## FA1-MS04-T01

**Ab Initio phasing with ARCIMBOLDO: Lost in translation.** Dayté Rodríguez, Iñaki M. de Ilarduya, Isabel Usón[a]. [a]*ICREA at Instituto de Biología Molecular de Barcelona (IBMB-CSIC), Barcelona Science Park, Spain.*
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*Ab Initio* phasing of macromolecular structures with no heavy atoms has been limited to cases with up to around 1000 atoms in the asymmetric unit, diffracting to atomic resolution [1].
Both the size and resolution barriers have been overcome in the case of several test and previously unknown structures. Thus, cases with a few thousand atoms, diffracting to 2Å have been solved through a combination of location of model fragments such as polyalanine alpha-helices with the program PHASER [2] and density modification with the program SHELXE [3]. Given the difficulties in discriminating correctly positioned fragments, the method has to test many putative groups of fragments in parallel, thus calculations are performed in a grid. The method has been called after the Italian painter Arcimboldo [4], who used to compose portraits out of fruits and vegetables. In the case of our program, most collections of fragments remain a "still-life", but some are correct enough for density modification to reveal the protein's portrait.
At the ECM we would like to report on the current successes but also on the limits of ARCIMBOLDO and how we are addressing them: especially, the difficulty to discriminate correct translations and how to overcome it.

[1] Sheldrick, G.M., Hauptman, H.A., Weeks, C.M., Miller, R. & Usón, I. International Tables for Macromolecular Crystallography vol. F, (eds., M.G. Rossmann and E. Arnold) 333–345 (Boston, 2001). [2] McCoy, A.J. et al. *J. Appl. Crystallogr*. 40, 658–674 (2007). [3] Sheldrick, G.M. *Z. Kristallogr.* 217, 644–650 (2002). [4] Tannenbaum, T., Wright, D., Miller, K. & Livny, M. in Beowulf Cluster Computing with Linux (ed., T. Sterling) 307–350 (MIT Press, Cambridge, Massachusetts, USA, 2002). [4] Rodríguez, D., Grosse, C., Himmel, S., González, C., M de Ilarduya. I., Becker, S., Sheldrick, G.M. & Usón, I. *Nat. Meth.* 6, 651–654 (2009).

**Keywords: ab initio phasing, macromolecules, grid computing**

## FA1-MS04-T02

**New tools for structure refinement in Phenix.** Paul Adams[a,b], Pavel Afonine[a], Nat Echols[a], Jeff Headd[a], Ralf Grosse-Kunstleve[a], Nigel Moriarty[a]. [a]*Physical Biosciences Division, Lawrence Berkeley Laboratory, USA.* [b]*Department of Bioengineering, University of California Berkeley, USA.*
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Phenix [1] is a Python-based software system for the solution and refinement of crystallographic structures using X-ray and/or neutron diffraction data. Recent developments in Phenix, especially in the refinement program phenix.refine, are presented. These include real space target functions for refinement, the use of torsion angle constraints, and the application of additional restraints to improve structure refinement at low resolution. The integration of automated side chain rotamer correction into the refinement process will also be described.

[1] Adams P.D., Afonine P.V., Bunkóczi G., Chen V.B., Davis I.W., Echols N., Headd J.J., Hung L.-W., Kapral G.J., Grosse-Kunstleve R.W., McCoy A.J., Moriarty N.W., Oeffner R., Read R.J., Richardson D.C., Richardson J.S., Terwilliger T.C., Zwart P.H., *Acta Cryst.* 2010, D66, 213. [2]

**Keywords: Phenix, crystallography, refinement**

## FA1-MS04-T03

**Experimental phasing with sticky triangles: how to deal with borderline cases.** Tobias Beck[a], Tim Gruene[a], George M. Sheldrick[a]. [a]*Department of Structural Chemistry, Georg-August-Universität Göttingen, Germany.*
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Experimental phasing is vital for the determination of protein structures using single-crystal X-ray diffraction. The compounds 5-amino-2,4,6-triiodoisophthalic acid (I3C) and 5-amino-2,4,6-tribromoisophthalic acid (B3C) represent a novel class of compounds that may be used for heavy-atom derivatisation of biological macromolecules. I3C and B3C contain an easily recognisable arrangement of three anomalous scatterers (iodine or bromine, respectively) and three functional groups for hydrogen bonding to the protein.
I3C was utilised for single-wavelength anomalous dispersion (SAD) phasing with in-house data [1,2]. The bromine derivative B3C, suitable for multi-wavelength anomalous dispersion (MAD) experiments, was employed for experimental phase determination using in-house and synchrotron data [3-5]. I3C has successfully been utilised to solve several novel protein structures, e.g. [6].
Different functional groups have been introduced to improve the binding capabilities of B3C. Synchrotron data were collected for several proteins and MAD phasing was successfully carried out.
The three halogen atoms present in I3C and B3C form an equilateral triangle that can be easily identified in the heavy atom substructure. Difficult cases will be presented where this information was taken into account for structure solution. For other examples, the main-chain autotracing algorithm incorporated in a beta-test version of SHELXE [7] was crucial for solving the structure.

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**Keywords: experimental phasing, heavy-atom derivatives, anomalous dispersion**