molecular sieves, as shape-selective catalysts, as dessicants, as ion-exchangers, and as hosts in advanced materials. A zeolite's suitability for a specific application is highly dependent upon its structure, so structure analysis is an intrinsic part of zeolite science. However, because most zeolites can only be prepared in polycrystalline form, standard methods of structure analysis cannot be applied.

Over the years, zeolite crystallographers have devised a number of different methods to overcome or circumvent this problem. Initially, physical model building based on information from various sources was the only option available. Interestingly enough, this is probably still the most powerful tool in the zeolite crystallographers toolbox, but it requires experience, talent and intuition. As computing capacity has increased, however, algorithms for automating the model building process have been created. At the same time, methods for improving the quality of reflection intensities extracted from powder diffraction patterns have been devised, and this in turn has allowed single-crystal methodology to be applied with greater success. An overview of some of the more recent developments in this field will be presented.

Keywords: zeolites, powder diffraction, structural analysis software

KN07.25

Acta Cryst. (2005). A**61**, C2

Structure Analysis of Modulated Crystals: Trends and Tendencies

Václav Petříček, Michal Dušek, *Institute of Physics, Praha, Czech Republic.* E-mail: petricek@fzu.cz

The superspace theory as developed by DeWolff, Jansen & Janner [1] gave to crystallographers a unique tool for generalization of structural analytical methods to be especially applicable to modulated structures. In many cases the structure analysis can now be performed almost routinely [2]. The superspace approach can also be used to find a systematic way of describing whole families of related structures [3]. The use of CCD and imaging plate systems changed considerably sensitivity of data collection for modulated structures and therefore a need for further improvement of the methods is obvious. The modulation of more complicated systems cannot be efficiently described as series of harmonic functions. Special discontinuous functions already introduced for 3+1 dimensions [4] are to be generalized to 3+2 and 3+3 superspace.

Recently modulations have been found in complicated organic structures including proteins. This opens a various new problems concerning efficiency of methods used for solution and refinement of modulated structures. New techniques such as maximum entropy [5] and charge flipping methods [6] give us a good chance to make such a generalization.

[1] Wolff de P.M., Janssen T, Janner A., *Acta Cryst.*, 1981, A**37**, 625. [2] Petříček V., Dušek M. *Z.,Kristallogr.*, **219**, 692. [3] Perez-Mato J.M., Zakhour-Nakhl M., Weill F., Darriet J. J., *Mat. Sci.*, 1999, **9**, 2795. [4] Petříček V., van der Lee A., Evain M., *Acta Cryst.*, 1995, A**51**, 529. [5] Smaaalen van S., Palatinus L., Schneider M., *Acta Cryst.*, 2003, A**59**, 459. [6] Palatinus L. *Acta Cryst.*, 2004, A**60**, 604.

Keywords: modulated crystal structures, structure analysis, superspace theory

KN08.25

Acta Cryst. (2005). A**61**, C2

High Throughput Technologies in Structural Biology

Raymond C. Stevens, *Department of Molecular Biology, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037 USA.* E-mail: stevens@scripps.edu

During the past few years, progress has been made in developing high throughput technologies for protein cloning, expression, purification, crystallization, crystal imaging, and synchrotron beamline data collection. Recently, we have been able to miniaturize, automate and parrallelize the structural biology processes significantly using nanoliter volume technologies (see http://stevens.scripps.edu/webpage/htsb for examples). Accordingly, significantly smaller amounts of materials can be used at all steps, and more parallel experiments can be engineered (genetic and mechanical) within the same space and time constraints. The next phase of this effort includes integration and improved system processing. A description of these technology developments, current status, and examples will be described.

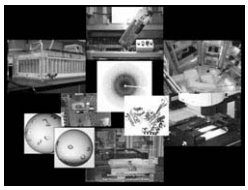

Figure 1. Sample of technologies that have been created in the past few years that include robotics systems for expression, protein purification, imaging, and analysis.

Acknowledgements: I am grateful for the cooperativity of the combined effort of researchers from the Joint Center for Structural Genomics (NIH PSI GM062411), JCIMPT (NIH Roadmap Initiative P50GM073197), Genomics Institute of the Novartis Research Foundation, The Scripps Research Institute, and Syrrx.

Keywords: structural genomics, structure based drug discovery, high throughput structural biology

KN09.25

Acta Cryst. (2005). A**61**, C2

Structure Solution of Pharmaceutical Compounds from Powder Diffraction Data

Peter W. Stephens, *Department of Physics and Astronomy, Stony Brook University, Stony Brook, NY 11794 USA.* E-mail: pstephens@stonybrook.edu

A significant part of contemporary medicine is based on the discovery and development of drugs, which are often molecules of ten to thirty non-hydrogen atoms. It is important to know the crystal structures of drug compounds and candidates for various reasons: fundamental understanding of structure and bonding vis-à-vis physiological action, the physical and chemical properties of polymorphs which are frequently encountered in drugs, and the relevance of polymorphism to patent protection and limits thereon. As it happens, many of these materials are available only as powders, and therefore any structural information must be obtained from powder diffraction.

