feedback are at the cutting edge of technology, and the conceptual design of autonomous systems represents a research frontier in mechatronics. We expect that the current operator-assisting UMR will evolve into a system endowed with progressively increasing autonomy capable of significantly increasing reliability of protein micro-crystal harvesting and reproducibility of cryo-cooling. In addition, advanced micro-manipulation robotics will open the field to new science and emerging crystallization technologies of far reaching impact. Major improvements in operational precision have given the UMR the capability of manipulating crystals significantly smaller than 10 microns thus facilitating nano-crystallization, harvesting from micro-fluidics, nano-diffraction techniques and novel seeding strategies.

Keywords: robotic crystal harvesting, cryotechniques, automation

P01.15.80

Facilitating low volume protein crystallography set-ups using the mosquito® liquid handler

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A prerequisite for efficient high throughput protein crystallisation screening is the accurate pipetting and positioning of the low volume drops used in hanging and sitting drop setups. Screening the many different conditions under which a protein crystal may form lends itself to automation, since it requires hundreds of similar experiments to be set up to find the few 'hits'. Automated solutions exist for low volume pipetting, however, the variable viscosities of protein and reservoir/screen solutions present significant challenges for many liquid handling systems. Another challenge is that of drop positioning. The mosquito® (TTP LabTech) offers fast positive displacement pipetting for accurate and reproducible aspiration and dispensing throughout the 50 nL - 1.2 μL range, producing CVs of < 8% at 50 nL irrespective of viscosity. This, plus its columnar arrangement of pipettes, allows it to automate hanging drop as well as sitting drop set-ups. Mosquito's micropipettes are also disposable, thus guaranteeing zero cross-contamination where required.
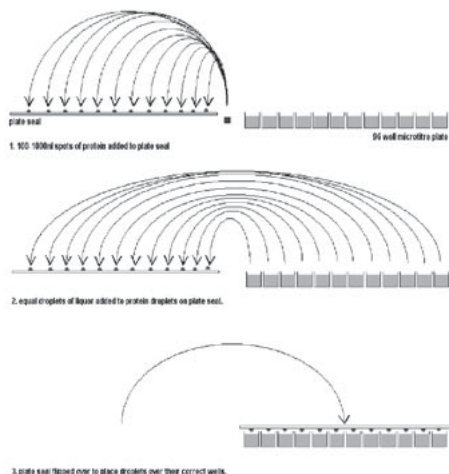
Keywords: protein crystallization, robots, laboratory automation

P01.02.81

A simplified unified approach for animations and movies using SBEVSL

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RasMol, Jmol, and PyMol, and many other molecular graphics programs are used to produce animations and movies. Each program takes a different approach making it necessary to use different commands and scripts when moving among programs, thereby making the development of lectures and tutorials more complex than necessary. The Structural Biology Extensible Visualization Scripting Language (SBEVSL) project is developing a common scripting language to access the common features of several molecular graphics packages. For some uses, the scripting language can be used as a black box, much the way we use Postscript for text documents, but, where feasible, SBEVSL is designed to be comprehensible to scientists by using simple menu-click-like commands and reasonable defaults. RasMol, PyMol and Jmol are being given "native" SBEVSL support and external translators will allow the approach to be applied to other packages, such as CCP4mg. For movies and animations the very useful but somewhat cryptic Jmol "moveto" command will be provided, but the SBEVSL version will be based on simple selection and recording of benchmark images using commands based on the PyMOL mset command combined with both time window and frame range based morphing. This work is part of the combined efforts of the SBEVSL groups at Dowling College and Rochester Institute of Technology. The people at Dowling are: Isaac Awuah Asiamah, Darina Boycheva, Georgi Darakev, Nikolay Darakev, John Jemilawon, Nan Jia, Petko Kamburov, Greg McQuillan, Daniel O'Brien, Georgi Todorov, Herbert J. Bernstein. The people at RIT are: Scott E. Mottarella, Brett Hanson, Charles Westin, Corey Wischmeyer, Paul A. Craig.

Keywords: animation, graphics, script

P01.02.82

Remote data collection and rapid scheduling at the Molecular Biology Consortium beamline ALS 4.2.2

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The Molecular Biology Consortium consists of academic institutions throughout the USA and Taiwan. The cost of making regular synchrotron trips to the Advanced Light Source in Berkeley is not trivial and Beamline 4.2.2 initially addressed this issue with the addition of Service Crystallography. Since February of 2007 the MBC has also offered full remote collection capabilities and this has significantly improved access to the beamline. A Rigaku ACTOR sample mounting system is at the heart of remote operations and has been integrated into the Blu-Ice collection interface. Onsite computers installed with NX server software allow users to connect remotely via free client software. Sample mounting, exchanges,

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