

Experience at the EMBL with Debian: the viewpoint of a scientist

Sandor Brockhauser

EMBL-Grenoble

Debian for Scientific Facilities Days

ESRF

Grenoble, France

June 24-26, 2012



EMBL



EMBL - ESRF





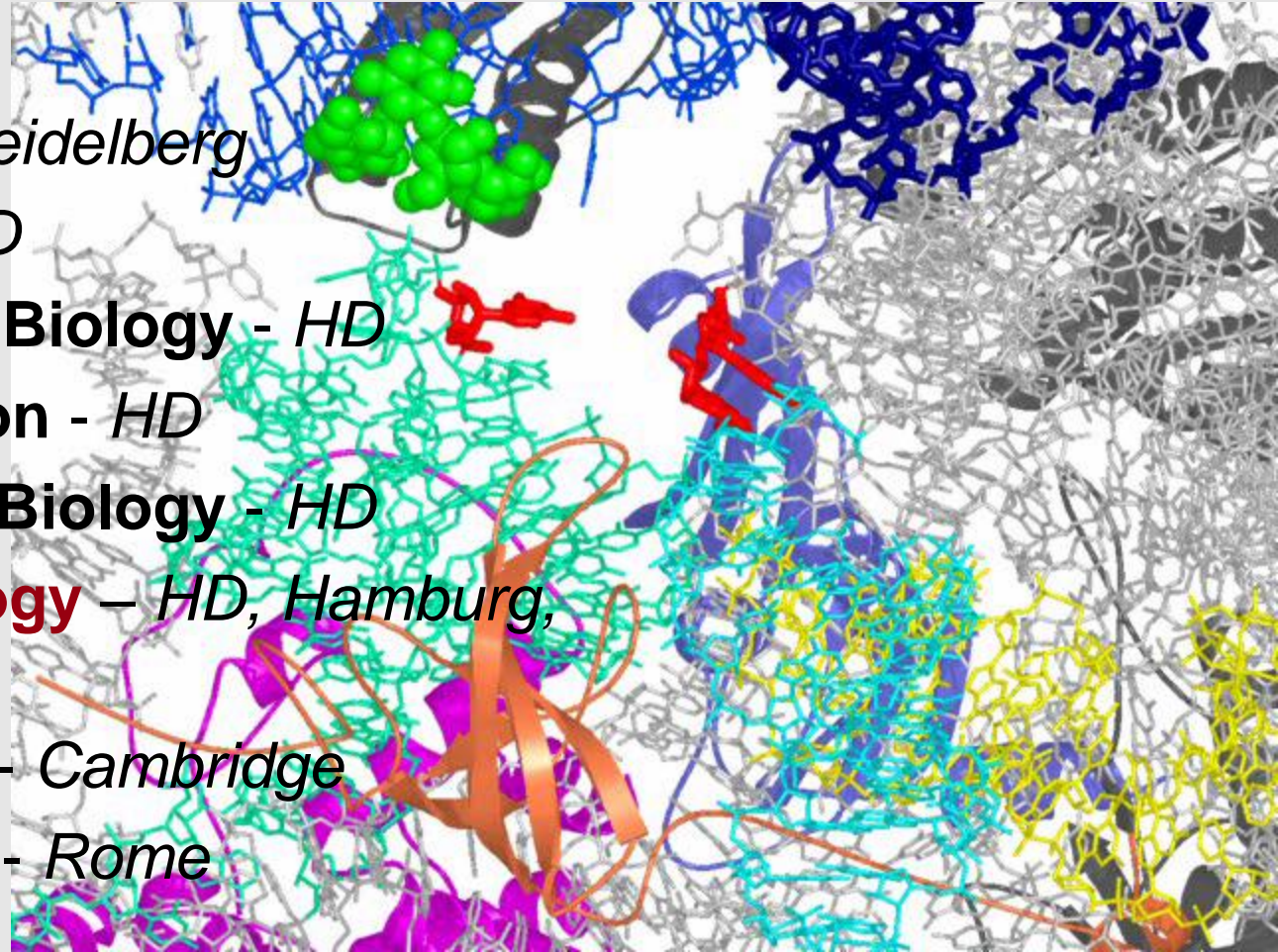
EMBL Units

- **Cell Biology**- *Heidelberg*
- **Biophysics** - *HD*
- **Developmental Biology** - *HD*
- **Gene Expression** - *HD*
- **Computational Biology** - *HD*
- **Structural Biology** – *HD, Hamburg, Grenoble*
- **Bioinformatics** - *Cambridge*
- **Mouse Biology** - *Rome*



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Paromomycin binding to 30S

http://www.mrc-lmb.cam.ac.uk/ribo/homepage/mov_and_overview.html

Techniques for Structural Biology

- Nuclear Magnetic Resonance (NMR)

