BECKMAN

T3 UPDATE

Volume 1, Issue 6 ◆ Winter 1997

New tips, tricks and techniques for users of Beckman laboratory automation systems

A CLUB BIOMEK BULLETIN

Multimek™ 96 provides rapid plate-to-plate fluid transfers

Susan Stone ◆ Beckman Instruments

This fall, Beckman replaces the Multi-Pette™ Automated 96-Channel Pipettor with an improved version — the Multimek 96. This instrument includes powerful software and major new safety features, and is sold and supported by the Beckman organization worldwide.

The Multimek 96 features a six-position work deck, high-precision pipetting, and the capability to transfer between 96-well and 384-well microplates without hardware reconfiguration or special programming.

The Multimek 96 is Beckman's solution for platewise microplate pipetting applications, including:

- Microplate replication
- Reagent addition
- Full-plate serial dilutions

The system can be configured with a standard safety shield for stand-alone use, or with a robot-friendly shield for integration into automated systems. There is also a choice of three pipette heads that feature disposable tips (200 µL or 20 µL) or fixed Teflon*-coated stainless-steel tips (400 µL).

Multimek Pro software is an intuitively easy-to-use graphical interface used to write and run methods.

Access to key pipetting parameters allows the user to execute liquid handling procedures as precisely as desired.

Specifiable parameters include pre- and post-dispense air gaps, multiple aspirations and multiple dispenses (even to or from multiple plates), aspirate and dispense speeds, aspirate and dispense heights, tip touches, liquid level tracking during aspirate and dispense, and mix volumes, speeds, cycles and air gaps.

Figure 1. Multimek 96 Automated 96-Channel Pipettor.

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INSIDE THIS ISSUE

From the Editor

John Gerace ◆ Beckman Instruments

Welcome to the sixth issue of T^3. I would like to start by thanking everyone who has faxed or e-mailed Biomek® methods or comments and suggestions.

This issue presents useful information about our liquid handling technologies and integrated robotic systems. It provides updates on developments that enhance the performance of our automation product portfolio and offers a glimpse into the future regarding assay miniaturization and plug-and-play technology.

We have expanded our liquid handling product line by introducing the new Multimek™ 96 Automated Pipettor, which replaces the SAGIAN Multipette™. The name change signifies some hardware changes that increase the instrument's safety and indicates that the product is now sold and supported by Beckman worldwide. The Multimek software, which was developed at SAGIAN under the direction of Carl Murray, Ph.D., has been instrumental in setting the Multimek above our competition. Our rapidly growing customer base agrees that the software is really fun and easy to use.

Multimek 96.

The Biomek 2000 continues to prove itself as a versatile workstation where sample preparation and assay procedures are quickly and easily automated. This issue of T^3 describes the features that our new BioWorks™ version 2.2 provides. BioWorks 2.2 is required to operate our newly released BioScript™ Pro advanced development software. As described in the last issue of T^3 (Vol. 1, Issue 5), BioScript Pro is a lower-level programming language based on Tool Command Language (TCL) that enables the user to perform complex functions that go beyond the basic capabilities of BioWorks software with standard BioScript.

BioScript Pro will be useful in expanding the functionality of the Biomek by integrating other devices within the Biomek work envelope. Dr. David Brandt describes the integration and use of Cartesian Engineering's Biodot solenoid inkjet dispenser in his assay miniaturization research using 384- and 1,536-well plates.

While assay miniaturization addresses issues of reducing reagent costs and increasing throughput in high-throughput-screening programs, we also address bottlenecks that can occur before and after the screening process within the drug development cycle. For example, John Hicks and Dr. Christian Oste describe a new menu of core devices that can be integrated to automate molecular biology applications used in functional genomics.

P/ACE System MDQ.

The success of high-throughput-screening programs has increased the number of lead compounds that proceed into pharmacological analyses (PkADM). To address the bottlenecks that may occur within this post-screening process, Jeff Chapman writes about a plug-and-play future where Beckman's micro-plate-based capillary electrophoresis instrument, P/ACE™ System MDQ, was designed to be integrated into an automated laboratory robotic system. Stay tuned for news on the integration of other analytical devices used in drug discovery.

Lastly, I would like to remind everyone about the Lab Automation '98 show to be held Jan. 17-21 in San Diego, Calif. We will be hosting another fun-filled Club Biomek event on the evening of Jan. 19. Keep an eye out for your invitation. We also will be previewing new landmark cross-platform Windows* NT laboratory automation software — another innovative software package developed at SAGIAN that we expect will become an industry standard.

Please read on and feel free to provide feedback via mail, e-mail or fax.

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New Products

From page 1

The software also includes advanced features such as looping, variables, and a macro control language for users wishing to program custom operations.

For more information on the Multimek™ 96, please contact your field sales representative.

