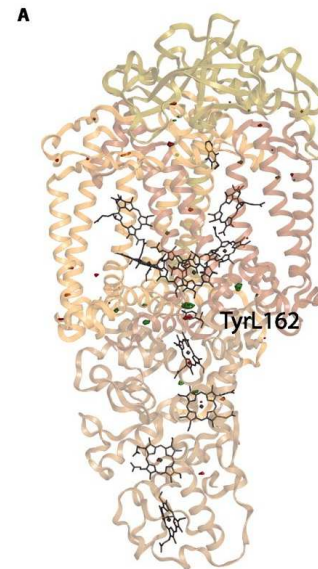
**100ps**  
Science **2003**:  
300, 1944-1947

## Photoactive Yellow Protein (PYP)



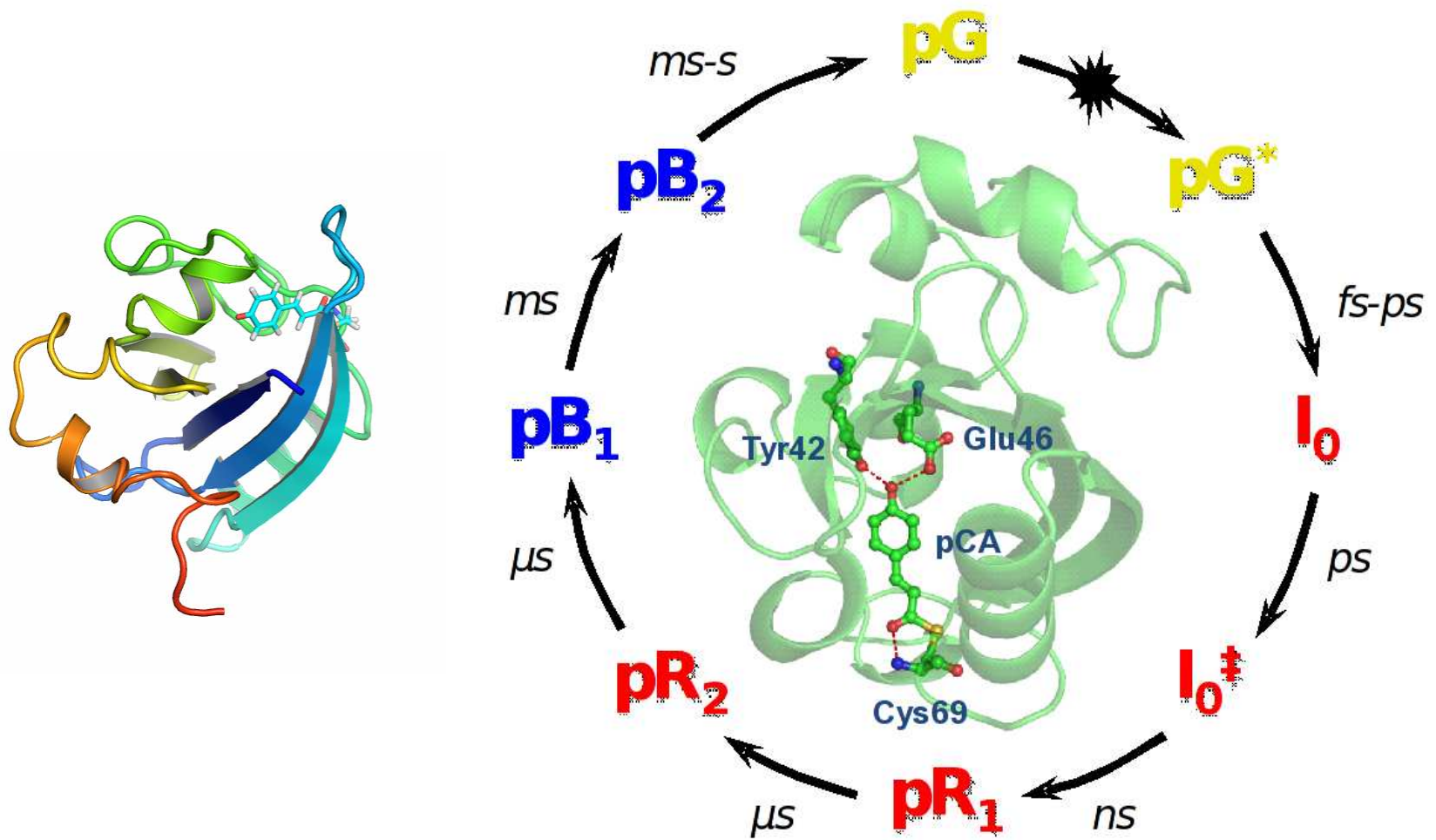
**1 ns**  
Science **1998**:  
279, 1946-1950

## Photosynthetic Reaction Center



**3 ms**  
Science **2010**:  
328, 630-633

## Transient structural changes in the PYP photoreceptor

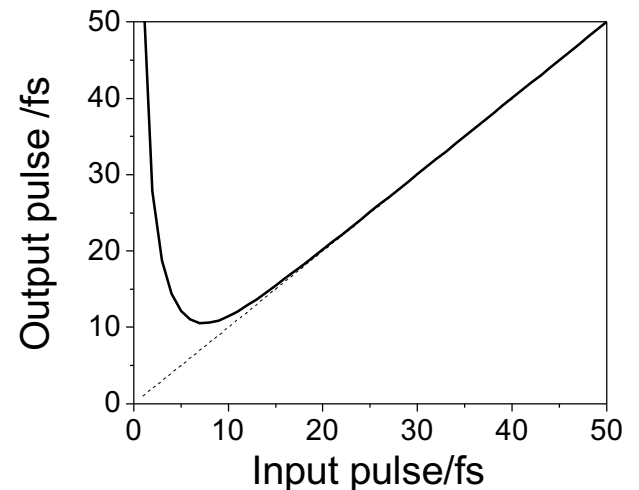
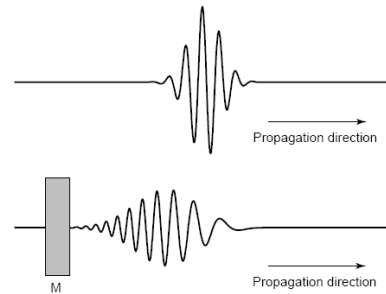
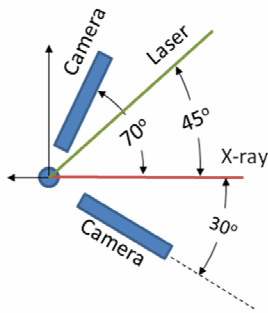
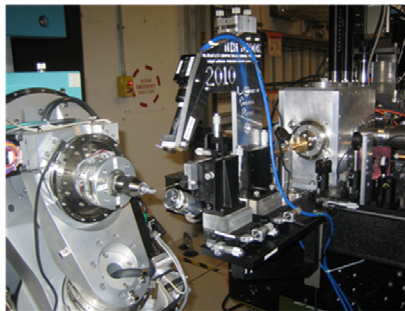


'Photocycle' of the 'Photoactive Yellow Protein'



## pump-probe fs X-ray diffraction

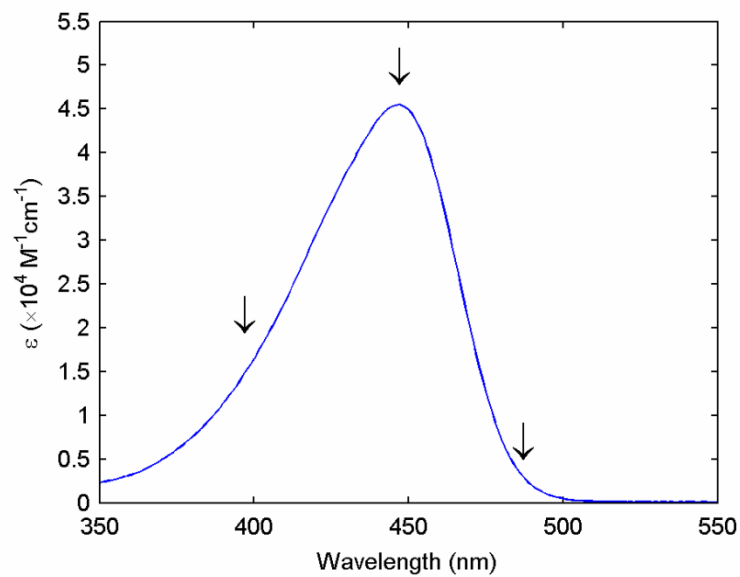
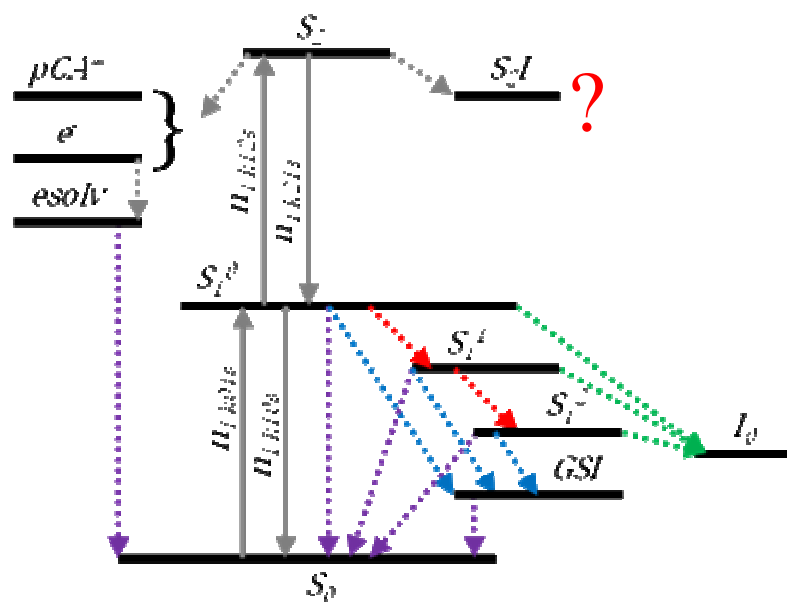
- Time resolution intrinsically limited to  $\sim 100\text{fs}$  as a result of (1) Multi-photon absorption and (2) group velocity mismatch VIS, X-ray  $\sim 133\text{ fs}/100\ \mu\text{m}$  (group index VIS  $\sim 1.4$ ) (3) very short intense pulses induce Kerr-effect, self-focussing
- So far, successful pump-probe experiments have relied on ~~stretching~~ stretching of optical pulses to avoid non-linear absorption (myoglobin-CO) and circumvents low quantum yield (Photoactive Yellow Protein): No femtosecond synchronisation of sufficient populations has been achieved. Fs time-resolution for X-ray diffraction is dictated by photochemical dynamics



Calculation using GVD  $20\text{ fs}^2 / 100\ \mu\text{m}$  of protein crystal ; only expected for  $< 20\text{ fs}$  pulse duration

# PYP

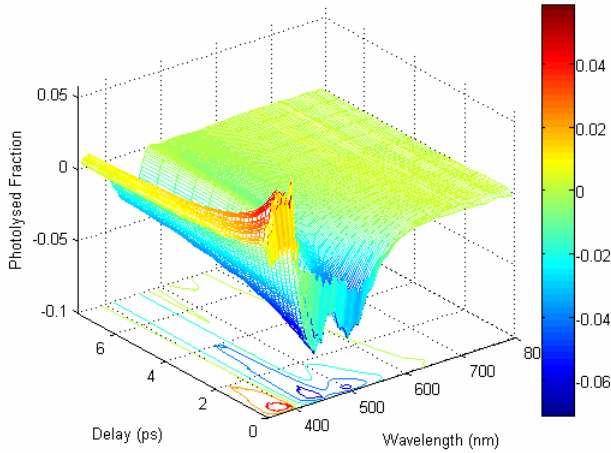
## primary photochemical reactions



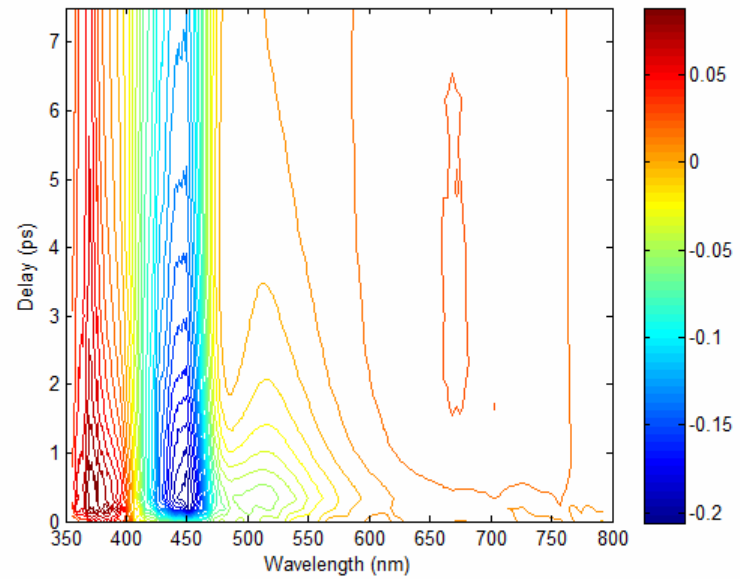
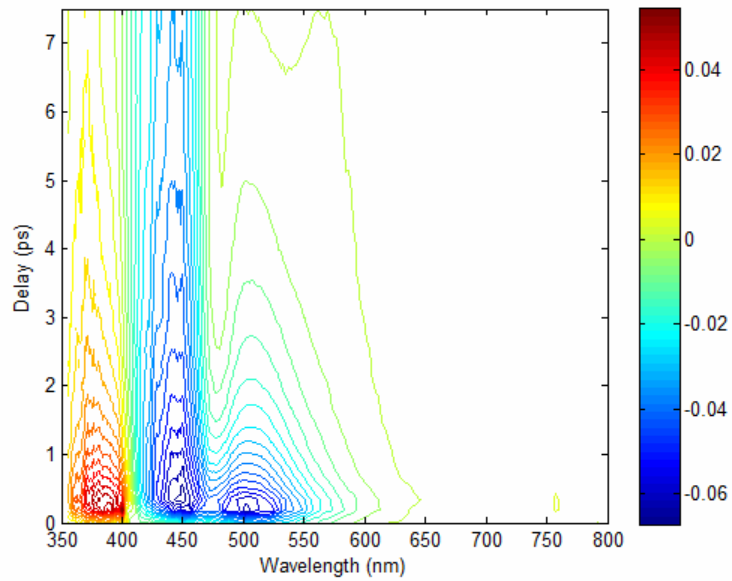
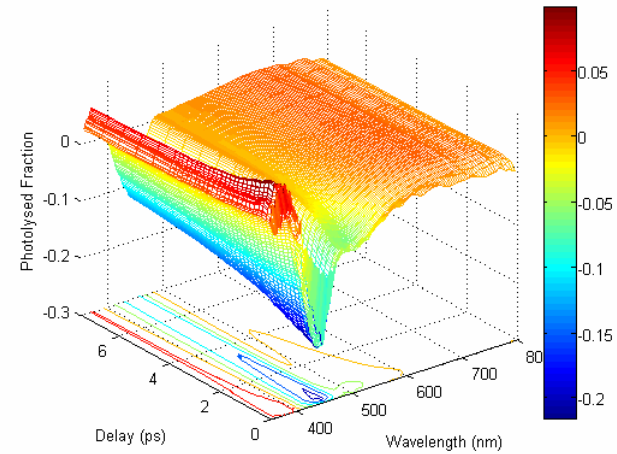
Lincoln et al. 2012. PCCP 14, 15752

# TA – 400 nm

Low Power



High Power



# Modelling cross sections from population transfer

$$\frac{d[S_0]}{dt} = -k_{01s}(t)[S_0] + k_{10s}(t)[S_1^0] + \varphi_{S_1^0 \rightarrow S_0} k_{s_1^0} [S_1^0] + \varphi_{S_1^1 \rightarrow S_0} k_{s_1^1} [S_1^1] + \varphi_{S_1^2 \rightarrow S_0} k_{s_1^2} [S_1^2] + k_{s_{GS1}} [S_{GS1}] + \varphi_{S_2 \rightarrow S_1} k_{s_2} [S_2] \quad (1a)$$

$$\frac{d[S_1^0]}{dt} = k_{01s}(t)[S_0] - k_{10s}(t)[S_1^0] - k_{12s}(t)[S_1^0] + k_{21s}(t)[S_2] - \varphi_{S_1^0 \rightarrow S_1^1} k_{s_1^0} [S_1^0] - \varphi_{S_1^0 \rightarrow I_0} k_{s_1^0} [S_1^0] - \varphi_{S_1^0 \rightarrow S_{GS1}} k_{s_1^0} [S_1^0] - \varphi_{S_1^0 \rightarrow S_0} k_{s_1^0} [S_1^0] \quad (1b)$$

$$\frac{d[S_1^1]}{dt} = \varphi_{S_1^0 \rightarrow S_1^1} k_{s_1^0} [S_1^0] - \varphi_{S_1^1 \rightarrow S_1^2} k_{s_1^1} [S_1^1] - \varphi_{S_1^1 \rightarrow I_0} k_{s_1^1} [S_1^1] - \varphi_{S_1^1 \rightarrow S_{GS1}} k_{s_1^1} [S_1^1] - \varphi_{S_1^1 \rightarrow S_0} k_{s_1^1} [S_1^1] \quad (1c)$$