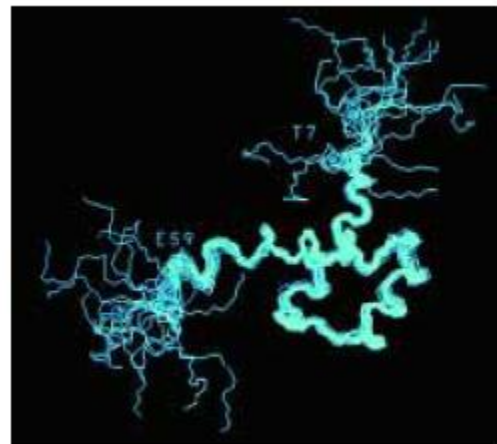


Figure 1. NMR structure of the *Antennapedia* homeodomain (1). A bundle of 20 superimposed conformers represents the polypeptide backbone. For the polypeptide segment 7–59 the tight fit of the bundle indicates that the structure is defined with high precision, whereas the two chain ends are disordered.

NMR STUDIES OF STRUCTURE AND FUNCTION OF BIOLOGICAL MACROMOLECULES

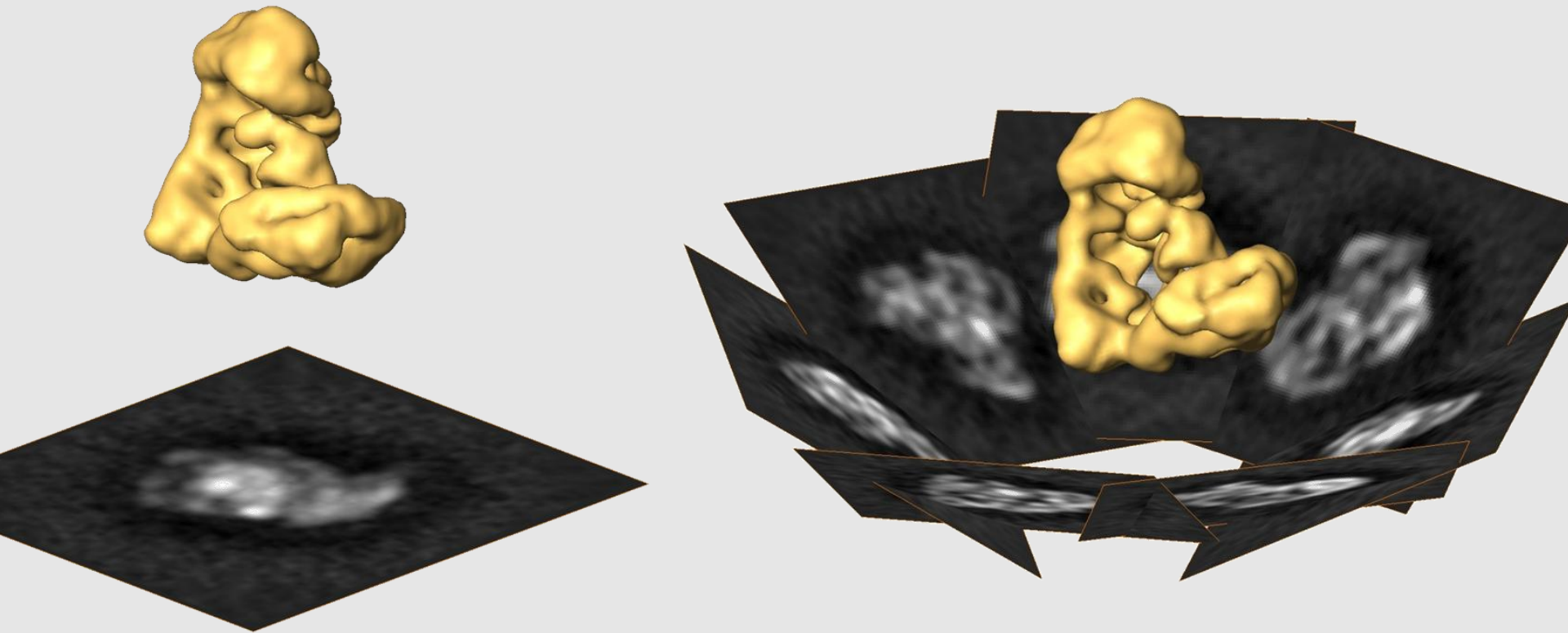
