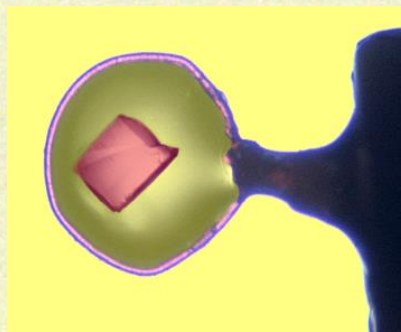
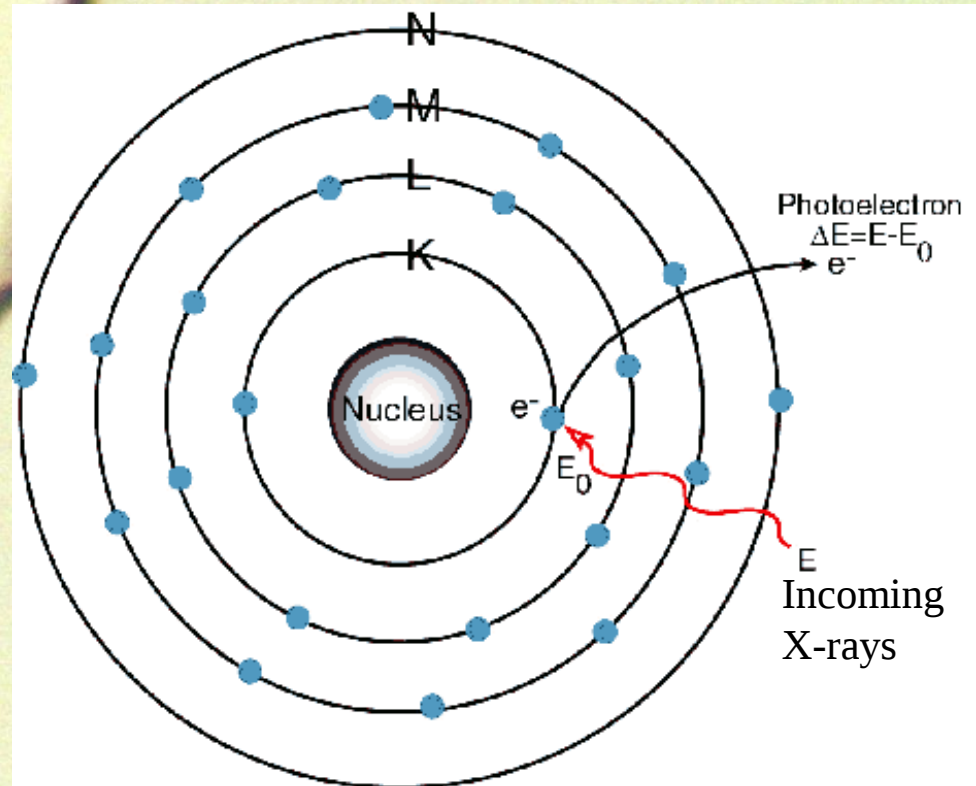
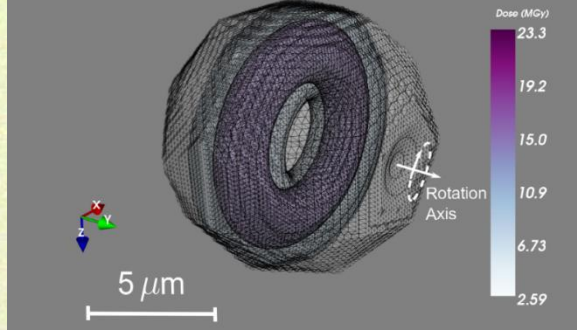
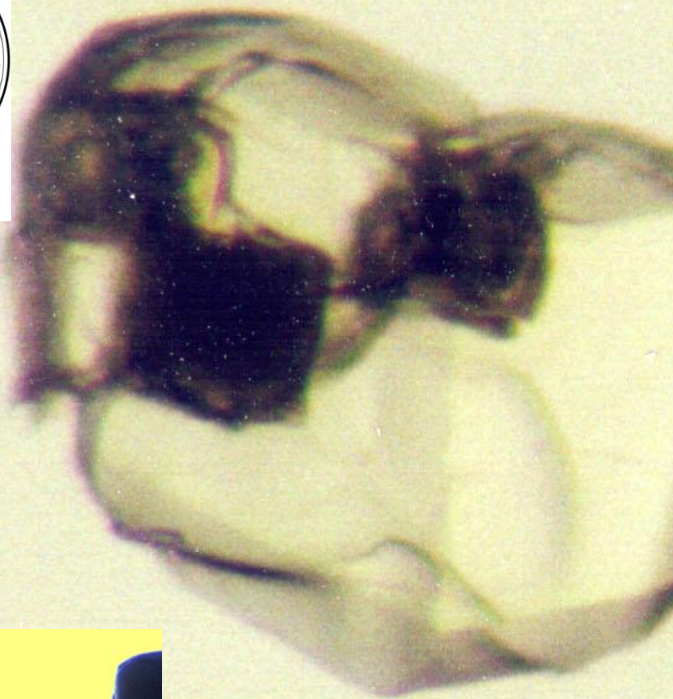
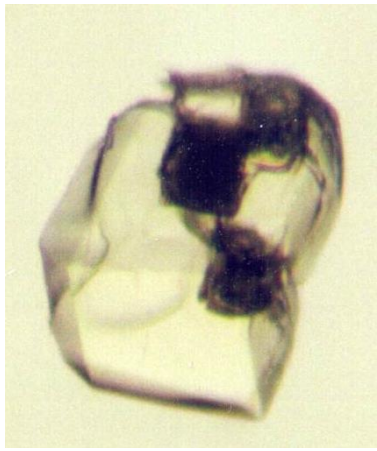


RADIATION DAMAGE:

why do we care?

CCP4/DLS
Workshop,
December 2018





Radiation damage:

The Plan:



- **What are the symptoms?**
- What is it?
- Why do we care? Effect on MAD/SAD.
- How do we calculate the Dose?
- What do we know/would like to know?

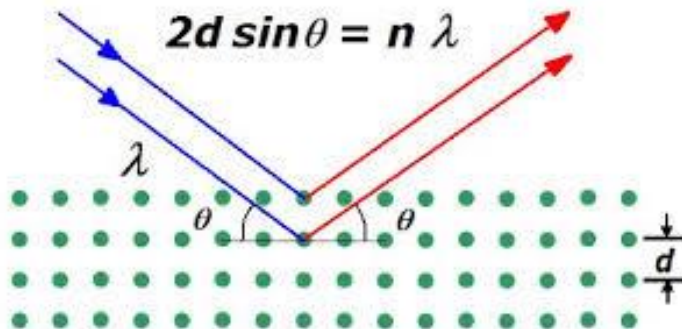
ROOM TEMPERATURE

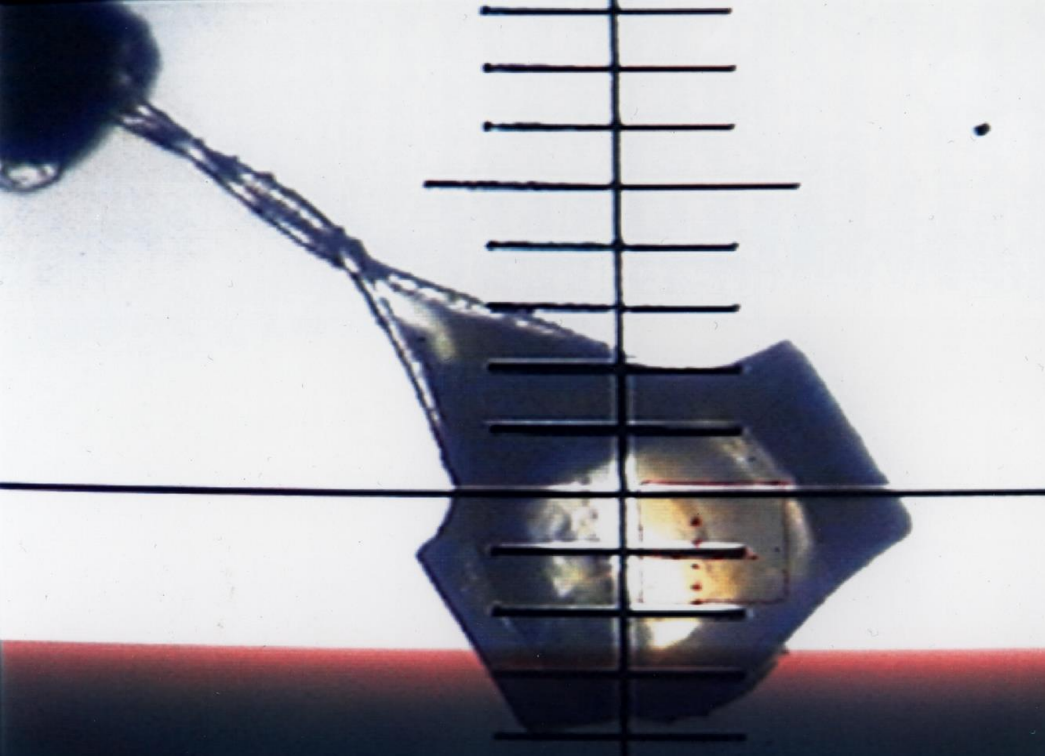
Intensity
decrease
with dose

Loss of
diffraction

Incomplete data
from crystals at
RT

$$2d \sin \theta = n \lambda$$





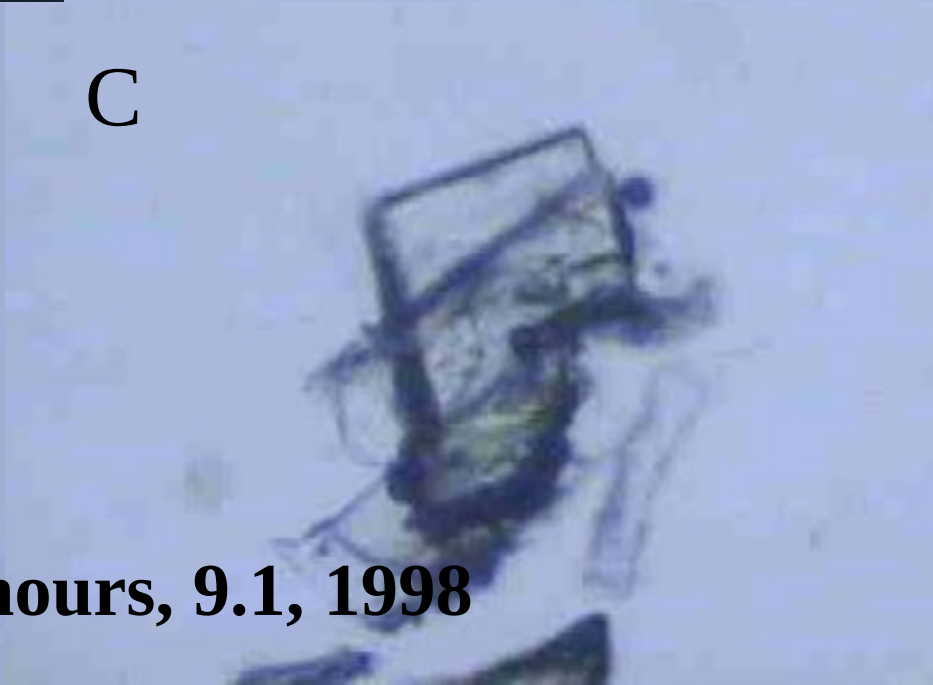
A



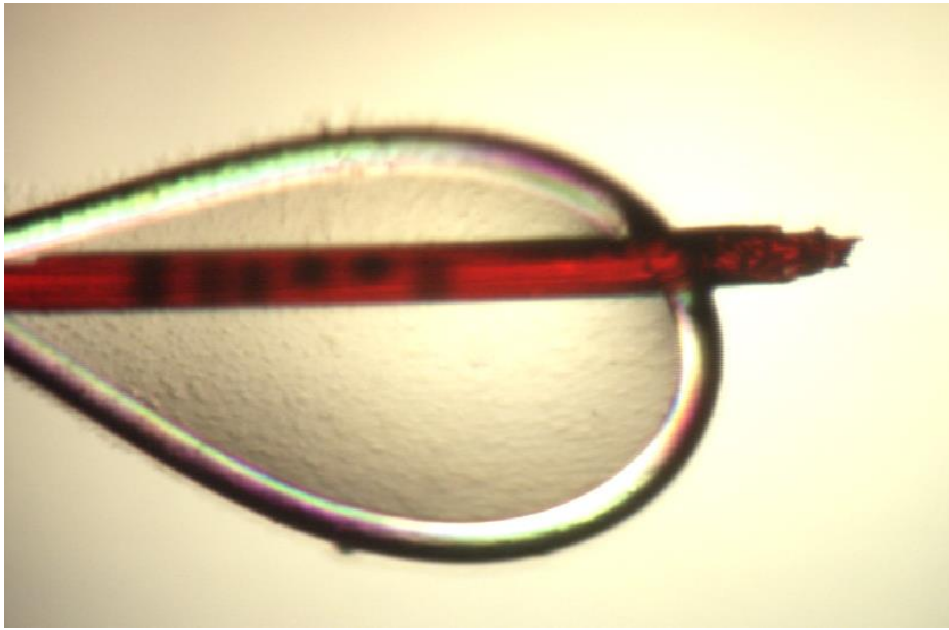
B



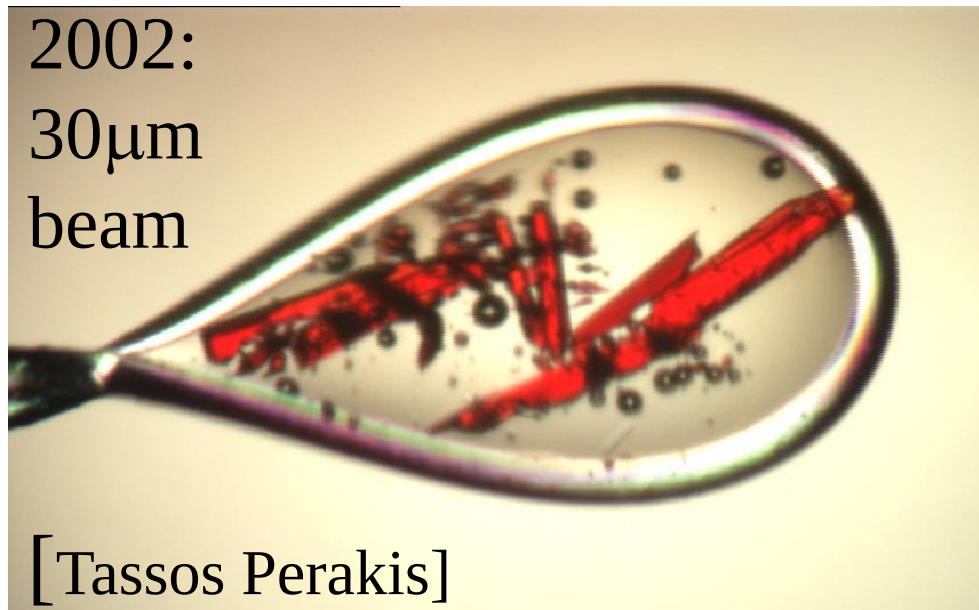
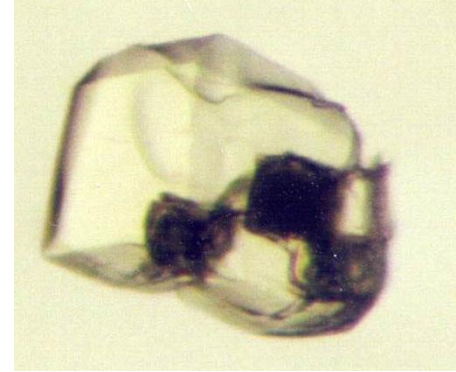
C



SSRL, 19 hours, 9.1, 1998



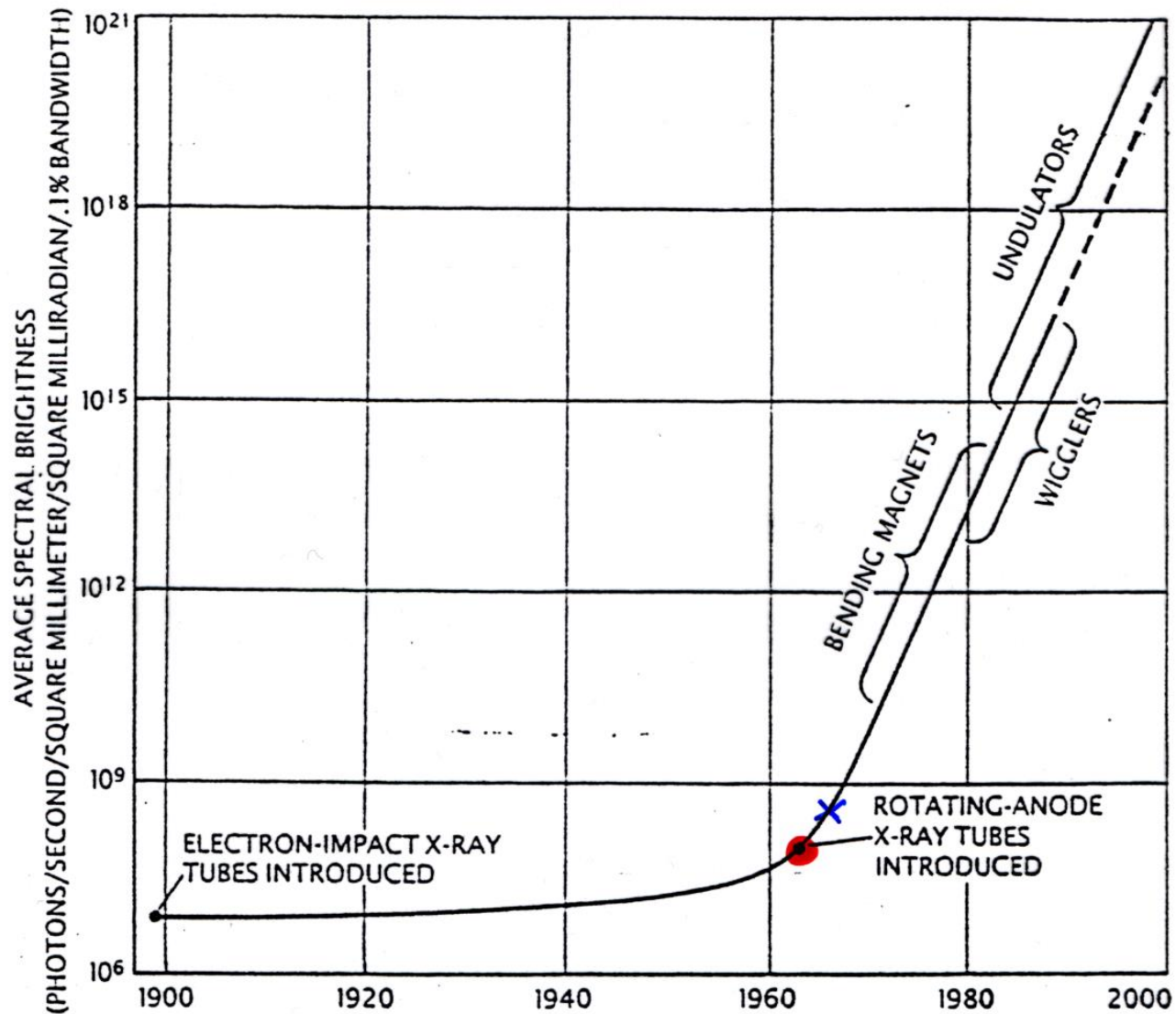
1995 onwards: 100 K
BUT THEN, 1999:



Also observe
spectral changes

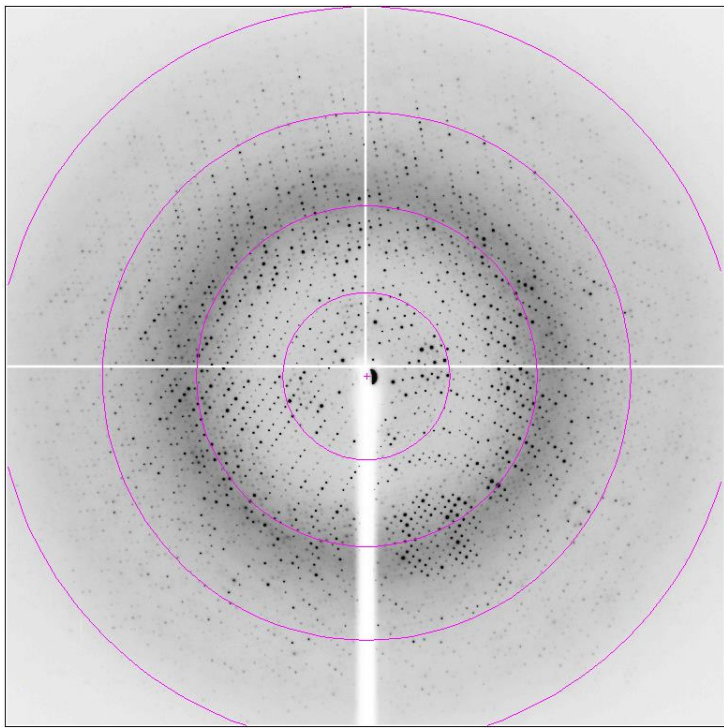
Iron containing protein, ESRF

Garman & Owen (2006), Acta D62



BRIGHTNESS OF X RAYS has increased by many orders of magnitude since the advent of synchrotron-radiation sources. Undulators in storage rings are the brightest source.

x multi-layer optics.

