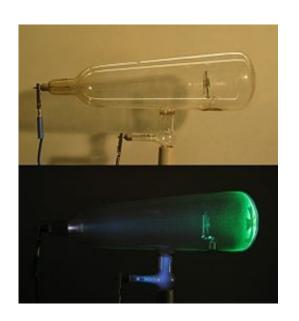
X-ray sources and detectors: past and present evolution

J-L Ferrer IBS/Synchrotron Group (Grenoble, France)

4ème École de Biologie Structurale Intégrative RéNaFoBiS Oléron – du 16 au 23 juin 2017

1895: First X-rays



Crookes tubes are cold cathode tubes: from a few kilovolts to about 100 kilovolts is applied between the electrodes. The Crookes tubes require a pressure from about 10-6 to 5×10-8 atmosphere.

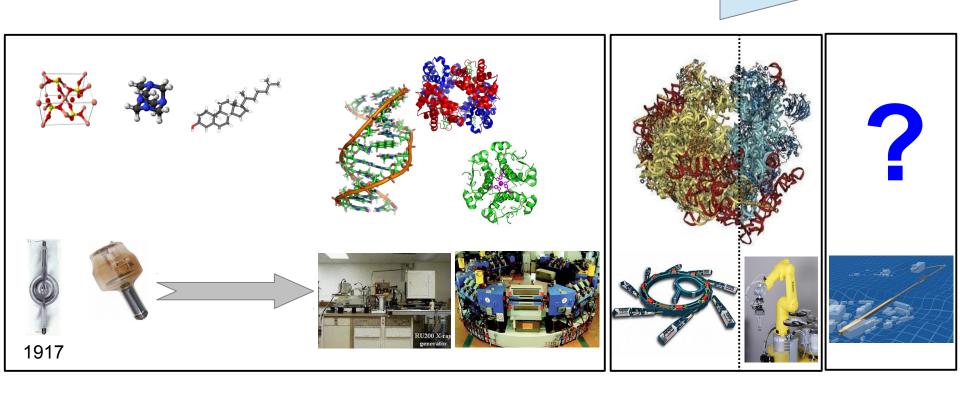


German physicist Wilhelm Röntgen, credited as the discoverer of X-rays in 1895

Wilhelm Röntgen's first "medical" X-ray, of his wife's hand, taken on 22 December 1895 and presented to Ludwig Zehnder of the Physik Institut, University of Freiburg, on 1 January 1896



1910 1920 1930 1940 1950 1960 1970 1980 1990 2000 2010

















1895-...: sealed tubes / rotating anodes 1-2nd generation synchrotrons

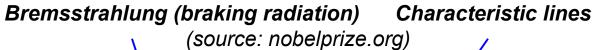
X-ray sources Films / IP

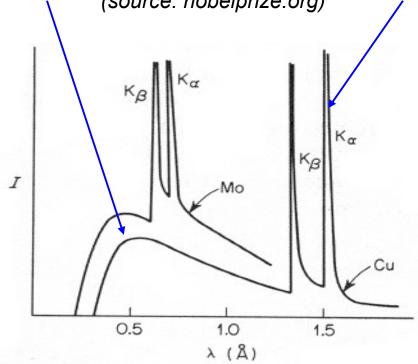
Capillaries

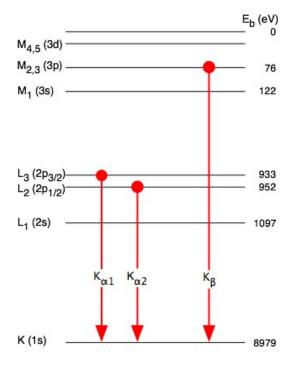
Isomorphous replacement

Lab sources







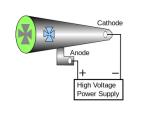


X-ray generation

Crookes (1869)

(cold cathode)
Ionization → e- from cathode to anode

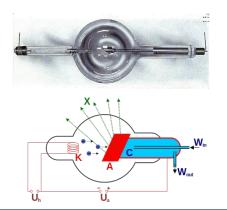




Coolidge (1917)

(hot cathode)