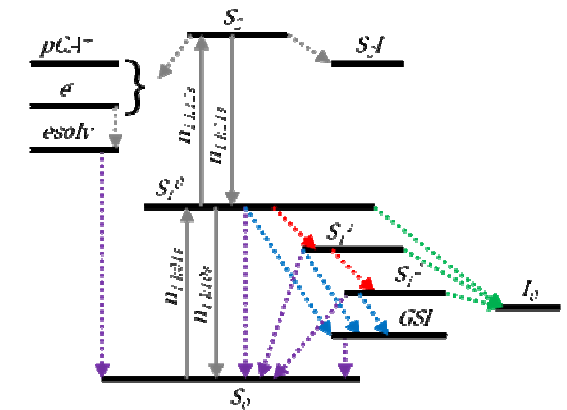
$$\frac{d[S_1^2]}{dt} = \varphi_{S_1^1 \rightarrow S_1^2} k_{s_1^1} [S_1^1] - \varphi_{S_1^2 \rightarrow I_0} k_{s_1^2} [S_1^2] - \varphi_{S_1^2 \rightarrow S_{GS1}} k_{s_1^2} [S_1^2] - \varphi_{S_1^2 \rightarrow S_0} k_{s_1^2} [S_1^2] \quad (1d)$$

$$\frac{d[I_0]}{dt} = \varphi_{S_1^0 \rightarrow I_0} k_{s_1^0} [S_1^0] + \varphi_{S_1^1 \rightarrow I_0} k_{s_1^1} [S_1^1] + \varphi_{S_1^2 \rightarrow I_0} k_{s_1^2} [S_1^2] - k_{I_0} [I_0] \quad (1e)$$

$$\frac{d[S_{GS1}]}{dt} = \varphi_{S_1^0 \rightarrow S_{GS1}} k_{s_1^0} [S_1^0] + \varphi_{S_1^1 \rightarrow S_{GS1}} k_{s_1^1} [S_1^1] + \varphi_{S_1^2 \rightarrow S_{GS1}} k_{s_1^2} [S_1^2] - k_{s_{GS1}} [S_{GS1}] \quad (1f)$$

$$\frac{d[S_2]}{dt} = k_{12s}(t)[S_1] - k_{21s}(t)[S_2] - \varphi_{S_2 \rightarrow e} k_{S_2} [S_2] - \varphi_{S_2 \rightarrow S_0} k_{S_2} [S_2] \quad (1g)$$

$$\frac{d[e^-]}{dt} = \varphi_{S_2 \rightarrow e} k_{S_2} [S_2] \quad (1h)$$

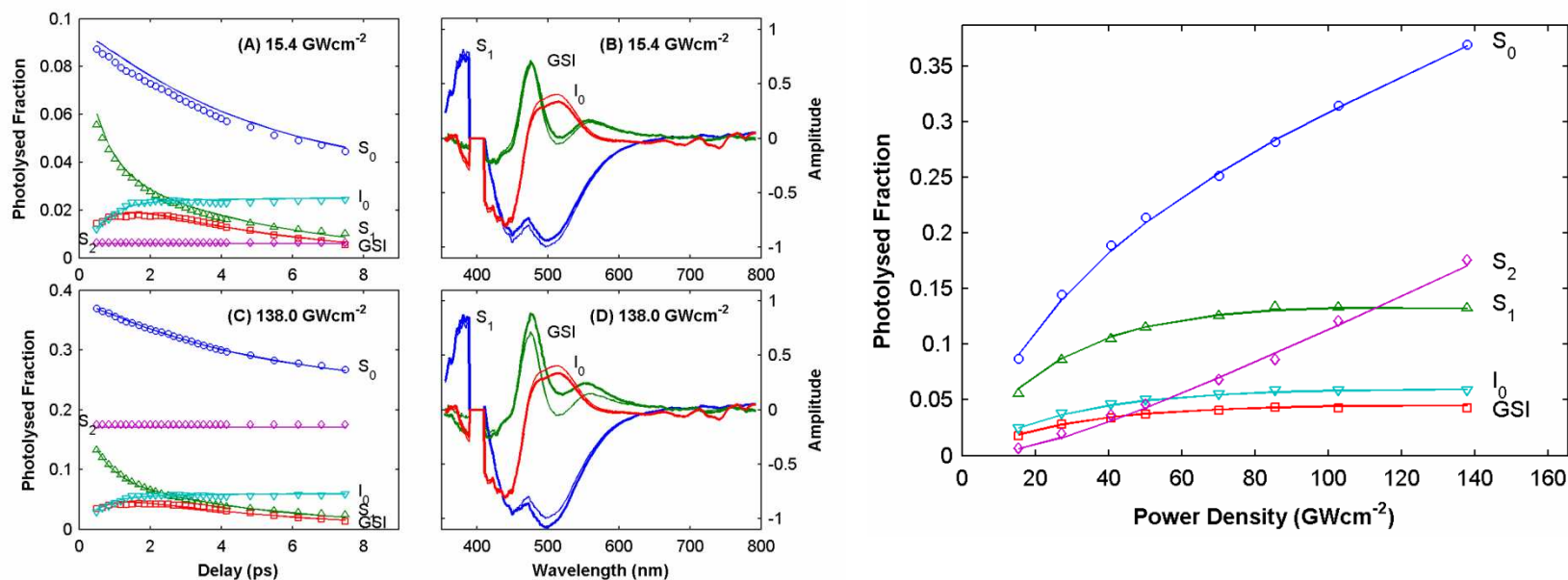


$$k_{ijS}(t) = 3J(t) \sigma_{ij} \Phi_{ij} \cos^2 \theta$$

$$\sigma_{ij} = \frac{1000 \times \ln(10) \times \epsilon_{ijS}}{N_A}$$



# Target Analysis - 400 nm



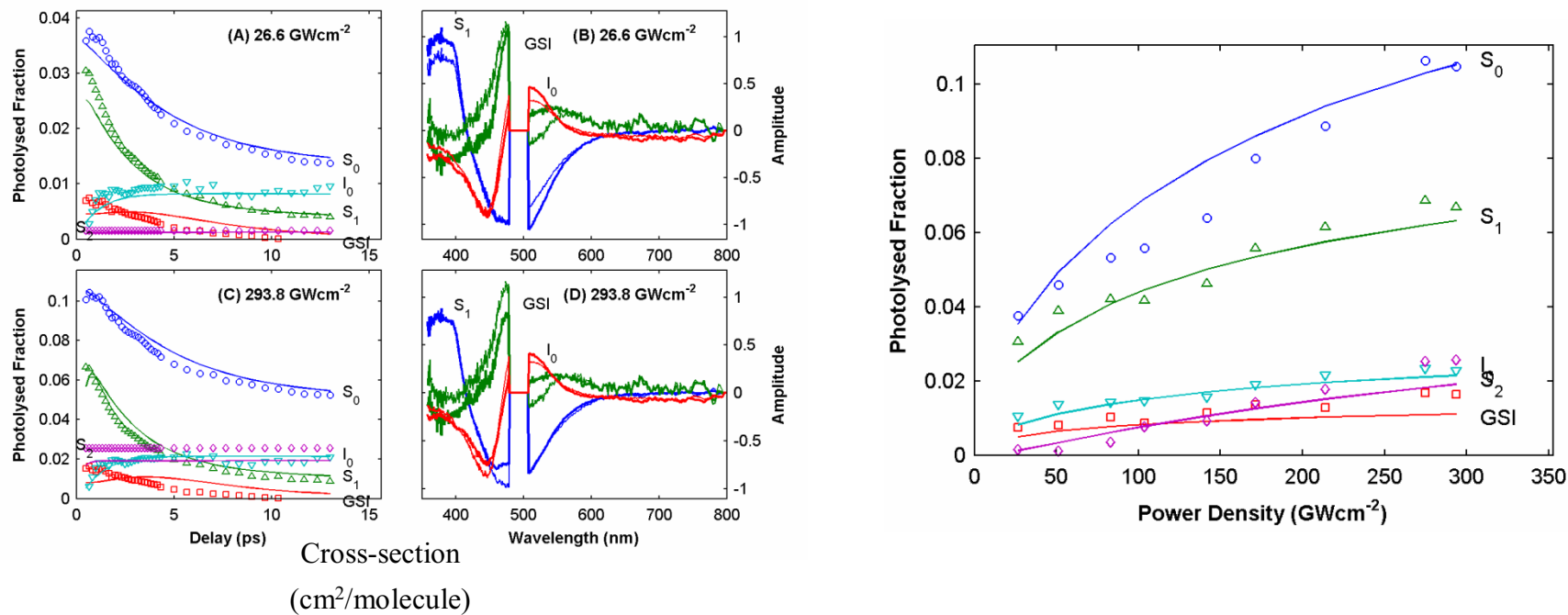
Cross-section  
(cm<sup>2</sup>/molecule)

$\sigma_{01s}$	$\sigma_{10s}$	$\sigma_{12s}$	$\sigma_{21s}$
6.31E-17	7.48E-17	3.11E-17	0.00

Branching Yields

States	S <sub>1</sub> <sup>0</sup>	S <sub>1</sub> <sup>1</sup>	S <sub>1</sub> <sup>2</sup>
S <sub>0</sub>	0.05	0.30	0.99
S <sub>GSI</sub>	0.28	0.61	0.00
I <sub>0</sub>	0.26	0.06	0.00
S <sub>1</sub> <sup>i+1</sup>	0.41	0.02	-
lifetime	0.6	4.6	40.0

# Target Analysis - 490 nm



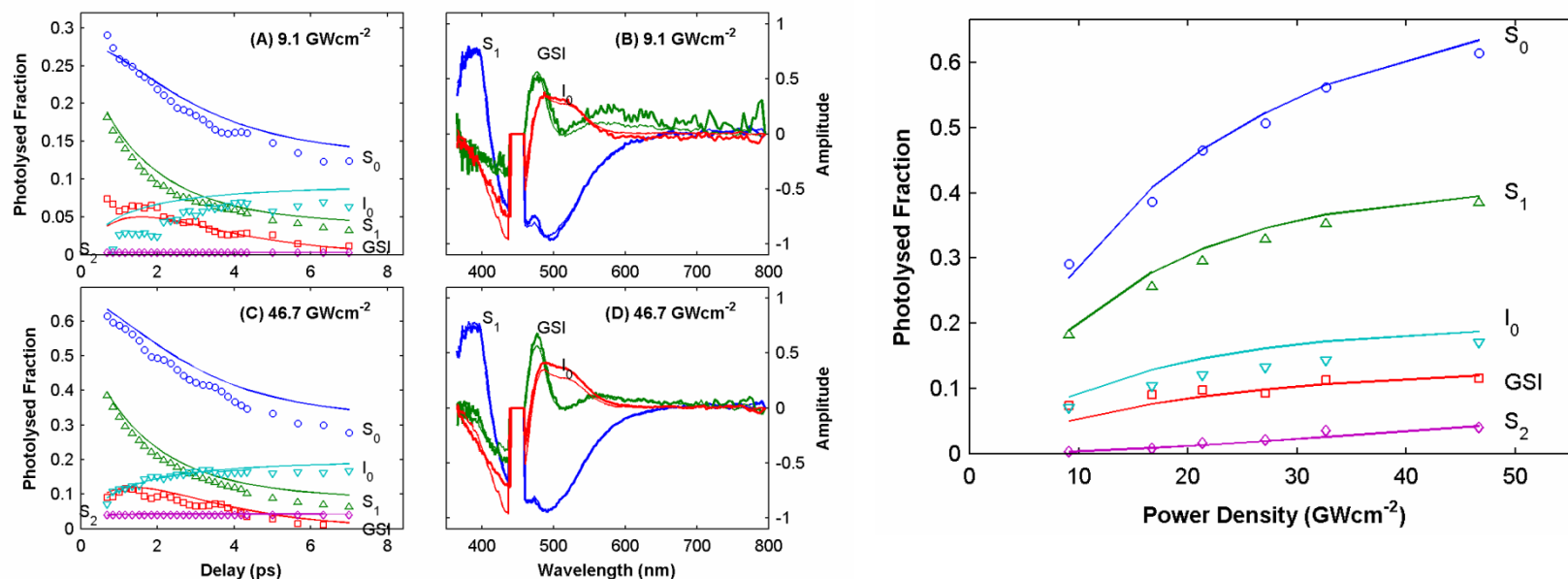
Cross-section  
(cm<sup>2</sup>/molecule)

$\sigma_{01s}$	$\sigma_{10s}$	$\sigma_{12s}$	$\sigma_{21s}$	$\sigma_{1gsi}$	$\sigma_{gsi2}$
1.26E-17	2.09E-16	8.41E-18	0.00	6.80E-17	2.48E-16

Branching Yields

States	S <sub>1</sub> <sup>0</sup>	S <sub>1</sub> <sup>1</sup>	S <sub>1</sub> <sup>2</sup>
S <sub>0</sub>	0.06	0.33	0.00
S <sub>GSI</sub>	0.00	0.41	1.00
I <sub>0</sub>	0.27	0.00	0.00
S <sub>1</sub> <sup>i+1</sup>	0.67	0.26	-
lifetime	1.1	2.5	40.0

# Target Analysis - 450 nm

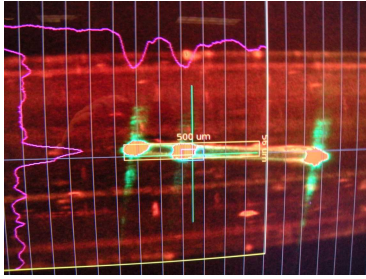


Cross-section  
( $\text{cm}^2/\text{molecule}$ )

$\sigma_{01s}$	$\sigma_{10s}$	$\sigma_{12s}$	$\sigma_{21s}$
1.68E-16	7.04E-17	1.33E-17	0.00

Branching Yields

States	$S_1^0$	$S_1^1$	$S_1^2$
$S_0$	0.00	0.02	0.18
$S_{\text{GSI}}$	0.13	0.52	0.08
$I_0$	0.15	0.22	0.74
$S_1^{i+1}$	0.72	0.24	-
lifetime	0.4	1.7	30.0

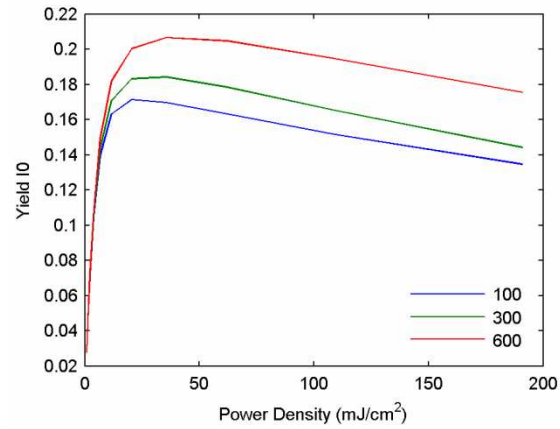
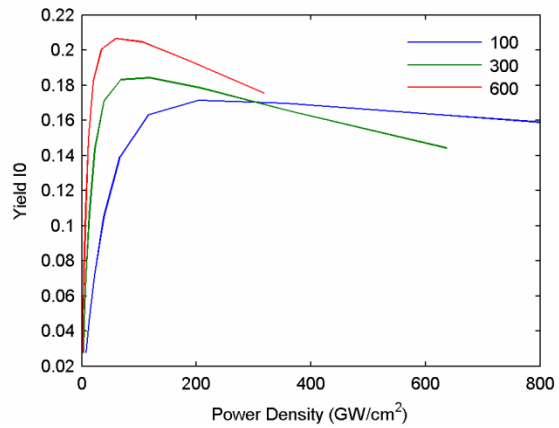
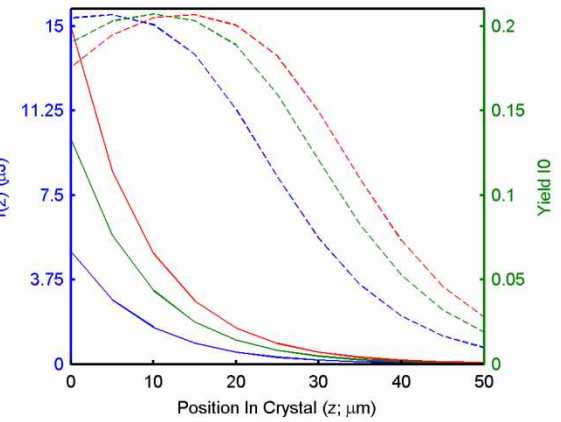
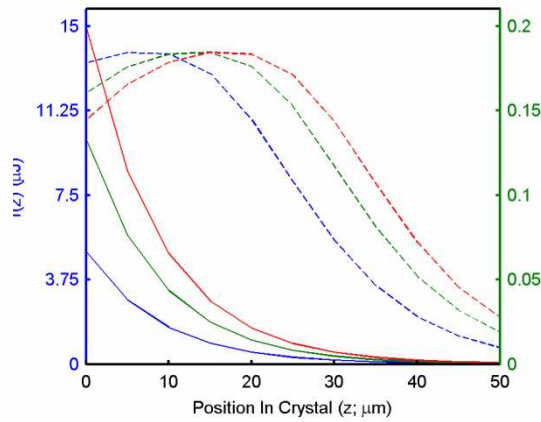
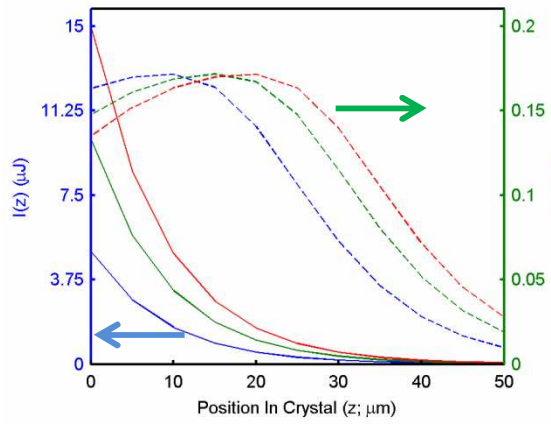