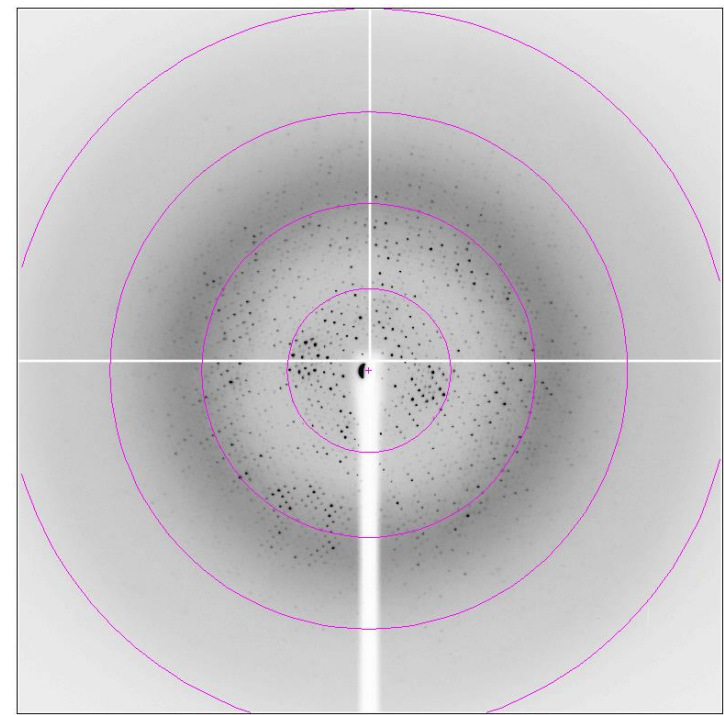


Intensity
decrease

Loss of
diffraction



Incomplete data
from crystals



Happens during 1 dataset at 100K for many crystals

Unit cell volume expansion

Increase in Wilson B factors, Rmerge

Increase in mosaicity

'GLOBAL' damage

ESRF 2000:

$1 \times 10^{12} \text{ ph s}^{-1}$ into
100 μm square slits

$3 \times 10^{13} \text{ ph s}^{-1}$ into
50 $\mu\text{m} \times 70\mu\text{m}$ [10¹⁴]

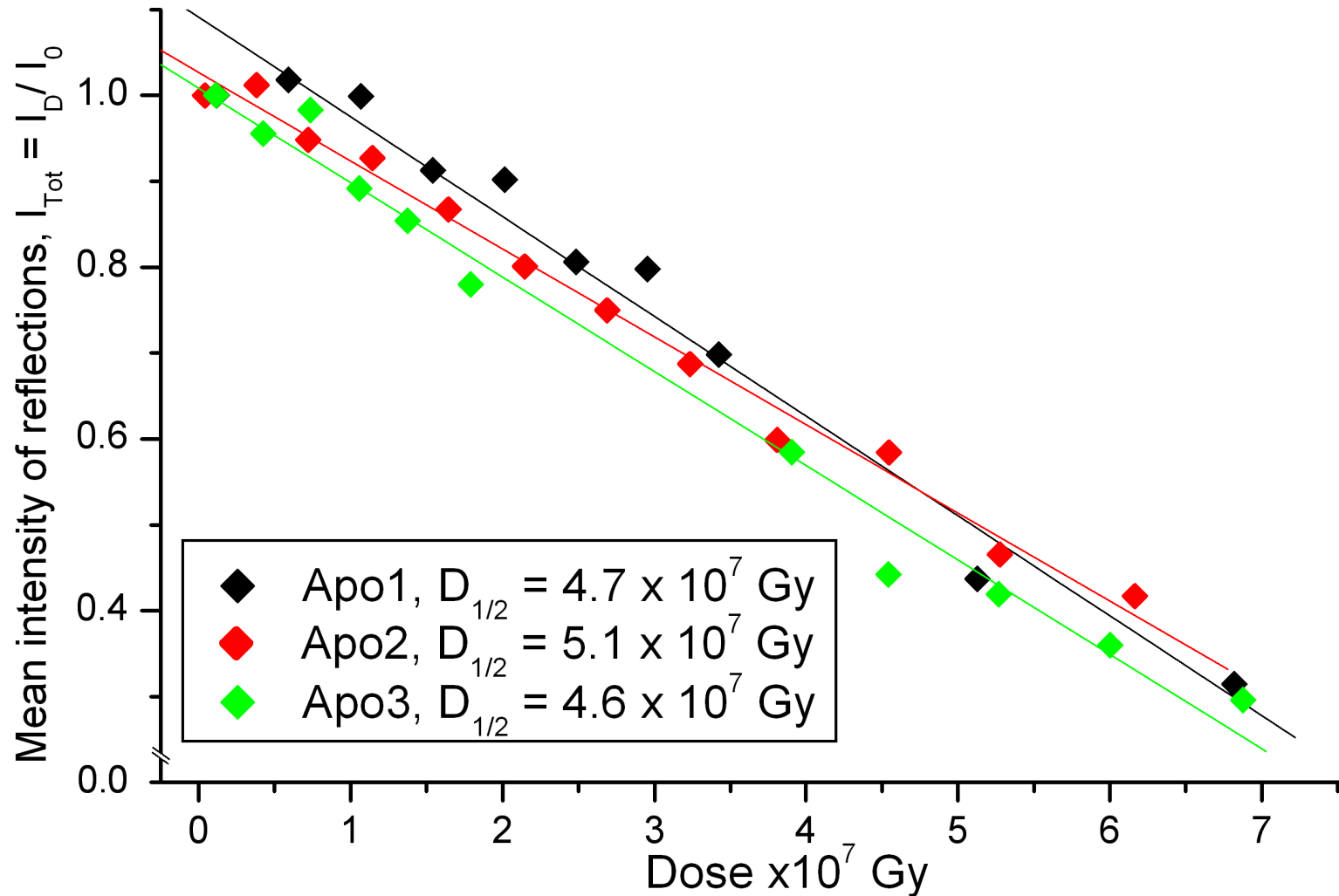


Diamond
Light
Source

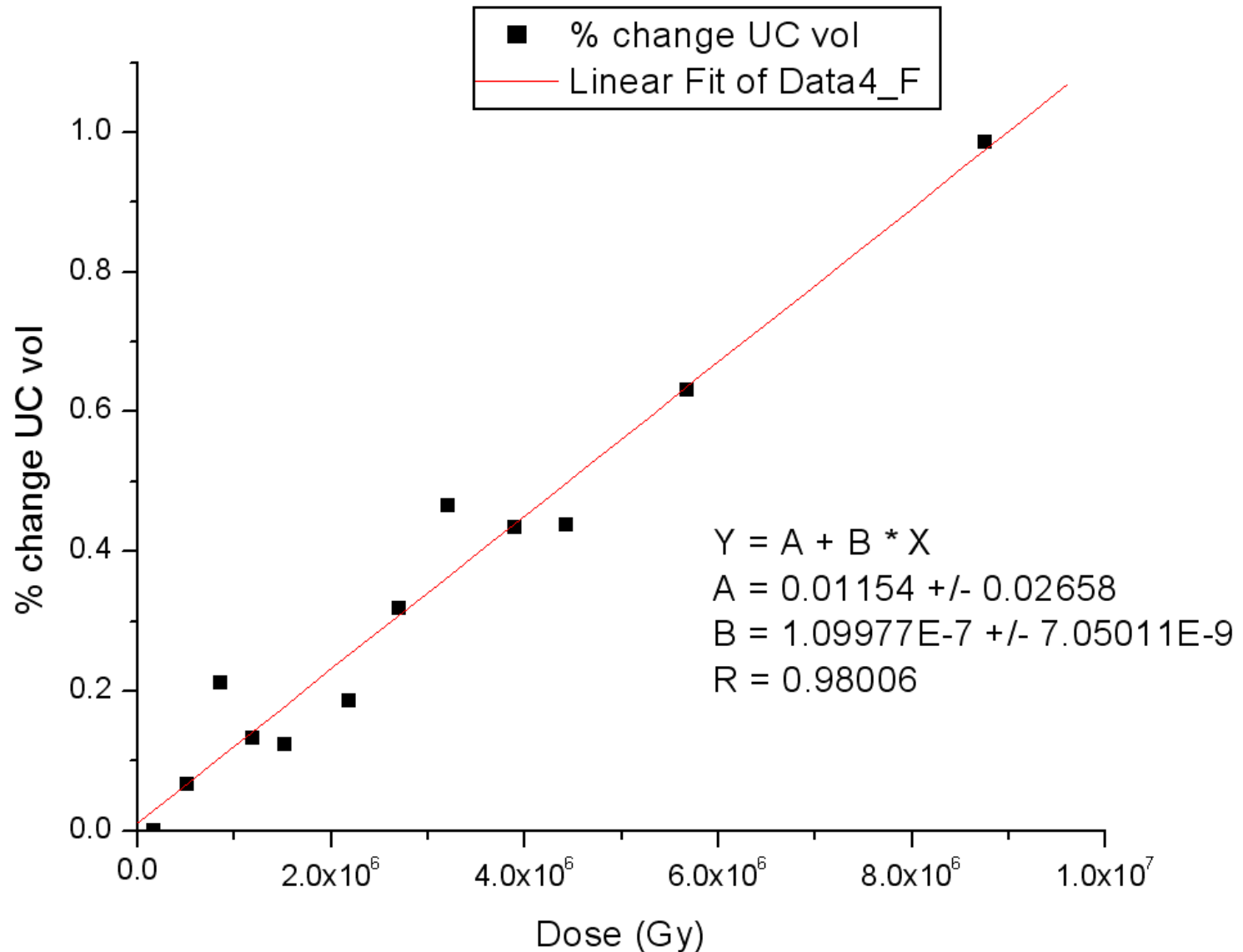


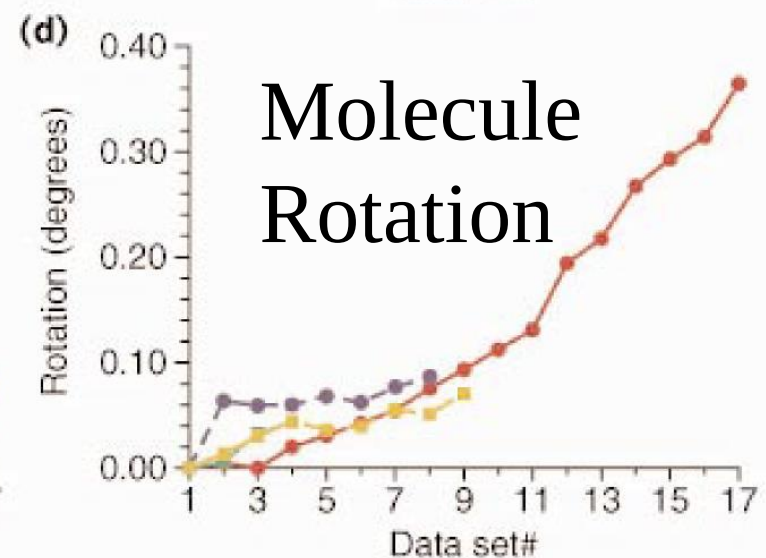
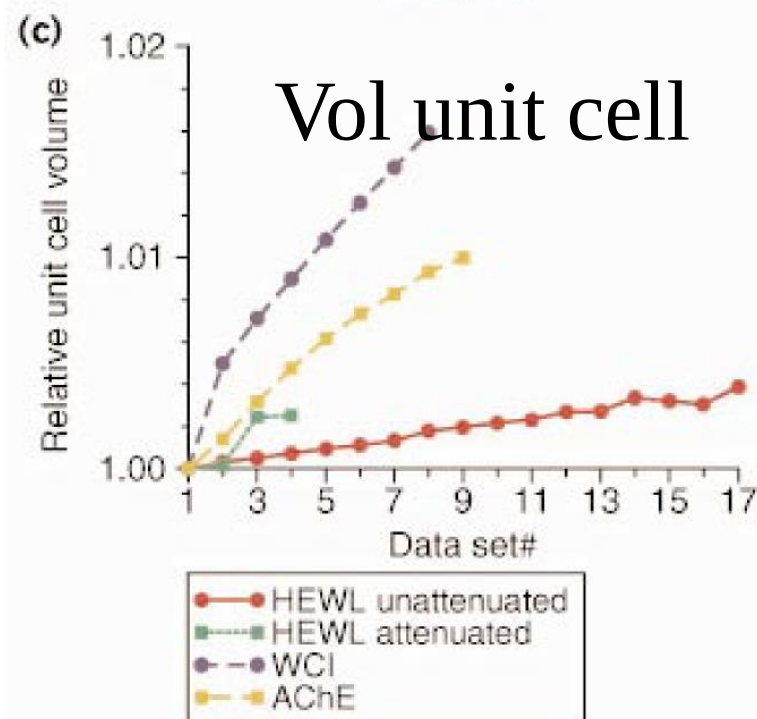
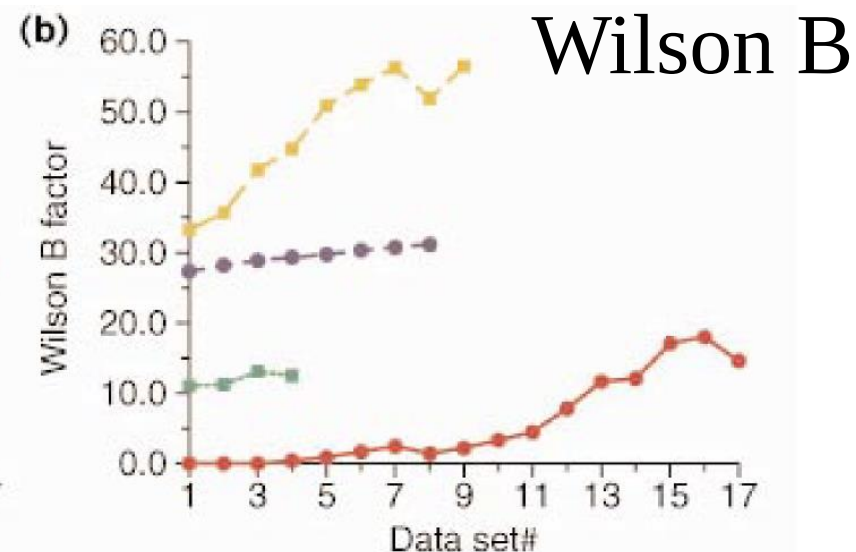
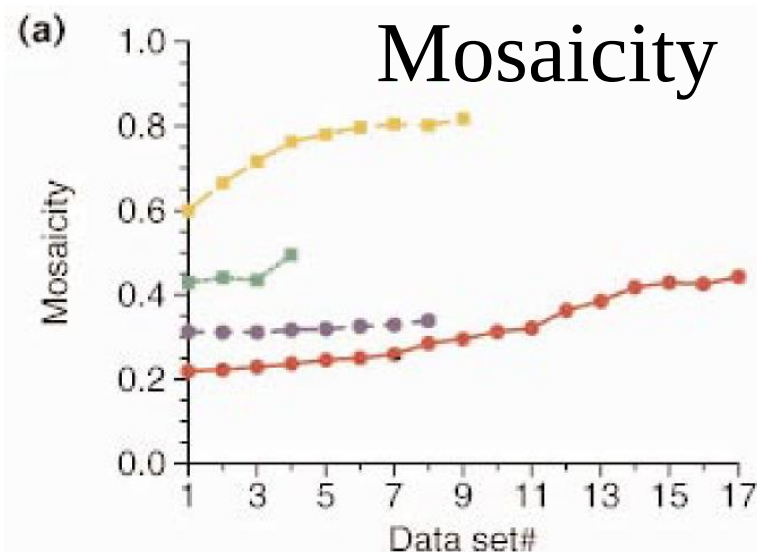
Intensity Decay at 100K

Normalised Intensity vs Dose: apoferritin



Unit cell volume increase





Structure

Data Parameters affected by Radiation Damage

- $I / \sigma(I)$ or resolution limit 
- R_{merge} 
- Scaling B factors 
- Mosaicity 
- Unit Cell expansion a) function of dose 
b) function of cryogen temperature 

Could this be an on-line damage metric?

[Ravelli and McSweeney, (2000) Structure]

No!

[Murray and Garman (2002), JSR, Ravelli et al (2002) JSR]

What global damage
metric should we use and against
what should we plot it?

- I_n/I_o
- Not $I/\sigma(I)$
- Scaling B factors?
- An R_{meas} type measure?