Cathode: heated filament



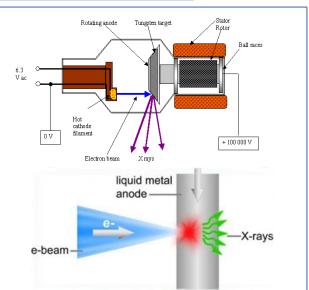
Moving target

Cathode: heated filamen

Anode: rotating/liquidt



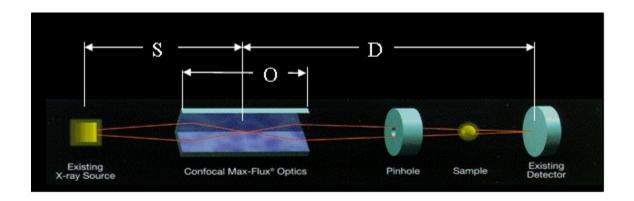
Siemens, 1933



Optics

Osmic confocal optics / Montel optics

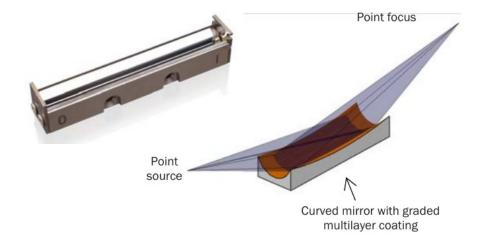
2 multi-layer mirrors at 90°





Ellipsoidal mirror

1 multi-layer mirror





excillum

70/160 kV Ga target



Lab sources





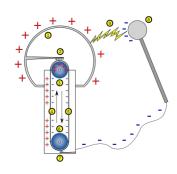




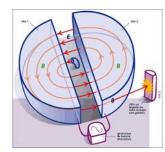


Particules accelerators

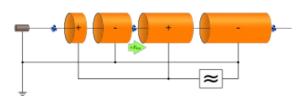
Electrostatic accelerator



Cyclotron

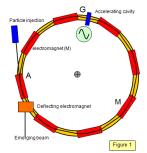


Linear accelerator

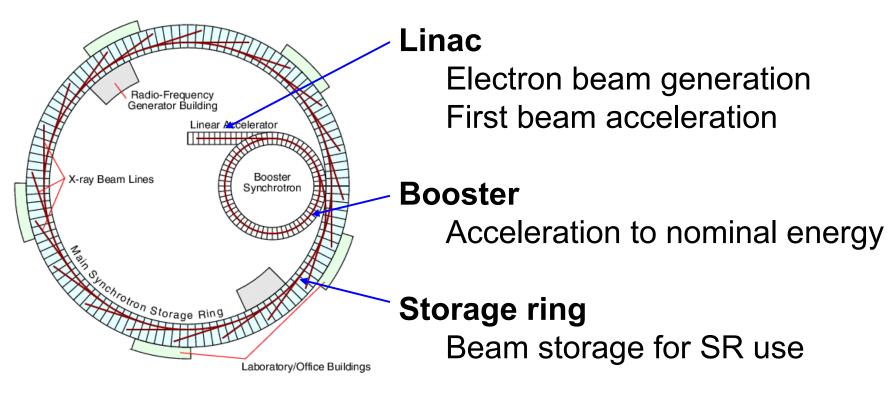


Synchrotron

- → high energy
- → store high current

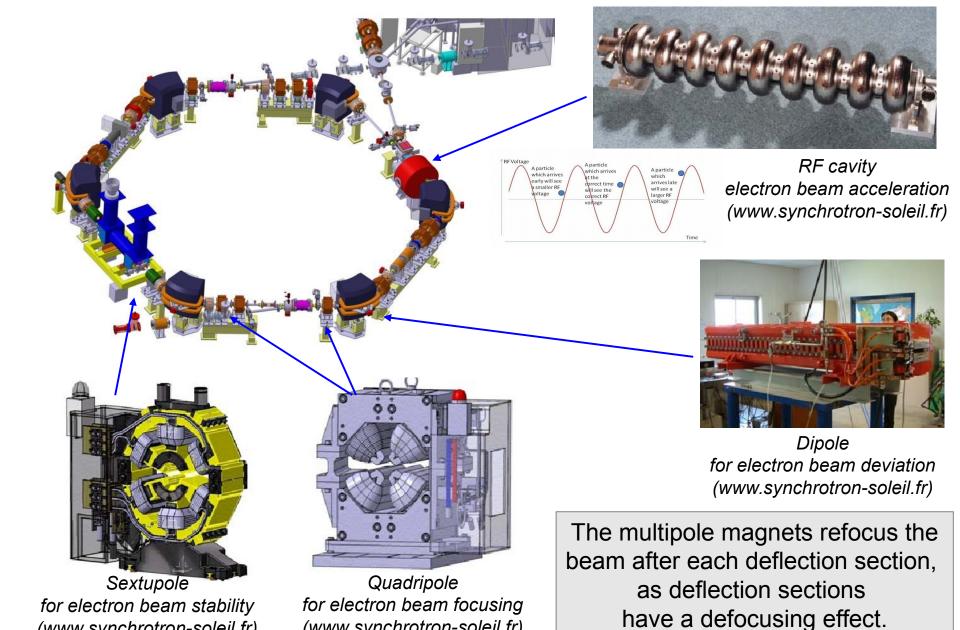


Synchrotron components



(http://pd.chem.ucl.ac.uk/pdnn/inst2/work.htm)

Synchrotron components



(www.synchrotron-soleil.fr)

(www.synchrotron-soleil.fr)

Synchroton generations

1st generation synchrotron: parasitic operation (50s to 70s)

ACO, DORIS, SPEARS...

ACO (www.media-paris-saclay.fr)

2nd **generation synchrotron**: dedicated to SR (80s)

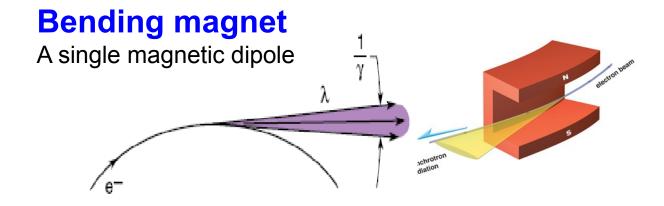
SRS, DORIS, NSLS, SuperACO...



DORIS (http://www.desy.de)

3rd generation synchrotron: ID with high brightness, low emittance ESRF, ALS,...

1st generation synchrotrons



Synchroton generations

1st generation synchrotron: parasitic operation (50s to 70s)

ACO, DORIS, SPEARS...



ACO (www.media-paris-saclay.fr)

2nd **generation synchrotron**: dedicated to SR (80s)

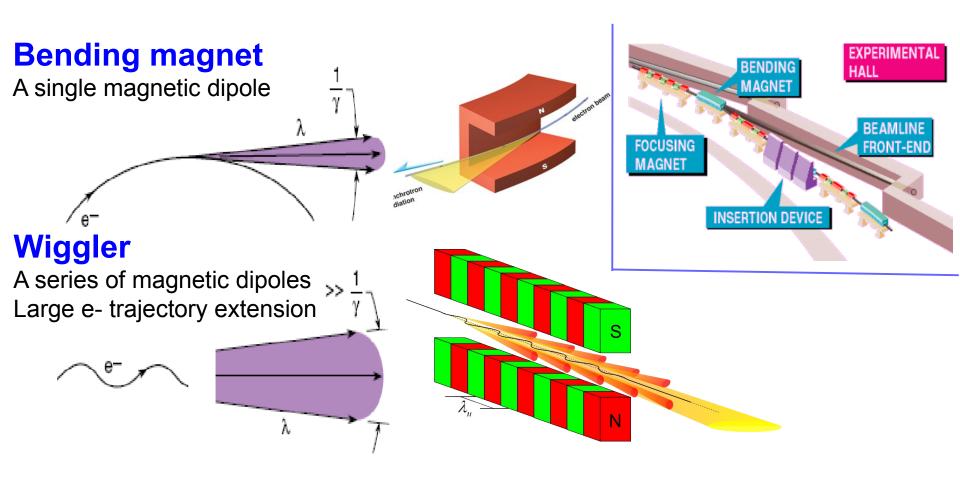
SRS, DORIS, NSLS, SuperACO...



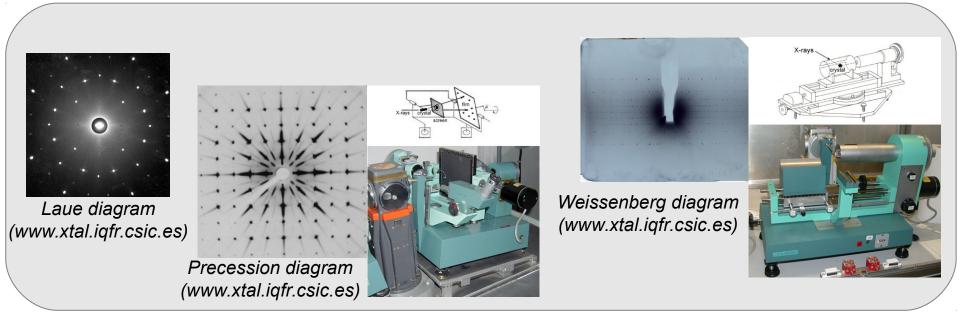
DORIS (http://www.desy.de)

3rd generation synchrotron: ID with high brightness, low emittance ESRF, ALS,...

2nd generation synchrotrons



Detectors: films and IPs



Upon exposure to X-ray:

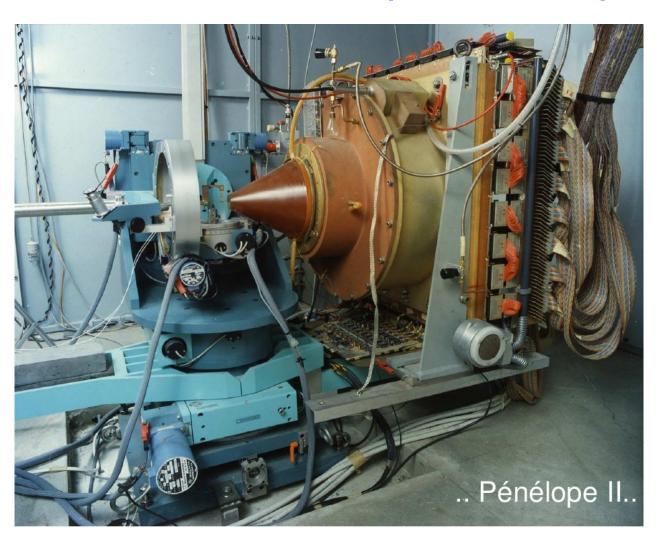
Storage of the signal in the phosphor plate over a prolonged period,

Upon readout:

Photostimulated luminescence (PSL) releases the stored energy within the phosphor by stimulation with visible light, to produce a luminescent signal.



A multi-wire chamber at LURE (1974-1992)



1st MAD structure!