Nobel Lecture, December 8, 2002

by

KURT WÜTHRICH

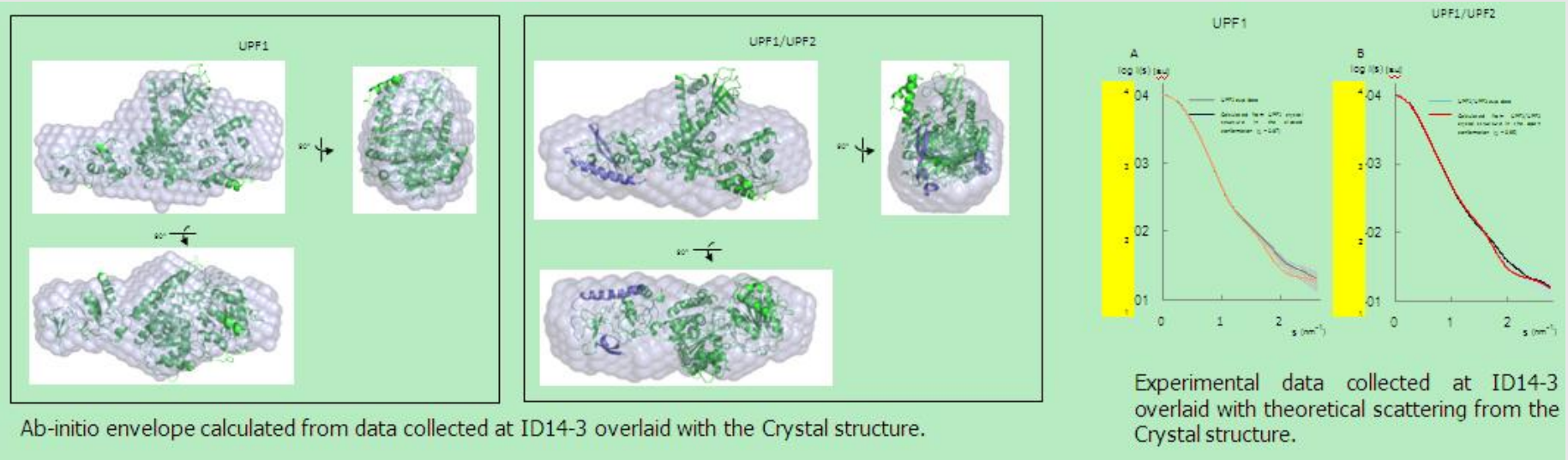
Techniques for Structural Biology

- Nuclear Magnetic Resonance (NMR)
- Electron Microscopy/Tomography (EM/ET)



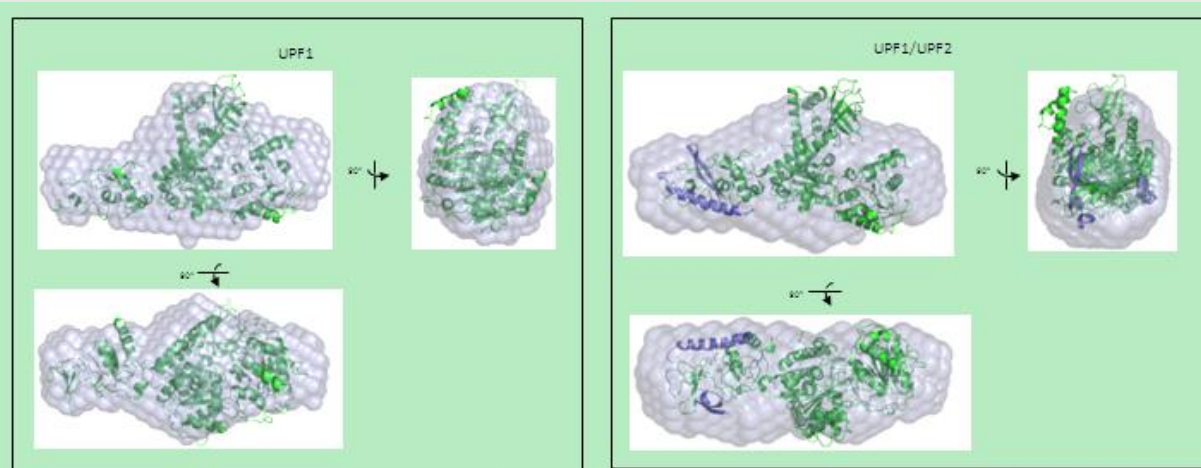
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- Nuclear Magnetic Resonance (NMR)
- Electron Microscopy/Tomography (EM/ET)
- Small Angle Xray/Neutron Scattering (SAXS/SANS)