To monitor the damage we need an x-axis!
Not time or image number...
Dose estimation

$$\begin{aligned}\text{Dose} &= \frac{\text{energy absorbed}}{\text{unit mass}} \\ &= \frac{\text{J}}{\text{kg}} = \text{Gy (gray)}\end{aligned}$$

Fundamental metric against which to measure damage.

Takes care of the physics but NOT the chemistry.

MX experiment

1 MGy/s absorbed by a 100 μm cubed
metal free crystal in a
100 $\times$ 100 μm^2 beam of
12.4 keV (1 $\text{\AA}$) X-rays
flux: 10^{13} photons s^{-1}

3 Gy

MX at 100 K: 30 MGy experimental
dose ‘limit’ reached in ~ 30 s:
4th generations sources $\ll 1$ s,
XFELs: < 80 fs



Intensity Decay at 100K

Normalised Intensity vs Dose:

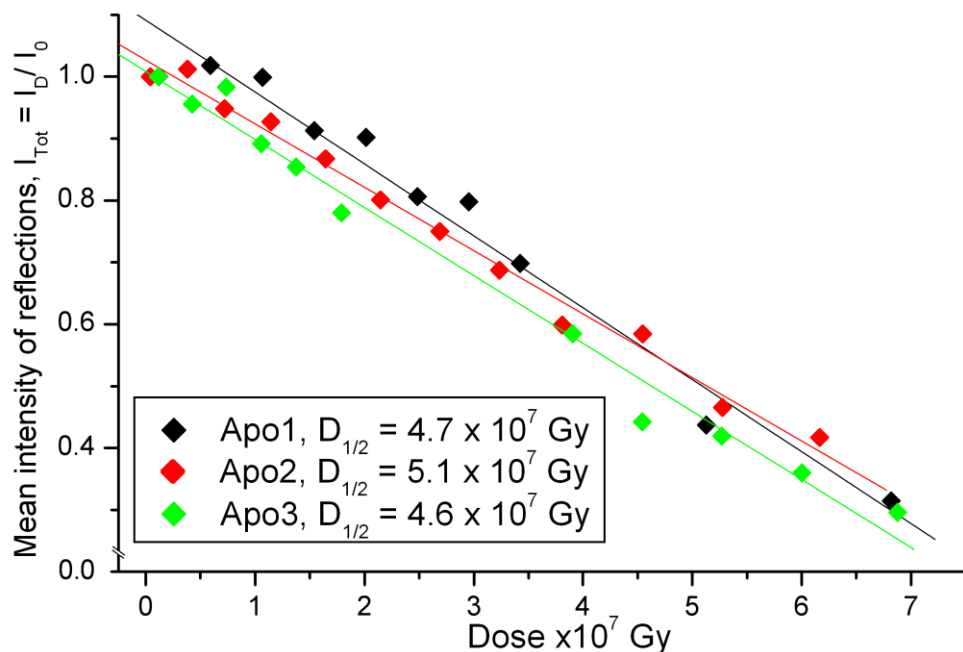
apoferritin

Coefficient of sensitivity $\propto$ change in
relative isotropic B factor:

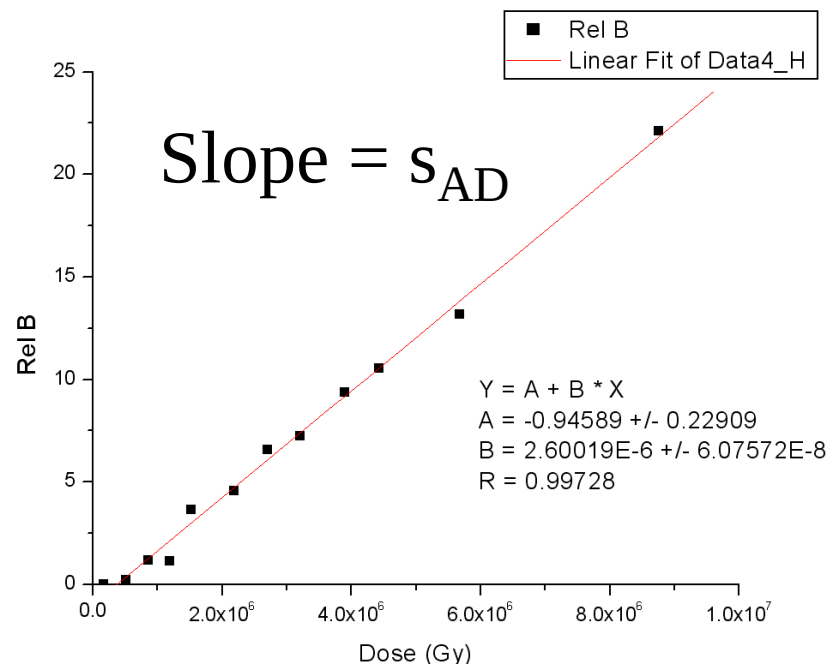
$$s_{AD} = \Delta B_{\text{rel}} / 8\pi^2 \Delta D$$

(e.g. HEWL@100 K = 0.012 Å²/Gy)

[Owen et al 2006, PNAS]

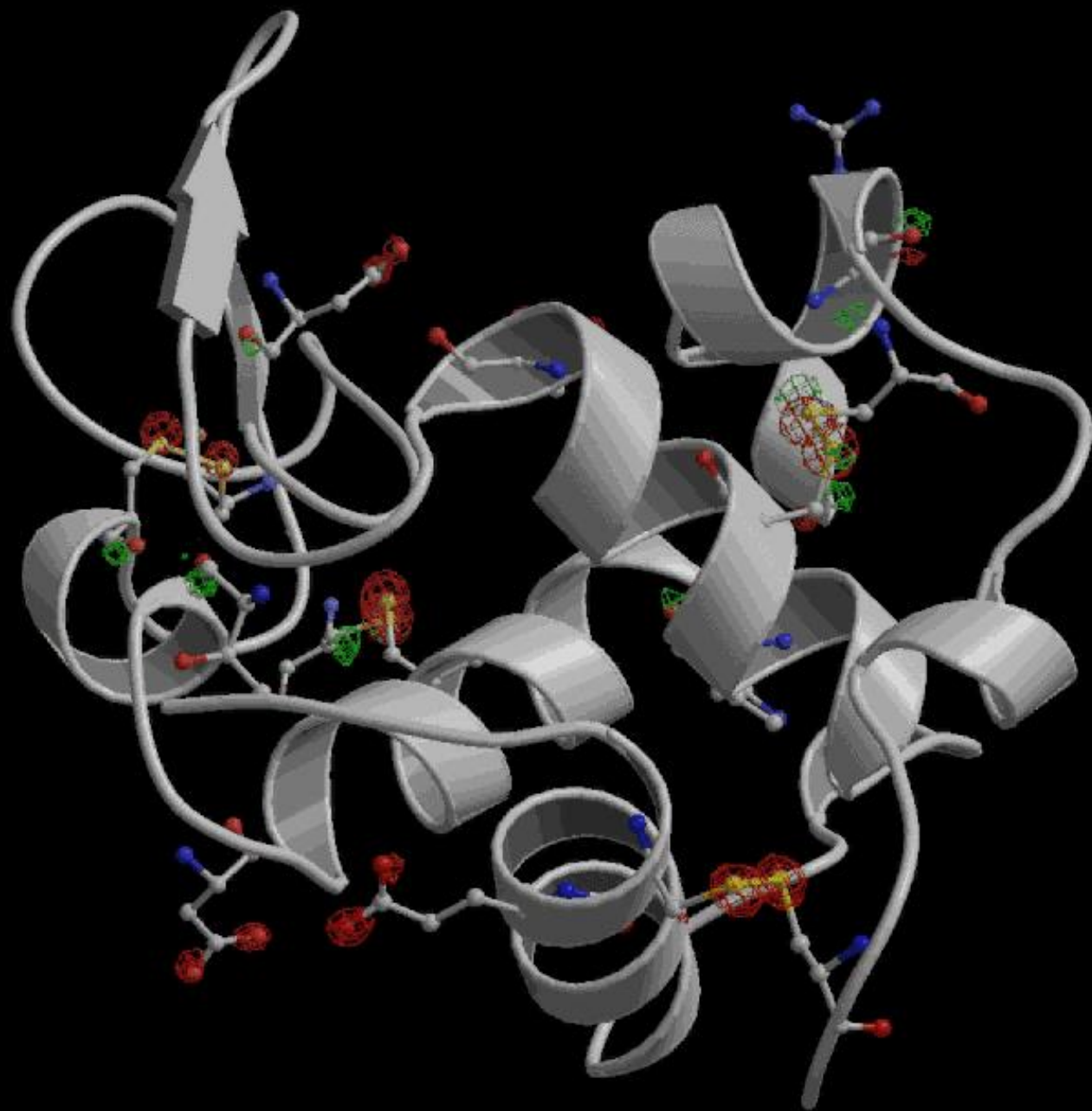


[Kmetko et al 2006, Acta D62]



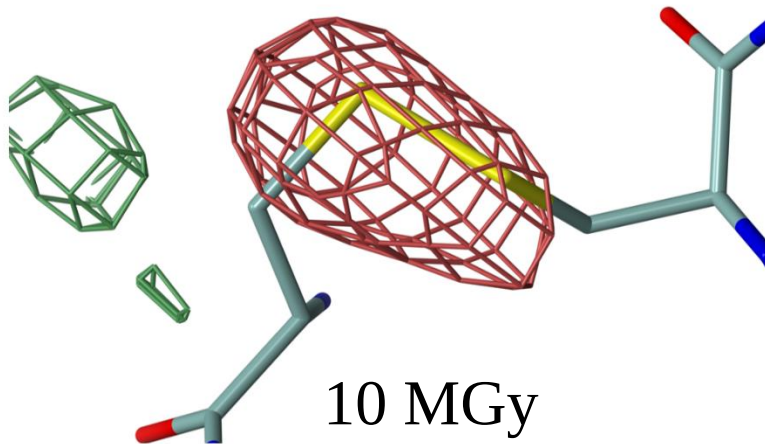
Global damage: summary

- Incomplete data/lost resolution/scaling ‘dip’
- Causes non-isomorphism within a dataset (unit cell grows)
- No significant ($< \times 2$) dose rate effect at 100 K at current flux densities (10^{15} ph/s/mm²).
- No significant ($< \times 2$) temperature dependence below 100 K, but weak minimum at around 50 K.
- Damage to lattice due to hydrogen abstraction and then build up?
- Heating not significant at current flux densities.
- For a particular system is predictable/can be modelled (using a sacrificial crystal)

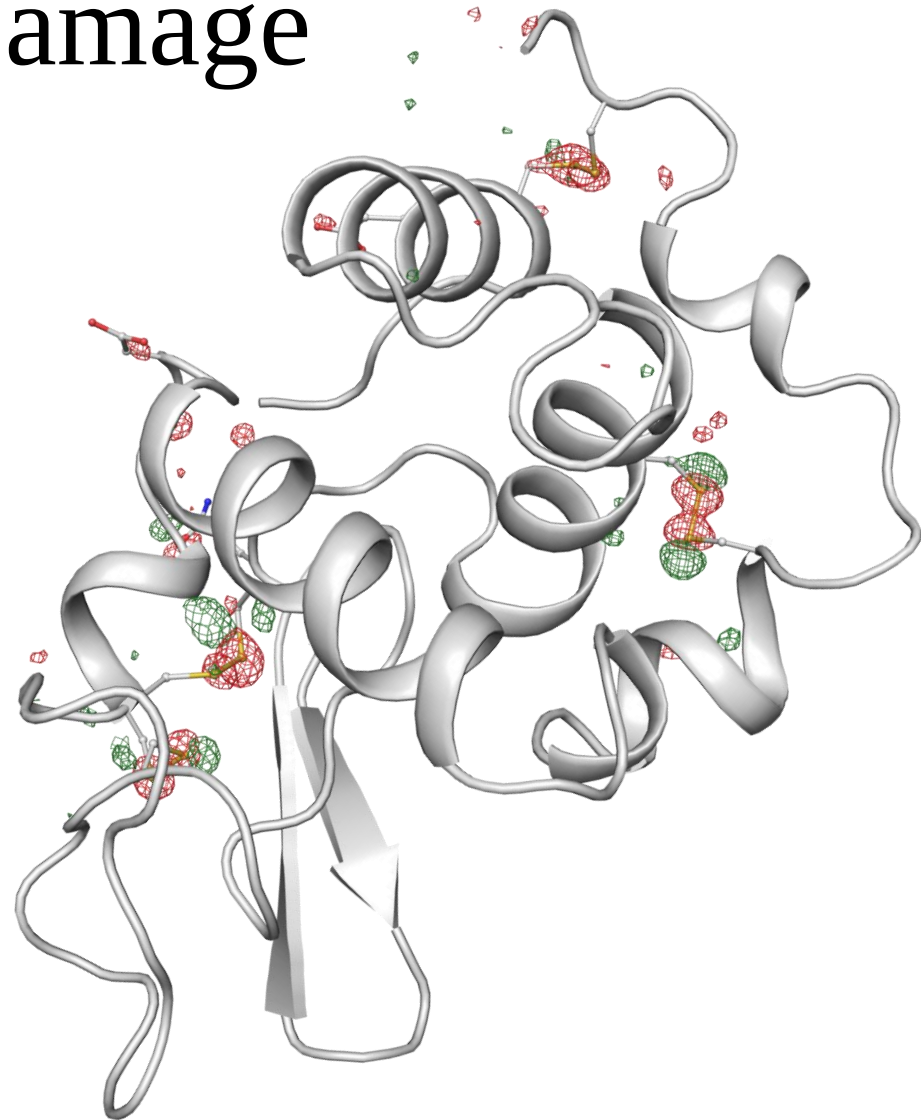


Specific Damage

- Specific damage occurs in a predictable hierarchy in proteins
- Reduction of metallocentres
- Breakage of disulphide bonds
- Asp and Glu decarboxylation



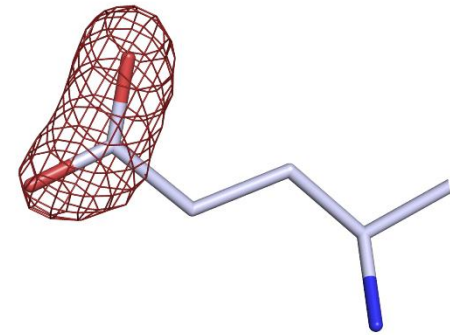
Difference map $\text{Fo}_4\text{-Fo}_1$



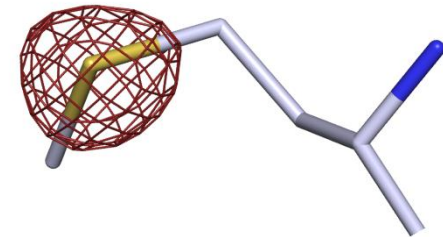
Weik et al. 2000, Burmeister 2000
Ravelli and McSweeney 2000,

Specific Damage

- Specific damage occurs in a predictable hierarchy in proteins
- Reduction of metallocentres
- Breakage of disulphide bonds
- Decarboxylation of ASP and GLU residues
- Cleavage of S—C bond in MET
- Rupture of covalent bonds to heavier atoms:
C-Br, C-I, S-Hg
- **Note** that if this were due to primary damage alone, damage would be in order of absorption cross sections of atoms, which it is not.



*GLU $\pm 4\sigma$ -level
difference map:
Red = negative density*



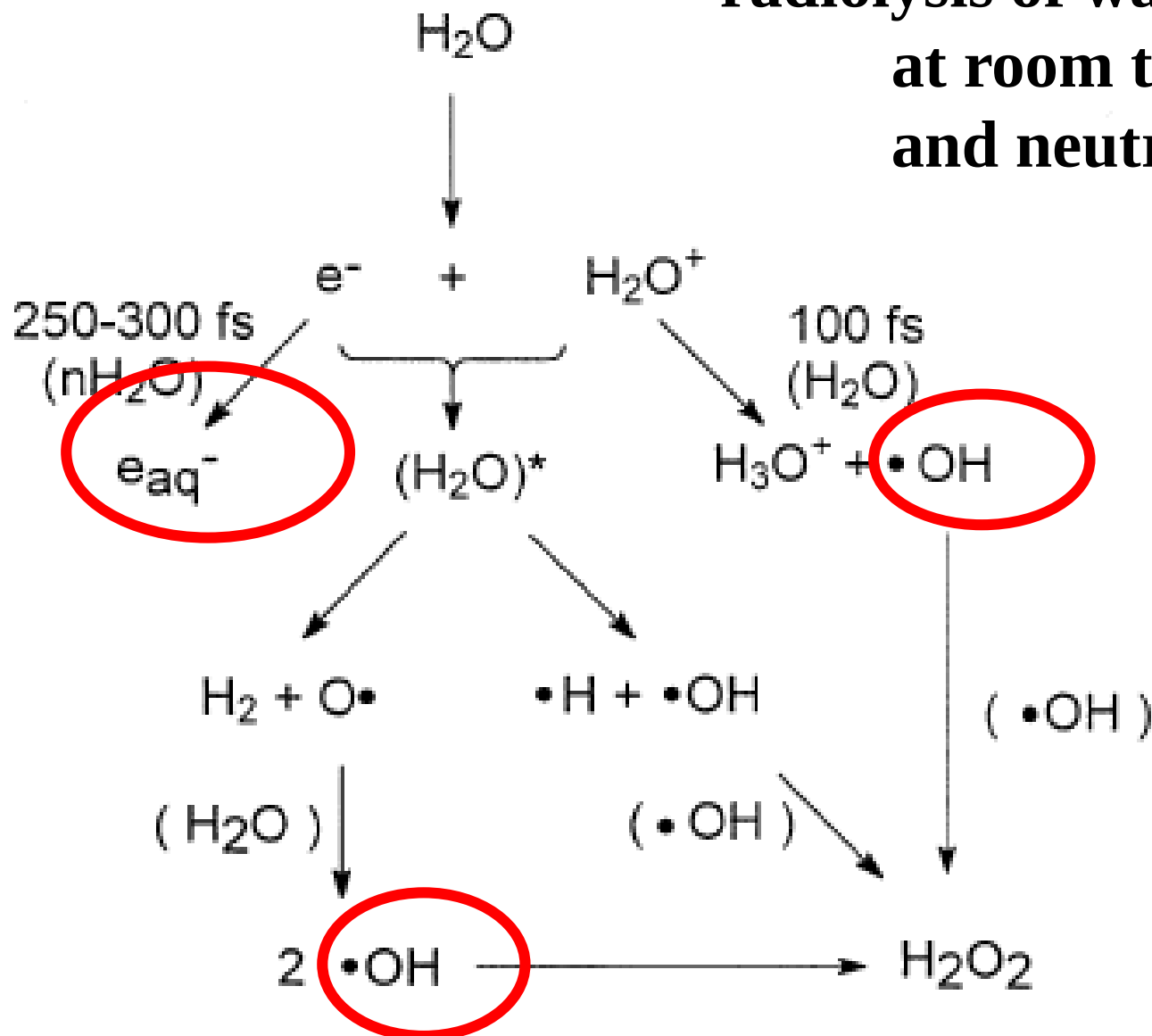
*MET $\pm 4\sigma$ -level
difference map:
Red = negative density*