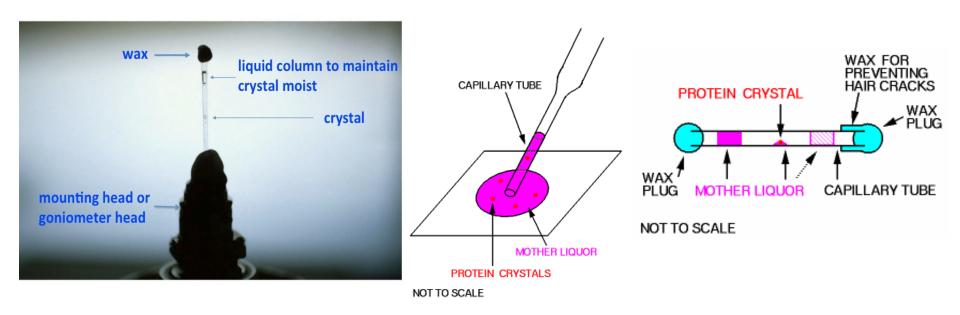
LURE:

R. Kahn, R. Bosshard, A.Bahri, G. Bricogne, A. Bentley, R. Fourme

CERN:

R. Bouclier, R. Million J.C. Santiard, G. Charpak

Samples in capillaries



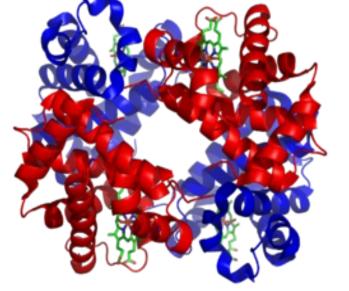


(www.mitegen.com/products/micrort/micrort.shtml)

1959: First protein structures

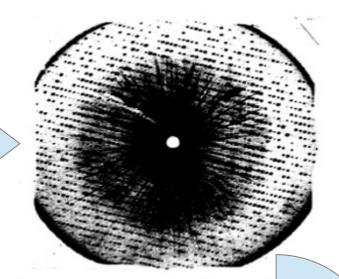
In 1953 **Max Perutz** showed that diffracted X-rays could be phased by comparing the patterns with and without heavy atoms attached. In 1959 he determined the structure of hemoglobin

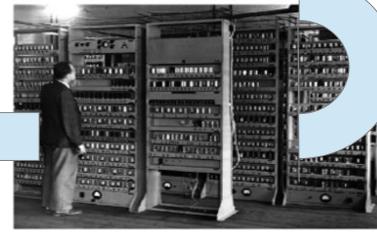
Max Perutz and John Kendrew shared the 1962 Nobel Prize for Chemistry for the structures of hemoglobin.



1969, **Dorothy Crowfoot Hodgkin** solved the 3D structure of insulin, on which she worked for over thirty years!!



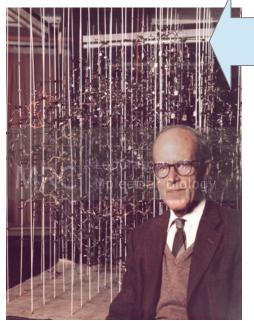






Myoglobin (1957)

Haemoglobin model 1957



To analyse the 25,000 reflections of haemoglobin data,
Perutz and Kendrew used the EDSAC I computer introduced in 1949

1990s: 3rd generation synchrotrons

X-ray sources CCD detectors / SS detectors

Freezing

Anomalous diffraction

3rd generation synchrotrons



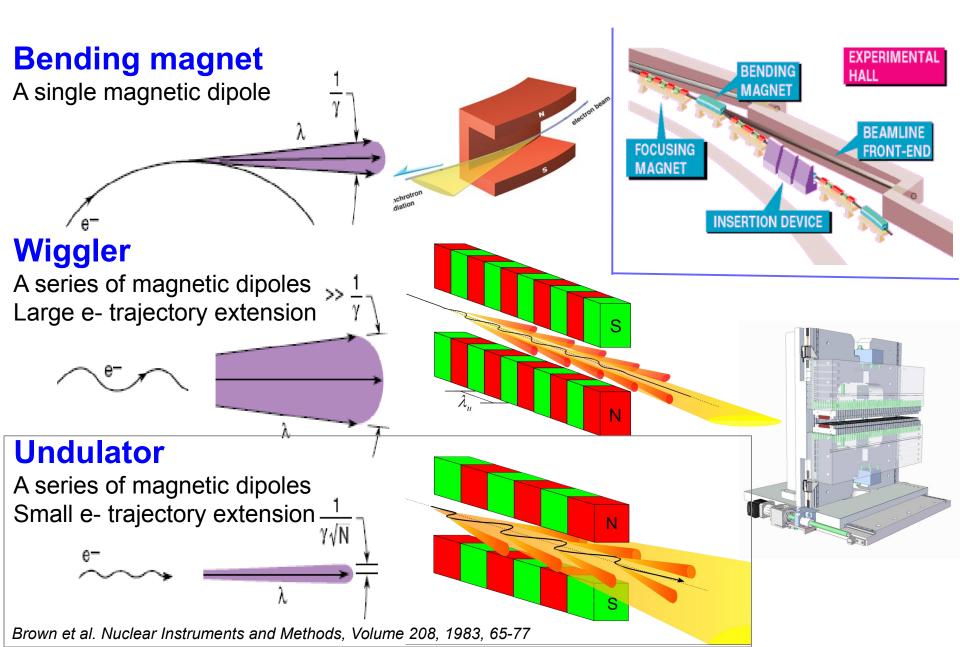
ESRF



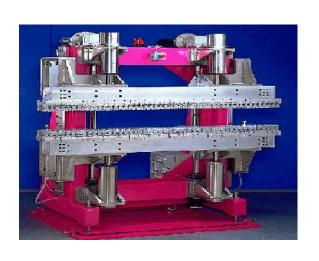
SOLEIL

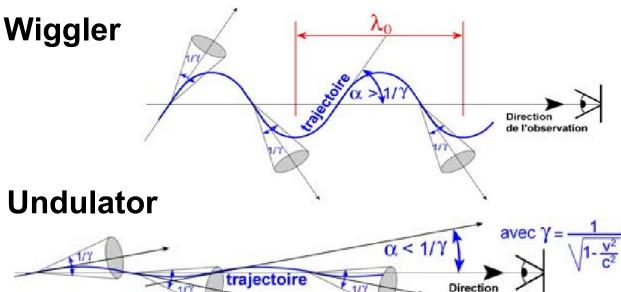


3rd generation synchrotrons



Wiggler vs undulator



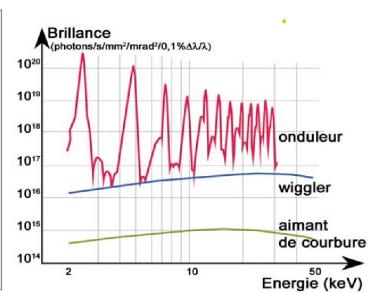


 α : angular extension of the e- traj.