Advances in instrumentation and data analysis techniques, both commercial and in the public domain, are proving equal to the task. However, judging from the literature, structure determination from powder data SDPD is still an obscure art, practiced by relatively few crystallographers. This is despite the outreach activities of a significant number of the innovators of SDPD, who have been working to develop and promulgate powder techniques.

I will review the state of the art and present some new results, such as the structures of chloramphenicol palmitate polymorphs.

Keywords: ab-initio powder structure determination, pharmaceutical structure determination, polymorphism

KN10.25

Acta Cryst. (2005). A**61**, C2-C3

Quasicrystal Structure Analysis. The State of the Art

Akiji Yamamoto, *Advanced Materials Laboratory, NIMS, Namiki, Tsukuba, Japan.* E-mail: Yamamoto.Akiji@nims.go.jp

The quasicrystal is an aperiodic solid showing Bragg peaks with noncrystallographic symmetry. It is recently clarified that the structure of quasicrystals can be analyzed by using a newly developed direct method and a structure refinement which is based on a higher-dimensional cluster model. They are equally applicable to decagonal and icosahedral quasicrystals since all quasicrystals seem to consist of some atom clusters (or building units)[1].

For the initial model building, the low-density elimination method (LDEM) is efficient [2]. This gives rough shape and size of occupation domains (OD) of a quasicrystal, which specify the location of atoms in a higher-dimensional space.

An initial model for the structure refinement is obtained from the rough ODs determined by LDEM by considering atom clusters, which are included in its crystal approximants. The distribution of atom clusters can not, however, be determined uniquely because of the existence of random phason strain, which is seen in all quasicrystals. This is usually inferred from high-resolution electron microscopy images or simply assumed based on a quasiperiodic tiling. The

random phason is taken into account as the phason displacement parameter in the refinement. The paper demonstrates structure determination of quasicrystals in the light of recently developed techiniques.

[1] Yamamoto A., Takakura H., *Ferroelectric*s, 2004, **305**, 223. [2] Takakura H., Shiono M., Sato T. J.,Yamamoto A.,Tsai A. P., *Phys. Rev. Lett.*, 2001, **86**, 236.

Keywords: quasicrystals, structure refinement, direct methods

KN11.26

Acta Cryst. (2005). A**61**, C3

Structure of Protein Assemblies by Comparative Modeling and Electron Microscopy

Andrej Sali[a], Maya Topf[a], Mathew L. Baker[b], Wah Chiu[b], [a]*University of California, San Francisco, CA.* [b]*Baylor College of Medicine, Houston, TX.* E-mail: sali@salilab.org

We explore structural characterization of protein assemblies by a combination of electron cryo-microscopy (cryoEM) and comparative protein structure modeling (1). Specifically, our method finds an optimal atomic model of a given assembly subunit and its position within an assembly by fitting alternative comparative models into a cryoEM map. The alternative models are calculated by MODELLER (2) from different sequence alignments between the modeled protein and its template structures. The fitting of these models into a cryoEM density map is performed by a new density fitting module of MODELLER (Mod-EM). Identification of the most accurate model is based on the correlation between the model accuracy and the quality of fit into the cryoEM density map. To quantify this correlation, we created a benchmark consisting of eight proteins of different structural folds with corresponding density maps simulated at five resolutions from 5 to 15 Å, with three noise levels each. Each of the proteins in the set was modeled based on 300 different alignments to their remotely related templates (12-32% sequence identity), spanning the range from entirely inaccurate to essentially accurate alignments. The benchmark revealed that one of the most accurate models can usually be identified by the quality of its fit into the cryoEM density map, even for noisy maps at 15 Å resolution. Therefore, a cryoEM density map can be helpful in improving the accuracy of a comparative model. Moreover, a pseudo-atomic model of a component in an assembly may be built better with comparative models of the native subunit sequences than with experimentally determined structures of their homologs.

[1] Topf M., Baker M.L., John B., Chiu W., Sali A., *J. Struct. Biol*.,*in press.* [2] Sali A., Blundell T.L., *J. Mol. Biol*.,1993, **234**, 779-815.

Keywords: comparative modeling, electron cryo-microscopy, fitting

KN12.26

Acta Cryst. (2005). A**61**, C3

Quantum Mechanical Simulation of the Vibrational Properties of Garnets

Roberto Dovesi[a], Roberto Orlando[b], Fabien Pascale[c], Javier F. Torres[a], [a]*Dipartimento di Chimica IFM, Università di Torino.* [b]*Dipartimento di Scienze e Tecnologie Avanzate, Università del Piemonte Orientale.* [c]*Laboratoire de Pétrologie, Modélisation des Matériaux et Processus, Université Pierre et Marie Curie.* E-mail: roberto.dovesi@unito.it

Structural, vibrational and electronic properties of pyrope, grossular and andradite have been simulated with the periodic *ab initio* CRYSTAL [1] program, that adopts a local variational basis set ("Atomic Orbitals") to build the crystalline orbitals. An *all-electron* basis and the B3LYP hamiltonian have been used.