Damage: the Radiation Chemistry

1) INDIRECT RADIATION DAMAGE :

radiolysis of water

at room temperature
and neutral pH:



OH thought not to be
mobile in glasses
below 110K

(Owen et al Acta D
2012)

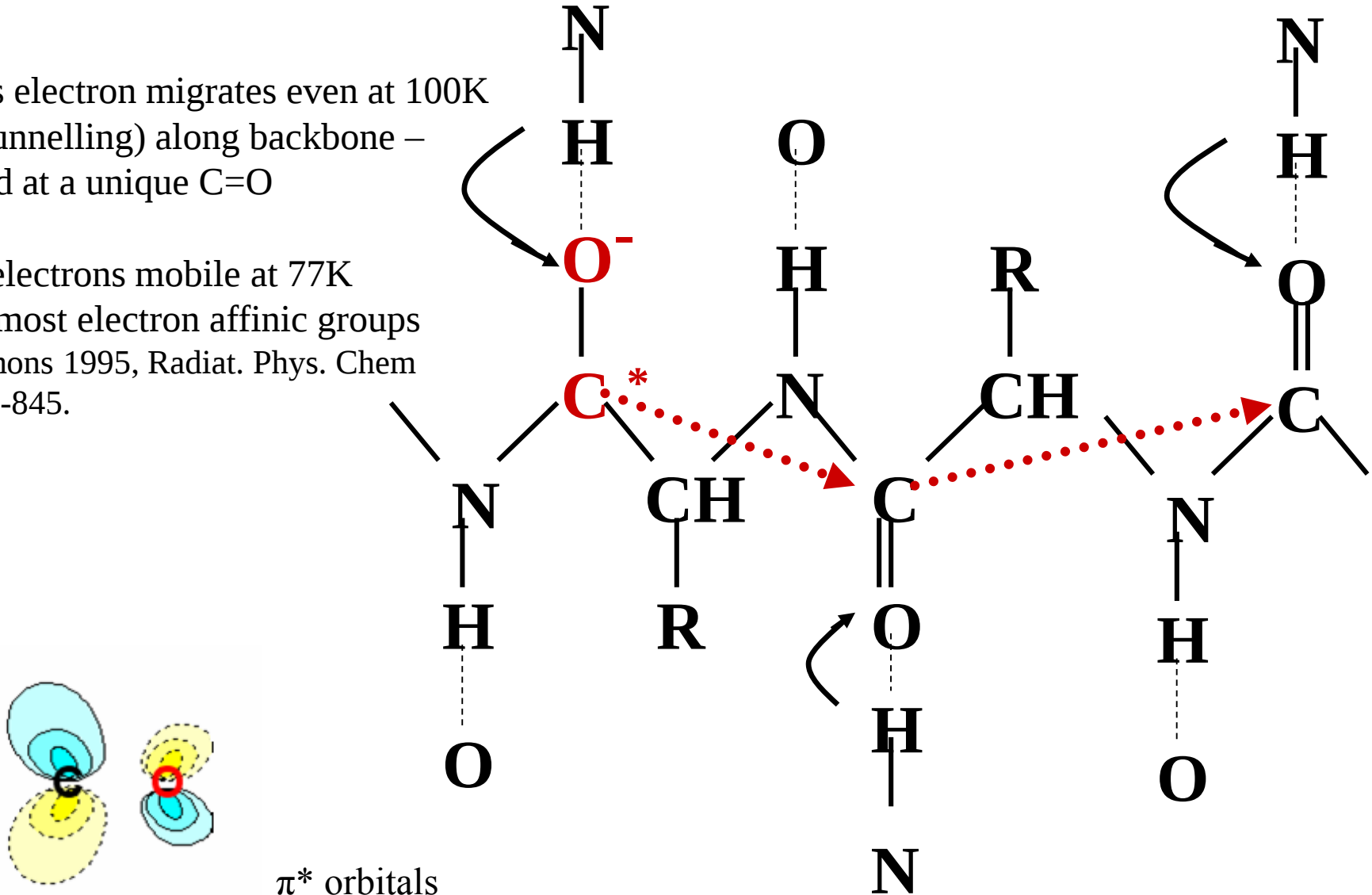
Hiroki, A. Pimblott, S. M.
LaVerne, J. A. (2002)
J Phys Chem A **106**,
9352-9358

2) DIRECT RADIATION DAMAGE. Protein Redox

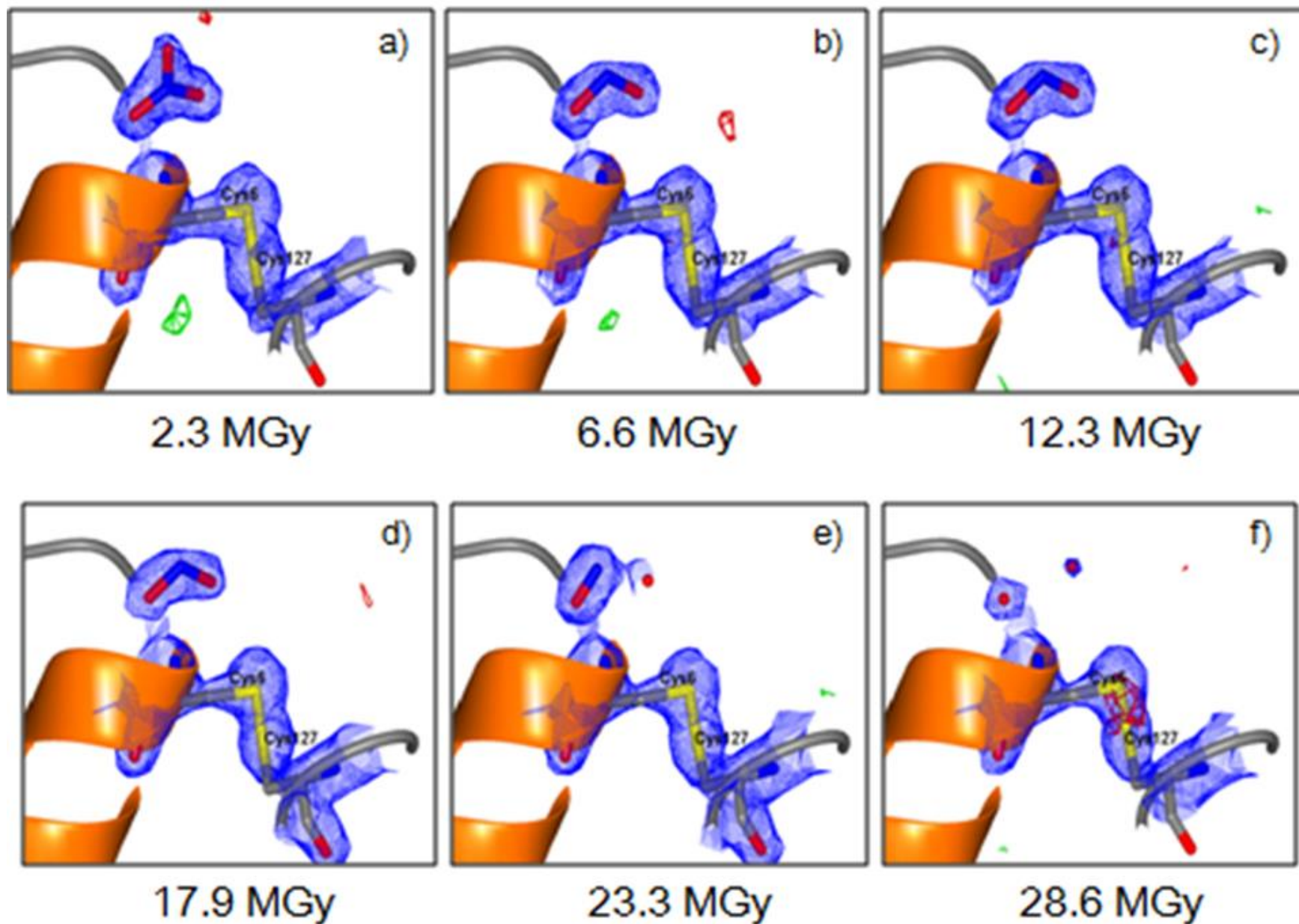
a) electron migration and trapping.

Excess electron migrates even at 100K
(q.m.tunnelling) along backbone –
trapped at a unique C=O

ESR: electrons mobile at 77K
Go to most electron affinic groups
M. Symons 1995, Radiat. Phys. Chem
45, 837-845.



Radiation Chemistry in action: Nitrate scavenger



Specific Damage: summary.

- Can compromise biologically relevant observations (e.g. damage enzymatically important glutamates).
- Metallo-enzymes are reduced by X-ray beam.
- Perhaps weakly dose rate dependent ($< \times 2$)
- Perhaps weakly wavelength dependent ($< \times 2$)
- Weakly temperature dependent (varying results) ($< \times 2$)
- Can be reduced with certain scavengers: but very conflicting results (mainly $< \times 2$, benzoquinone RT $\times 9$)
- We DON'T understand pecking order of damage within an amino acid group pH? Solvent accessibility? Neighbouring amino acids?

Radiation damage:

The Plan:

- What are the symptoms?
- **What is it?**
- Why do we care? Effect on MAD/SAD.
- How do we calculate the Dose?
- What do we know/would like to know?

PHYSICS of the interaction of X-rays with crystals.

A) Diffraction

B) Absorption = Energy loss

N.B. $> 90\%$ of the beam does not interact at all,
but goes straight through.

A) Primary X-ray interaction processes with crystal and solvent.

Thomson (Rayleigh, coherent) scattering

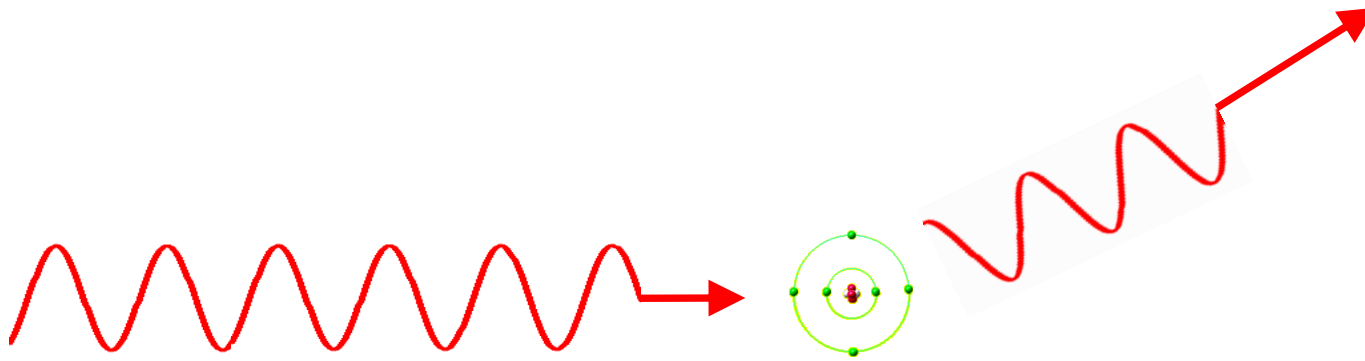


[8% at 1Å]

ELASTIC - no energy loss.

Primary X-ray interaction processes with crystal and solvent.

Thomson (Rayleigh, coherent) scattering

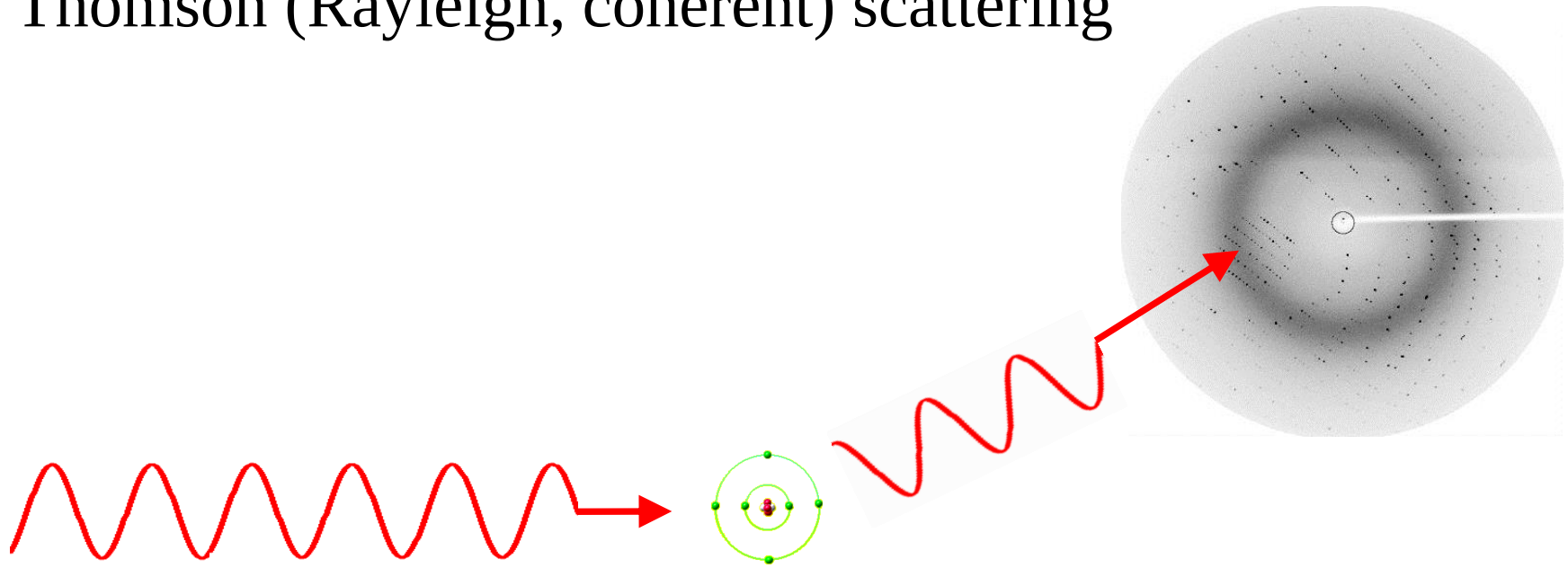


[8% at 1Å]

ELASTIC - no energy loss.

Primary X-ray interaction processes with crystal and solvent.

Thomson (Rayleigh, coherent) scattering



ELASTIC - no energy loss.

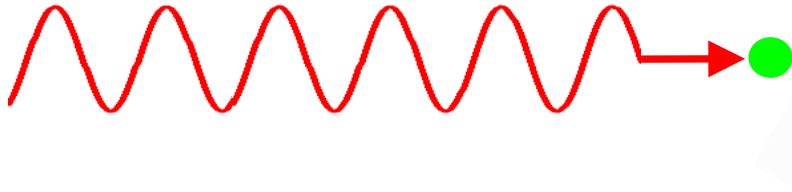
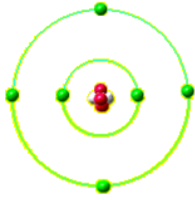
Coherent – adds vectorially and gives diffraction pattern.

Small proportion of total scattering: 8% at 1Å

BUT IT IS THE BIT WE WANT!!

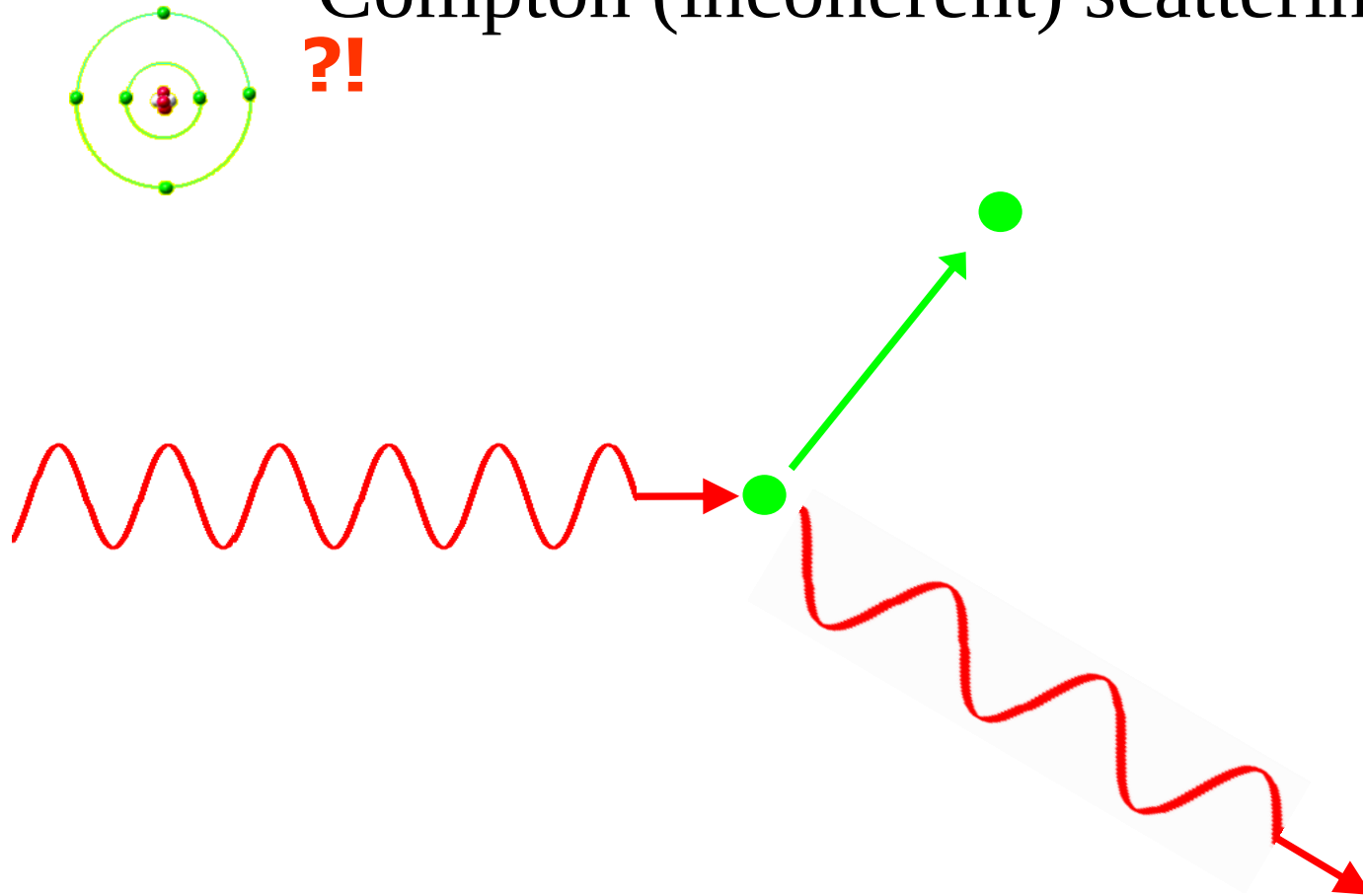
Compton (incoherent) scattering

?!