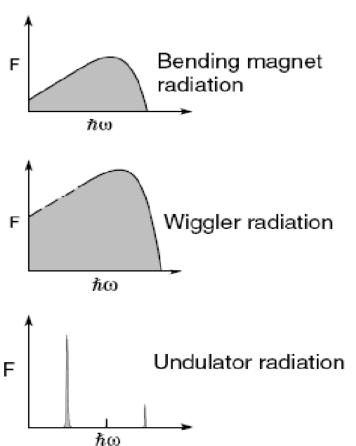
 γ : emission cone aperture

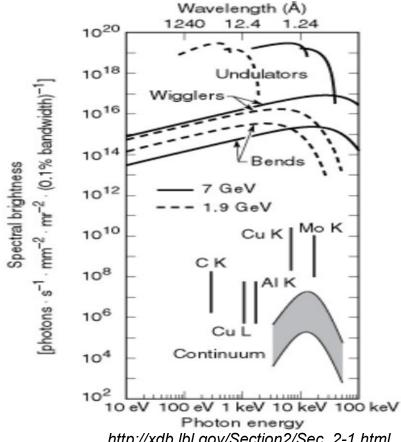
In an undulator: α < 1/ γ

- => emission in presence of the beam
- => constructive interferences
- => spectral lines (brightness in N²)
- => beam divergence in N^{-1/2}



generation synchrotrons



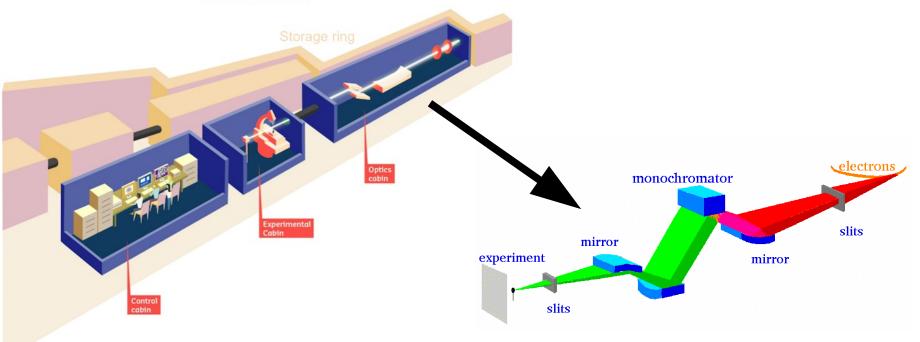


http://xdb.lbl.gov/Section2/Sec 2-1.html

Jim Clarke, ASTeC, SRS					Bending magnet		Wiggler		Undulator	
Ring	Energy (GeV)	ρ (m)	$I_b \ (\mathrm{mA})$	$P_{ m total} \ ({ m kW})$	$dP/d\theta$ (W/mrad)	$\frac{dP/d\Omega}{(W/\mathrm{mrad}^2)}$	$dP/d\theta$ (W/mrad)	$\frac{dP/d\Omega}{(W/\mathrm{mrad}^2)}$	$dP/d\theta$ (W/mrad)	$\frac{dP/d\Omega}{(W/\mathrm{mrad}^2)}$
SRS (2nd genera	tion) 2	5.56	2 00	50.9	8.1	20.8	4.0	0.6	1.0	2.2
DIAMOND	3	7.15	3 00	300.7	47.9	184.4	13.7	4.9	3.5	16.8
ESRF	6	25.0	200	916.5	145.9	1124.0	36.4	52.5	9.3	179.1

Beamline optics

Beamlines



Reflecting elements

- → collimating / focusing
- → high energy cutoff (harmonic rejection, ...)

Refracting elements

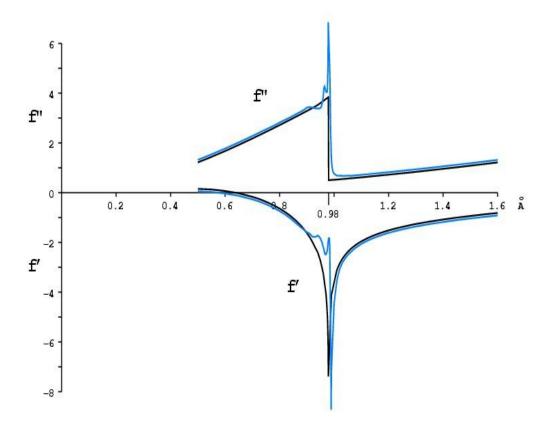
- → energy selection
- → focusing

The anomalous signal

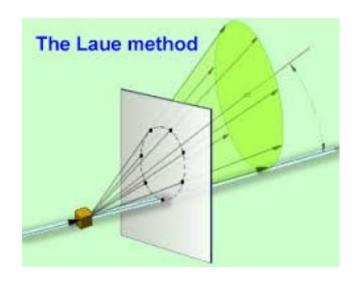
$$F(h) = \sum_{j} f_{j} \exp (2\pi i h \cdot r_{j})$$

$$f_{j} = f_{j}^{\circ}(\theta) + f_{j}^{\prime}(\lambda) + i \cdot f_{j}^{\prime\prime}(\lambda)$$

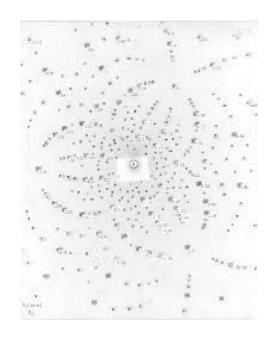
Anomalous correction f" is proportional to absorption and fluorescence and f' is its derivative



Laue



Complete dataset in 1 frame
→ real time experiment



Detectors: automated IPs

Upon exposure to X-ray:

Storage of the signal in the phosphor plate over a prolonged period,

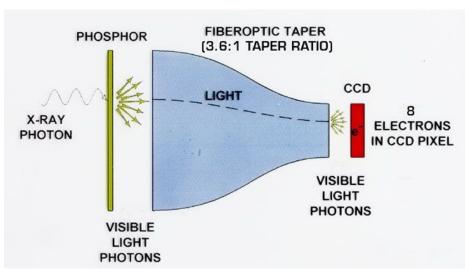
Upon readout:

Photostimulated luminescence (PSL) releases the stored energy within the phosphor by stimulation with visible light, to produce a luminescent signal.





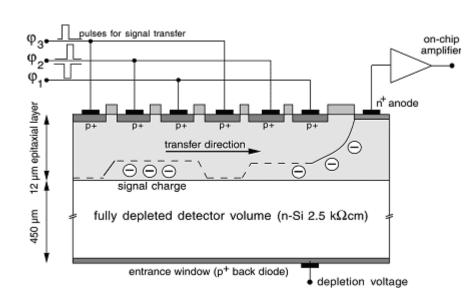
CCD detectors



http://proteincrystallography.org

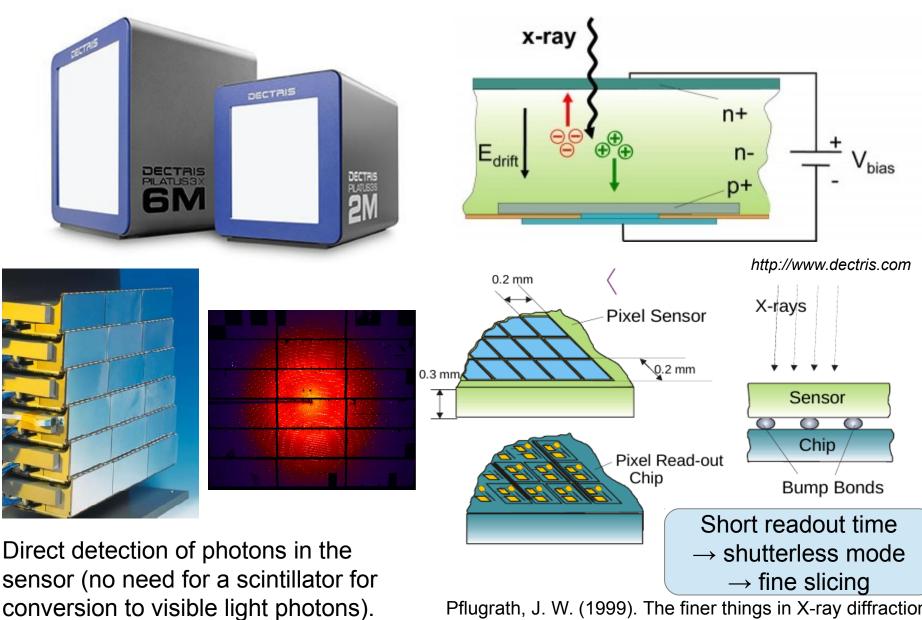
A scintillator converts X-ray photons to visible light photons. The image is demagnified to match the CCD size.