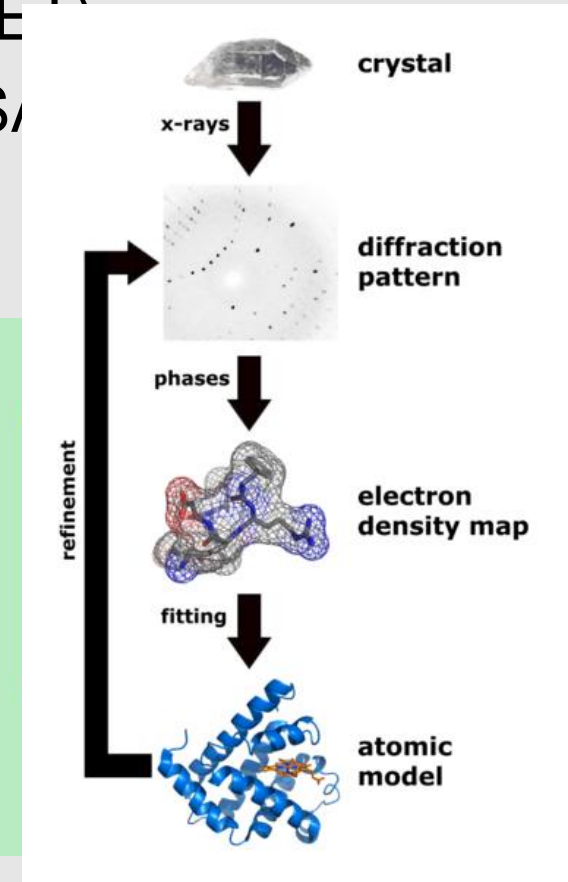


Techniques for Structural Biology

- Nuclear Magnetic Resonance (NMR)
- Electron Microscopy/Tomography (EM/ET)
- Small Angle Xray/Neutron Scattering (SAXS/SANS)
- Macromolecular Crystallography (MX)

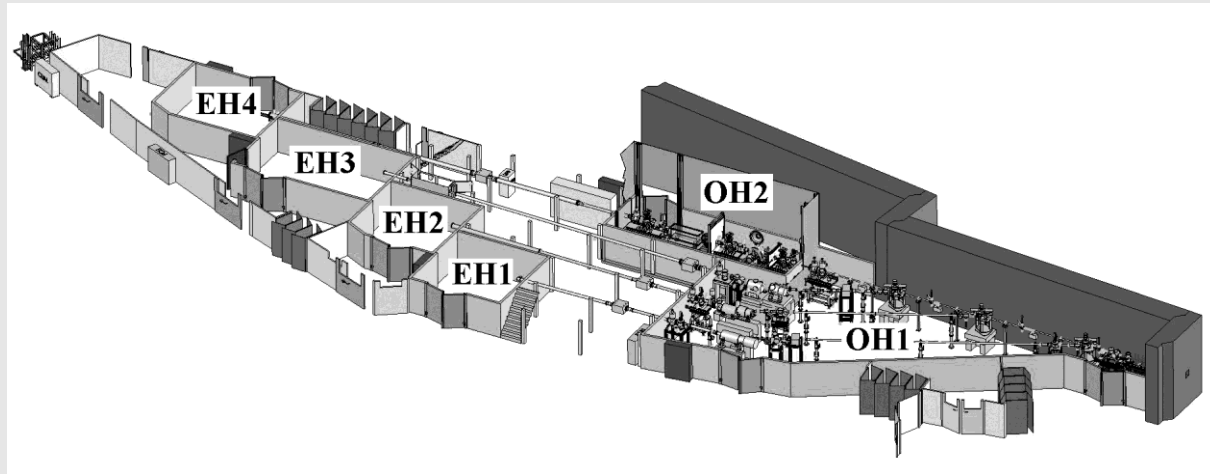


Ab-initio envelope calculated from data collected at ID14-3 overlaid with the Crystal structure.