X-ray transfers some energy to atomic electron and thus has lower energy (higher wavelength).

Compton (incoherent) scattering



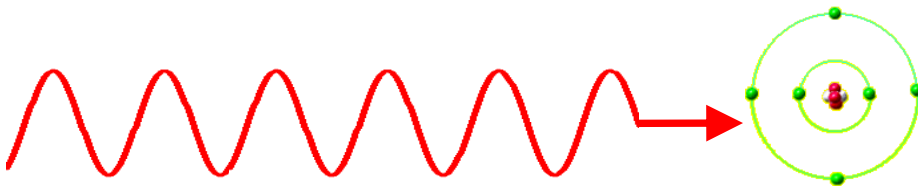
X-ray transfers some energy to atomic electron and thus has lower energy (higher wavelength).

Incoherent – part of X-ray background in images.

Also a small proportion of total scattering: 8% at $1\text{\AA}$

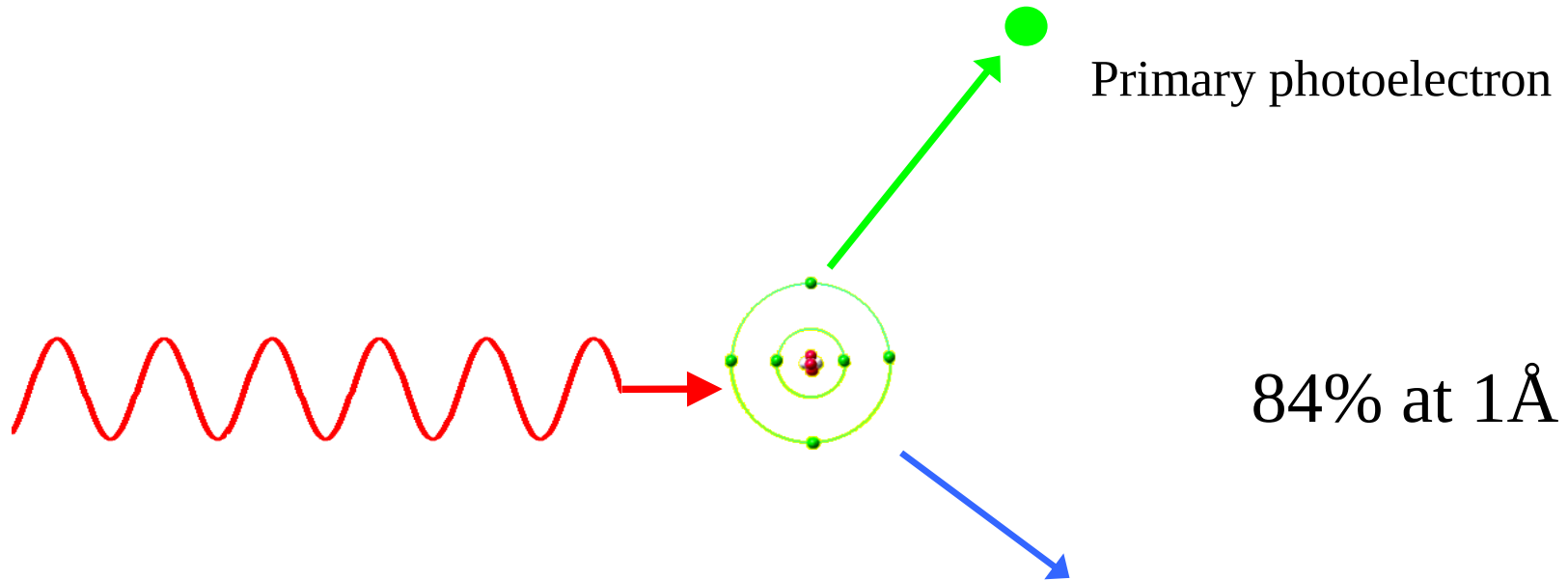
Photoelectric Absorption

84% at 1Å



INELASTIC.

Photoelectric Absorption

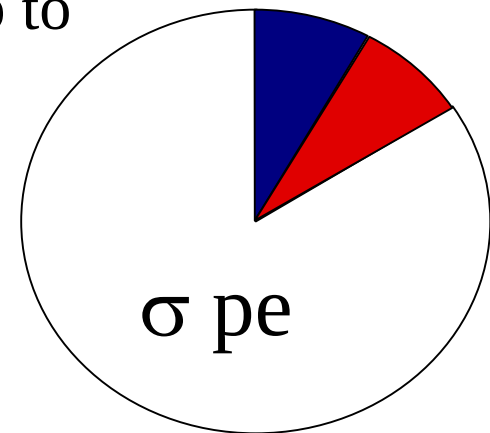


INELASTIC.

X-ray transfers all its energy to an atomic electron, which is then ejected. Each 12 keV primary photoelectron can give rise to up to 500 ionisation events.

Atom can then emit a characteristic X-ray or an Auger electron to return to its ground state.

$$\begin{aligned}\sigma_{\text{tot}} &= \sigma_{\text{pe}} + \sigma_{\text{inc}} + \sigma_{\text{coh}} \\ &84\% + 8\% + 8\%\end{aligned}$$



Photoelectric Cross Sections (barns/atom) at 13.1 keV

[1 barn= 10^{-28}m^2]

A few heavy atoms can
make a big difference.

.

H

Photoelectric Cross Sections (barns/atom) at 13.1 keV

[1 barn= 10^{-28}m^2]

A few heavy atoms can
make a big difference.

.



H

C

Photoelectric Cross Sections (barns/atom) at 13.1 keV

[1 barn= 10^{-28}m^2]

A few heavy atoms can
make a big difference.

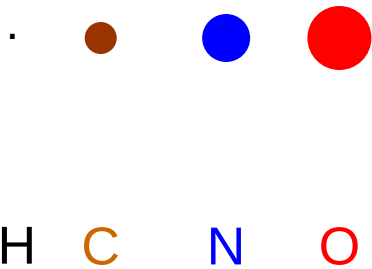


H C N

Photoelectric Cross Sections (barns/atom) at 13.1 keV

[1 barn = 10^{-28}m^2]

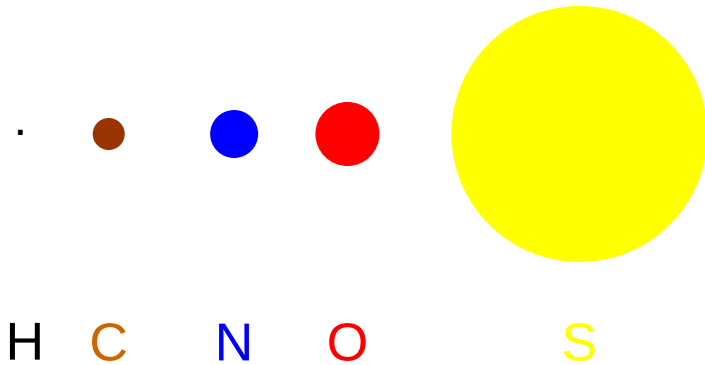
A few heavy atoms can
make a big difference.



Photoelectric Cross Sections (barns/atom) at 13.1 keV

[1 barn=10⁻²⁸m²]

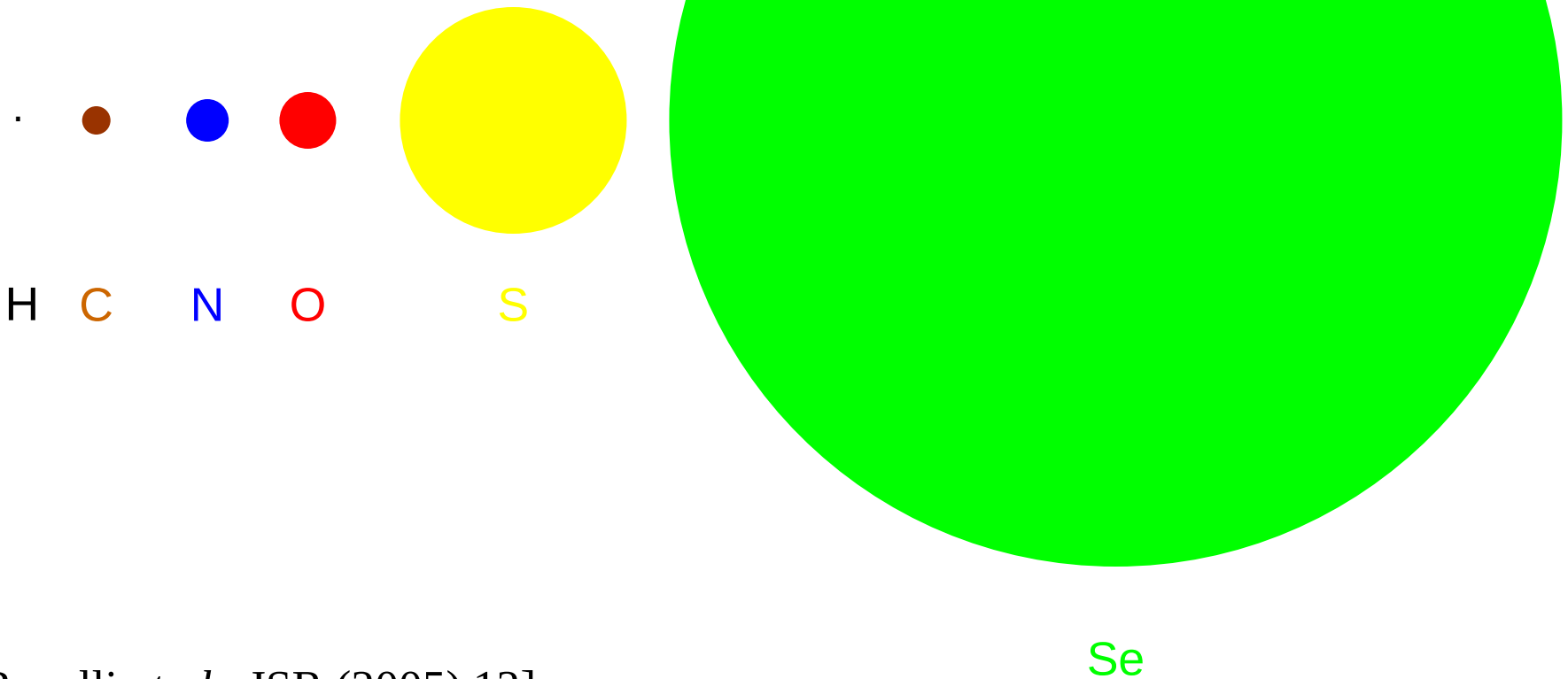
A few heavy atoms can
make a big difference.



Photoelectric Cross Sections (barns/atom) at 13.1 keV

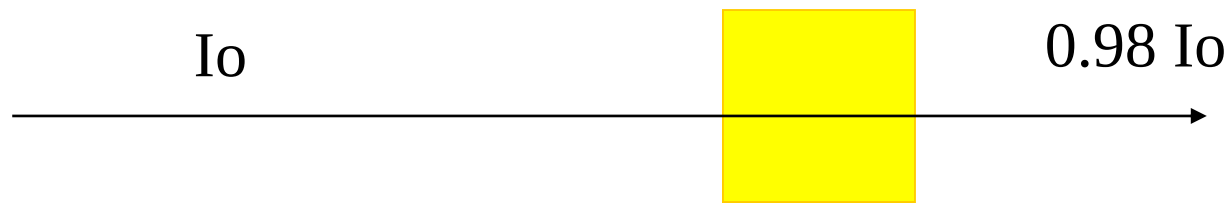
[1 barn=10⁻²⁸m²]

A few heavy atoms can
make a big difference.

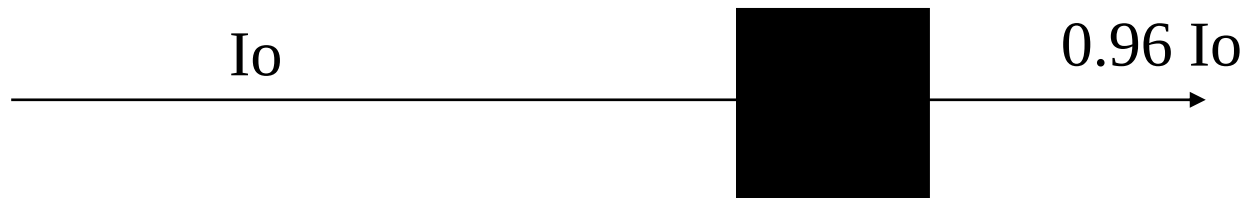


Beam absorption ($\lambda=1\text{\AA}$) by a protein crystal

Native HEWL 100 μm thick



Platinum derivatised (1/molecule)
HEWL 100 μm thick



N.B. INCIDENT FLUX is the SAME but the absorbed dose is DOUBLE

A few heavy atoms in the solvent can make a BIG difference to the absorption cross section and this the dose rate for the SAME flux.

e.g. Cacodylate buffer (arsenic, mass 75 cf selenium = 79)

BACK SOAKING to REMOVE

Non-specifically bound heavy atoms

e.g. a brominated DNA-protein complex will radiation damage much faster than a native crystal, and will de-brominate during data collection [Ennfar et al, Acta Cryst D (2002) 1263-1268].

Radiation damage:

The Plan:

- What are the symptoms?
- What is it?
- **Why do we care? Effect on MAD/SAD.**
- How do we calculate the Dose?
- What do we know/would like to know?

Effect on MAD/SAD phasing methods.

- Failure of structure determination (Multi-wavelength anomalous dispersion MAD, SAD)
due to creeping non-isomorphism –
 - a) cell expansion and
 - b) movement of molecule in unit cell
 - c) structural changes DURING experiment.i.e. **MAD/SAD phasing** signals (<5%)
washed out completely.

Non-isomorphism: DISASTER!

Crick and Magdoff (1956) showed that for a 0.5% change in all three unit cell dimensions of 100Å, the intensity would change by

15% at 3Å

for general reflections

[Crick and Magdoff (1956) Acta Cryst **9**, 901-908]

i.e. **MAD/SAD phasing** signals (<5%) washed out completely.

Radiation damage:

The Plan:

- What are the symptoms?
- Why do we care? Effect on MAD/SAD.
- What is it?
- **How do we calculate the Dose?**
- What do we know/would like to know?

DOSE Postulate (Henderson 1990):

- There is a MAXIMUM dose

(Energy absorbed/unit mass: Joules/kg = Gy)

which protein crystals can tolerate which depends only on the PHYSICS of the situation.

- Crystal might not reach that limit due to chemical factors, but it is unlikely to last BEYOND the limit.
- Need to be able to calculate the DOSE:

RADDOSE

V1: Murray, Garman & Ravelli (2004) JAPC, 37, 513-522

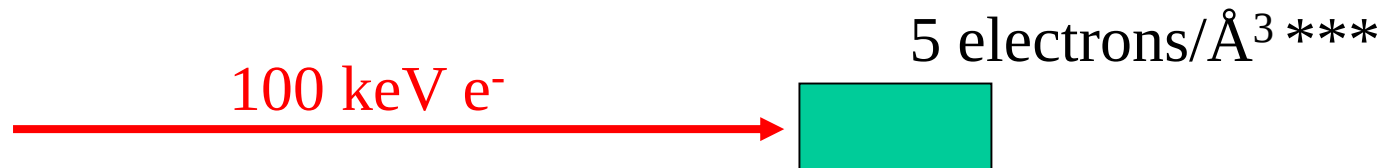
V2: Paithankar, Owen & Garman, (2009) JSR 16, 152-162

V3: Paithankar & Garman (2010), Acta D 66, 381-388

Calculated radiation dose limit for biological specimens at 77K from analogy with electron microscopy.

[Henderson (1990) Proc. R. Soc. Lond. B **241**, 6-8.]

- For 100 keV electrons, diffraction from protein crystals at 77 K fades to half the intensity with 5 electrons/Å²
- This corresponds to a dose of: 5×10^7 Grays
[say 2×10^7 Grays in first part of depth-dose curve ($\sim 50\mu\text{m}$)] ***
(1 Gray = 1Joule kg⁻¹)

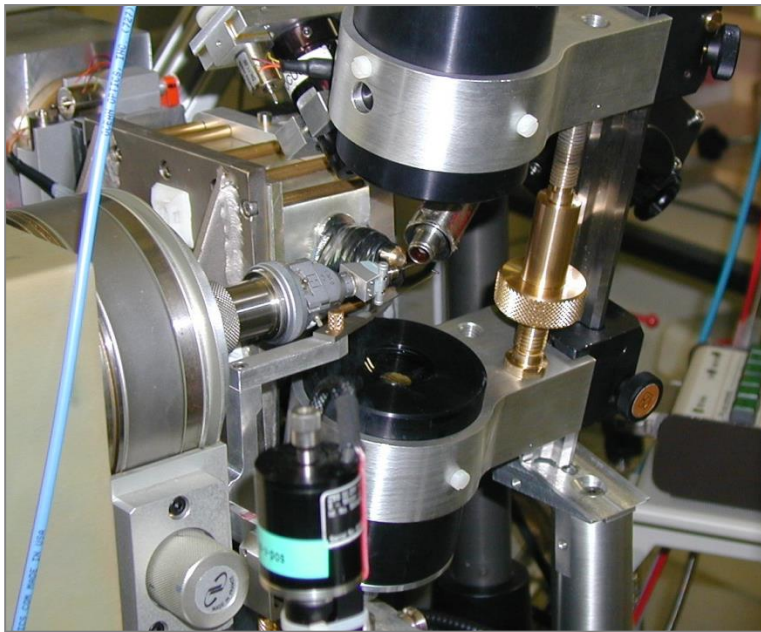


Absorbed energy to take diffracted I_0 $\longrightarrow$ $I_0/2$

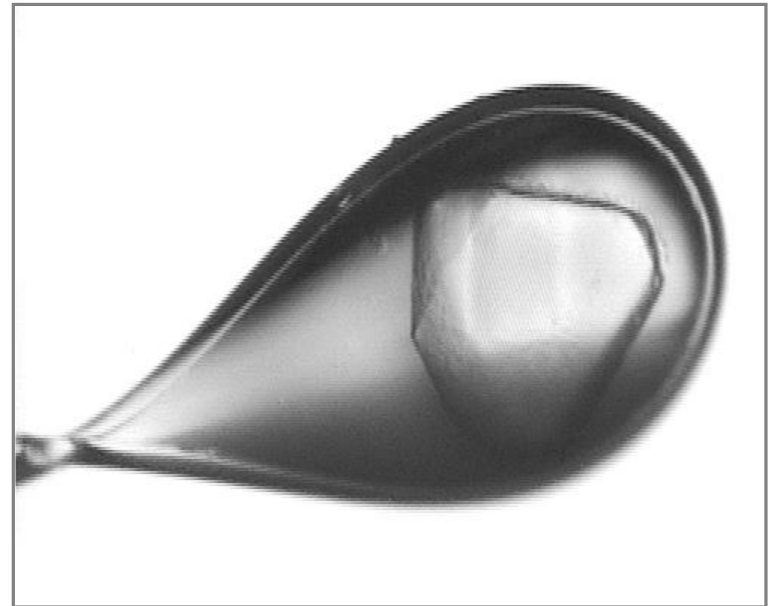
Make this dose calculation convenient for MX (include solvent contribution in mM and heavy atoms explicitly: RADDDOSE)