Readout time compatible with synchrotron exposure time + high dynamic





Pixel detectors



Pflugrath, J. W. (1999). The finer things in X-ray diffraction data collection, Acta Cryst. D 55, 1718-1725.

Last evolutions

Present fast detectors dead time ~1 msec



Pixel: 75 um

Frame rates : 25 Hz

1 ms readout time

Pilatus (Dectris)

Last generation dead time ~3 usec



Eiger (Dectris)

Pixel: 75 um

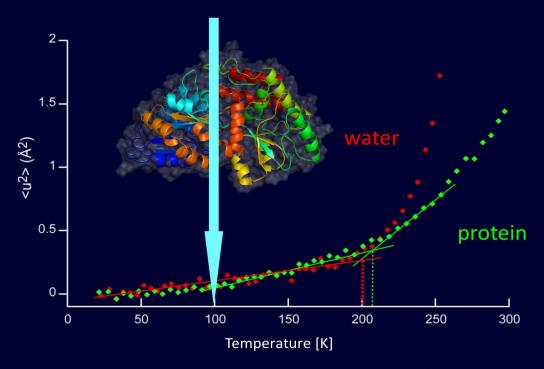
Frame rates : 10³ Hz

3 us readout time

Cryo-cooling

Temperature-dependent side-chain flexibility from neutron scattering

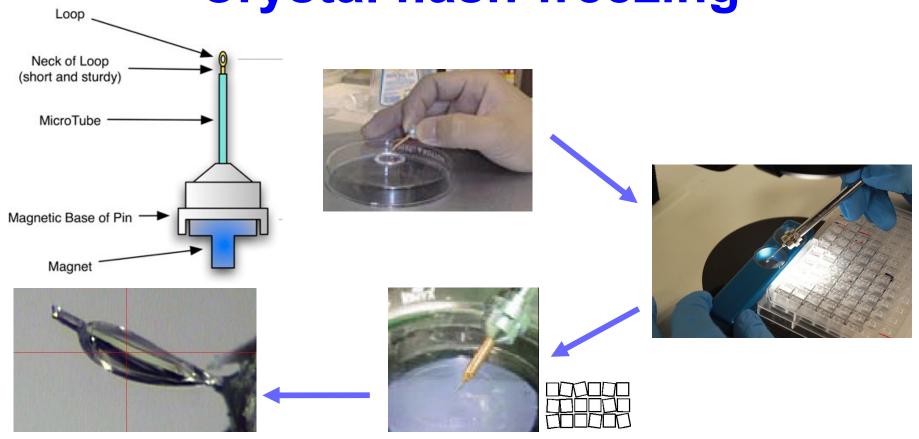
Cryo X-ray data collection



Wood, Frölich, Gabel, Moulin, Haertlein, Paciaroni, Zaccai, Tobias & Weik (2008) JACS 130, 4586

Cryo-cooling at 500 K / s : protein conformational changes quenched at 200 K Halle (2004) PNAS 2004, 4793

Crystal flash-freezing



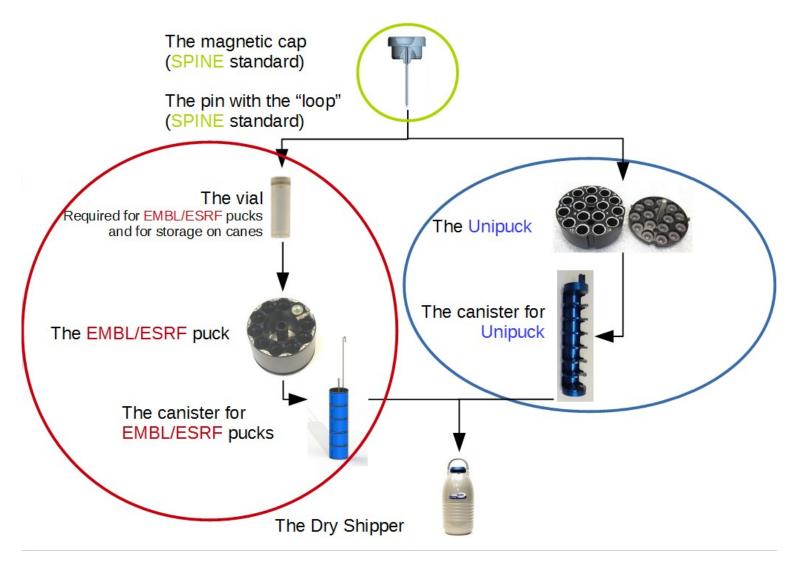
Possible improvements:

Optimized cryo-protectant

Absence of liquid (Pellegrini et al., Acta Cryst. (2011). D67, 902-6)

High speed freezing (Warkentin et al., J Appl Cryst. (2006) 39, 805–11)

Freezing in propane, etc...



EMBL/ESRF pucks are required for example on:

- ESRF (BM30A, and all ID MX beamlines)
- BESSY (BM14.1-14.2)
- SLS (all MX beamlines)
- ALBA (XALOC)

Unipucks are required for example on:

- SOLEIL (Proxima1 & 2)
- ESRF (BM30A, ID30B)
- BESSY (BM14.2)
- DLS (all MX beamlines)

Other formats:

SSRL: "pineapple"

ALS: similar to Unipuck

Rigaku: used by the Actor









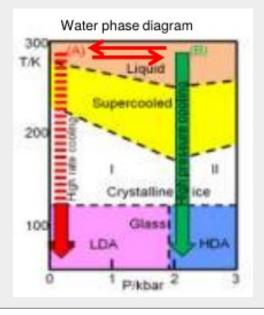
MiniSpine: new format, under evaluation at the ESRF