# I0 Yield

100 fs

300 fs

600 fs





December 2010:xpp23410

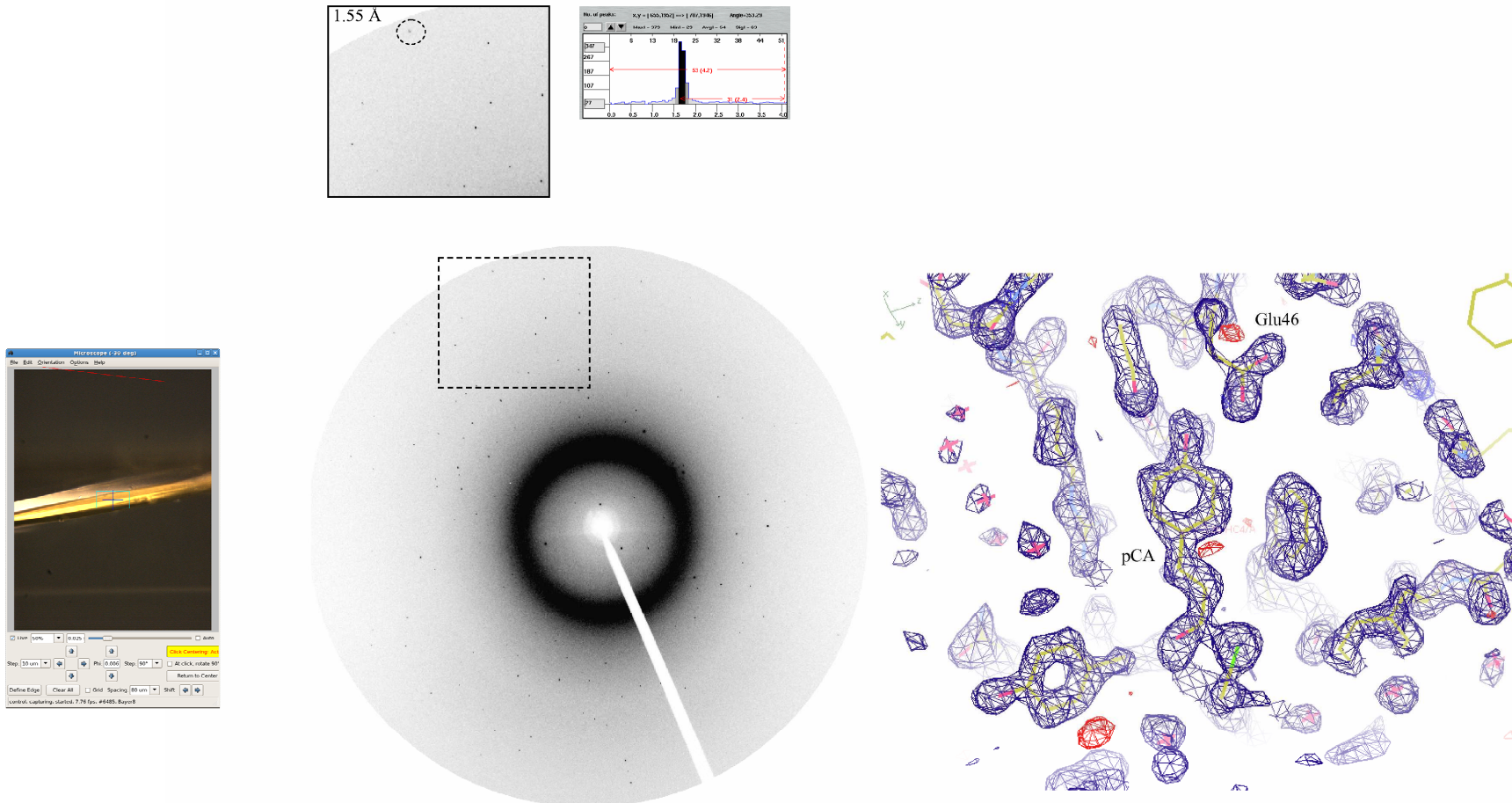


Figure 4. Diffraction of P63 PYP crystals at the XPP beamline, at 8.989 keV, 75 fs and a 2eV bandpass using the 111 monochromator at a detector distance of 68.8mm (1.55 Å resolution). Data was scaled, merged (40 degree range at 0.2 degree interval, 85% completeness, 15026 unique reflections, 1.55 Å resolution) and phased by rigid body refinement ( $R = 0.38$ ,  $R_{\text{free}} = 0.38$ ). Preliminary maps are shown for the ground state (2Fo-Fc; blue) and Fourier difference density at 5 ps delay ( $F_{\text{5ps}} - F_{\text{off}}$ ; red), with signals visible at the chromophore (pCA) and Glu46. Poor statistics of the preliminary data are caused by collecting with rotations larger than the mosaic spread (which is 0.1 degree)

April 2012: xpp44112

## Signal to noise considerations for single crystal femtosecond time resolved crystallography of the Photoactive Yellow Protein

Jasper J. van Thor,<sup>a\*</sup> Mark M. Warren,<sup>a</sup> Craig N. Lincoln,<sup>a</sup>  
5 Matthieu Chollet,<sup>b</sup> Henrik Till Lemke,<sup>b</sup> David M. Fritz,<sup>b</sup> Marius  
Schmidt,<sup>c</sup> Jason Tenboer,<sup>c</sup> Zhong Ren,<sup>e</sup> Vukica Srajer,<sup>e</sup> Keith  
Moffat<sup>d,e</sup> and Tim Graber<sup>e,f</sup>

<sup>a</sup> Imperial College London, Division of Molecular Biosciences, South Kensington Campus, Lo  
SW7 2AZ

10 <sup>b</sup> LCLS, SLAC National Accelerator Laboratory, Menlo Park, California 94025, USA

<sup>c</sup> Department of Physics, University of Wisconsin-Milwaukee, 1900 E. Kenwood Blvd, Milwau  
WI 53211, USA

<sup>d</sup> Department of Biochemistry and Molecular Biology, and Institute for Biophysical Dynamics,  
University of Chicago, 920 East 58th Street, Chicago, Illinois 60637, United States

15 <sup>e</sup> Center for Advanced Radiation Sources, The University of Chicago, 5640 South Ellis Avenue  
Chicago, Illinois 60637, United States

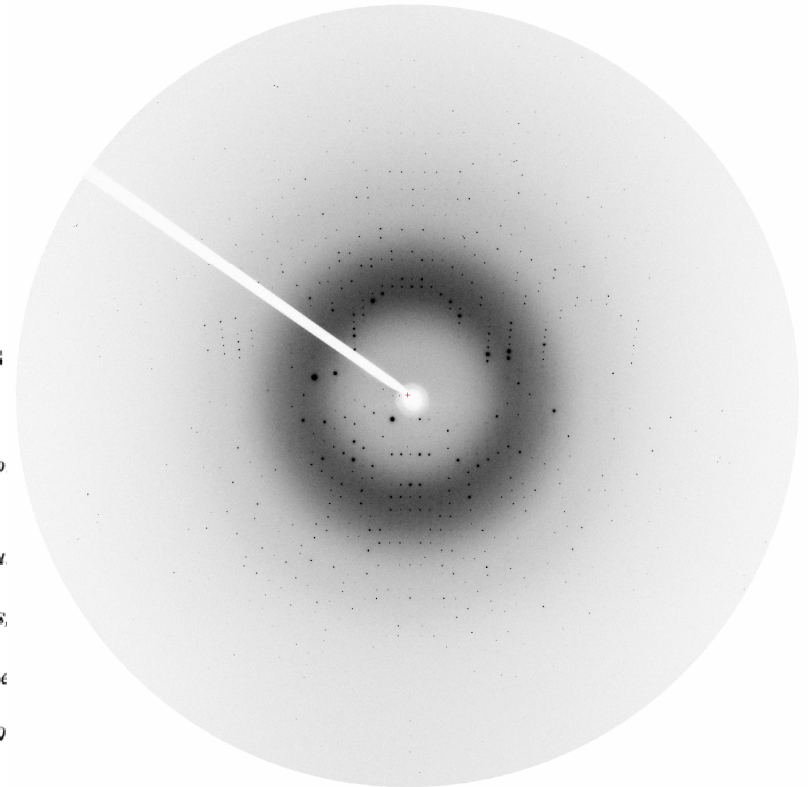
<sup>f</sup> Current address: Washington State University c/o Argonne National Laboratory Bld. 438F9  
Cass Ave Argonne, IL 60439