To find the energy deposited per unit mass in the
crystal, need to characterise two things:

The Beam

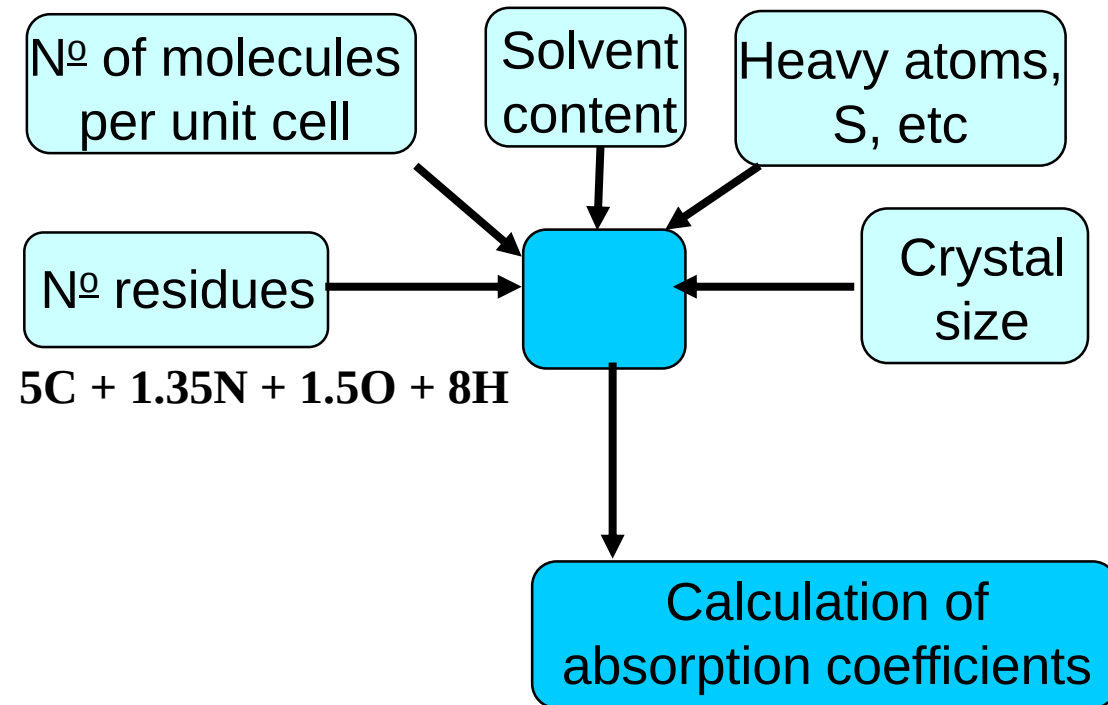


The crystal

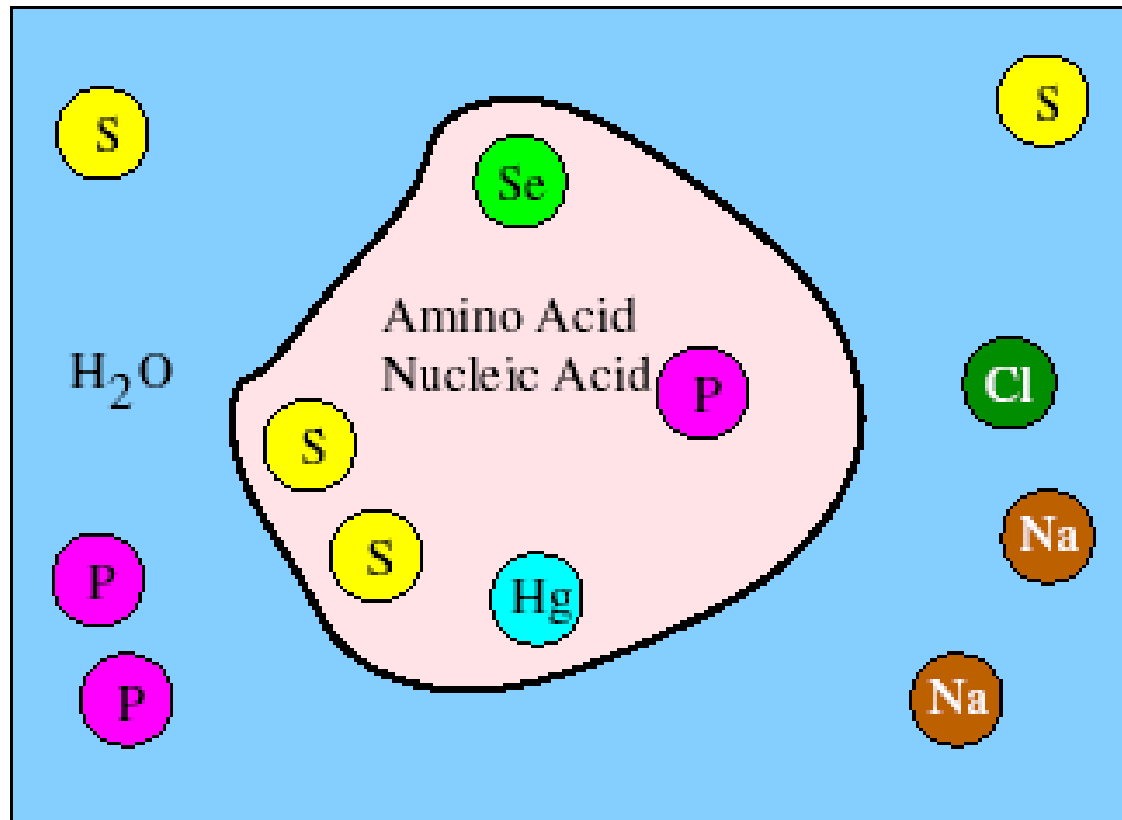


Calculating Dose (*RADDOSE*)

Crystal Characteristics



absorption coefficients
e.g. apoferritin: 0.406mm^{-1}
holoferritin: 1.133mm^{-1}



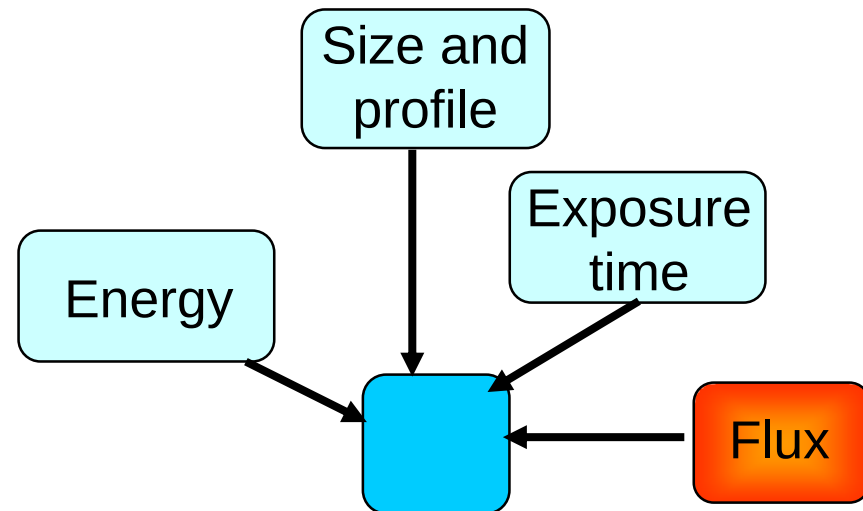
Number of Amino Acids

'HA' atoms per monomer, *e.g.* S, Se, Hg

Solvent - concentrations of components, *e.g.* Na⁺, Cl⁻

Calculating Dose (*RADDOSE*)

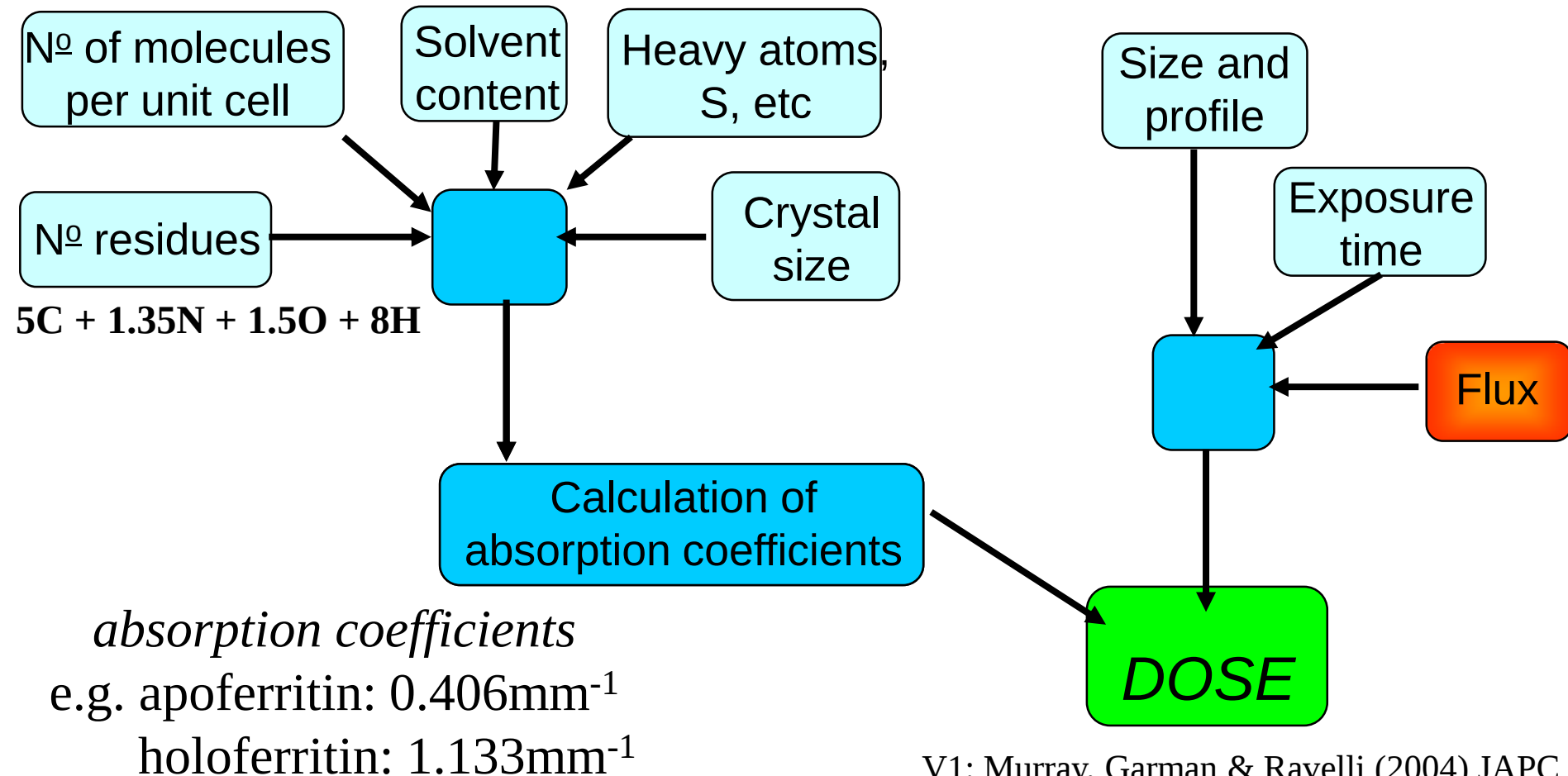
Beam Characteristics



Calculating Dose (*RADDOSE*)

Crystal Characteristics

X-ray Beam Characteristics



V1: Murray, Garman & Ravelli (2004) JAPC
V2: Paithankar, Owen & Garman, (2009) JSR
V3: Paithankar & Garman (2010), Acta D

MX experimental dose limit (@ 2Å) measurement: Ferritin

N.B. INCIDENT FLUX is the SAME but the absorbed dose is DOUBLE

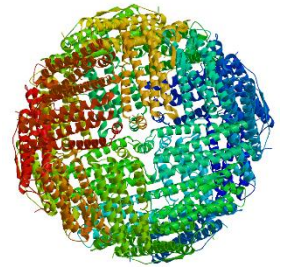
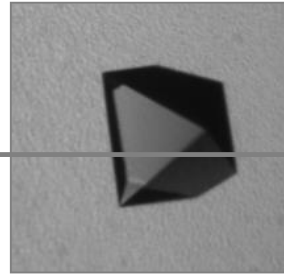
The heavy atom ($z \geq 16$) content of a crystal is not crystallographically defined, but we need it.

Apo ferritin

I_0

$0.98 I_0$

absorption coefficient
 0.406mm^{-1}



Holo ferritin

I_0

$0.96 I_0$

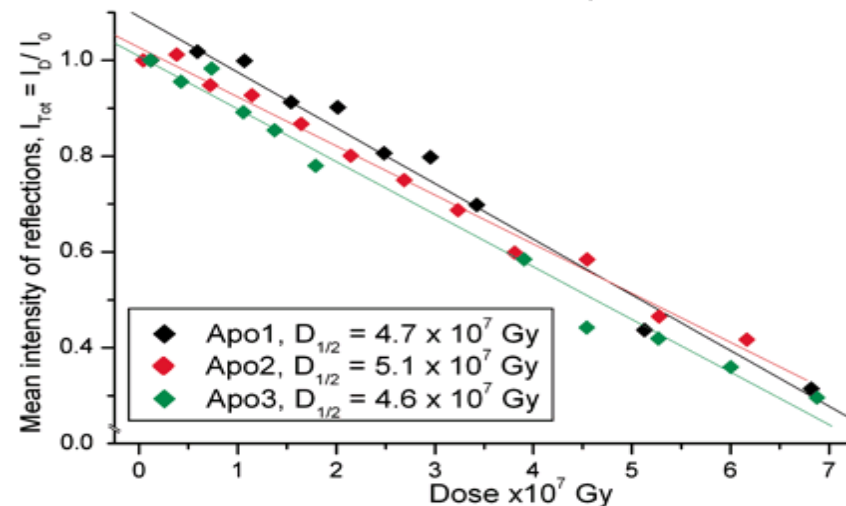
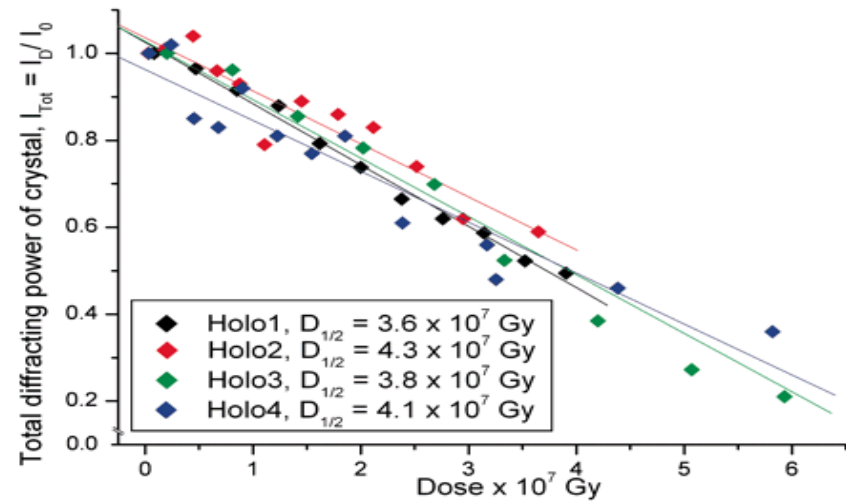
absorption coefficient
 1.133mm^{-1}



$\lambda = 1 \text{\AA}$
100 μm thick xtal

Dose Limit Quantification at 100 K

- Holoferitin & Apoferritin as model: absorption coefficients differ by factor of 2
- Intensity: $\sim$ linear dependence on dose
- $D_{1/2}$ is dose to $I_0/2$
- $D_{1/2} = 4.3 (\pm 0.4) \times 10^7$ Gy
= 43 MGy
- **Henderson limit, $D_{1/2} = 20$ MGy**
- Howells et al (2005): resolution dependent limit of 10 MGy/ Å

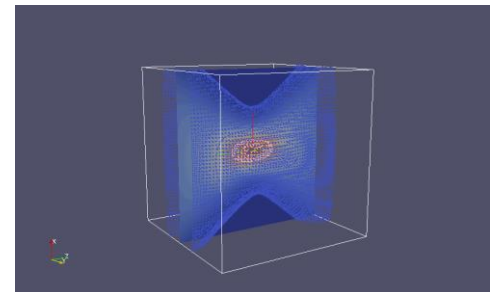


Suggested limit to retain biological 'fidelity'

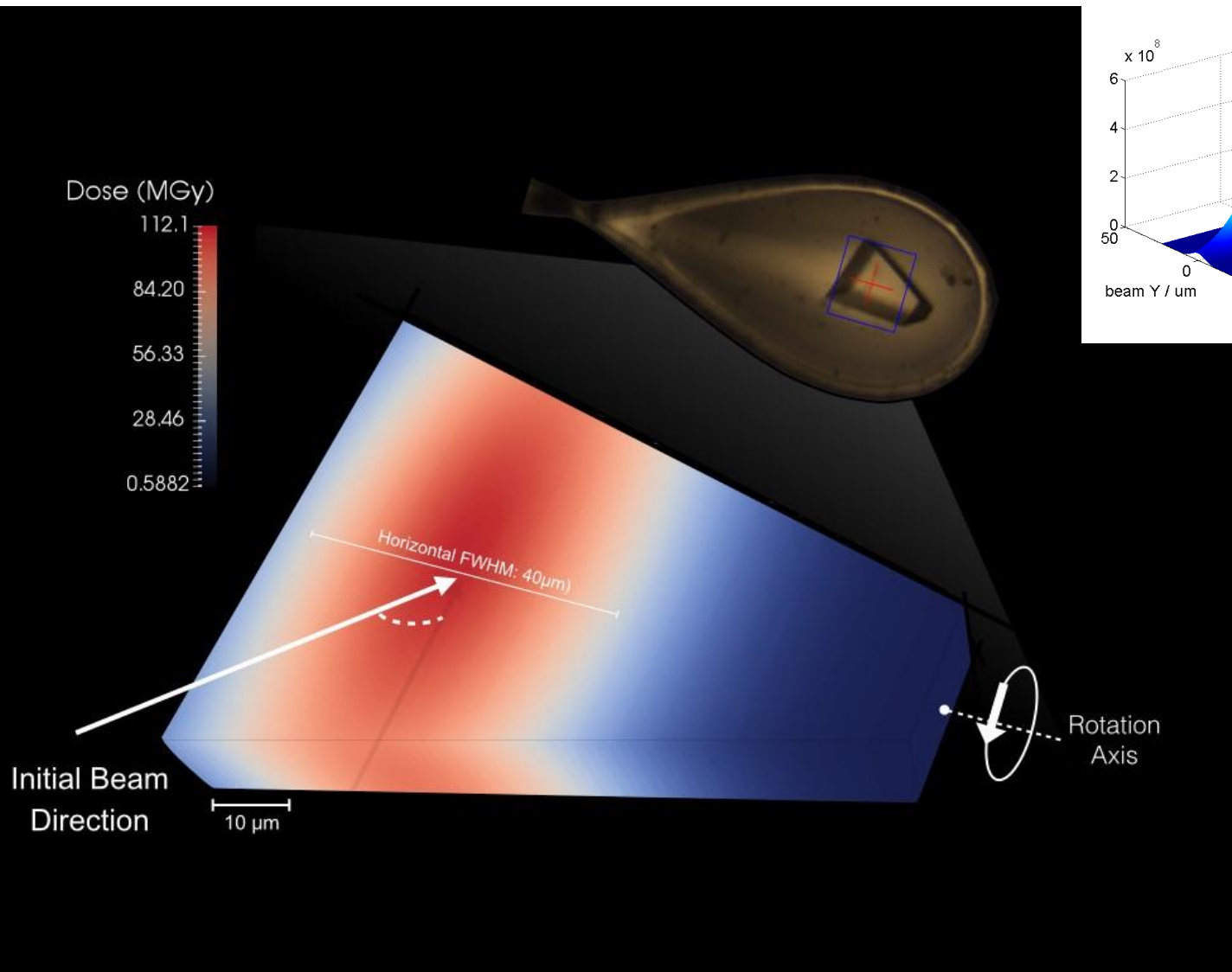
$$D_{0.7} = 3.0 \times 10^7 \text{ Gy} = \mathbf{30 \text{ MGy}}$$

RADDOSE-3D

- Full 3-D simulation of dose absorption by the crystal.
- Can deal with multiple wedges of data and different energy beams (e.g. MAD).
- Models beam as Top-Hat or Gaussian or can use experimental profiles
- Gives information on dose DISTRIBUTION and TIME COURSE, not just average dose.
- Engineered for easy extendibility: can read beam profile now, and actual crystal shape in the future.
- On server: www.raddo.se (!!)



