

m34.p12**Bijvoet revisited. A Python class to check Friedel pairs**

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The determination of absolute configurations is a task of major importance on the characterization of optically active molecules. The use of X-ray to 'ab initio' assign absolute configurations was first explored by Bijvoet. Nowadays the Rogers's parameter [1] and mainly the Flack's parameter [2] are used to determine the right absolute configurations.

In spite of the Flack's parameter is strong and reliable, in some cases the comparison of a strong set of Friedel's pairs is in our experience very useful to solve the uncertainty resulted from the Flack's parameter calculation. In order to check the Friedel pairs for a particular crystal the Dirdif package [3] uses the Bijvoet program [4] developed some time ago by professor Paul Beurskens.

A Python based graphical interface has been developed to use Bijvoet as an independent tool. This procedure will be presented along with a collection of test cases where the combination of Flack's parameter weak indications are solved, based on the direct investigation of the Friedel pairs through the Bijvoet coefficient (B).

[1] Rogers, D., *Acta Cryst.*, 1981, A37, 734.[2] Flack, H. D., *Acta Cryst.*, 1983, A39, 876.[3] Beurskens, G.; Noordik, J. H.; Beurskens, P. T., *Cryst. Struct. Commun.*, 1980, 9, 23.

[4] Beurskens, P. T.; Beurskens, G.; Bosman, W. P.; de Gelder, R.; García-Granda, S.; Gould, R. O.; Israël, R.; Smits, J. M. M., The DIRDIF-99 program system (1999). Crystallography Laboratory, University of Nijmegen, The Netherlands.

m34.p13**The CRYSTALBUILDER project: an easy way for single crystal structure analysis**

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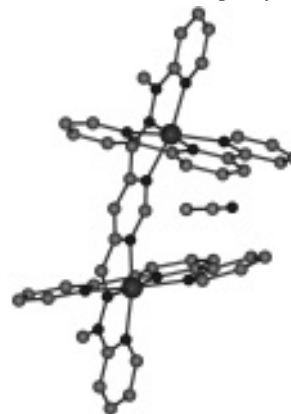
*DECOMET lab., UMR-CNRS 7177, Institut de Chimie de l'Université Louis Pasteur Strasbourg I, 4 rue Blaise Pascal, F-67070 Strasbourg Cedex, France. E-mail: welter@chimie.u-strasbg.fr***Keywords: single X-ray diffraction, molecular visualisation, free academic software**

A new graphical software for the single crystal structure refinement is presented in this communication. This free software, called CRYSTALBUILDER [1], uses SHELXL-97 [2] software for the refinement, and facilitates the analysis of single crystal X-ray diffraction data. The main objective of the CRYSTALBUILDER project is to give chemists a simple tool, usable with a personal microcomputer and free of charge for the X-ray crystallographic investigation. Objective-C programming language is used for the software development. Links with both PLATON [3] and MERCURY [4] softwares have been implemented.

To date, the software has been developed for MACOS 10.X UNIX operating system [5], known for his high stability.



Screen view of CRYSTALBUILDER during a refinement process



Pov-Ray image generated by CRYSTALBUILDER

[1] <http://www-chimie.u-strasbg.fr/~decomet>.[2] G.M. Sheldrick, SHELXL97, *University of Gottingen, Germany*, (1997).[3] A.L. Spek, PLATON 98, *Utrecht University, The Netherland*, (1998).[4] Bruno I. J.; Cole J. C.; Edgington P. R.; Kessler M. K.; Macrae C. F.; McCabe P.; Pearson J.; Taylor R. *Acta Crystallogr.*, 2002 389-397, B58.[5] <http://www.apple.com/macosx/>