*Faraday Disc.*, 2014, DOI: 10.1039/C4FD00011K

X-rays: 1.3009 Å, ~70 fs, 1.6 eV bandpass, 40x40 μm

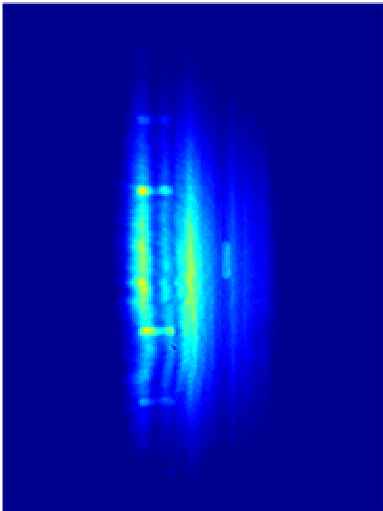
Pump-probe cross-correlation: ~ 280fs

Pump-probe delays: 600 fs & 900 ns

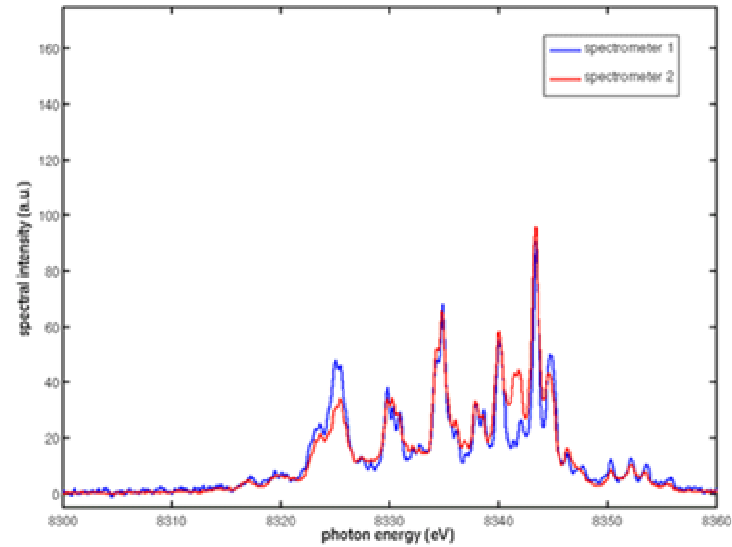


# Crystallographic data quality and reflection amplitude noise

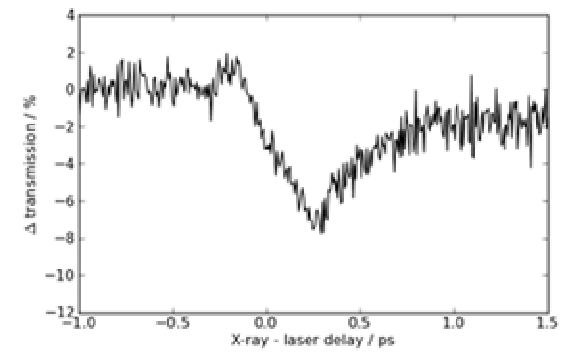
Spatial



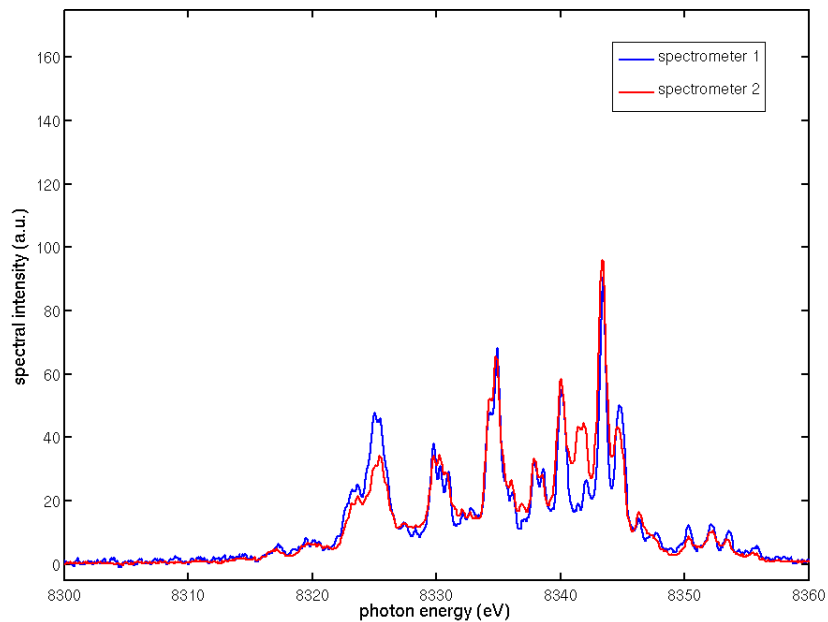
Spectral



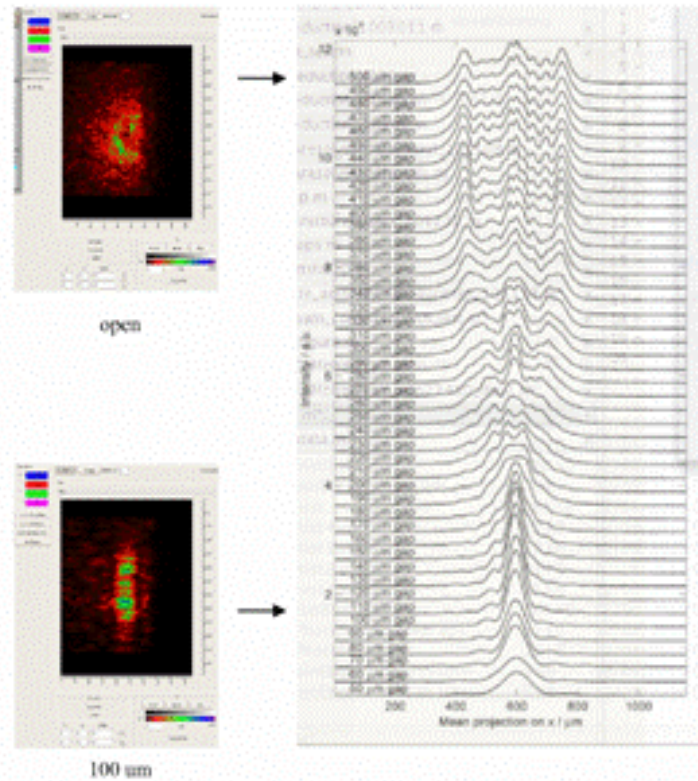
Temporal



# Crystallographic data quality and reflection amplitude noise: Energy selection and spatial selection



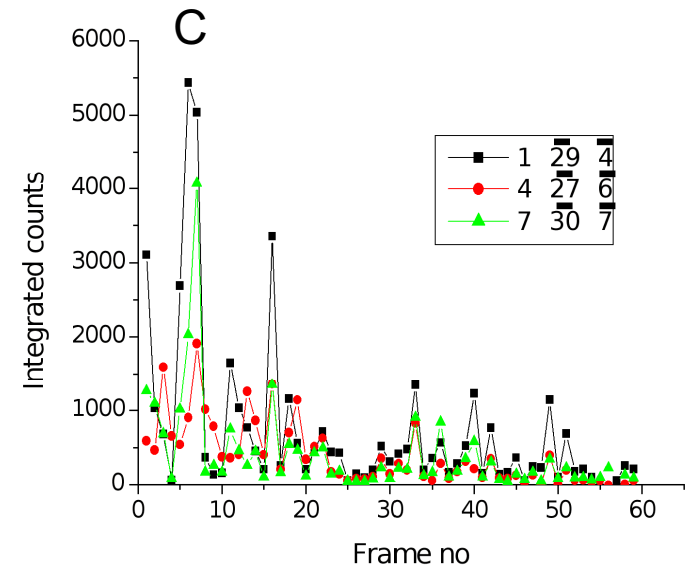
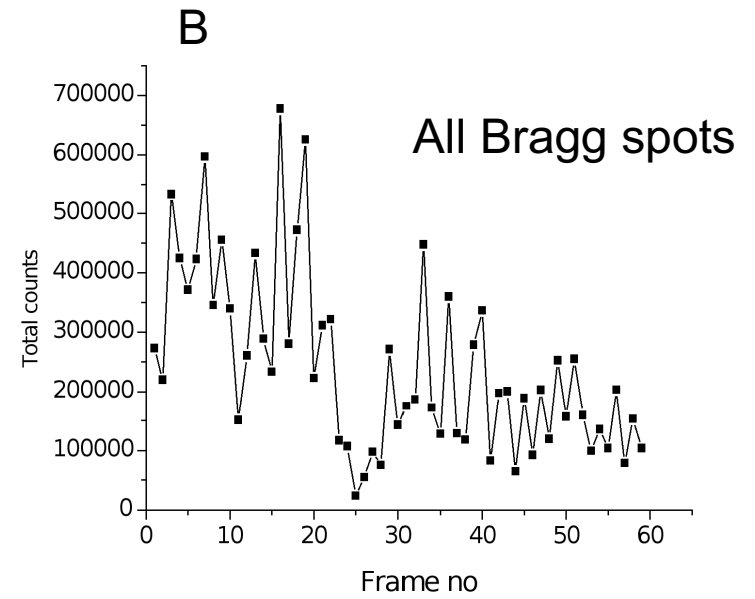
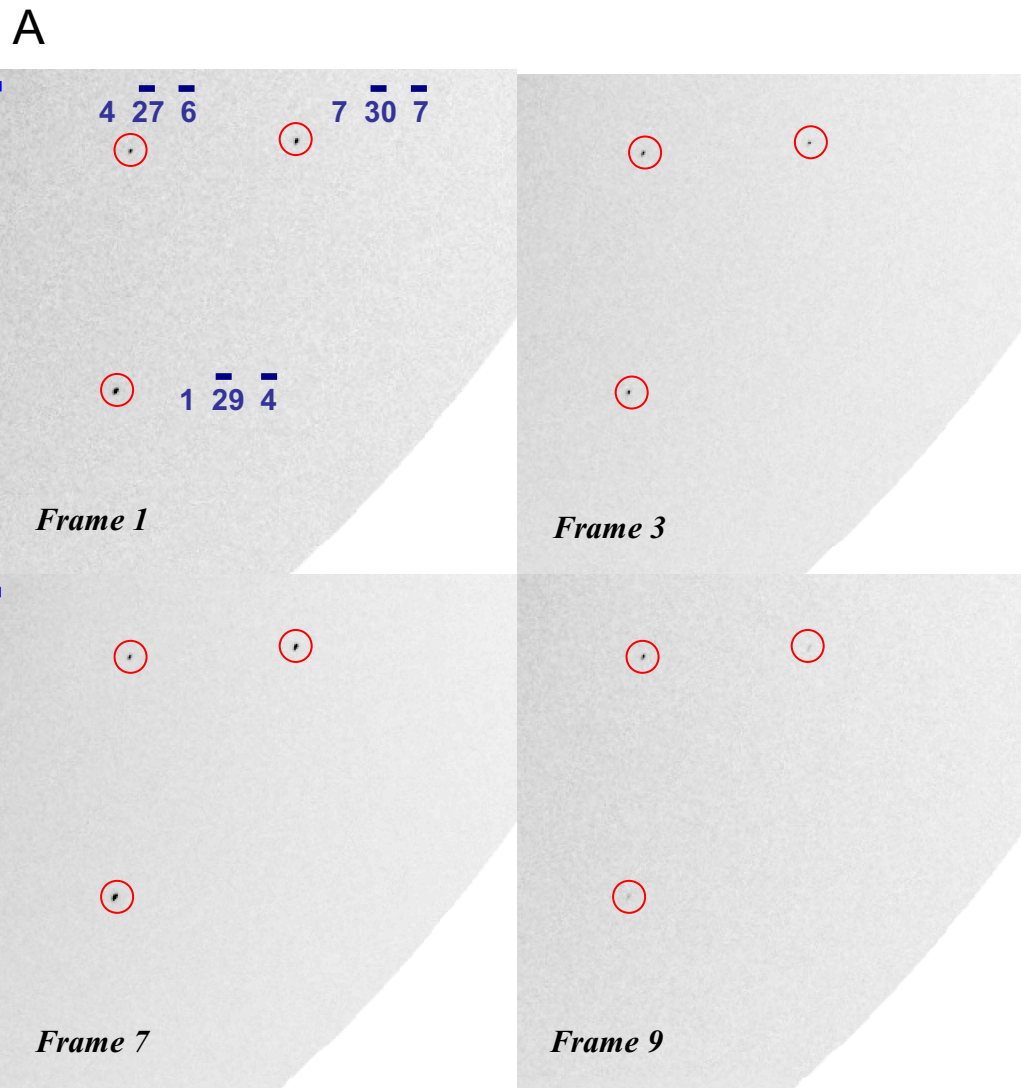
***Spectral Jitter***



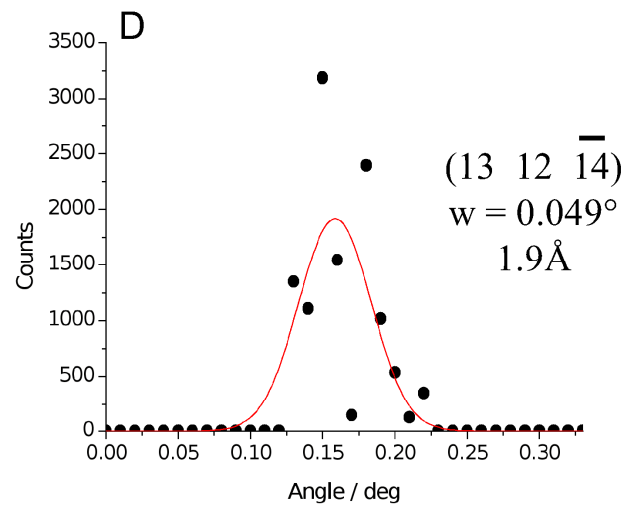
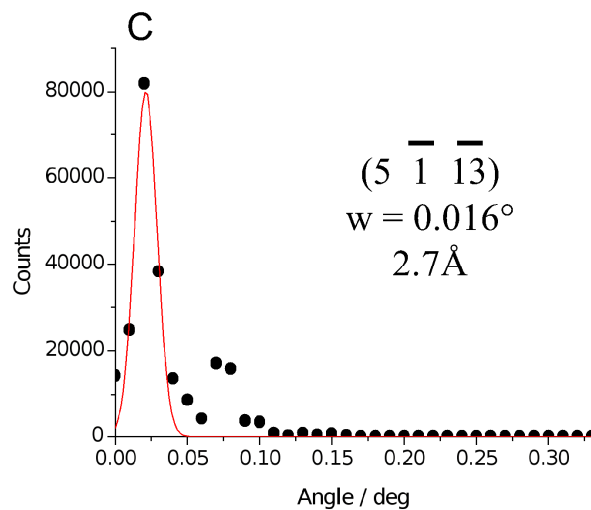
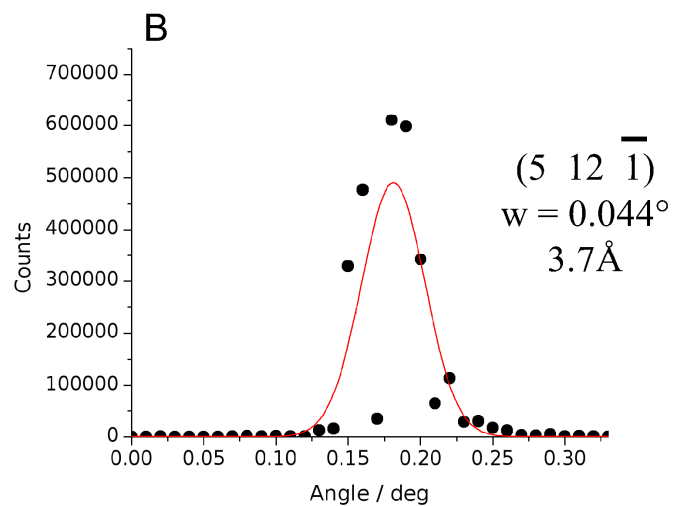
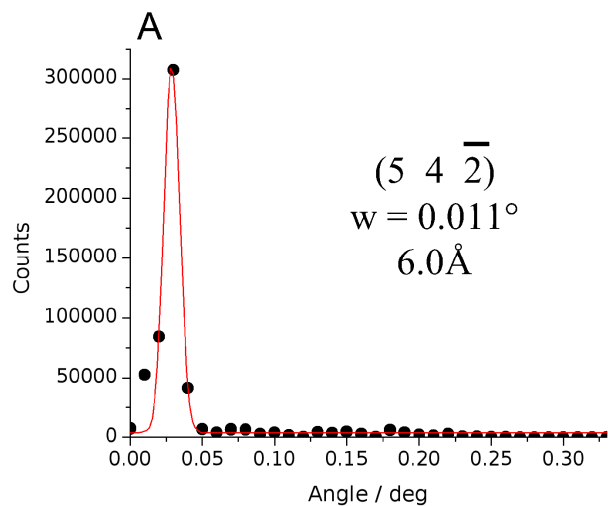
***Mode distortions***



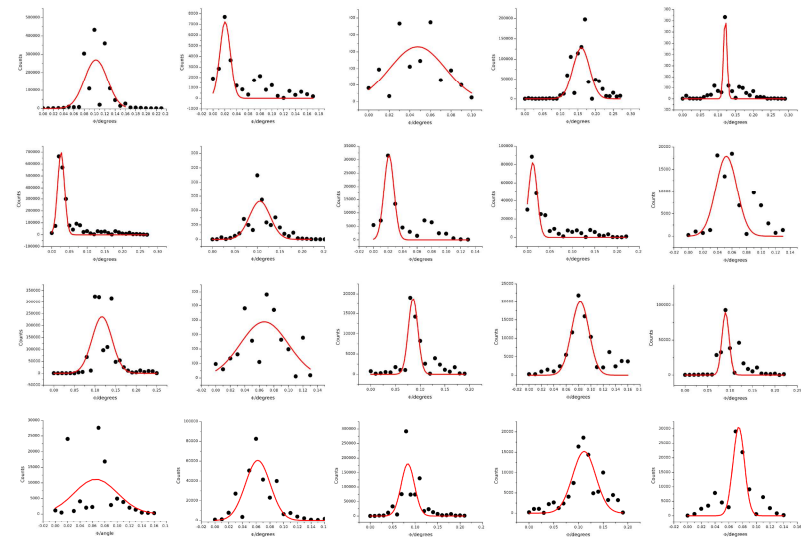
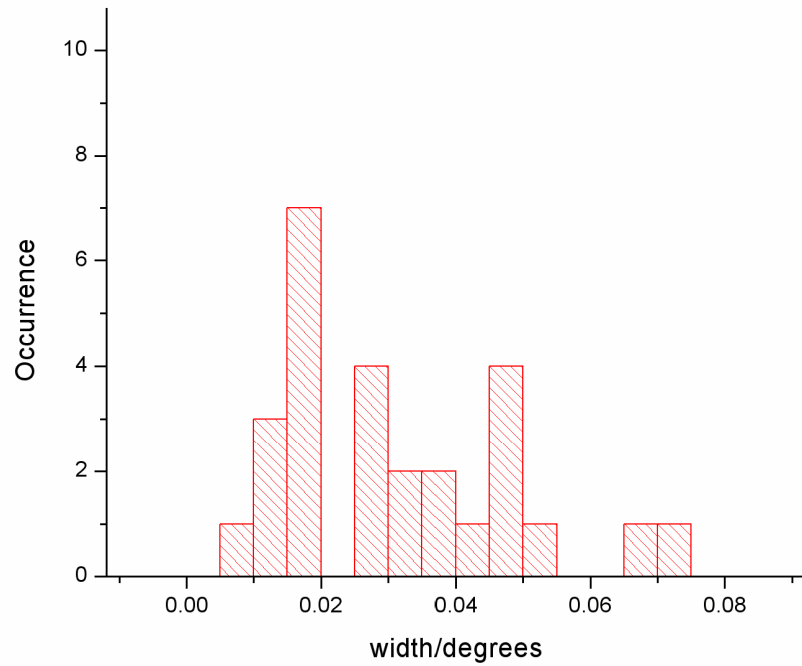
Static crystal orientation, monochromator energy selection 1.6 eV bandpass



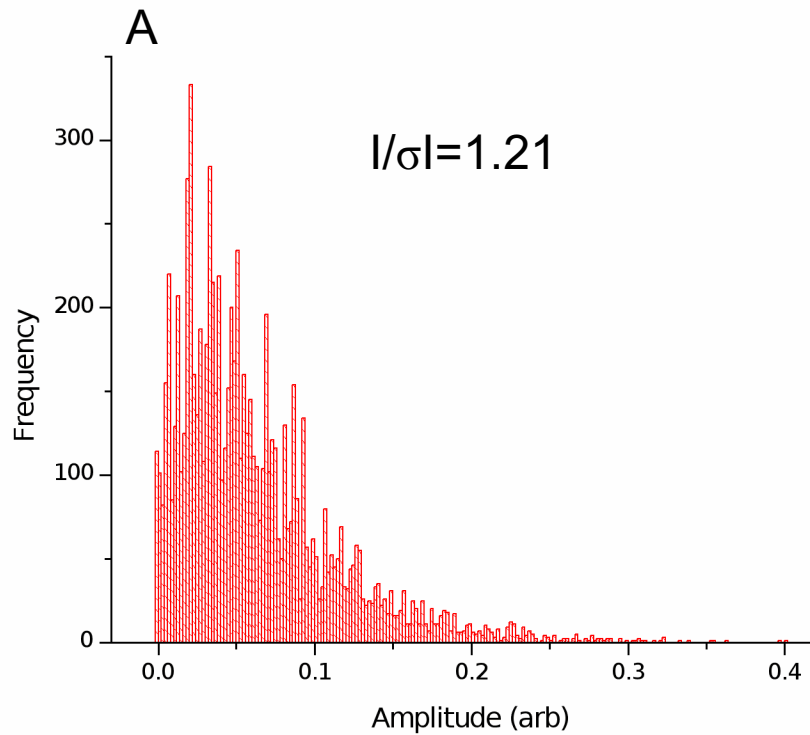
A convergence of  $0.007^\circ$  allows rocking curve measurements



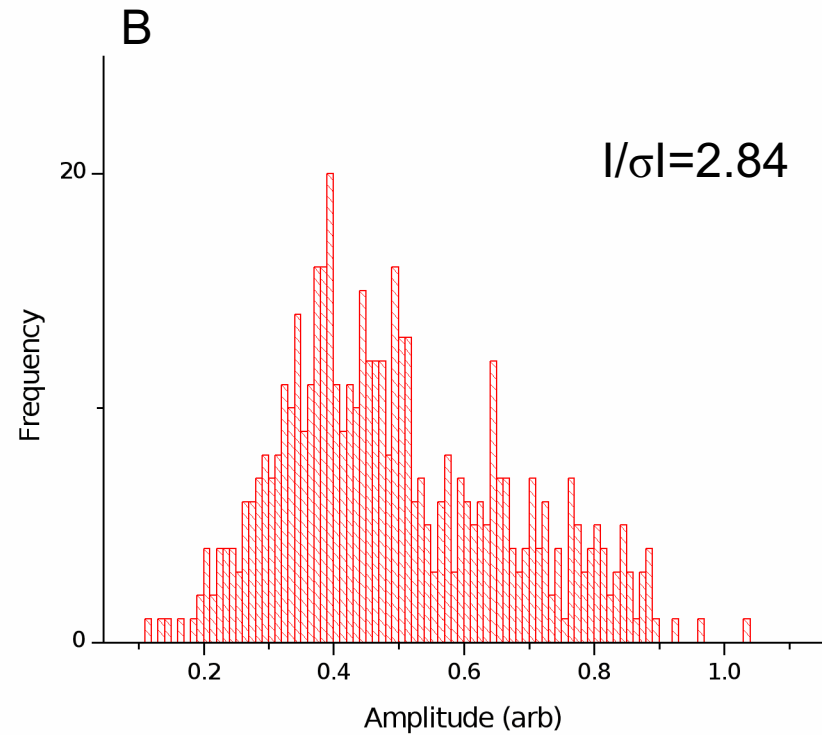
# Spread and line defects of rocking curve widths



## X-ray intensity noise



xpp44112  
8,475 pulse intensities  
from SASE mode at  
9.47 keV with a  
monochromator.



