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The possibilities offered by the Java language to run on any computer platform linked to Internet has motivated a large number of scientists in creating interactive applications or applets, aiming at a better understanding of scientific phenomena.

Crystallographers have been early adopters of the new possibilities offered by Internet with the aim to illustrate various concepts specific to crystallography. Presently, a quick search on the Internet reveals already the existence of numerous web sites containing interactive applets dedicated to crystallographic teaching .

The current generation of personal computers equipped with the most recent graphical hardware and software and the enormous local CPU capacity, allows to create very powerful applets which were not conceivable with previous generations.

Almost all the aspects of crystallographic teaching can be currently accessed on the web. Notions of point and space group symmetry, Fourier transform and diffraction theory, crystal structures and many others related topics are covered on various sites, freely accessible on the web.

However, for the student wishing to learn more about crystallography, the problem is to find the logical path among all the possible sites and applets providing the best sequence of subjects in order to acquire the expected knowledge.

We are currently setting up a web-based interactive environment on crystallography, building not only on our own developments but also on the vast amount of already existing tools available on Internet.

Keywords: teaching of crystallography, simulation software, web resources

MS96.30.5

Acta Cryst. (2005). A**61**, C122

Teaching Crystallography with a Laser, Two Lens and …Einstein's Tongue

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Teaching crystallography to students in Biology is a difficult task, particularly because many of them arrived there because '*there are no more Maths or Physics in Biology*'. After 10 years of practice, we have tried as much as possible to limit (not suppress !) the recourse to Mathematics and, also, to show really what diffraction means.

For that goal we make use of a classical optical bench requiring a LASER (λ=0.6328 μm), a pinhole as a beam expander and two lens. We use as crystals 24x36 B&W photographs of a 80×60 repeats of the well-known 'Eistein's tongue' (cell parameters a = 0.45 mm, b = 0.4 mm.). This allows to record a diffraction pattern on films mounted in the back focal plane of the second lens. The diffraction data extend to order 21 (more than 500 visible Bragg's spots), which correspond to 20 μm resolution.

In order to illustrate the principle of the MIR method, we have made 'heavy atom derivatives' by adding small dots on Einstein's face (one site per derivative), and we have 'collected new data'. Our hope is to go really all the way through with experimental data to 'solve the structure'. For now, this structure solution step is illustrated with calculated data. This shows very well how a recognizable picture is obtained after 'MIR phasing' with only 50 reflections, and what is the effect of experimental noise.

All programming was performed with *Mathematica* (Wolfram Research), which allowed to develop very rapidly the necessary code. This aspect will also be shown in the oral presentation.

Keywords: teaching, optical diffraction, mathematica

MS97 BIO-INORGANICS IN BIOLOGICAL MACROMOLECULES

Chairpersons: Adriana Bigi, Enrico Rizzarelli

MS97.30.1

Acta Cryst. (2005). A**61**, C122

Structural Biology of Ligninolytic Enzymes: Laccases and Heme Peroxidases

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Laccases (Lac) and certain peroxidases, e.g. lignin peroxidase (LiP), manganese peroxidase (MnP), and versatile peroxidase (VP) are employed by filamentous fungi to degrade the recalcitrant bio-polymer lignin a major constituent of woody plants. While LiP, MnP, and VP are heme-containing glycoproteins utilizing hydrogen peroxide as co-substrate to attain the redox state needed for activity, laccase is a blue multi-copper oxidase using molecular oxygen for activation. These fungal metalloenzymes are used in biotechnological applications and have a high potential to be employed in other industrial processes. We have been engaged in structural-functional work on LiP/MnP and VP since many years. This work resulted in the finding of a unique, unprecedented amino acid modification in LiP, which initiated further investigations employing crystallography, protein chemistry, site-directed mutagenesis, spectroscopy, and spin-trapping. The conclusions drawn from the outcome of these experiments had far reaching consequences for the understanding on LiP substrate interaction and on the redox behavior. More recently, we have extended our interest towards fungal laccases, yielding the first crystal structure of a laccase in its glycosylated, fully functional form, containing a full complement set of coppers. In this presentation the current state on structural-functional aspects of the above metallo-enzymes is reviewed, spanning from the description and analysis of 3D-structures to mechanistic aspects, e.g. substrate binding and specificity and redox potential.

Keywords: ligninolytic enzymes, radicals, substrate binding

MS97.30.2

Acta Cryst. (2005). A**61**, C122

Inhibitor Binding to Aldose Reductase Studied at Subatomic Resolution

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Aldose reductase (ALR2; EC 1.1.1.21), which reduces D-glucose into D-sorbitol, is believed to cause the development of severe degenerative complications of *diabetes mellitus*. Therefore, ALR2 is the target of an extended effort in inhibitor development. We have solved the X-ray structure of complexes with ALR2 and a large number of inhibitors, of which several are at atomic and subatomic resolution, with either a carboxylate head (IDD 594, 0.66 Å) or an hydantoin head (fidarestat, 0.92 Å; minalrestat, 1.10 Å). Inhibitors bind to a charged "anionic site" in the active site cleft. The structure of IDD 594 showed very precise details, with departures from standard stereochemistry, as well as hydrogen atoms and unusual contacts for a Br atom in the inhibitor. The structure of fidarestat showed the presence of Cl^- ions replacing buried water molecules in the active site. The Cl^- ion has been clearly identified in an anomalous difference map. These observations explain inhibitor binding, which is crucial for drug design.

Keywords: aldose reductase, inhibitor interactions, diabetes