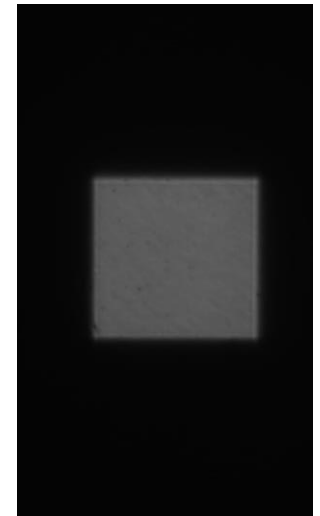
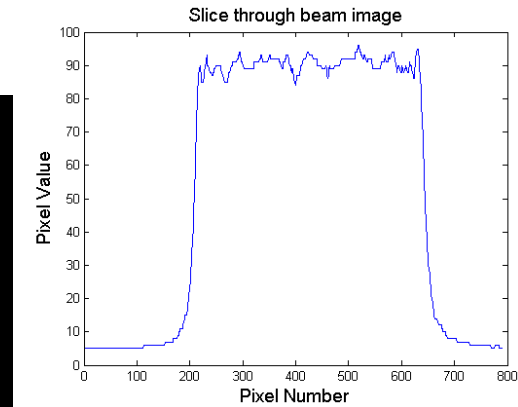
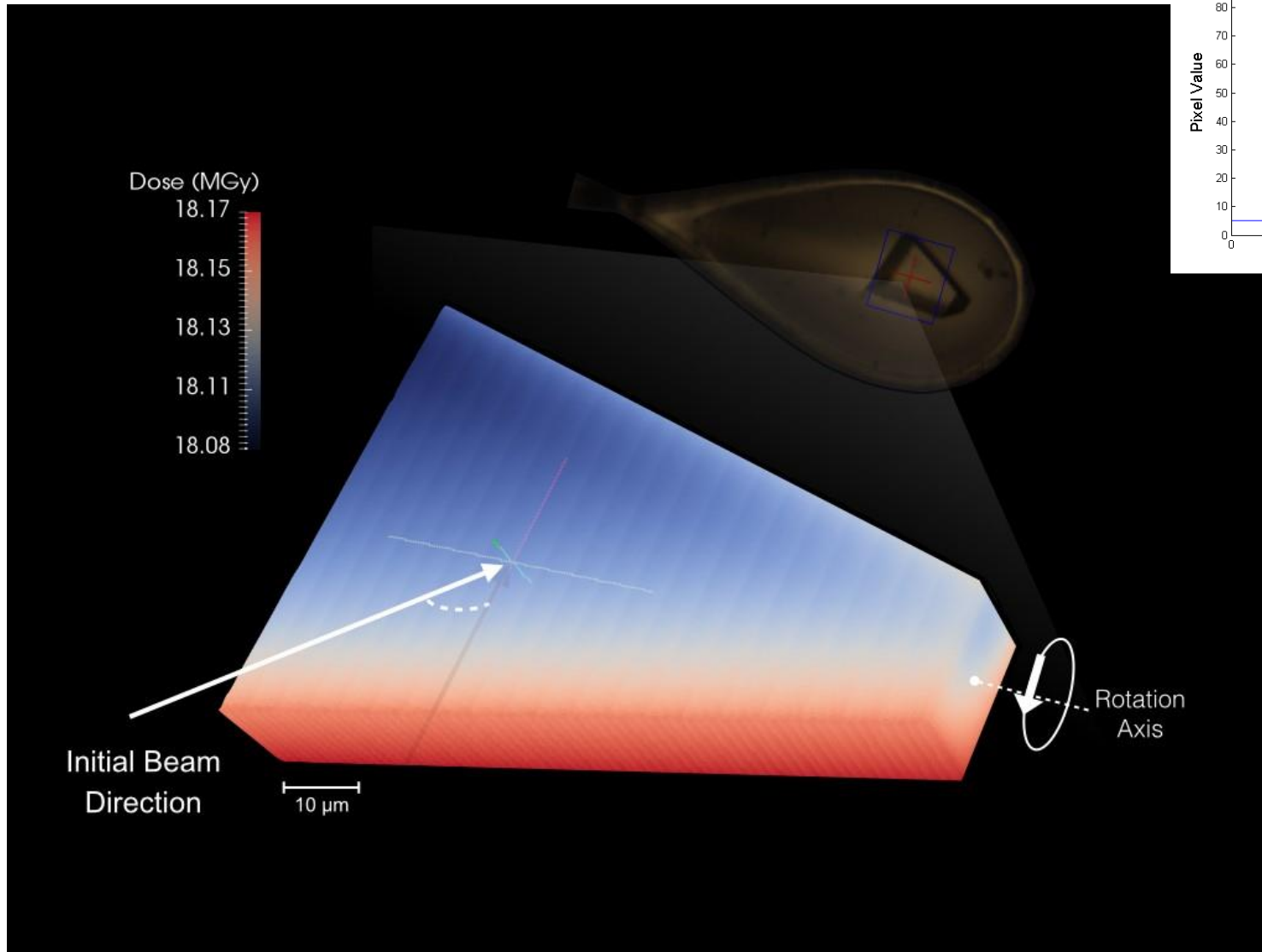
Gaussian Beam Profile



Differential irradiation may lead to differential damage:
get data which merge poorly and are a population of substates

13.2 keV, 60(v)×40μm²(h) FWHM, 100(h)×160μm²(v) coll., 5e11 ph/s

Top-Hat profile



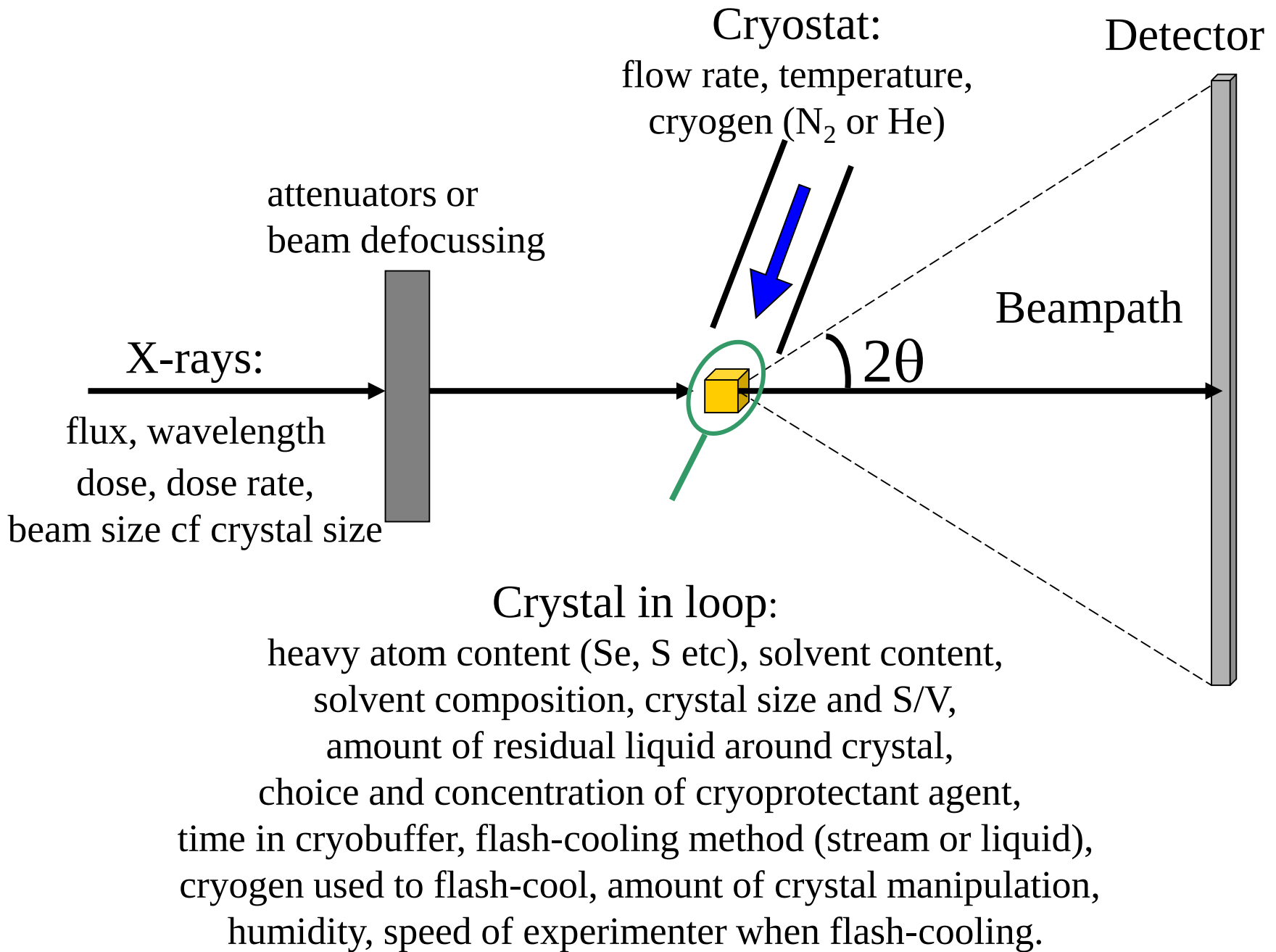
Imaged beam
PETRA III,
Bourenkov,
Schneider

13.2 keV, 100(h) x $160\ \mu\text{m}^2$ (v) coll., $5e11\ \text{ph/s}$

Radiation damage:

The Plan:

- What are the symptoms?
- Why do we care? Effect on MAD/SAD.
- What is it?
- How do we calculate the Dose?
- **What do we know/would like to know?**



PROBLEM: how do we know that we are making any difference?

- In order to investigate the effects of various parameters on the radiation damage process, we need a robust radiation damage METRIC which is preferably ON-LINE during the diffraction experiment.

No unanimous metric currently/ results from different metrics do not agree.

- Structural changes occur before degradation of diffraction quality is obvious.

Work so far / ongoing:

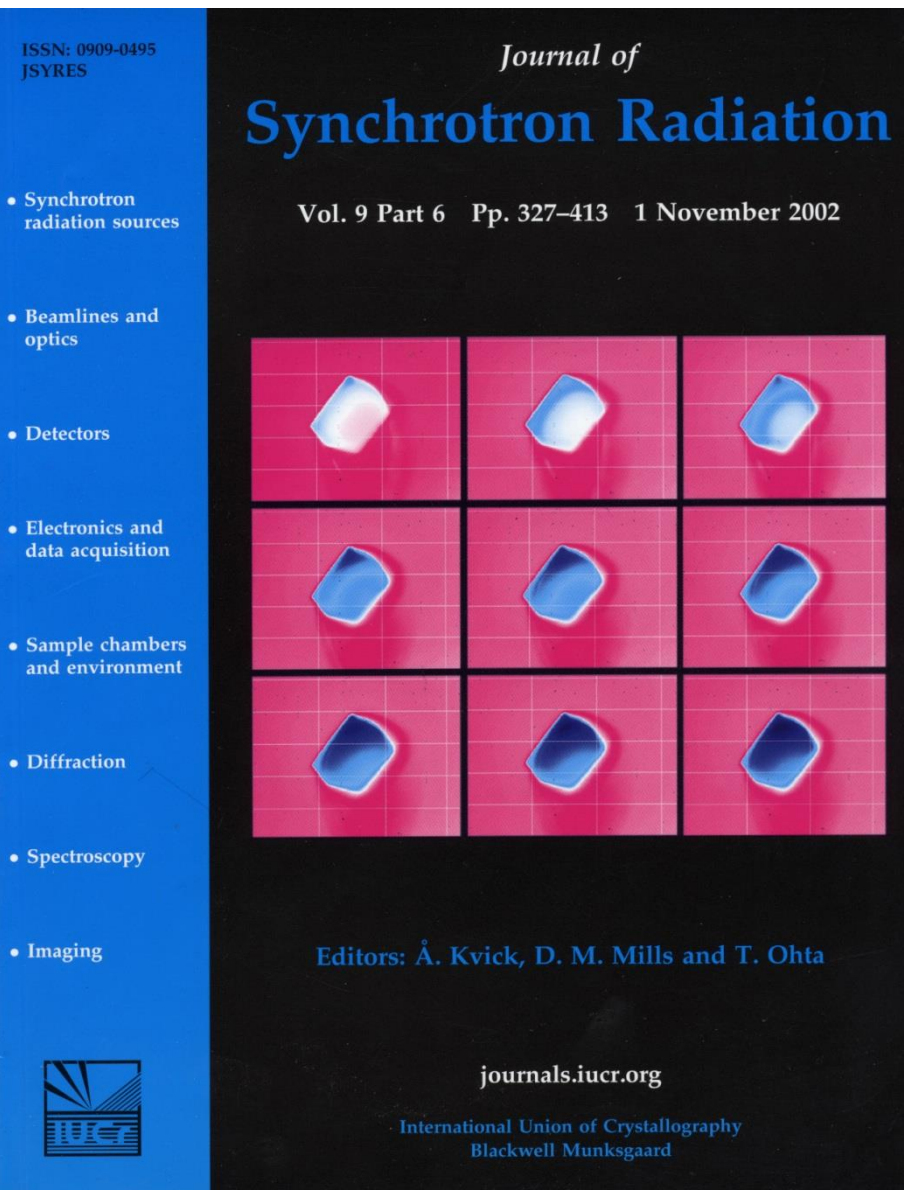
- Lower the cryogen temperature? 40K? 50K? 16K? 140K (no!). **Less than a factor of 2 improvement.**
- Lower the wavelength? Lots of anecdote + now some systematic results: **no effect on damage rate.**
- Unit cell expansion as a metric? **No!**
- Change/ regulate the dose/dose rate regime? **No, not at current!**
- Effect on MAD/SAD? Order of data collection?
- Minimum crystal size? Several papers. (see Holton 2009)
- Beam heating. **Not a big factor at current flux**

Work so far / ongoing:

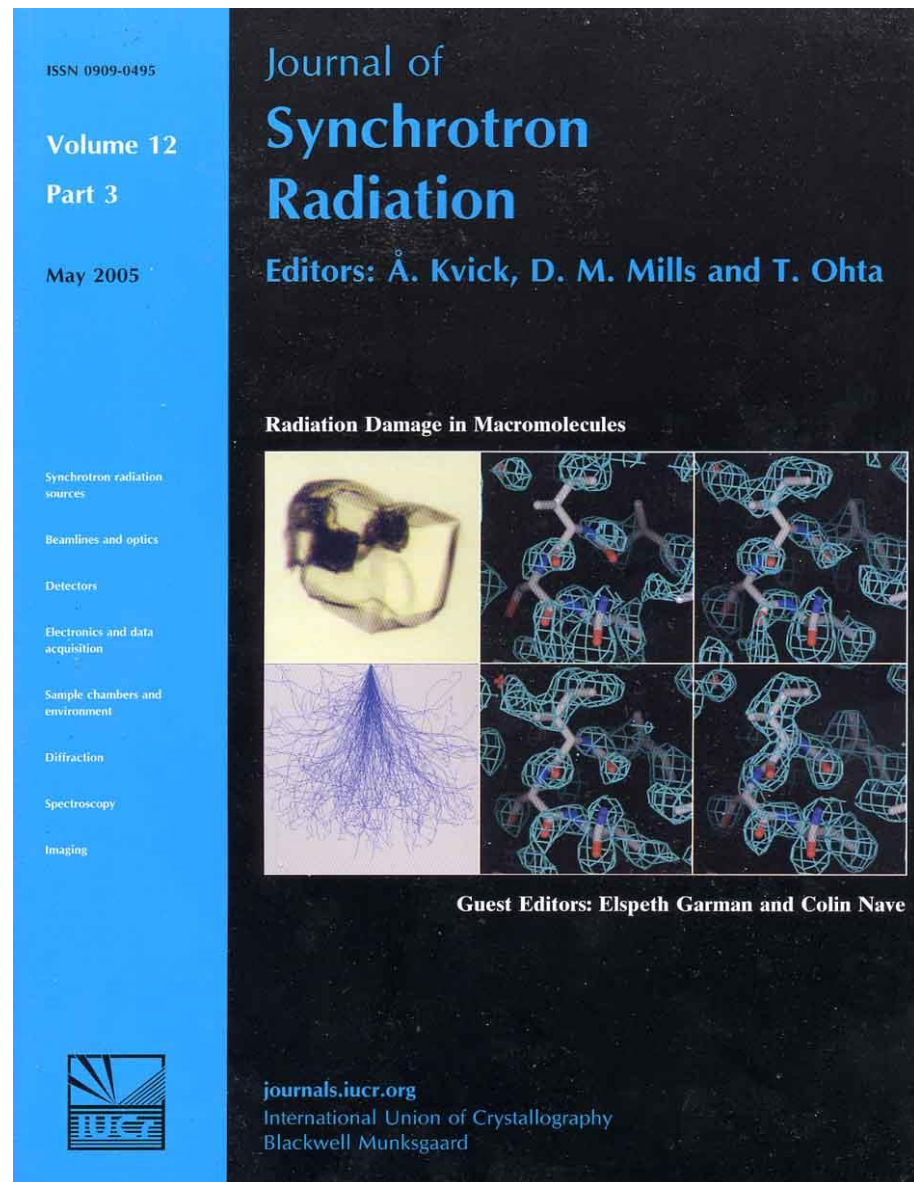
- X-ray absorption – **important parameters defined.**
- Remove oxygen? **Nothing yet.**
- Radiation damage Induced Phasing (RIP)
- Software developments – **big progress.**
- Add radical scavengers: **results disagree.**
- Biological implications/applications to mechanistic studies. **Now many.**
- Room temperature studies: dose rate effects? **Results disagree.**
- N.B. Need for **systematic statistically significant** experiments.
- **Series of Radiation Damage Workshops**