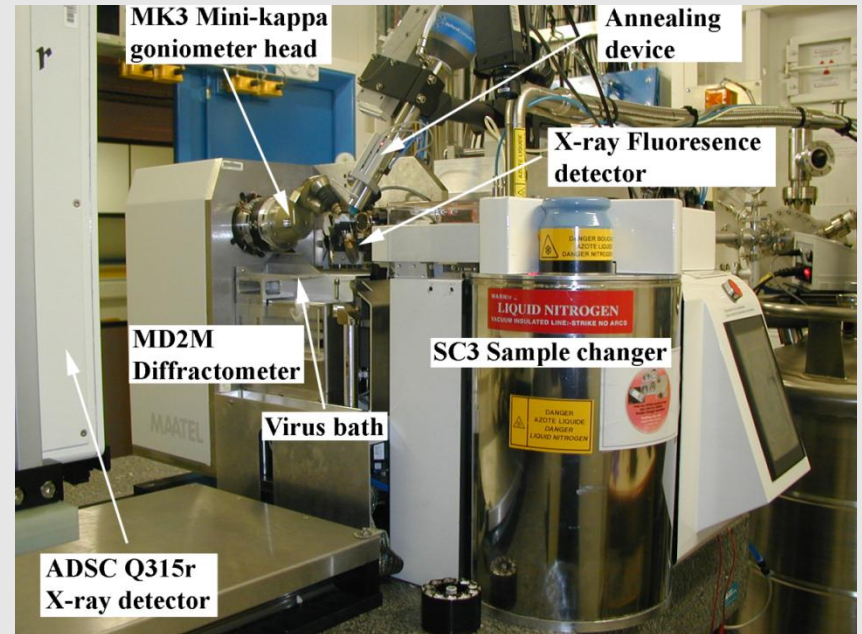
EMBL at the SB Beamlines

- MX:
 - Hassan Belrhali, Babu Manjasetty
 - Sandor Brockhauser, Andrew McCarthy
 - Max Nanao
 - BM14, ID14-1, ID14-4, ID23-1, ID23-2, ID29
- BioSAX:
 - Adam Round, Petra Pernot (ESRF)
 - BM29



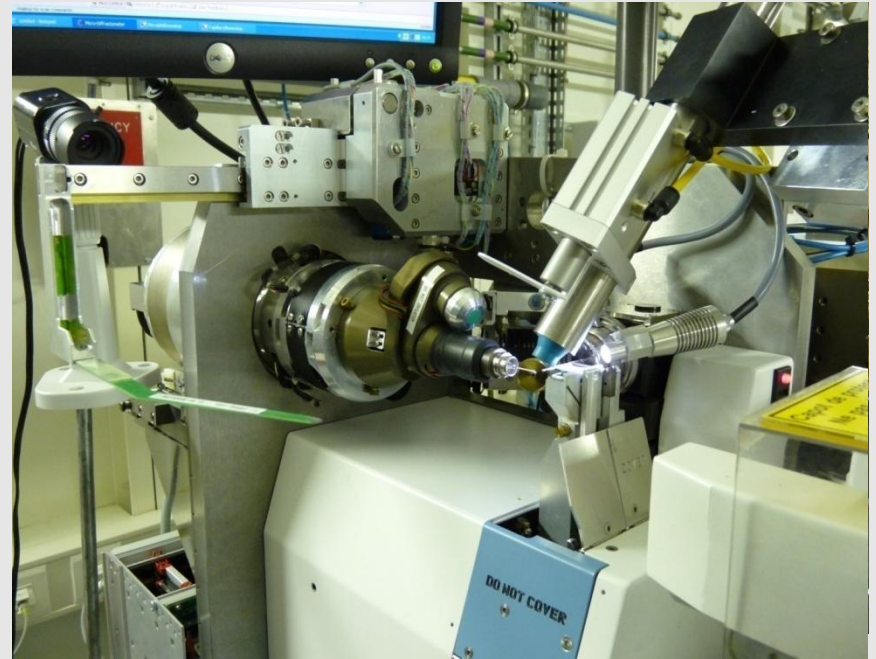
EMBL/ESRF developments

- Diffractometer
- On-axis-view
- Sample Changer



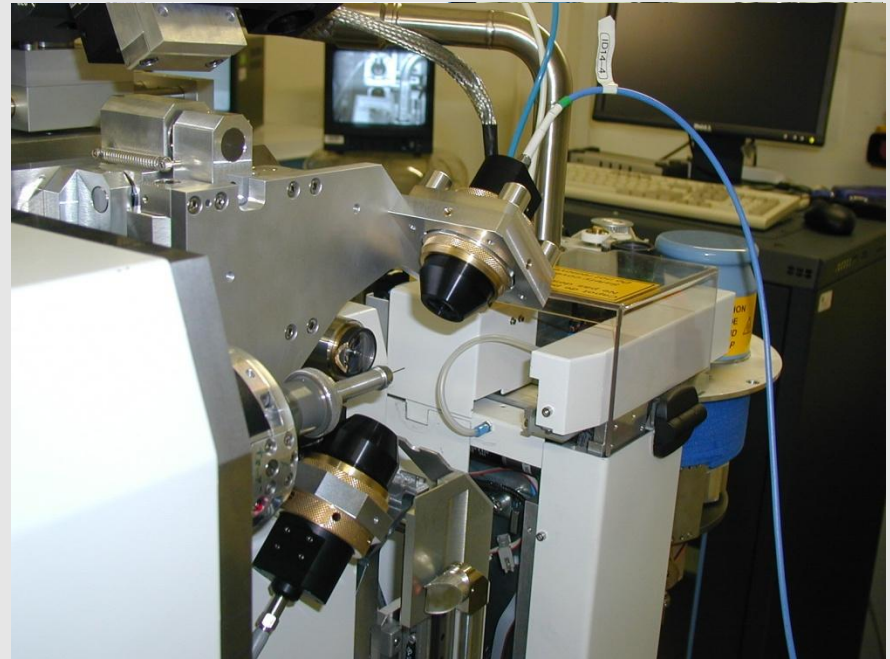
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- Diffractometer
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- Sample Changer
- MiniKappa
- Low-resolution beamstop