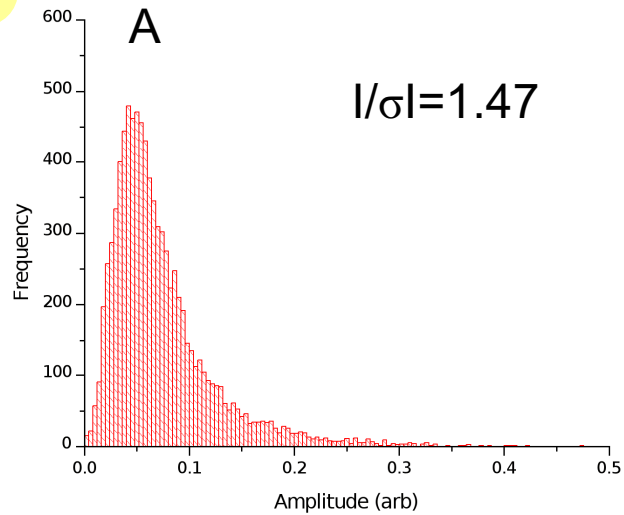
500 pulses from **self-seeded**  
mode at 8.4 keV using the entire  
length of the undulator  
Courtesy of Paul Emma and  
Alberto Lutman, LCLS



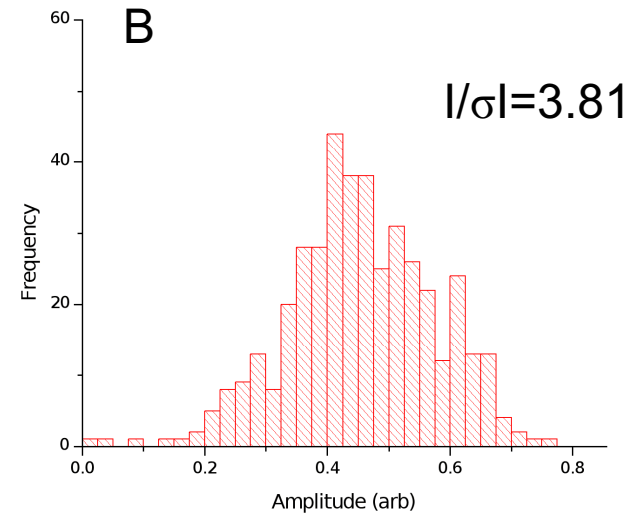
**MODEL:**  
Integrated intensity  
0.01° rotation/shot

0.04° mosaic  
spread

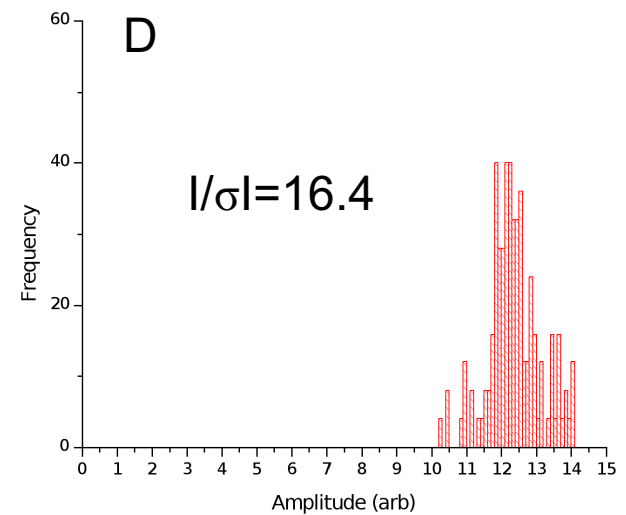
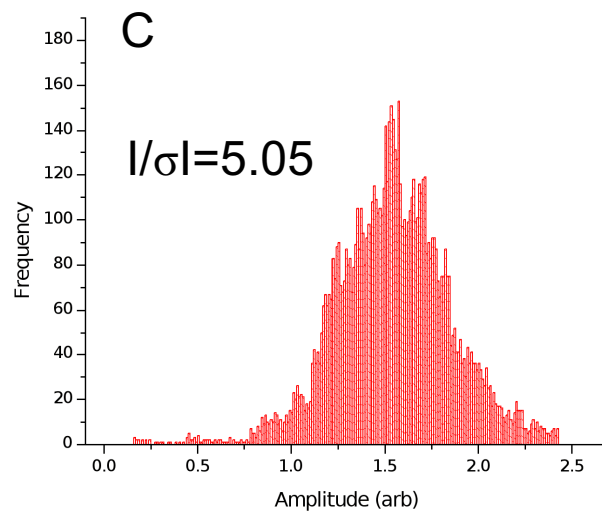
SASE



Self seeded



0.4° mosaic  
spread



**Table 1** Data reduction statistics

	Multi-crystal dataset	Single-crystal dataset
# of frames / # of crystals	96/6	23/1
Space group	P6 <sub>3</sub>	P6 <sub>3</sub>
Unit cell (a,b,c(Å);α,β,γ(°))	66.934, 66.934, 40.986 90.000 90.000, 120.000	66.867, 66.867, 40.985 90.000 90.000, 120.000
Resolution range (Å)	57.97-1.60	100-1.50
Reflections (Total/Unique)	137,459/13,877	20,145/16,947
Rejected outlier (#/%)	9,986/7.3	1,286/6.4
Completeness <sup>a</sup>	84.3(63.6)	51.4(21.6)
I/σI	3.1(1.4)	7.1(1.5)
Average Multiplicity	4.8	1.2
R <sub>merge</sub> <sup>b</sup>	0.400 (0.534)	0.239 (0.470)
R <sub>meas</sub> <sup>c</sup>	0.445 (0.614)	N.D.
R <sub>p.i.m.</sub> <sup>d</sup>	0.190 (0.289)	N.D.
PCV <sup>e</sup>	0.635 (0.822)	N.D.
R <sub>cryst</sub> /R <sub>free</sub> (%)	0.26 (0.23)	N.D.

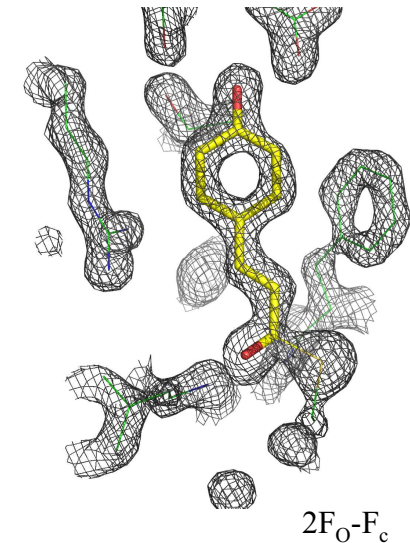
<sup>a</sup>Numbers appearing in parenthesis are for the high resolution shell.

$$^b R_{merge}(I) = \frac{\sum_{hkl} \sum_i |I_i(hkl) - \langle I(hkl) \rangle|}{\sum_{hkl} \sum_i I_i(hkl)}$$

$$^c R_{meas}(I) = \frac{\sum_{hkl} \sum_i \left(\frac{n}{n-1}\right)^{1/2} |I_i(hkl) - \langle I(hkl) \rangle|}{\sum_{hkl} \sum_i I_i(hkl)}$$

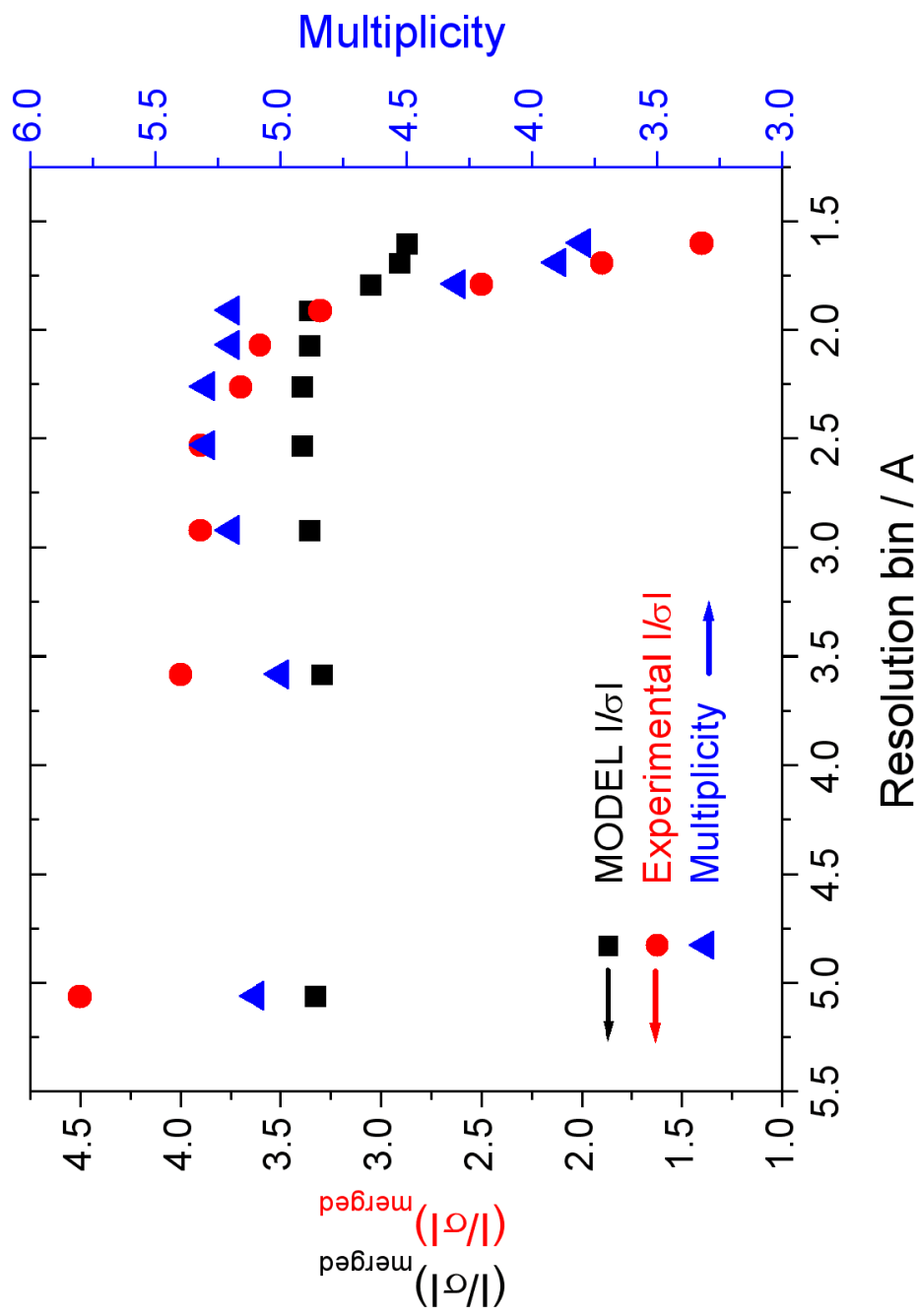
$$^d R_{p.i.m.}(I) = \frac{\sum_{hkl} \sum_i \left(\frac{1}{n-1}\right)^{1/2} |I_i(hkl) - \langle I(hkl) \rangle|}{\sum_{hkl} \sum_i I_i(hkl)}$$

$$^e PCV(I) = \frac{\sum_{hkl} \left(\frac{1}{n-1} \sum_i (I_i(hkl) - \langle I(hkl) \rangle)^2\right)^{1/2}}{\sum_{hkl} \langle I(hkl) \rangle}$$



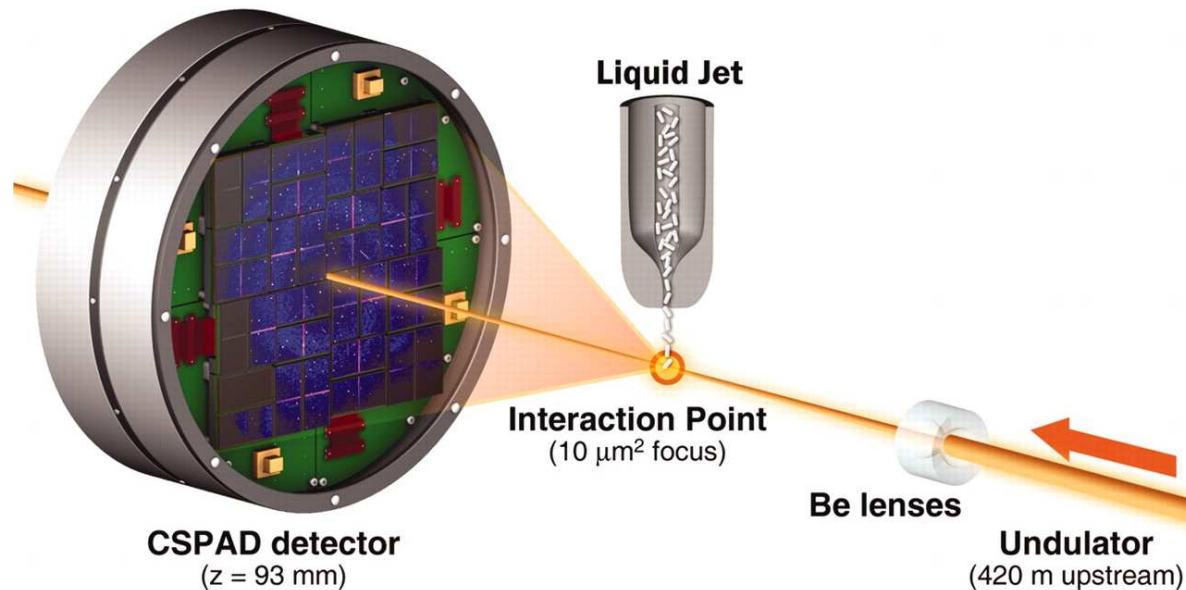
$$\left(\frac{\langle I_o \rangle}{\langle \sigma I \rangle}\right)_{merged} = n^{1/2} \left(\frac{\langle I_o \rangle}{\langle \sigma I \rangle}\right)_{unmerged}$$

$$\text{e.g. } \sqrt{4.8} \left(\frac{I}{\sigma I}\right) = 3.22$$



$$\left(\frac{\langle I_o \rangle}{\langle \sigma I \rangle}\right)_{merged} = n^{1/2} \left(\frac{\langle I_o \rangle}{\langle \sigma I \rangle}\right)_{unmerged}$$

## Serial Femtosecond Crystallography: Monte-Carlo approach to time resolved measurements



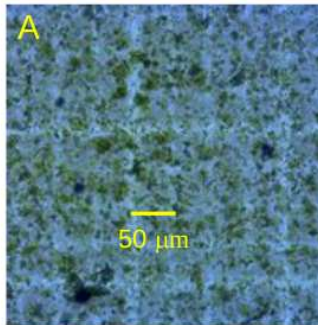
Barends et al. Nature **505**(7482), 244-247 (2013).

-SAD Phasing of gadolinium complex of lysozyme resolves  $\Delta/I \sim 20\%$

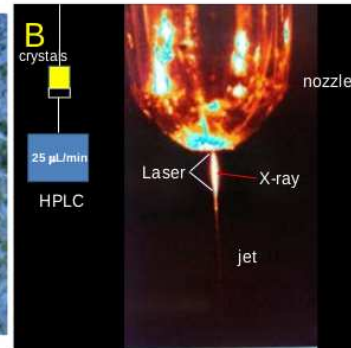
-2,402,199 diffraction patterns.

-59,667 of which were indexed and integrated

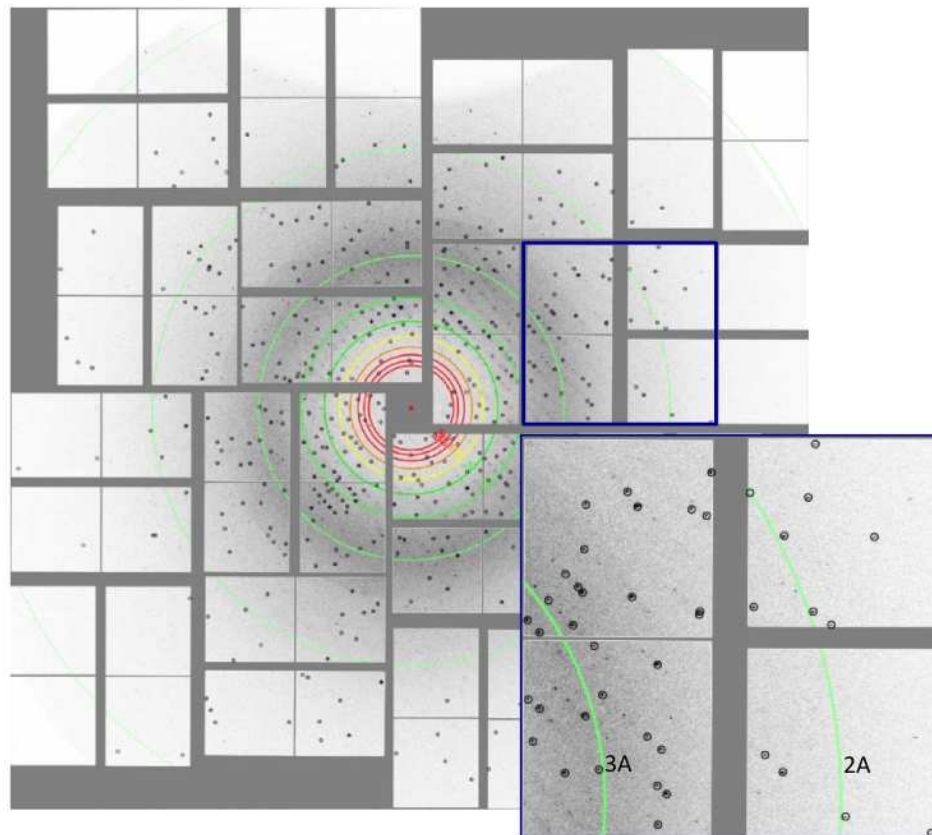
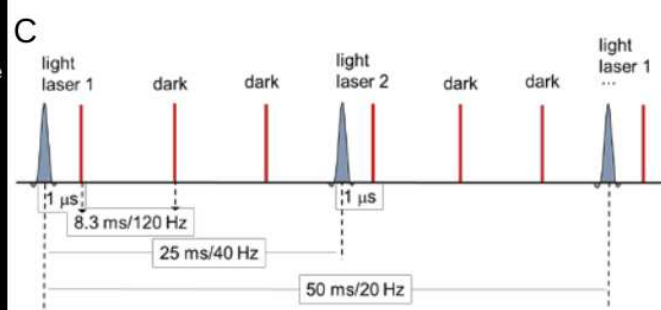
### Micro-crystals