The full spectrum at the Γ point (97 frequencies) [2] and the IR intensities have been evaluated, along with the symmetry of the modes, which is automatically determined. The eigenvectors of the dynamical matrix have been analyzed with different tools, including direct inspection, isotopic substitution, animations; classification-interpretation questions raised by previous studies are discussed.

The 17 IR and 25 RAMAN active modes are compared with available experimental data [3], [4]. The agreement is excellent in most of the cases (6-8 cm^{-1} the mean absolute difference).

[1] Saunders V.R., Dovesi R., Roetti C., Orlando R., Zicovich-Wilson C., Harison N.H. Doll K., Civalleri B., Bush I.J., D'Arco Ph., Llunell M., *CRYSTAL2003 user's manual. University of Torino*, *Torino*, 2003. [2] Pascale F., Zicovich-Wilson C., Orlando R., Dovesi R. J., *Phys. Chem.*, 2005, *in press*. [3] Kolesov B., Geiger C., *Phys. Chem. Min*, 2000, **27**, 645. [4] Hofmeister A., Chopelas A., *Phys. Chem. Min*, 1991, **17**, 503.

Keywords: ab-initio calculations, garnets, vibrational frequencies

KN13.26

Acta Cryst. (2005). A**61**, C3

***In Situ* X-ray Study of Hydrothermally Prepared Titanates and Silicotitanates**

Abraham Clearfield, Akhilesh Tripathi, Dmitri Medvedev, *Department of Chemistry, Texas A&M University, College Station, TX, USA*. E-mail: clearfield@mail.chem.tamu.edu

In a typical ex-situ hydrothermal or solvothermal reaction the investigator knows what is input and what the end result is but has no experimental evidence of what transpires in between. In situ methods, whether using X-ray, NMR, IR or other techniques aims to follow the reaction through this in-between stage. For crystal growth studies, in-situ X-ray diffraction is eminently satisfactory. We will describe our crystal growth studies of titanium silicate phases and the ion exchange mechanism of Cs^+ ion uptake in their tunnel structures.

One of the most vexing problems facing the nuclear industry and countries with nuclear weapons is the safe disposal of the generated nuclear waste. Huge quantities of nuclear waste arising from weapons manufacture are stored at the Hanford and Savannah River sites. The general method of remediation involves the removal of Cs-137, Sr-90 and actinides from a huge quantity of salts, principally $NaNO_3$, organics and complexing agents. It has been found that a sodium silicotitanate is able to remove Cs^+ selectively from the waste and certain sodium titanates remove Sr^{2+} and actinides. These compounds have been prepared by ex-situ hydrothermal methods. We have studied the in situ growth of these materials at the National Synchrotron Light Source, Brookhaven National Laboratory.* In addition we will describe the mechanism of ion exchange in the titanosilicate as observed by in situ methods and how the combination of these techniques coupled with an intimate knowledge of the structure of the solids is helping to solve the remediation process. In general, the in situ method allows the investigator to follow the nucleation and crystal growth or phase transformations occurring in hydrothermal reactions, and as a result of ion exchange reactions.

* In collaboration with Aaron J. Celestian, Department of Geosciences and John B. Parise and Jonathan Hanson, Department of Chemistry, SUNY Stony Brook, NY, USA.

[1] Medvedev D.M., Tripathi A, Clearfield A., Celestian A.J., Parise J.B., Hanson J., *Chem. Mater.*, 2004, **16**, 3659.

Keywords: hydrothermal synthesis, in situ reactions, in-situ powder diffraction

KN14.26

Acta Cryst. (2005). A**61**, C3-C4

Catalysts of *De Novo* Disulfide Bond Formation

Deborah Fass, Einav Gross, Nimrod Heldman, Elvira Vitu, *Department of Structural Biology, Weizmann Institute of Science, Rehovot, Israel.* E-mail: deborah.fass@weizmann.ac.il

Disulfide bonds are crucial for the folding and stability of many cell-surface and secreted proteins. In addition, disulfides can be used for redox control of protein activity. *De novo* disulfide bond formation by enzymes such as those that drive oxidative protein folding requires transfer of electrons from dithiols to non-thiol electron acceptors. We have determined the structures of representatives of the two known eukaryotic enzyme families that catalyze this process. These enzymes, Ero1 and Erv2, are flavoproteins that share similar structural and mechanistic features despite a lack of sequence similarity. In particular, our crystallographic and enzymological studies suggest that both enzymes operate by a "disulfide shuttle" mechanism, in which a dithiol motif on a mobile segment of each enzyme transfers electrons from cysteines in substrate proteins to the rigid active-site disulfide. In