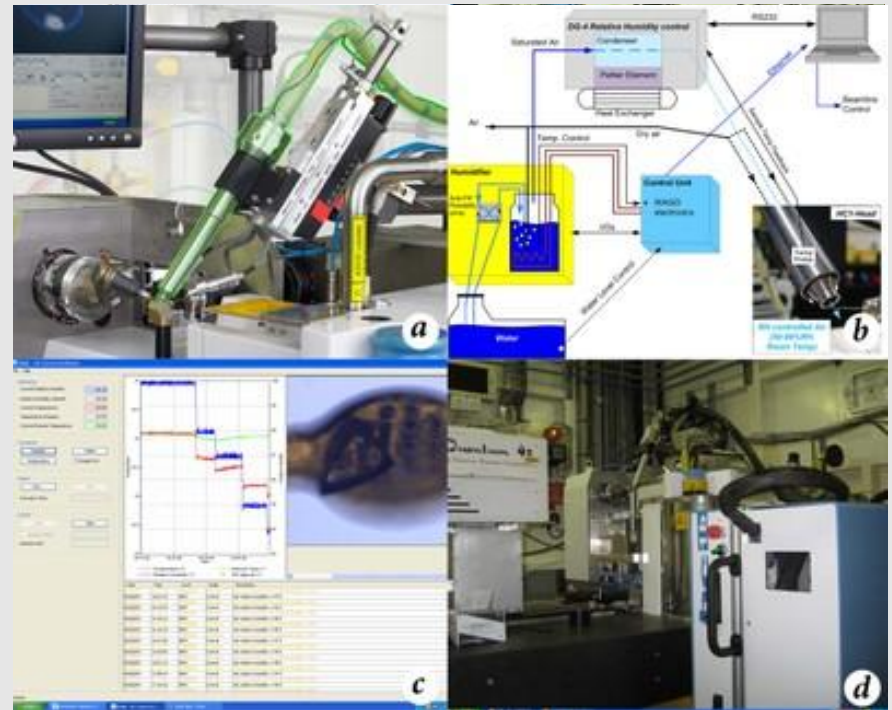
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- **On-line Microspec**



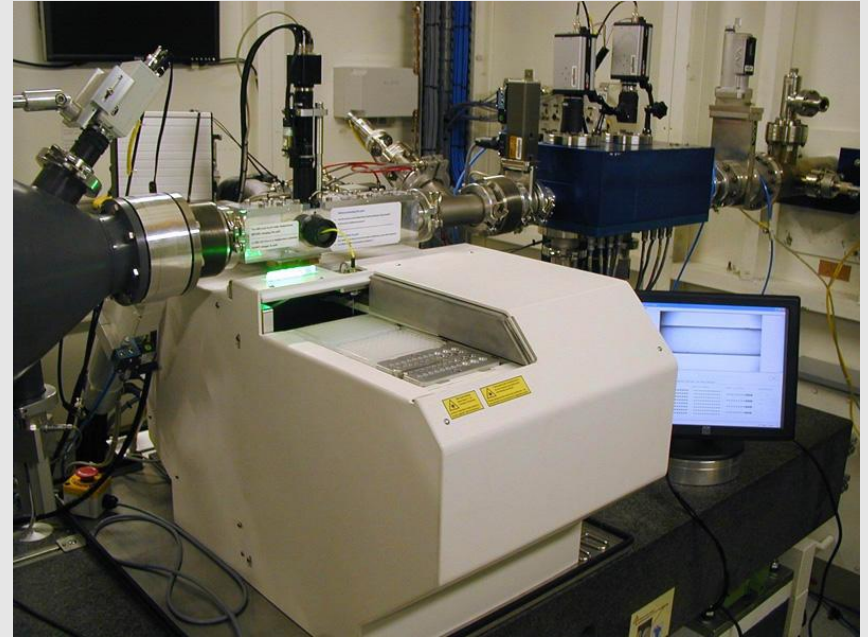
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- Humidity Control Device