### Jet



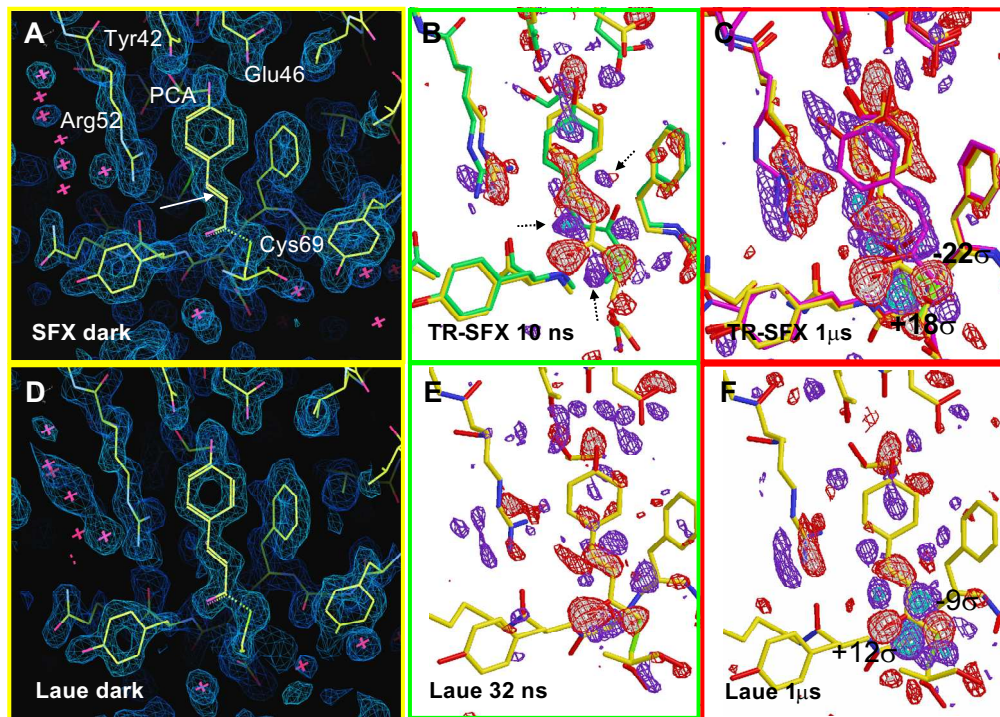
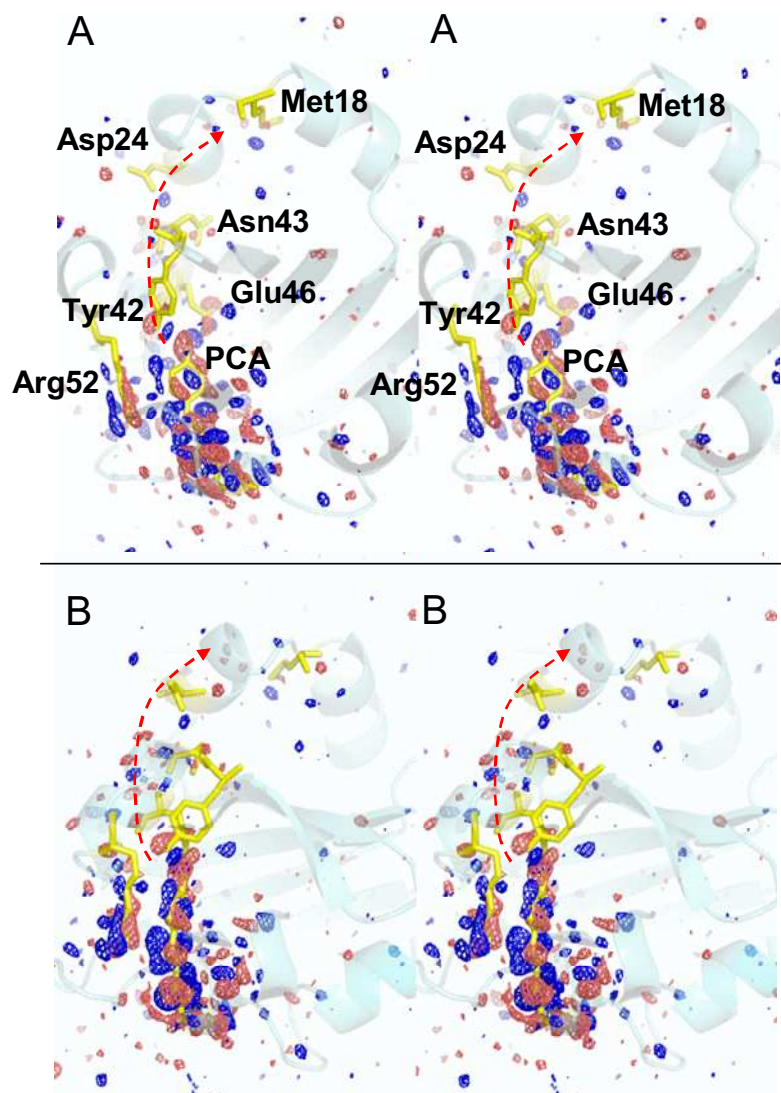
### Timing



CSPAD image of PYP diffraction

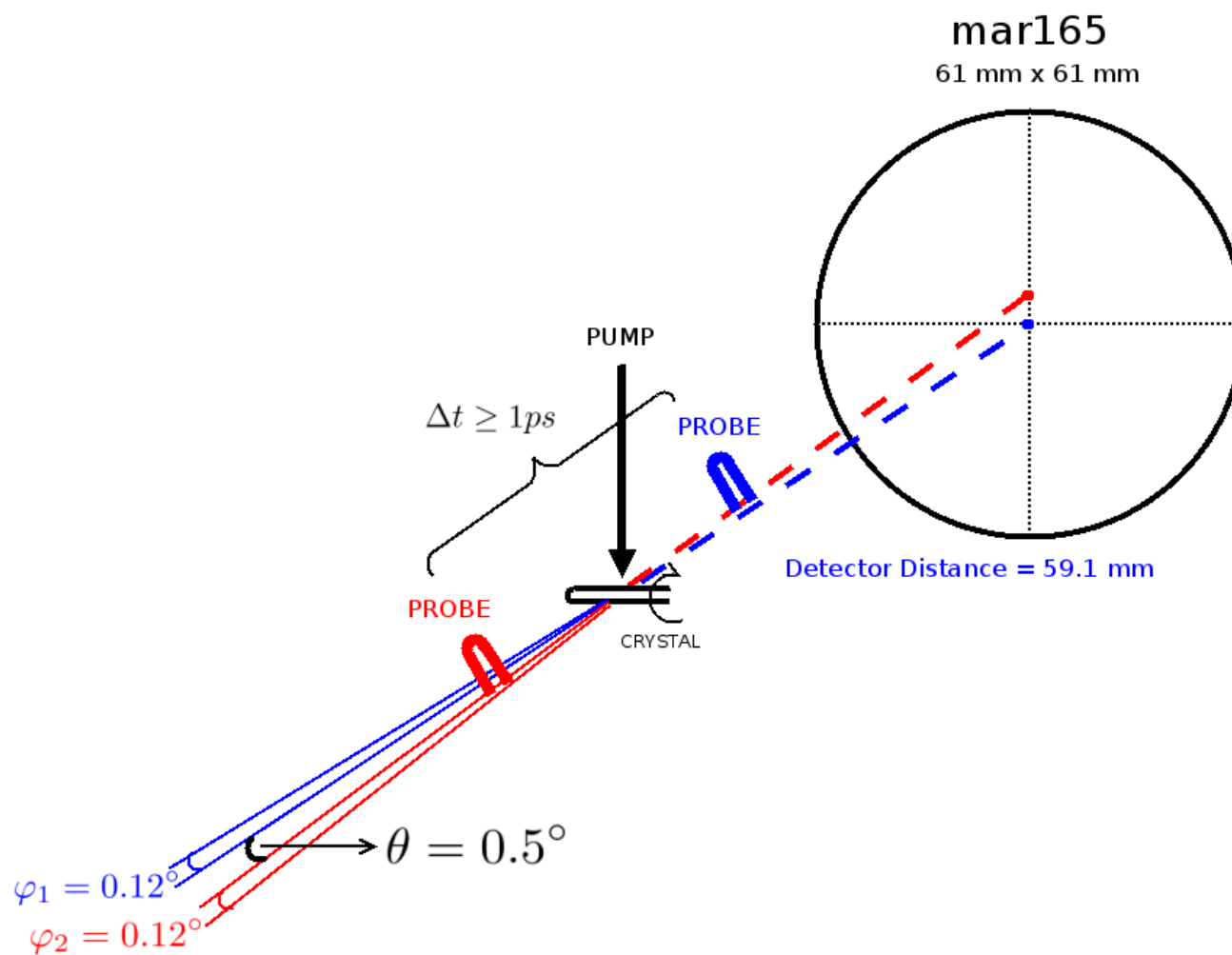


# Microsecond intermediates in PYP at 2Å resolution from SFX

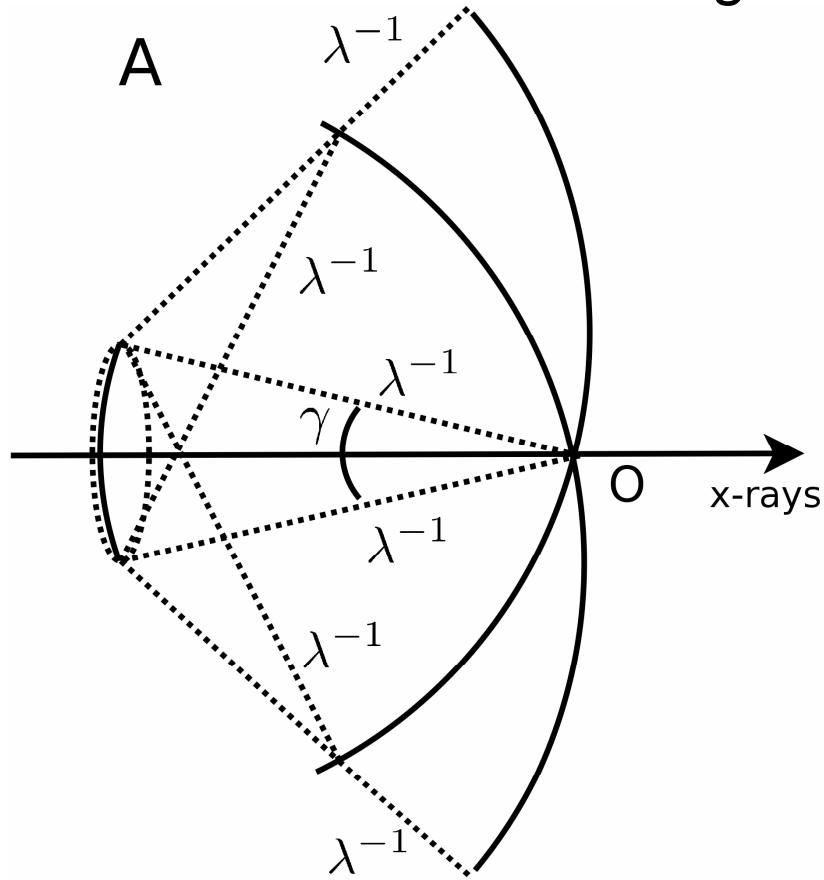




# Proposal for a Probe-Pump-Probe scheme: Ratiometric detection of $\Delta F$

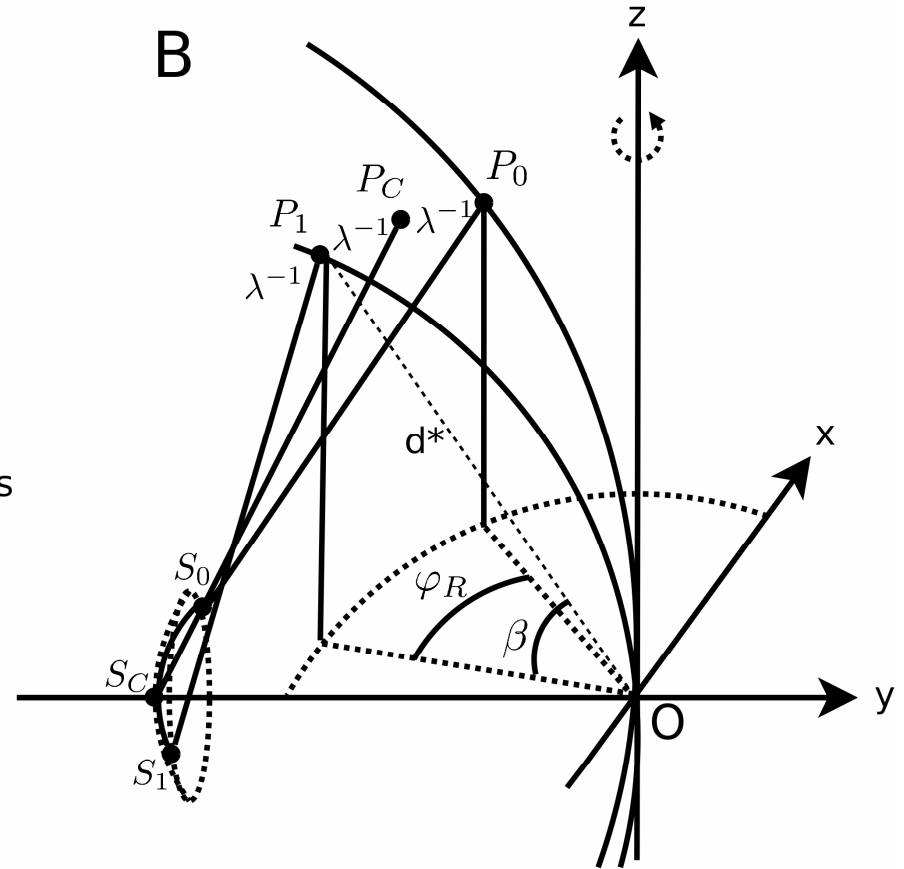


# Convergent Beam Method



$$\cos\left(\beta + \frac{\gamma}{2}\right) \leq \frac{\lambda d^*}{2} \leq \cos\left(\beta - \frac{\gamma}{2}\right)$$

Bragg conditions



$$\varphi_R \simeq L\left(\Delta d^* \cos\theta + \frac{\delta\lambda}{\lambda} d^* \sin\theta\right)$$