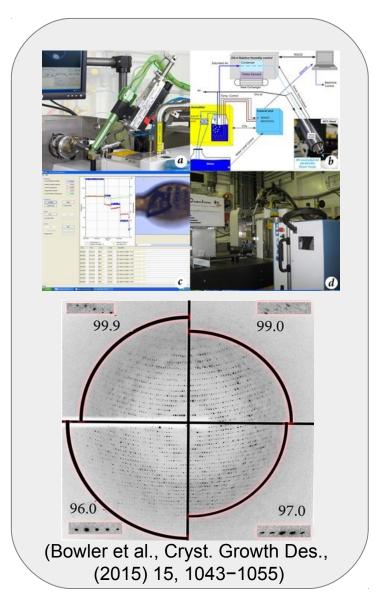


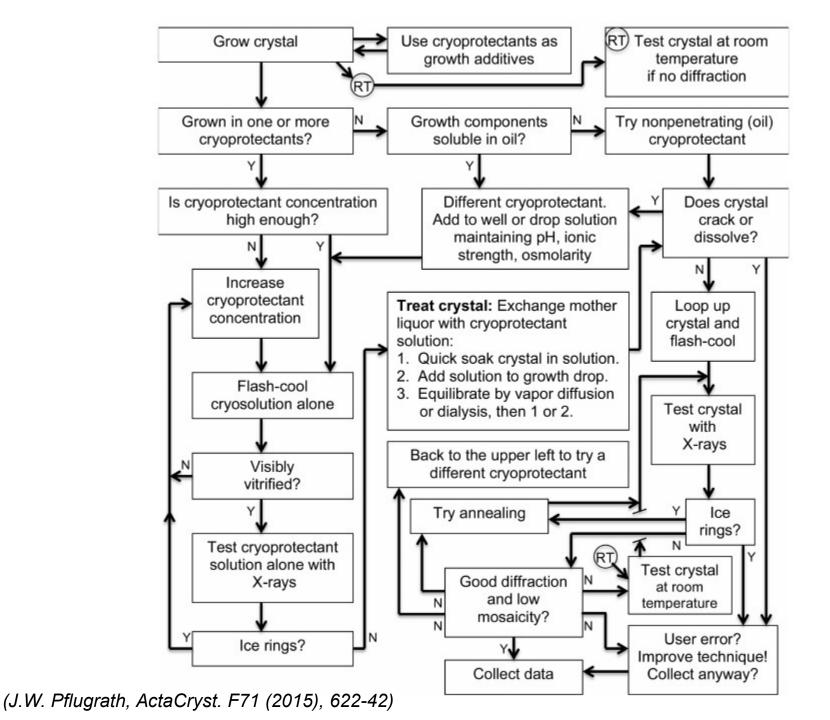
Crystal flash-freezing Last improvements



P. Carpentier, ESRF





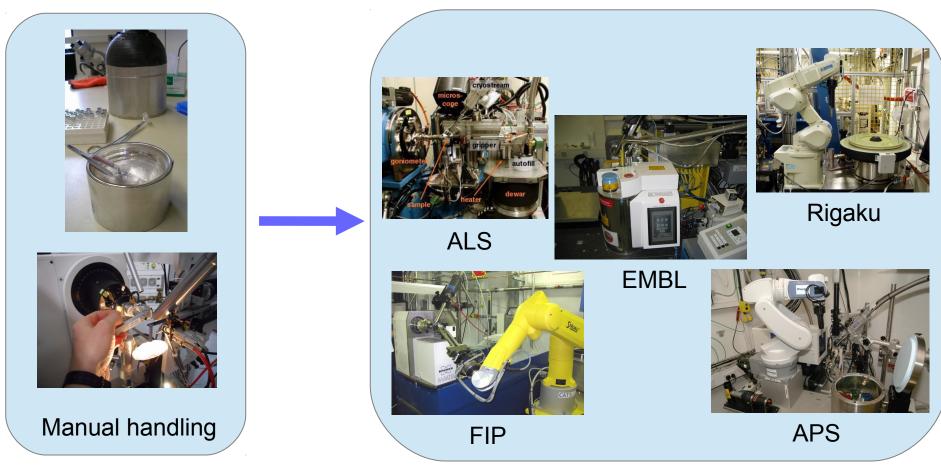


2000s: Automation

Crystallization / nanodrops

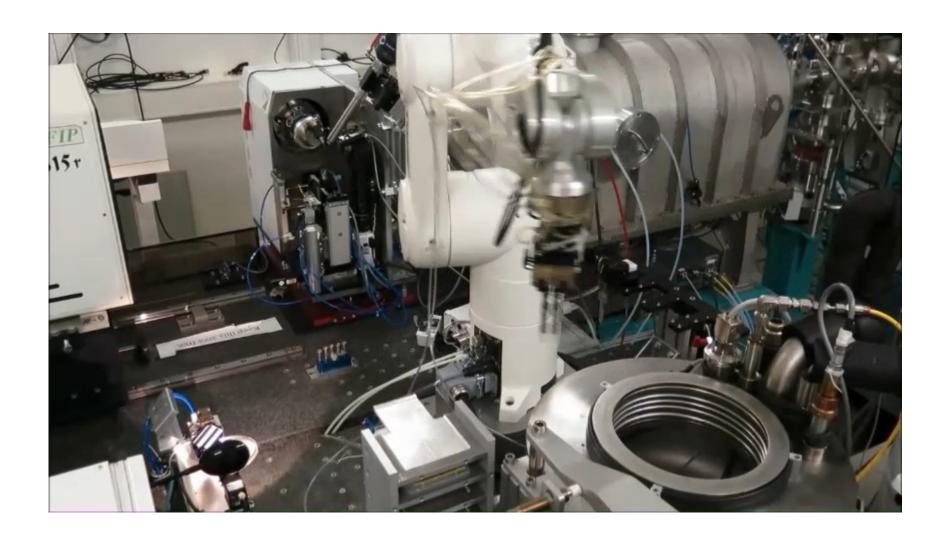
Sample changers / sample holder standard

Automation: Sample changer



Higher reliability
Better reproducibility
=> screening, to find the best crystal



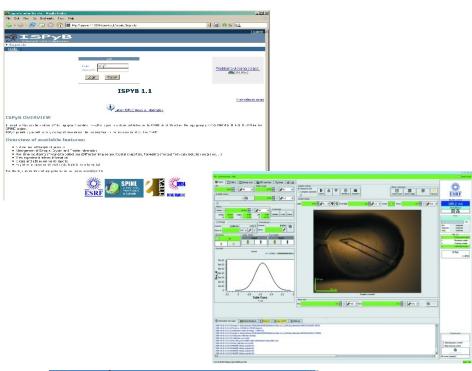


AutomationSoftware

- MxCube

- ISPyB

- EDNA / xdsadp, meXDS, etc.





RT experiments

RT + ensemble

Flash cooling of protein crystals

- biases structural collective motions;
- remodels > 35% of side chains;
- induces bias toward smaller, overpacked,

and unrealistically unique models.

Instead, **room-temperature** X-ray crystallography helps in revealing

- motions crucial for catalysis,
- ligand binding,

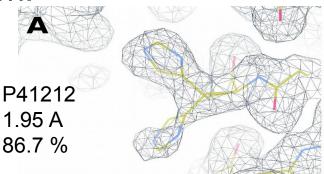
Resol:

- allosteric regulation.

Spacegroup:

Completness:

Automated *in situ* experiment on cyclophilin D

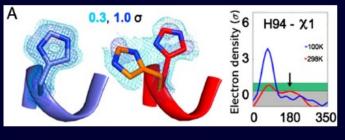


Structure of cyclophylin D at room temperature (A) and with flash-frozen crystals (B).

When His173 exhibits a single conformation in the later,
clear density is observed for a double conformation at room temperature (unpublished data).

Protein conformational heterogeneity greater in RT than in 100 K structures

Fraser, van den Bedem, Samelson, Lang, Holton, Echols & Alber (2011) PNAS 108, 16247

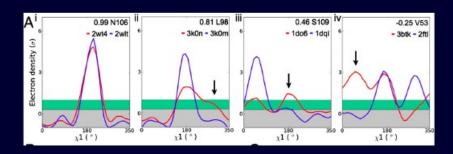


Alternate conformation of H94 In H-Ras at RT, but not at 100 K

100 K

RT

Cryo-cooling remodels conformational distributions in 35% of all protein side-chains



Tools to analyse conformational heterogeneity in crystal structures:

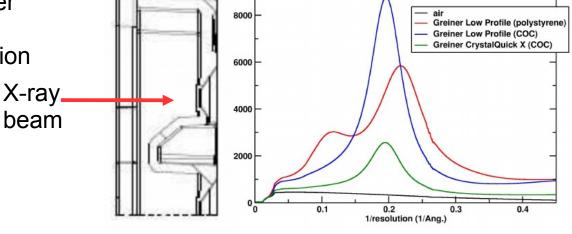
- RINGER: samples e- density around side-chain dihedrals below 1σ level (Lang et al. (2010) Protein Sci. 19, 1420)
- qFit: automates building of alternative polypeptide conformations (van den Bedem et al. (2009) Acta Cryst. D65, 1107)
- Time-averaged crystallographically restrained MD refinement of ensembles (Burnley et al. (2012) eLife 1, e00311)
- END, RAPID: place e- density maps on absolute scale and calculate noise at each position in the map (Lang et al. (2014) PNAS 111, 237)