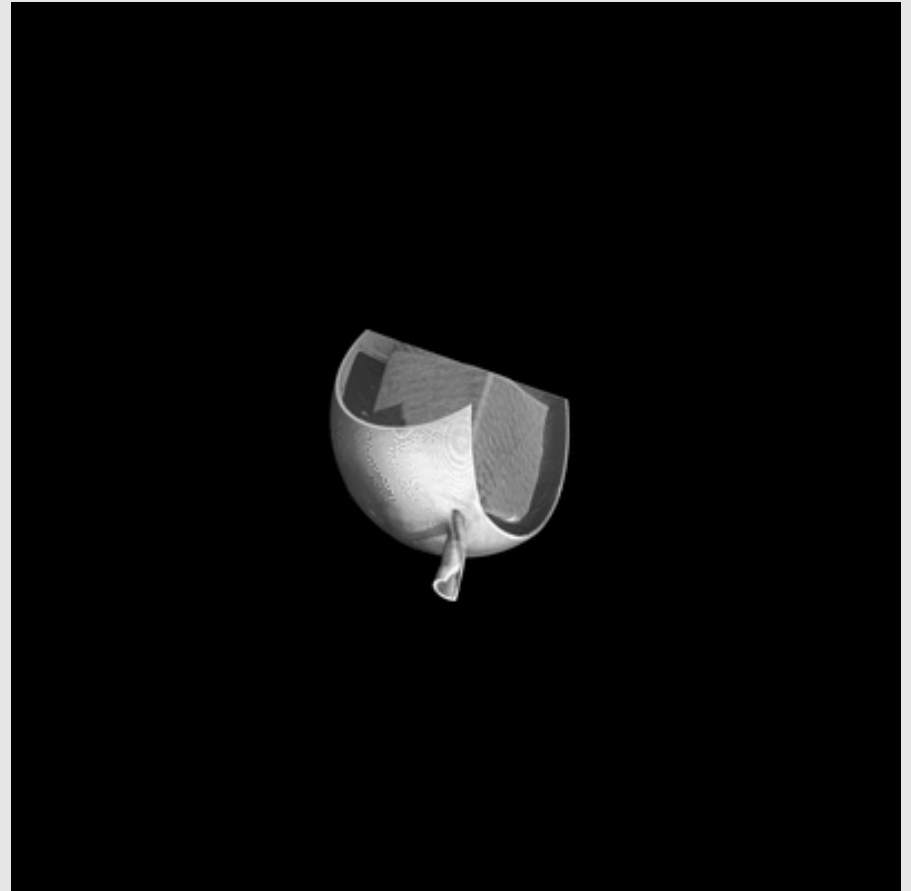
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- **SAX Sample Changer**



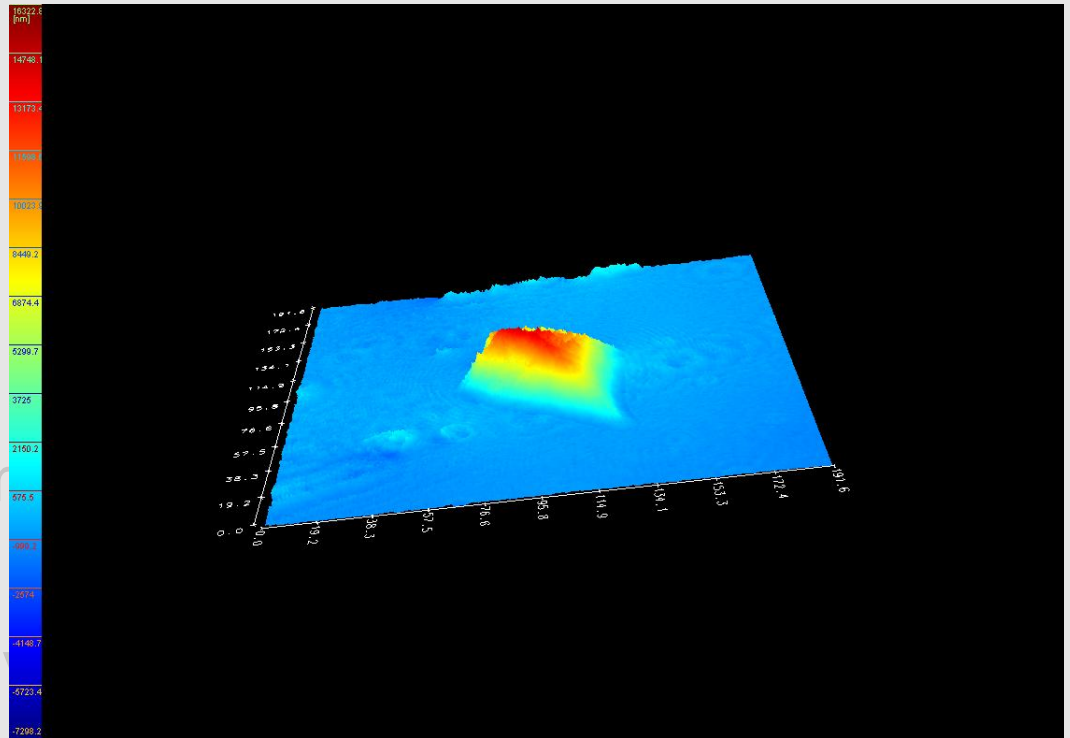
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- Tomography