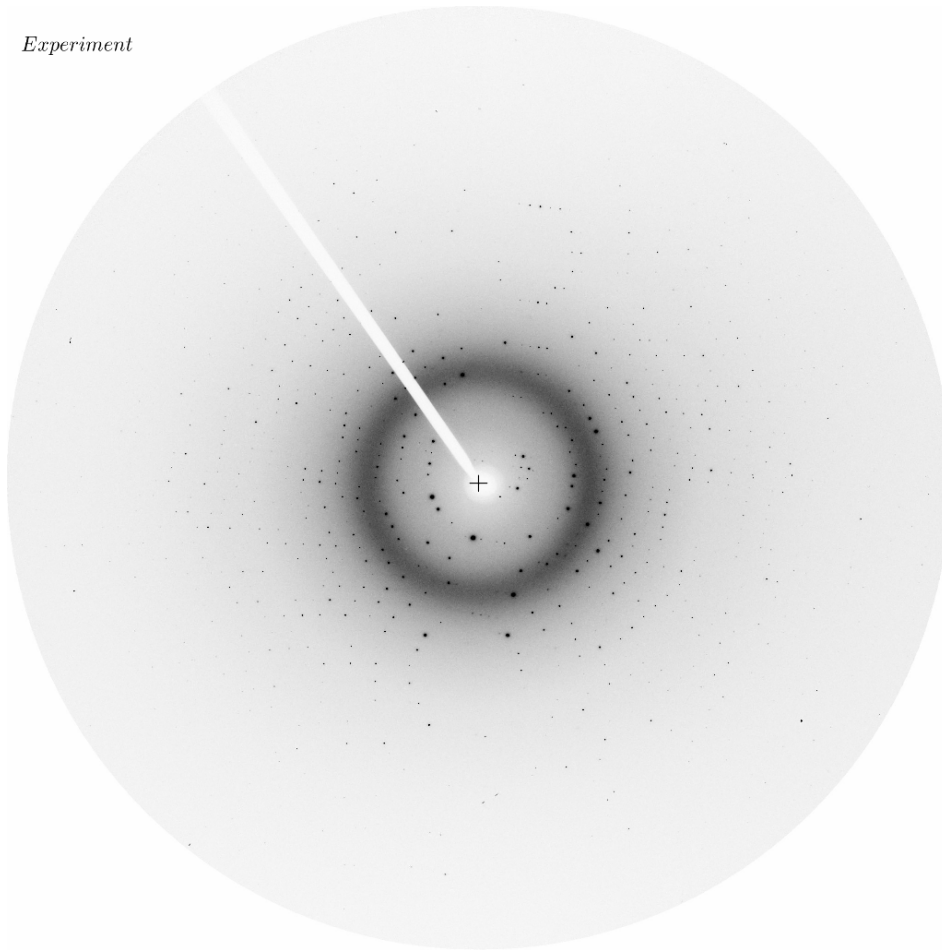
Reflecting Range

$$\Delta = \gamma + \eta$$

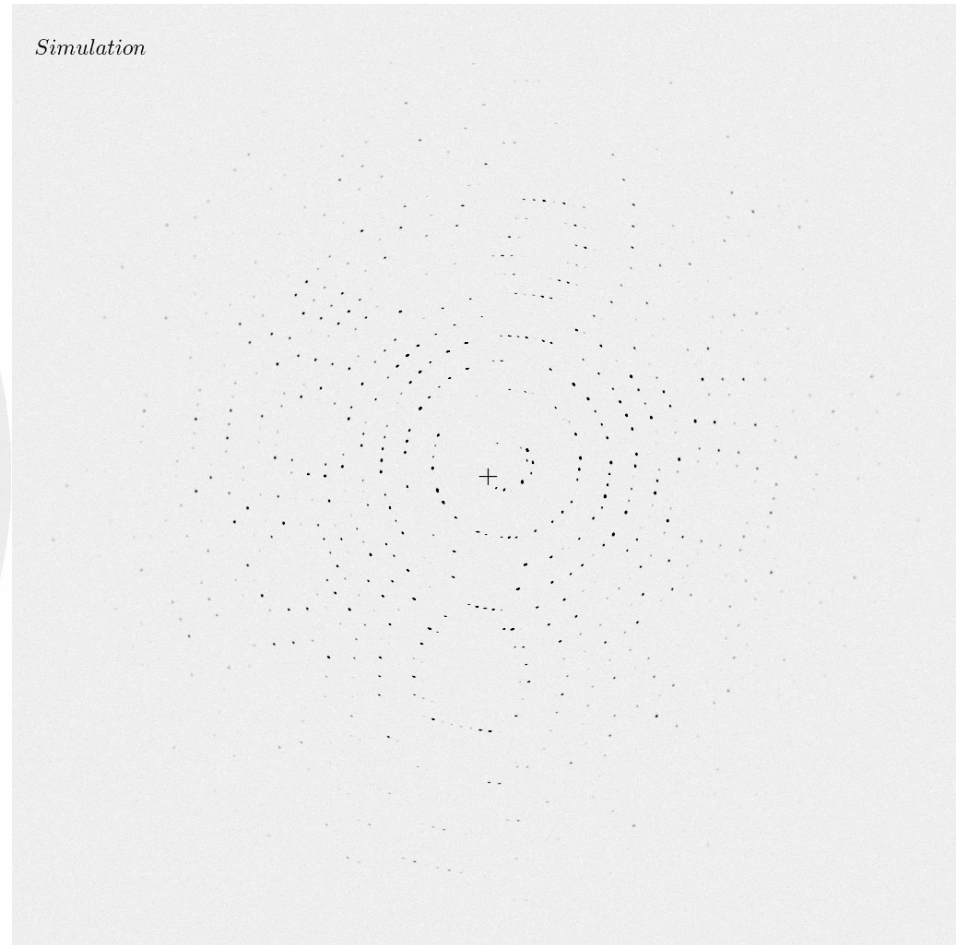
Cross-fire **and** mosaic spread

# Ray-tracing simulations of LCLS/XPP diffraction data Monochromatic and Rotation Method

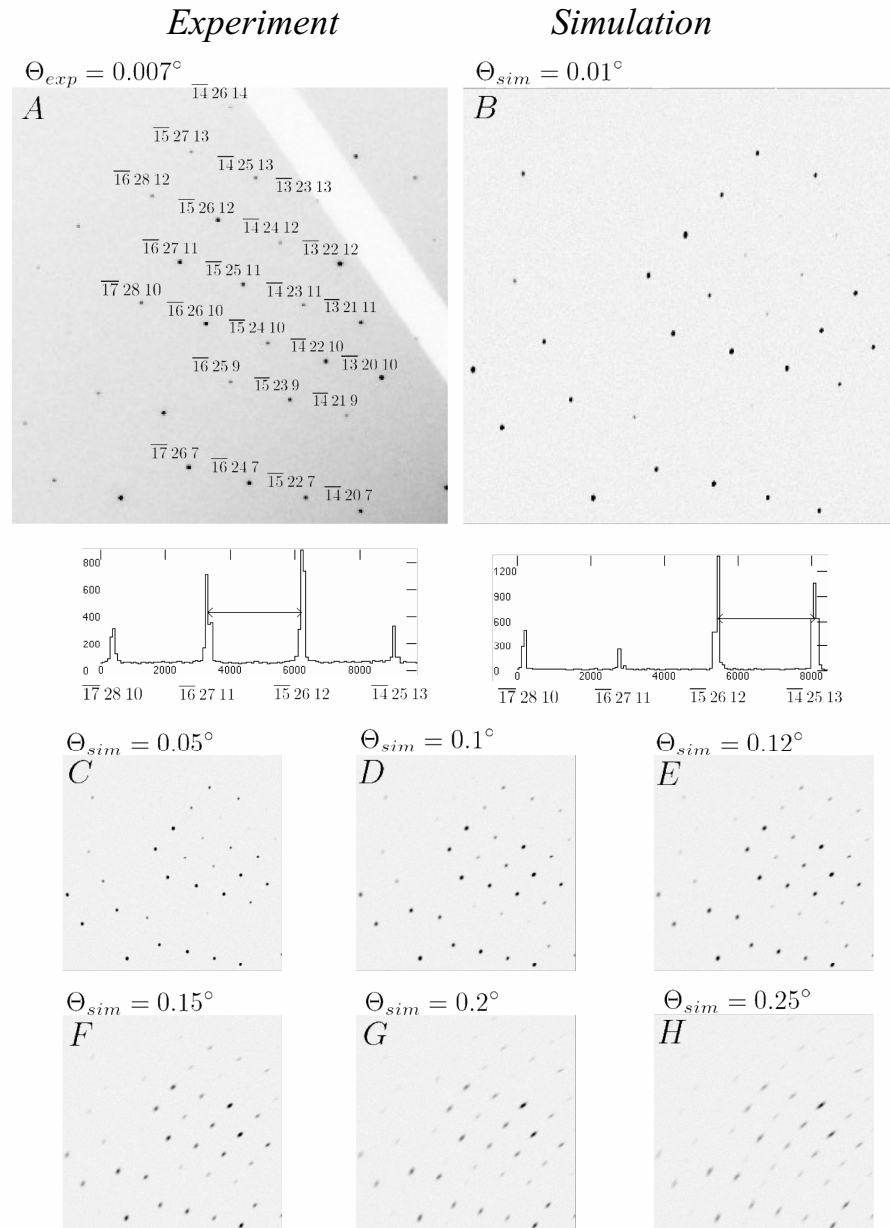
*Experiment*



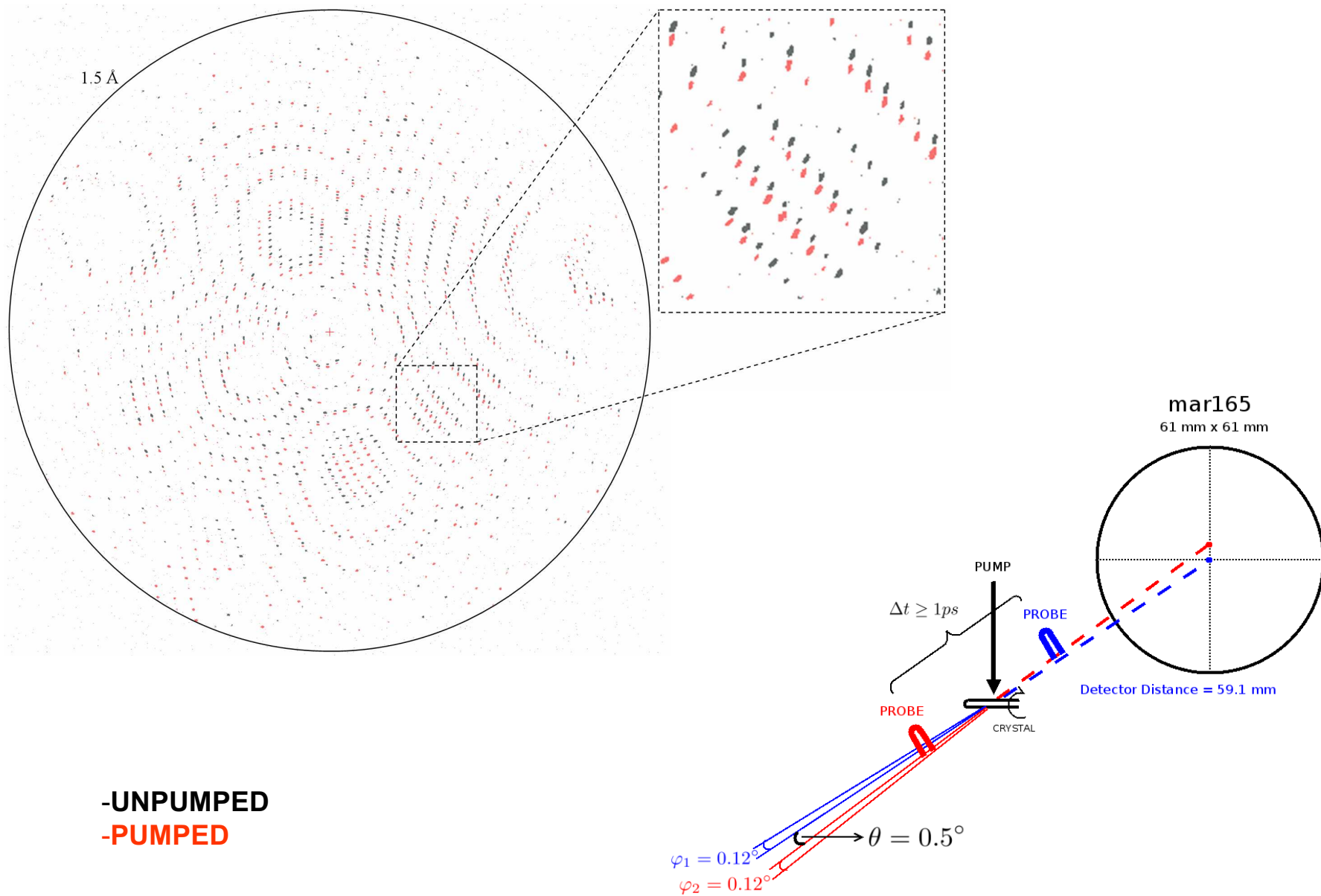
*Simulation*



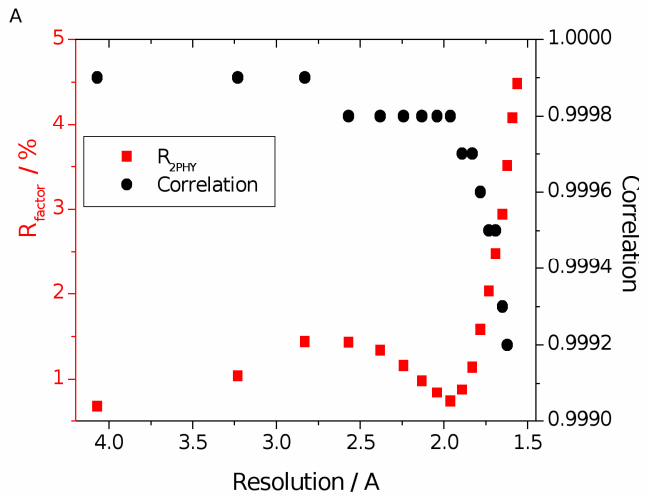
# Ray-tracing simulations of LCLS/XPP diffraction data: Convergence angle



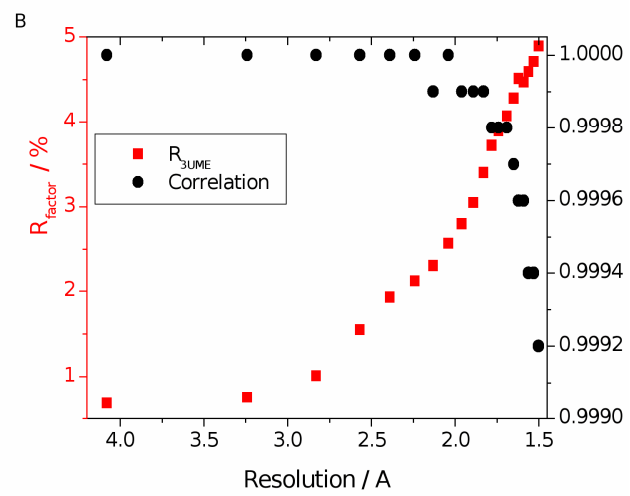
# Probe-Pump-Probe (Simulation to 1.5 Å resolution, 9.4 keV)



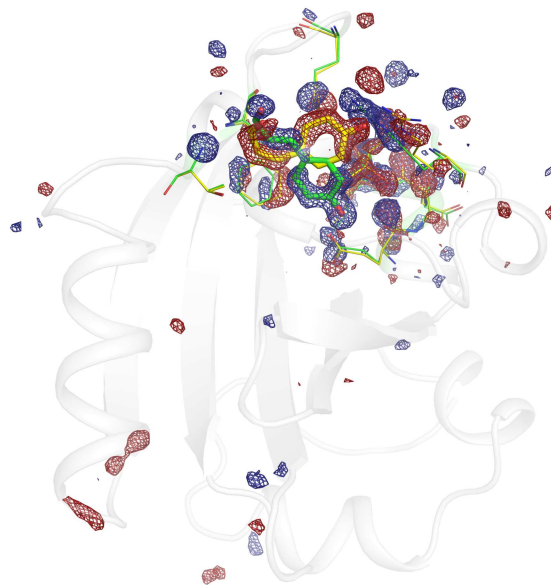
Unpumped



Pumped



Data correlation



Retrieved synthetic  
 $F_{\text{PUMPED}} - F_{\text{UNPUMPED}}$



## A split-beam probe-pump-probe scheme for femtosecond time resolved protein X-ray crystallography

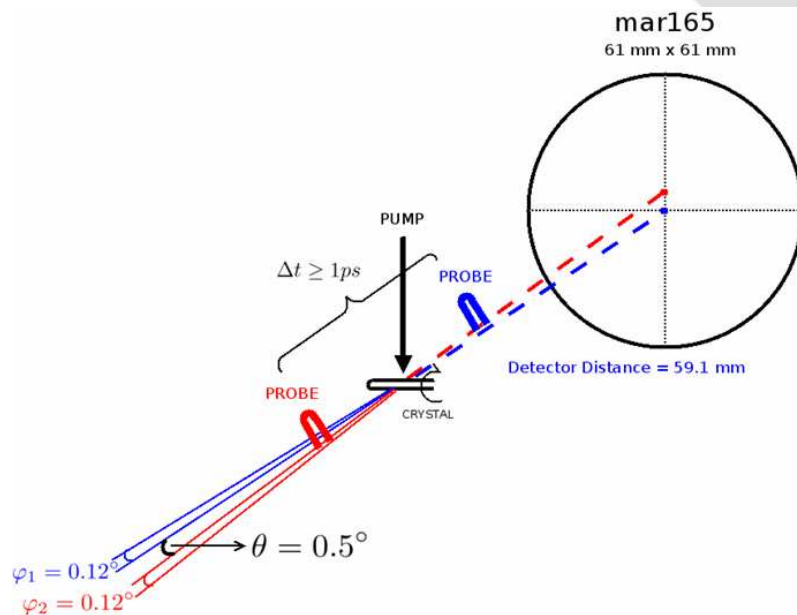
Jasper J. van Thor<sup>1,a)</sup> and Anders Madsen<sup>2</sup>

<sup>1</sup>*Division of Molecular Biosciences, Imperial College London, South Kensington Campus, SW7 2AZ London, United Kingdom*

<sup>2</sup>*European X-Ray Free-Electron Laser Facility, Albert-Einstein-Ring 19, 22761 Hamburg, Germany*

(Received 30 August 2014; accepted 9 January 2015; published online xx xx xxxx)