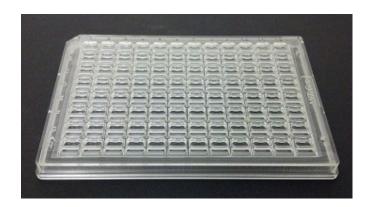
Optimized plates for in situ X-ray diffraction

CrystalQuick X from Greiner

- molding technique
- 2 drops location per condition





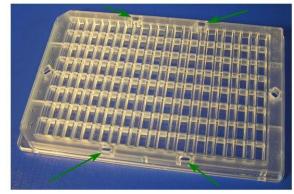


CrystalDirect from EMBL

- tapes on both side
- positioning marks

In-situ-1 from Mitegen

- tapes on both side
- small volume for the reservoir





In situ screening / data collection

Diffraction "in the plate" => no crystal handling

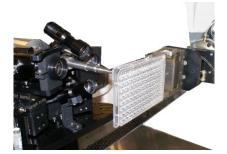
Great for fragile crystals (larges complexes...), RT, ligand screening

in situ screening & data collection

- SBS micro-plates (sitting/hanging drops)
- SBS high density batch plates
- micro-chips
- high pressure cells

Applications

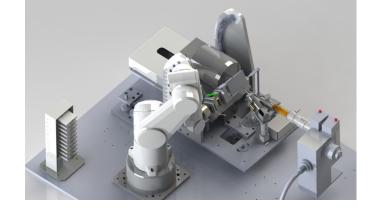
- rapid crystallization screening
- data collection on fragile crystals, significantly degraded upon freezing
- data collection at room temperature on series of crystals
- automated screening of compounds, fragments, heavy atoms



96-well crystallization plate

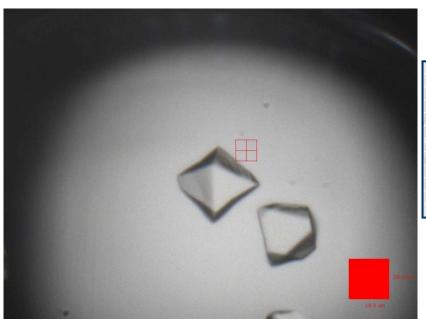


1536-well micro-batch plate

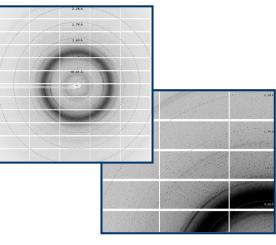


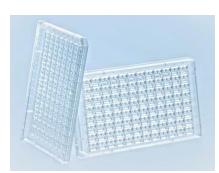
FIP-BM30A (ESRF) CBS (Montpellier)

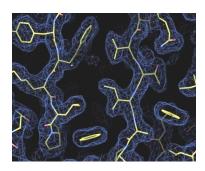
A new virus structure: Bovine enterovirus 2 crystallization plate screening on I24 at DLS



CrystalQuick X plate





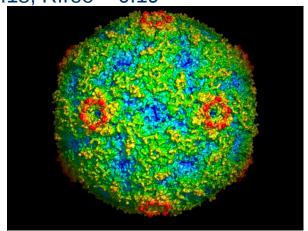


Data collected at DLS, I24
Beam size 20 microns, focus at detector (P6M)

exposure time 0.1 sec, 0.1° oscillation, detector distance = 480 & 645 mm, resolution at edge of detector 2.28 & 2.97 Å

E.E. Fry, J.S. Ren, A. Kotecha, T.S. Walter, C. Porta, D.I. Stuart, The Wellcome Trust Centre for Human Genetics, University of Oxford (UK),

D.J. Rowlands, Institute of Molecular and Cellular Biology, University of Leeds (UK) and Gwyndaf Evans, Robin Owen, Danny Axford, Jun Ashima, I24, Diamond Light Source (UK) 2.2 Å resolution R= 0.18, Rfree = 0.19





MXIS

Nov.-Dec. 2017 IBS-ESRF-CBS-EMBL

A workshop on in situ technique With special focus on small molecules screening







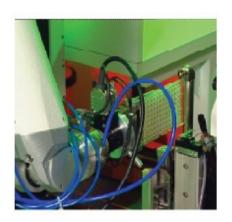


Plate pre-coating Ligand **Crystal mounting Protein and** in DMSO and freezing mother liquor dispensing dispensing (Diffraction @ 100 K) Quick Ligand evaporation **Re-solubization** Crystal X-ray **Transfer** beam (soaking) In situ diffraction

« Dry co-crystallization » of CypD

- proline isomerase
- crystallized in P4₁2₁2
- validated target in ischemia (Alam et al., 2015)

Cyclophilin D (CypD)

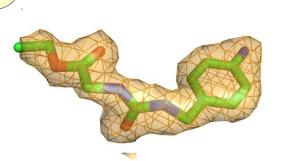
=> new inhibitor detected

- micromolar range
- MW: 251 and XlogP: 0.37

Further chemical derivations

- => nanomolar inhibitors
- => pre-clinical trials (Guichou et al., 2011).

F428 (μM)



In situ In house (2.23 Å) 2 crystals

Labesse G, Gelin M, Guichou J-F, CBS Montpellier)

