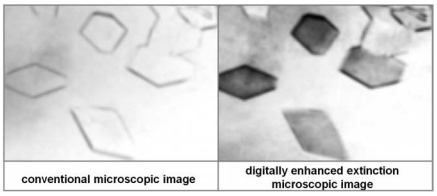
Weinheim, Germany, 2002. [2] Boese R., Kirchner M. T., Billups W. E., Norman L. R., *Angew. Chem. Int. Ed.*, 2003, **42**, 1961.
Keywords: ionic liquid, cryo-crystallization, polymorphism

P.16.15.1
Acta Cryst. (2005). A**61**, C446
Improved Crystal Detection of Protein Crystals by Bulk Contrast Enhancement
Peter Nollert, Mark Mixon, *deCODE biostructures, Bainbridge Island, WA, USA*. E-mail: pnollert@decode.com

We present a computer-enhanced microscope that improves the reliable detection of small and colorless protein crystals in their native crystallization environment. Careful observation and evaluation of crystallization experiment pose a substantial burden on operator-based resources especially in high throughput crystallization operations. The presence of crystals is usually established by the observation of - frequently disguised - crystal facets, i.e. crystal edges in images. It is desirable to add a further contrasting method. Polarization microscopy does provide bulk color but this contrast is severely attenuated owing to the use of polymer-based birefringent crystallization trays.



We show how bulk contrast of micro crystals (grown in birefringent plastic trays and in lipidic cubic phase matrices) can be enhanced dramatically by digital processing of images that are captured with an automated extinction microscope (see figure). At first, images of crystallization experiments with different rotations of locked polarization extinction settings are captured. Then the colors are decomposed and numerical operations are applied on the respective grey-value matrices. The final combined false-color image shows protein crystals with enhanced bulk contrast. The configuration of the automated extinction microscope, its image processing algorithms and its usefulness for the detection of colorless protein crystals will be shown. We conclude that bulk contrast enhancement substantially aids the confident identification of crystals.
Keywords: crystal detection, image processing, lipidic cubic phase

P.16.15.2
Acta Cryst. (2005). A**61**, C446
How a new Chemical Compatibility Test Facilitates Protein's Crystallization
Jean-Pascal Viola, Steve Tétreault, Christian Houde, *Nextal Biotechnologies, Montreal, QC, Canada, H3K 1G6.* E-mail: jpviola@nextalbiotech.com

In early stages of a macromolecule's crystallization, when little information is known about a protein's solubility versus various chemicals, the selected strategy is to setup usual initial screens at protein concentration selected from past experience. Factors such as availability of protein or intrinsic protein physical properties can be used as guidelines, but again, they provide little help in selection of initial screens conditions.

During development of new optimization procedures and initial screens, we needed to find a new startegy which would address this question, and enable us to orient crystallization appropriately. Presented here is a new method to test a macromolecule's solubility against many chemicals which can be applied straightforwardly at experimental setup. Using this method, not only did we obtain a reasonable and necessary high level of precipitation in any selected initial screens, but results from this test can also be applied directly to optimization strategies like "Pro-Active" or "The Optimizer Series" presented earlier.

This strategy was applied to a series of 10 proteins, where solubility was tested against a series of salts, polymers, organics and buffers. From results obtained, initial screens and optimization methods were selected. This preliminary solubility evaluation, performed prior to crystallization setup, benefited not only initial screening results but also accelerated optimization process, using less protein compare to the classical optimization method.
Keywords: biomacromolecular crystallization, optimization, crystal growth apparatus design