DOI: 10.1063/1.4906354

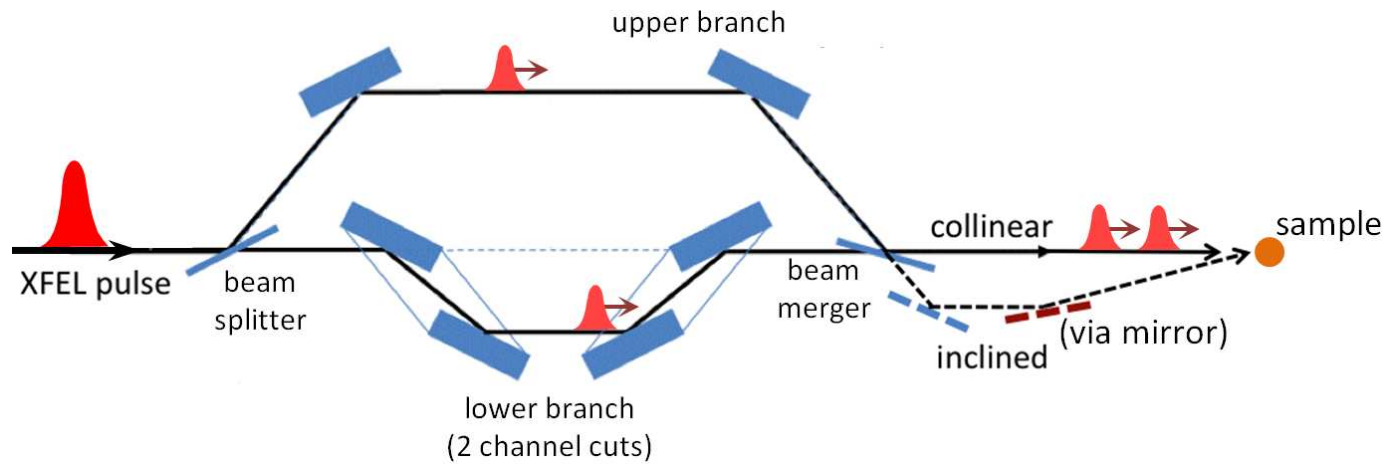


# MID station XFEL : SDL design

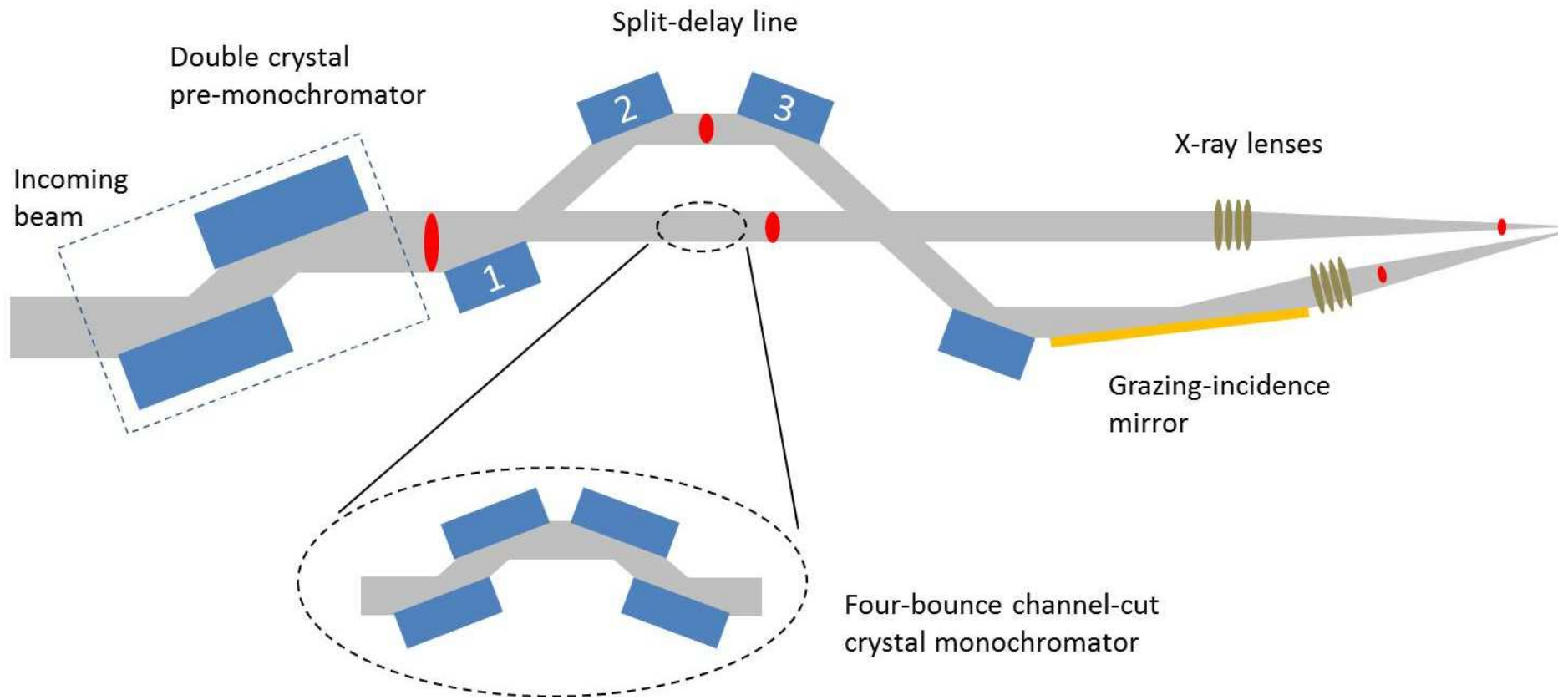
*Technical Design Report: Scientific Instrument MID*

*Madsen, A.; Hallmann, J. ; Roth, T. ; Ansalidi, G.*

*XFEL.EU Technical Report 1-191 (2013) [10.3204/XFEL.EU/TR-2013-005]*



# MID station XFEL : SDL design



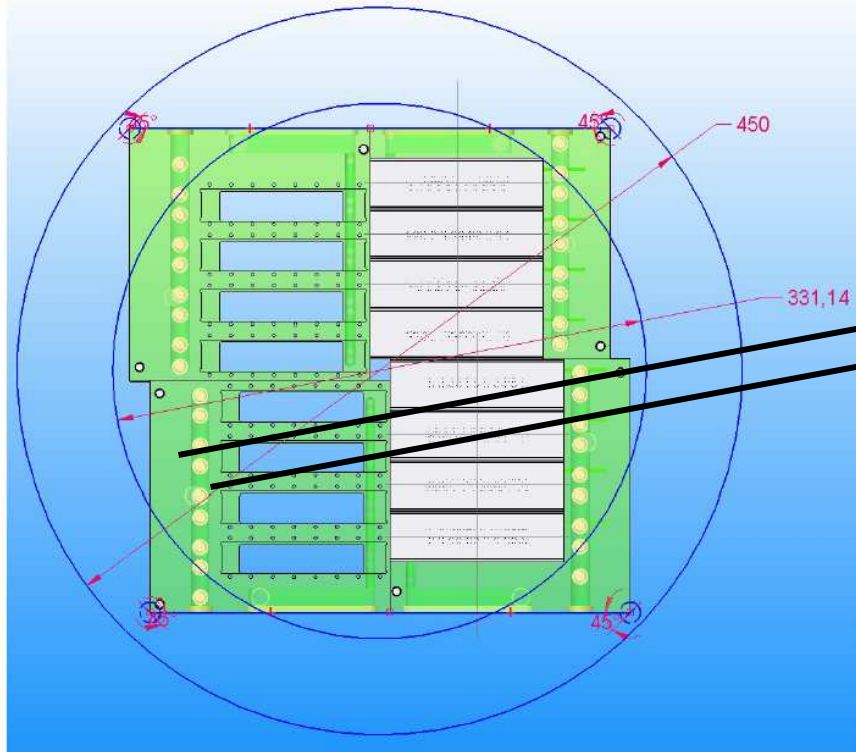
**Table 2.** Proposed parameters for a split and delay unit

	Single crystal application	SFC application	SDL/MID (XFEL.EU)
Convergence angle (both beams)	0.12° (optimized value; 0.15° max, no convergence potentially tolerable)	0 - 0.12° (Non-convergent beam acceptable for high-throughput SFC measurement)	Up to ~0.12°, depending on the focusing optics
Angle between beams	0.5° (based on MAR165 detector, and experimental parameters used during XPP44112 ). Control of the value would allow big and small unit cells (0.1 – 0.8 degrees range)	0.5°	Up to ~0.6°, depending on the mirror material chosen (Si/Pt)
Time delay between pulses	>1 ps. Ideally controlled 1-10 ps	>1 ps.	Design specs: 0-800 ps +/- 3 fs
Bandwidth	1.6 eV	1.6 eV	~6 x 10 <sup>-5</sup> (0.3-0.6 eV) (Si 220 reflection)
Photon energy	9-9.5 keV	9-9.5 keV	5-10 keV (adjustable)
Photons / pulse	> 10 <sup>10</sup> – 10 <sup>11</sup> each beam	< 1.5 x 10 <sup>9</sup> each beam (Non-destructive)	10 <sup>8</sup> - 10 <sup>11</sup> per pulse, tunable, depending on SASE/seeding
Source stability	Not intrinsically required	Not intrinsically required	Desirable
Repetition rate	Up to full LCLS rate. For PYP: 2 Hz	Detector limited	3.5 kHz, detector limited
Spot size on target	40 μm, round or up to 150 x 40 μm aperture	~1 μm	<1-100 μm, variable
Overlap between beams on target	Better than 5 μm precision	Better than 100nm precision	Design specs: better than 80% overlap area



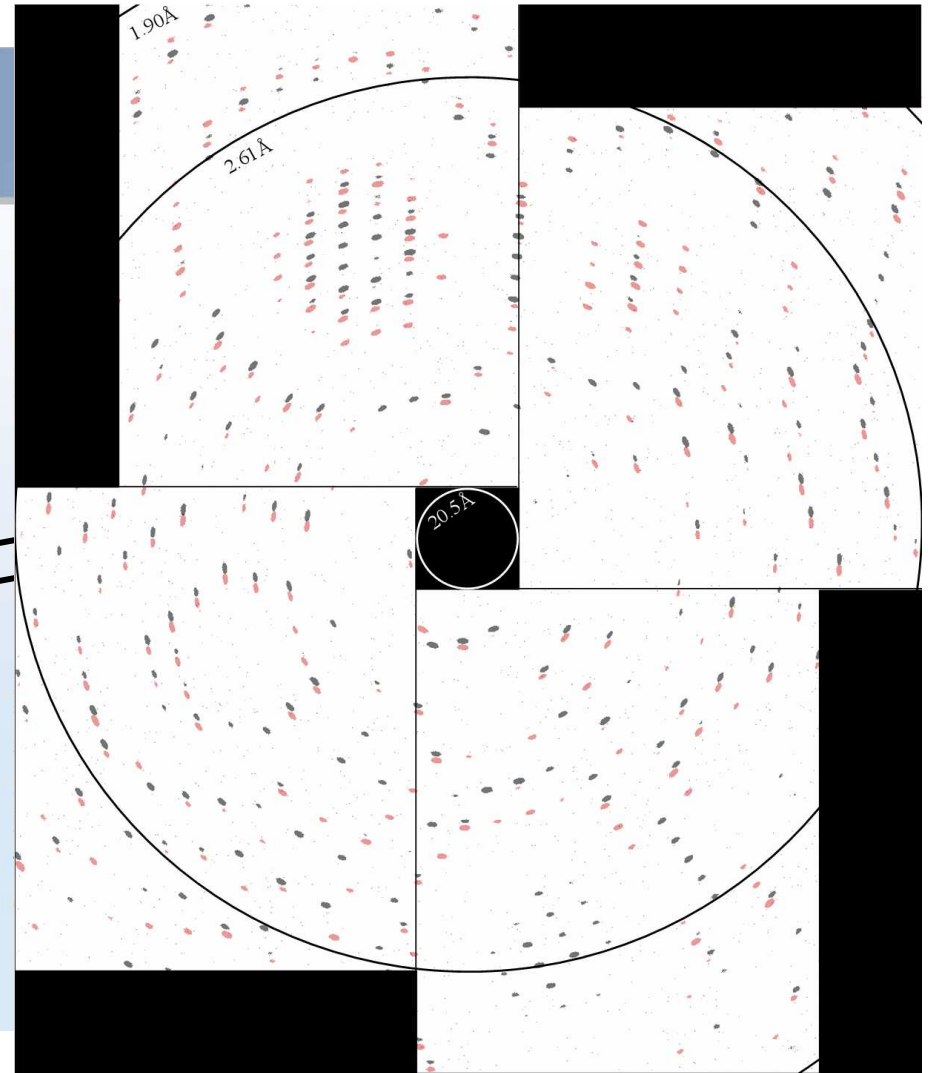
# AGIPD detector: 2.5 Å resolution limit

## Image plane



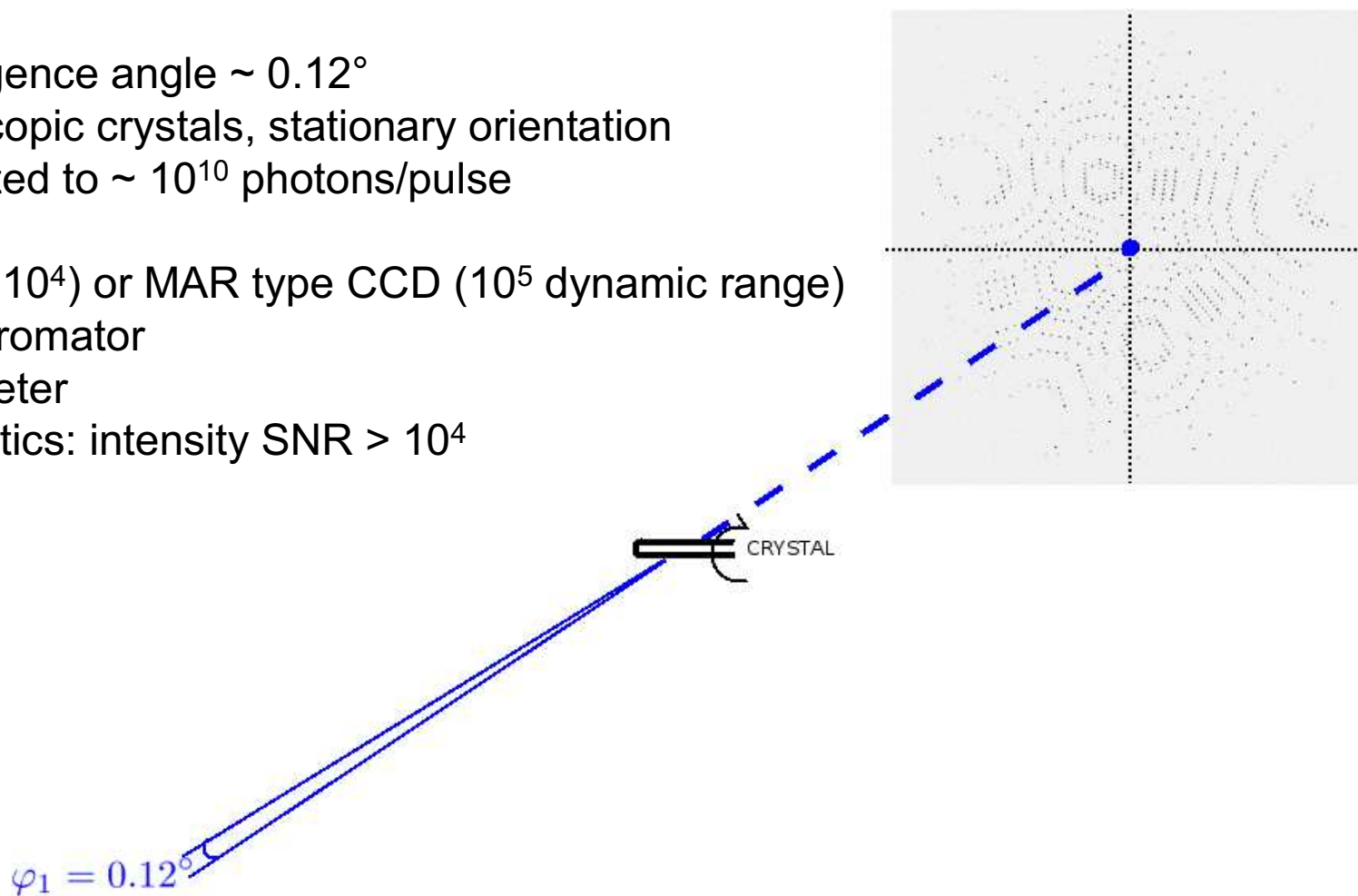
9.4.2013

J. Becker, S. Rah, H. Hirsemann



# Day-1 proposed experiment at MID: Convergent Beam method

- Convergence angle  $\sim 0.12^\circ$
- Macroscopic crystals, stationary orientation
- Attenuated to  $\sim 10^{10}$  photons/pulse
- 9 keV
- AGIPD ( $10^4$ ) or MAR type CCD ( $10^5$  dynamic range)
- Monochromator
- Goniometer
- Diagnostics: intensity SNR  $> 10^4$





@Imperial  
Craig Lincoln  
Mark Warren

@European-XFEL  
Anders Madsen

@APS/BioCARS  
Keith Moffat  
Tim Graber  
Zhong Ren  
Vukica Srajer  
Robert Henning

@LCLS/XPP  
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David Fritz  
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@Milwaukee  
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<sup>1</sup>Physics Department, University of Wisconsin, Milwaukee, WI 53211, USA. <sup>2</sup>Department of Chemistry and Biochemistry, Arizona State University, Tempe, AZ 85287, USA. <sup>3</sup>Department of Physics, Arizona State University, Tempe, AZ 85287, USA. <sup>4</sup>Linac Coherent Light Source, SLAC National Accelerator Laboratory, Sand Hill Road, Menlo Park, CA 94025, USA. <sup>5</sup>Lawrence Livermore National Laboratory, Livermore, CA 94550, USA. <sup>6</sup>Centre for Ultrafast Imaging, University of Hamburg, 22761 Hamburg, Germany. <sup>7</sup>Center for Free Electron Laser Science, Deutsches Elektronen Synchrotron DESY, Notkestrasse 85, 22607 Hamburg, Germany. <sup>8</sup>Hauptman-Woodward Institute, State University of New York at Buffalo, 700 Ellicott Street, Buffalo, NY 14203, USA. <sup>9</sup>Center for Advanced Radiation Sources, University of Chicago, Chicago, IL 60637, USA. <sup>10</sup>Department of Biochemistry and Molecular Biology and Institute for Biophysical Dynamics, University of Chicago, Chicago, IL 60637, USA. <sup>11</sup>Faculty of Natural Sciences, Life Sciences, Imperial College, London SW7 2AZ, UK. \*Present address: Linac Coherent Light Source, SLAC National Accelerator Laboratory, Sand Hill Road, Menlo Park, CA 94025, USA. †Present address: Physics Department, University of Wisconsin, Milwaukee, WI 53211, USA. ‡Corresponding author. E-mail: m-schmidt@uwm.edu



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