RD2: Dec 2001

RD3: Nov 2003

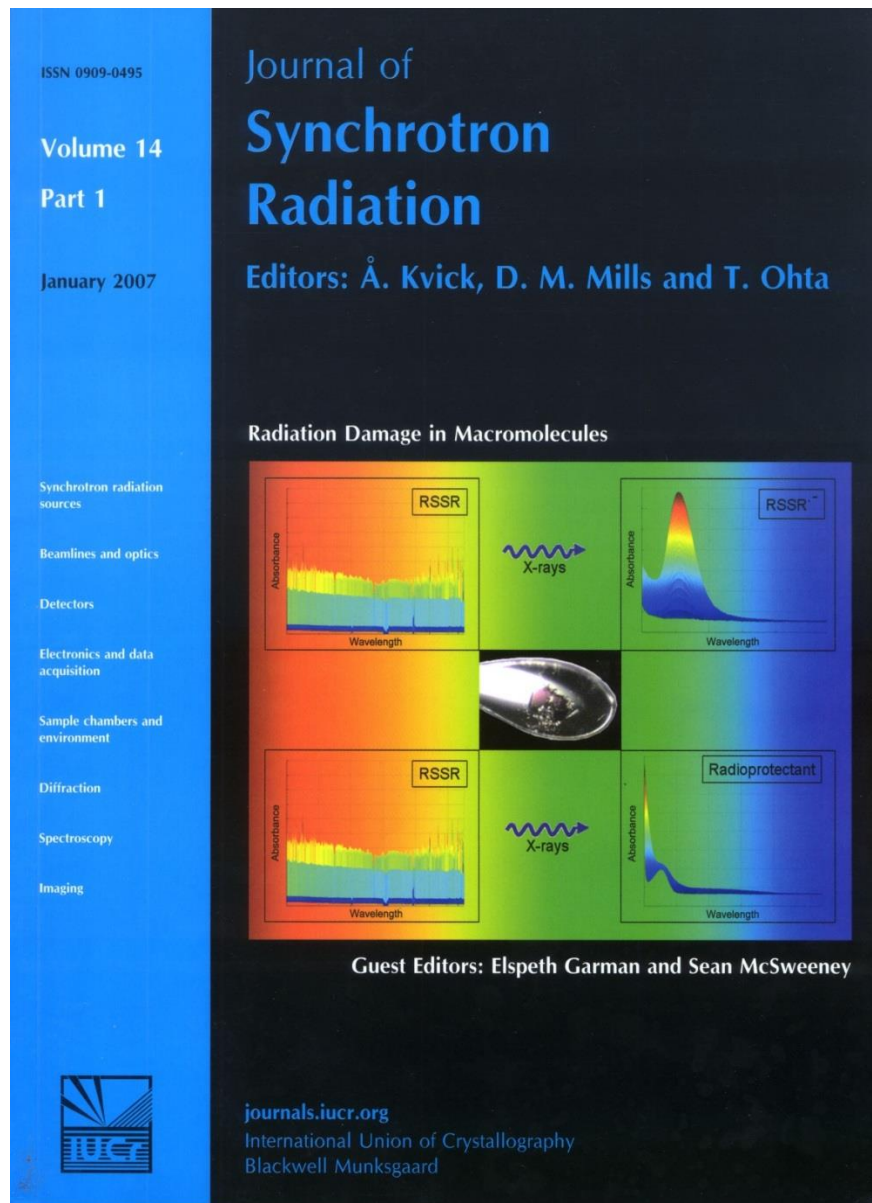


JSR, Nov 2002, 8 papers

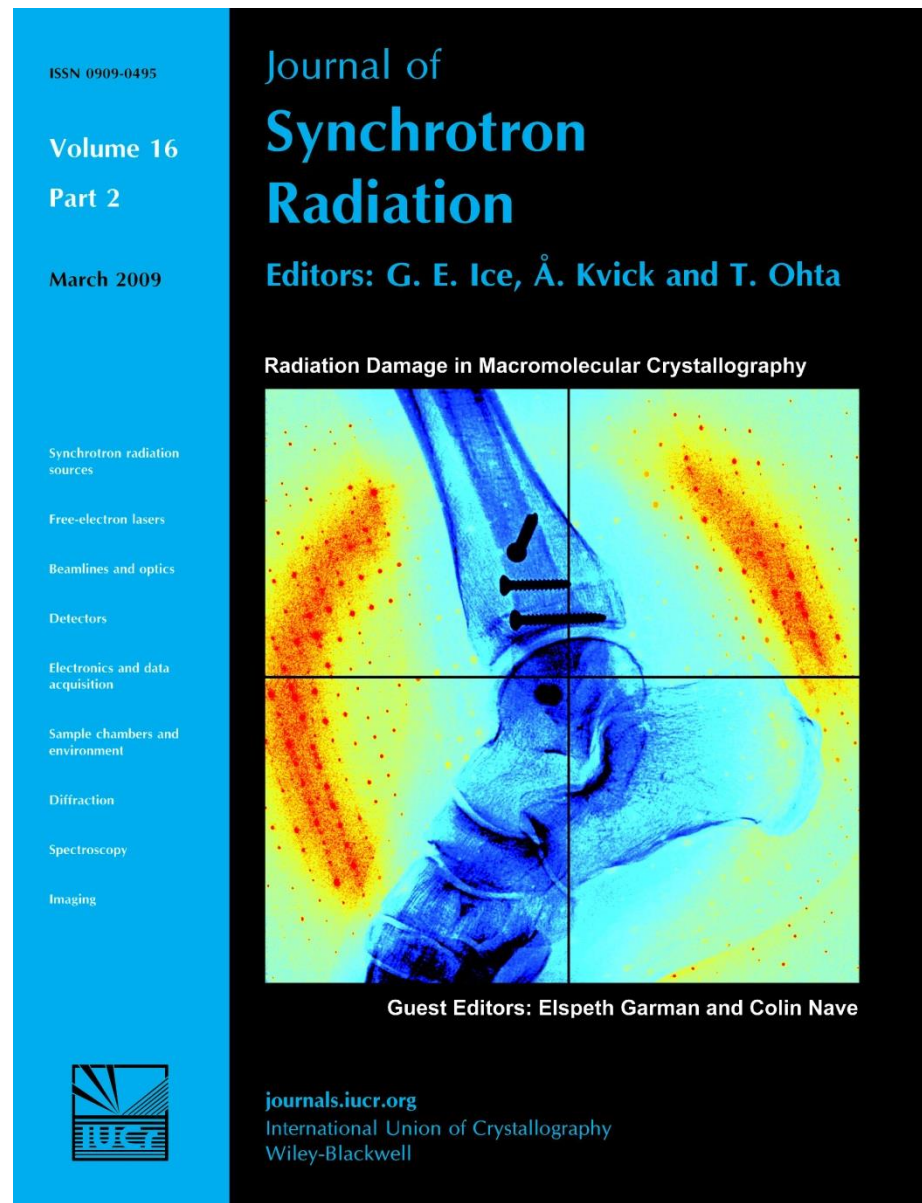


JSR, May 2005, 9 papers

RD4: March 2006



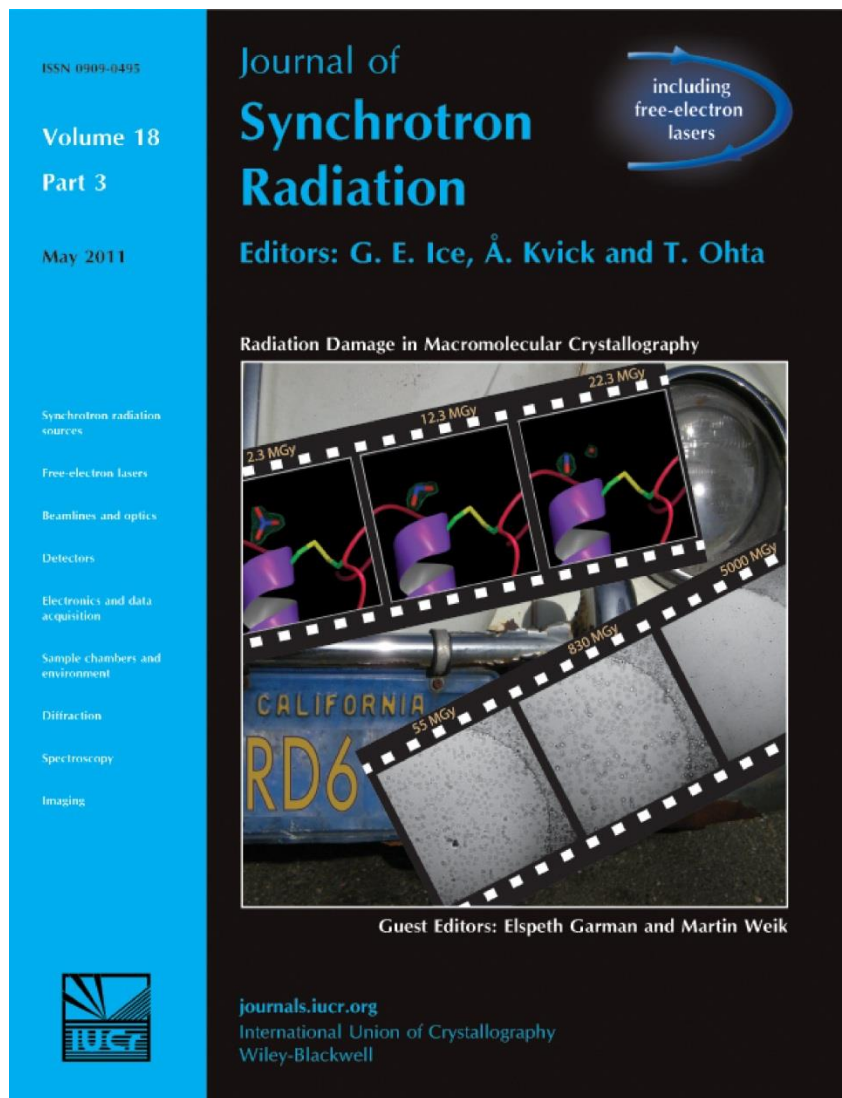
RD5 March 2008



JSR, Jan 2007, 14 papers

JSR, March 2009, 8 papers

RD6: March 2010



JSR, May 2011, 10 papers

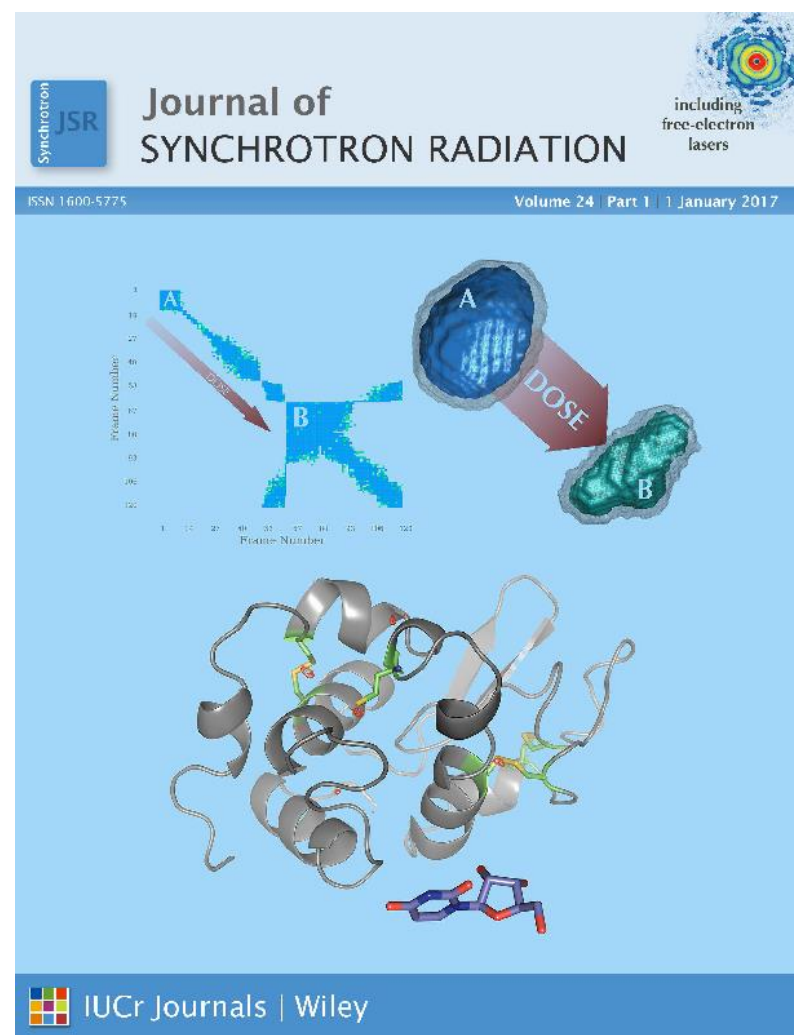
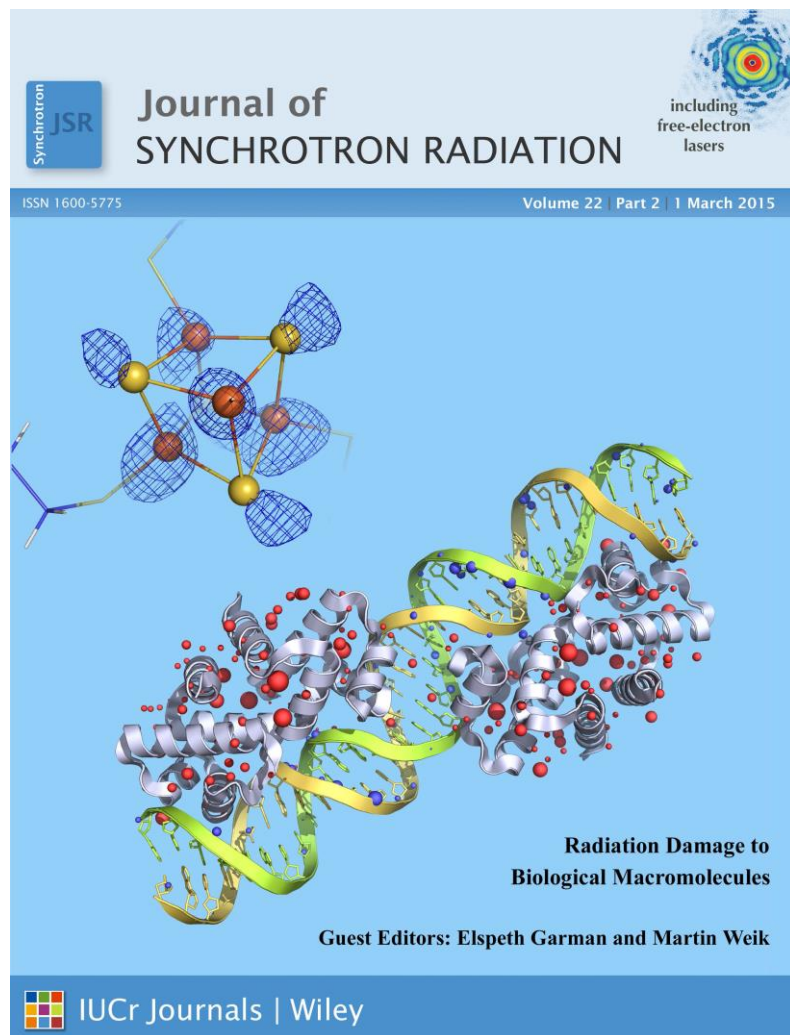
RD7, March 2012



JSR, Jan 2013, 6 papers

RD8 (PETRA III): April 2014

RD9 (MAX IV): March 2016



JSR, March 2015, 8 papers

JSR, January 2017, 8 papers

RD10, NSLSII Sept 2018, Special JSR Issue 2019

‘Beginner’s guide to
RD’ in Holton (2009) JSR
16,133-142

General summary in:
Garman Acta D (2010)
66, 339-355

Summary 1: what can YOU, the experimenter do?

- Do not be afraid to merge data taken from different isomorphous crystals which all had lower doses.
- Back soak non-specifically bound heavier atoms out of your crystals.
- Be ‘absorption aware’ of the contents of your crystal (e.g. Se and buffer) and if possible, avoid cacodylate buffer (arsenic mass=75).
- Match beam size to crystal size

Summary 2: what can YOU, the experimenter do?

- Scavengers: try electron scavengers at 100 K (nitrate/ascorbate/benzoquinone).
- Dose ‘spreading’: use a tophat profile beam if possible. Consider Helical/Translational data collection.
- So you can estimate the dose, ASK at the beamline:
 - What is the flux today at this energy and with this slit size (‘flux density’)?
 - What is the beam profile today at this beam energy? FWHM in x and y ?

Current status: radiation damage in protein crystals

- Understand a lot more than eighteen years ago, but still not nearly enough...
- Understand how to do experiments better.
- Research has prompted some very exciting new approaches.
- Many complementary methods now being used on the problem in concert with crystallography
- Experiments must involve more than one sample (!) to get statistically significant results: labour intensive and time consuming. Also MUST know incident FLUX density...
- **Radiation damage has DEFINITELY become a mainstream concern**

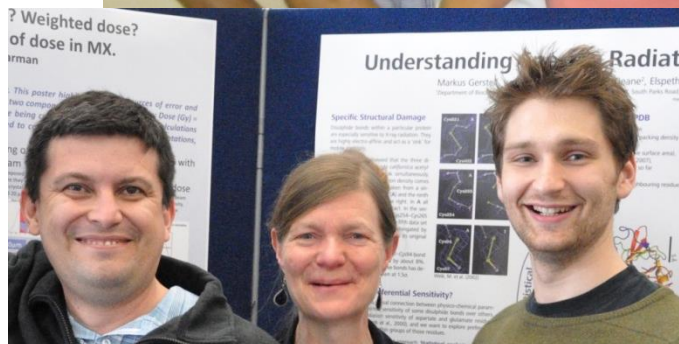
Many thanks to my Research Group and our collaborators

EPSRC

Engineering and Physical Sciences
Research Council



John McGeehan
(Portsmouth)
Ian Carmichael (NDRL)
James Holton (USF)



Garman Group Graduate students and postdocs 2000-15



Drs Jonny Brooks-Bartlett
and Charlie
Bury, RIDL

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Kathryn Shelley, RABDAM



Ed Lowe X-ray
Facilities Manager



Radiation
Damage
Josh
Dickerson