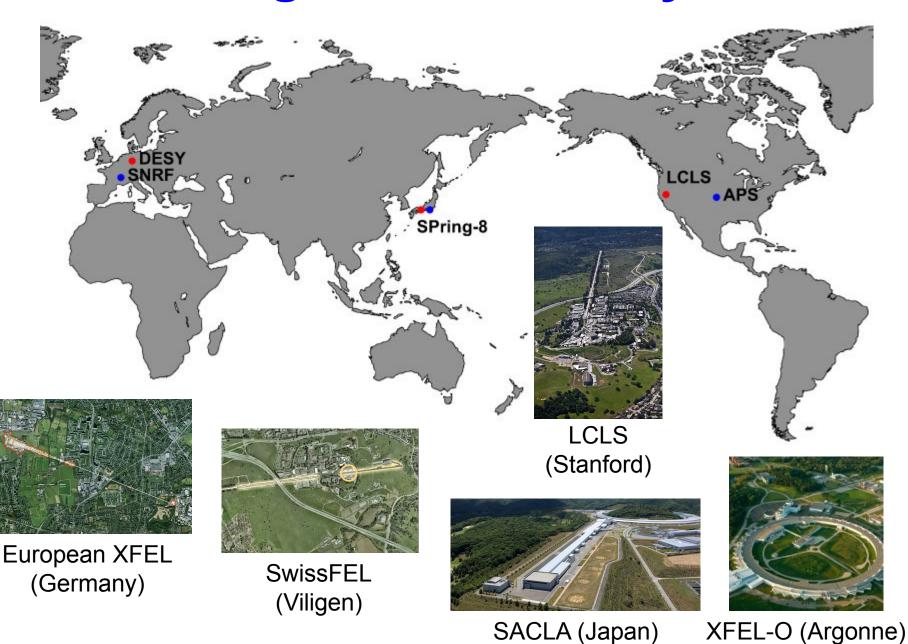
2010s: 3rd+/4th generation sources

X-ray sources Fast SS detectors

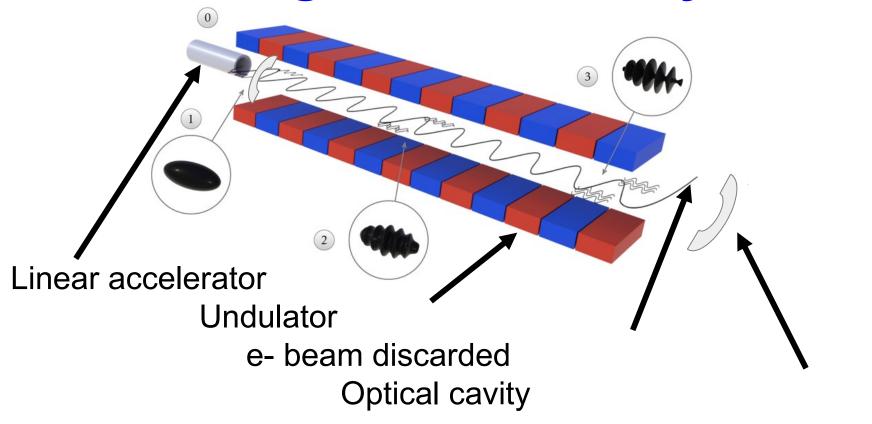
Micro/nano crystals

Room temperature / serial data collection

XFELs: 4th generation X-ray sources



XFELs: 4th generation X-ray sources



Long undulator => micro-bunching of the electron beam => self amplificating spontaneous emission e- in undulator field \rightarrow X-ray beam e- in X-ray beam field \rightarrow X-ray beam exponentially Transverse and longitudinal coherent beam

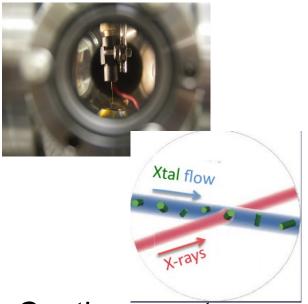
4th generation X-ray sources: Sample dispensing

Sample destroyed upon exposure to the beam (1 frame /sample)

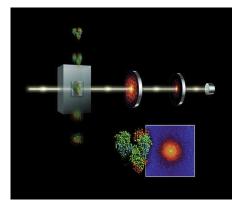
- → samples to intercept the beam at an high frequency
- → merging of many randomly collected diffraction frames



Crystals in droplets ejected with sonic waves



Continuous stream of nano-crystals solution

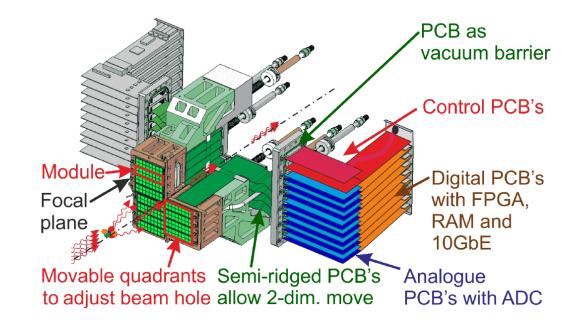


Up to single particules analysis?

4th generation X-ray sources: Detectors

To come...

3.5 MHz frame rate!



AGIPD (DESY, PSI)

(Allahgholi et al., Journal of Instrumentation, 10 2015)

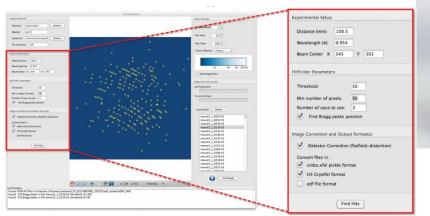
3 and 3+rd generation X-ray sources: Serial data collection

Convergence between in situ approach on 3rd gen. sources and high rate sample dispensing on X-FELs

A large number of small crystals used to collect partial dataset at room temperature

- →multiple crystals on a single support
- →clustering and merging data

Spectra quality
Small crystals
RT
Access



The X-ray offer on large facilities

Synchrotron beamlines in France

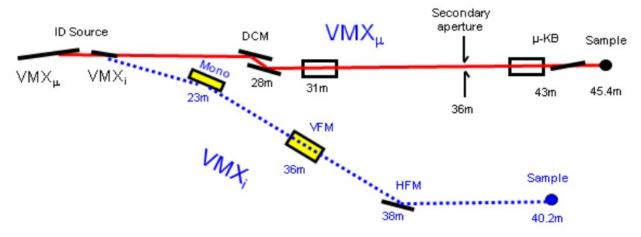
Synchrotro	on / Station	Beam	Main equipments	Experiments
ESRF				
ID23-1	40x30um/0.6-	-2.5Å	MD2/SC3/Pilatus6M	SAD, MAD
ID23-2	8x6um/0.873/	Å	MD2/SC3/Mosaic225	single wav.
ID29	10x75um/0.7-	2.1Å	MD2/SC3/Pilatus6M	SAD, MAD
ID30A-1	100x65um/0.	968Å	RoboDiff/Pilatus2M	single wav.
ID30A-2	~100um/0.98	4Å	?	single wav.
ID30A-3	15um/0.984Å		MD2/SC3/Eiger4M	single wav.
ID30B	20x20um/0.6	2-2.1Å	MD2/SC3/Eiger?	SAD, MAD
ВМ30А	300um/0.7-1.	8Å	MD2/G-Rob/ADSC315	in situ/SAD/MAD
SOLEIL				
Proxima1	40x20um/	0.84-2.5/	A Kappa/CATS/Pilatus6	M SAD, MAD
Proxima2	2A 10um/0.84	1-2.5Å	MD2/CATS/ADSC315	SAD, MAD

Synchrotron beamlines in Europe

Synchrotron	Station	Beam	Experiments
SLS	PXI-X06SA	10x40um/0.72-2.2Å	SAD/MAD
	PXII-X10SA	50x10um/0.62-2.07Å	SAD/MAD
	PXIII-X06DA	80x45um/0.71-2.07Å	SAD/MAD/in situ
DLS	I 02	80x20um/0.5-2.5Å	SAD/MAD
	I 03	80x20um/0.5-2.5Å	SAD/MAD/in situ
	I04-1	???/0.92Å	single wav./in situ
	I 04	10x5um/0.88-2.07Å	SAD/MAD
	123	1.5-4Å	sulphur SAD
	I 24	10x10um/0.7-2.0Å	SAD/MAD/in situ
	VMXi / VMXu	. (I02)	
BESSY	MX14-1	40-30um/0.8-2.5Å	SAD/MAD
	MX14-2	180x70um/0.8-2.5Å	SAD/MAD
	MX14-3	180x110um/0.91Å	single wav.
PETRAIII	P13	30x20um/0.7-2.7Å	SAD/MAD
	P14	5x5um/0.6-2.1Å	SAD/MAD
MAX IV	commissioning	•	
ELETTRA	XRD1	200um/0.6-3.15Å	SAD/MAD
ALBA	BL13-XALOC	50x10um/0.6-2.4Å	SAD/MAD

3+rd generation X-ray sources and sub-micron beams

Project of sub-micron beams, such as VMXu at DLS, ...



High flux, very small beam size

- → small crystals
- → short exposure

makes possible complete data collection at RT before decay

Ultrafast (ms) data collection with ultra-high dose rate at RT could reduce radiation sensitivity to the one at 100 K Warkentin et al. (2013) JSR 20, 7 Owen et al. (2012) Acta Cryst D68, 81

Large wavelength beamline at DLS

ID23 is dedicated to anomalous phasing at large wavelength (S/P-SAD, anom. from Ca, S, ... atoms)







Experiment under vacuum!
Cylindrical pixel detector