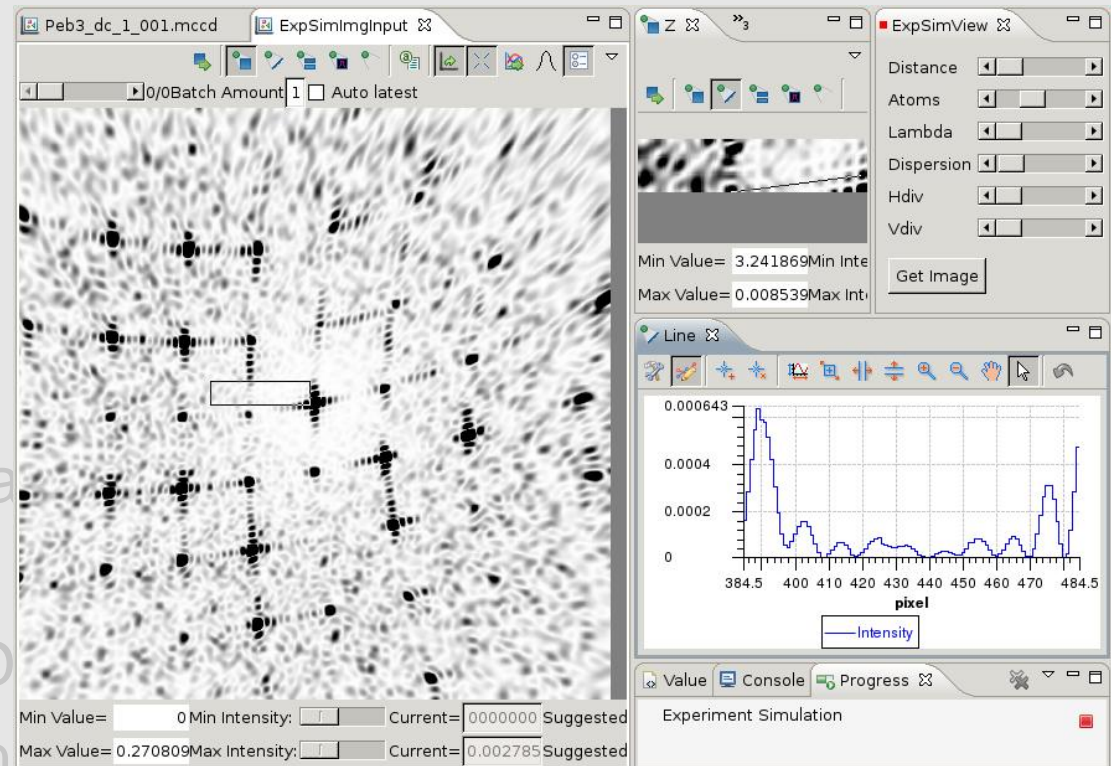
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- Diffractometer
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- Low-resolution beam
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- Humidity Control D
- SAX Sample Changer
- Tomography
- Holography
- **Experiment Simulation**



Computing diversity

- Hardware:
 - motion control: PMAC/Galil/V-DPAP
 - generic computing: i686, x86_64, tesla/fermi
- OS: Windows/MacOS/Linux (suse, redhat, centos, ubuntu, debian, gentoo)
- Local developments
 - mostly for specific target platform
 - cross platform: java (3D stereo beamline modeling)
- PXSOFT (for *linux* with full support for *multiple versions*):
 - applications compiled from source, or
 - binary distributions maintained with required libs



Using Debian

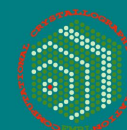
- Open development platform
Academic spirit
Democratic management

HAD problem with redhat

Using Debian

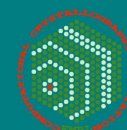
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- Wide package coverage

Centos fails even on libfftw



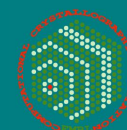
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convergence in configuration settings (eg: conf.d)



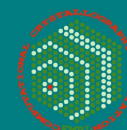
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powerful packaging system (localisation support:
EMBLrepos / EMBLws / EMBLserver packages)



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easy and robust distribution upgrades
not too slow updates

The release of Redhat6 was already slow and
Centos followed it with an extra 9 months of delay

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convergence in configuration settings (eg: conf.d)
powerful packaging system (localisation support:
EMBLrepos / EMBLws / EMBLserver packages)
easy and robust distribution upgrades
not too slow updates
- Binary compatibility with other distributions
can be an issue, but DC

Future directions at EMBL

- Up-to-date upgrades for both binary/source packages
- Maintain all configuration and customisation settings as .deb packages

Single Linux OS
DEBIAN 7

Thank you for your attention!