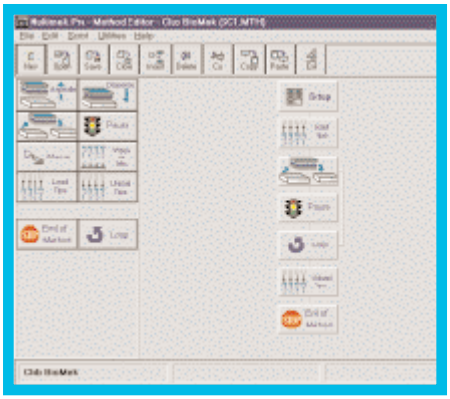

Figure 2. Multimek Pro software offers drag-and-drop programming.

BioWorks™ Version 2.2 Released

We've made several improvements from BioWorks 2.1. Following is a list of of the new features that can be found in BioWorks 2.2. Please note that this is a necessary upgrade for use of the newly released BioScript™ Pro lower-level programming language for the Biomek® 2000.

Edit

- A 96-well square plate permits the user to place a lid on it.
- Reservoir holders that have had their module configurations altered after the original setup will display correctly using the right-mouse click.
- Lab book changes in Edit after editing and closing a method no longer cause a program fault.
- BioWorks will validate placing a tip rack holder and tip rack in location A4 with a Side Loader in the system. However, the Side Loader still cannot move a tip rack in A4 because the arm cannot reach far enough to open the latch.
- The minimum aspirate and dispense heights have been modified to correct problems with collisions, and have been corrected for situations where the labware is below a vacuum collar. The minimum height is now 0.5 mm below the computed limit where the tool will come into contact with the labware, and 1.5 mm below the limit where a tip will make contact. For more titerplates, this is the same or better tolerance than the 10% previously permitted. For test tubes, this change should prevent breakage. The 0.5-mm and 1.5-mm tolerances permit user adjustments to compensate for labware and alignment variances.
- Printing device parameters will print the offsets, top width and height, as displayed in the Device Edit dialog.
- Printing labware parameters for titerplates and HDR gels will now print the grip parameters.

Run

- The "Reset All Tip Racks" menu item is no longer overridden by the BIOMEK.INI setting at the start of each run.
- Side Loader "portals" now will have the arm move entirely clear of the location before the next method step is executed.
- The HDR tool is now moved to its "parked" position correctly for Side Loader access.
- Tip/labware Disposal Collision Avoidance values have been adjusted to prevent MP20/MP200 collision with the right edge of the disposal shoot.
- Side Loader grip sensing has been improved to perform automatic retry if no labware is sensed at the source.

Edit, Run and Lab Book Manager

- A user can launch Run, select a lab book, load and start a method. Then the user can launch Edit, select another lab book, and edit it while continuing to run the method from another lab book.
- If "Edit" is busy, i.e., it has any methods open or any edit dialog boxes (Edit Labware, Devices, etc.), then neither Run nor Lab Book Manager will be able to change lab books. Instead, the user will get a message stating that Edit is busy.
- If more than one BioWorks application is running (but Edit is not busy), then changing the current lab book in one application will automatically switch all other applications to that lab book. The exception here is that if Run is running a method, it will continue to use the same lab book throughout that method.
- If run is Exited during a running method, in order to re-synchronize with the running workstation method the operator will need to use the Lab Book Manager or Edit to switch back to the lab book that the run was started with, before launching Run.
- If lab books are switched in Edit while Run is occurring, it is not possible to run that method from Edit without first closing the Run application (allowing it to be re-synchronized with the current lab book).
- This operational mode is similar to BioWorks 1.4a, but additional precautions were added to prevent lab book damage. Also implemented is an automatic synchronization between two applications using the same lab book, in case one application changes the default. Care must be taken by the user to bring both applications into synchronization, after the run is complete, when editing and running from different lab books at the same time.

BIOMEK® 2000 ENHANCEMENTS

Figure 3. Biomek® 2000 with Biodot solenoid inkjet system.

What's up with Cartesian Engineering?

David W. Brandt, Ph.D. ◆ Beckman Instruments

At the recent conference of the Society for Biomolecular Screening (SBS), we announced a collaborative project between Beckman and Cartesian Engineering on the integration and validation of the Biodot solenoid inkjet system with the Biomek 2000. The objective of the project is to co-develop the software interface between the two instruments and test the validity of using the High-Density Replicating Tool for the transfer of compounds in 100 percent DMSO and the transfer of other assay components with the Biodot into high-density microplates — 384- and 1,536-well formats.

Objectives completed:

- The software interface has been finished. Marketing Specialist Jeff Cahlik has written a program that allows the initiation of Biodot methods via a command-line protocol within a BioWorks™ method.
- The Biodot platform has been modified to accept modified Biomek labware holders so that the Gripper Tool can place microplates on the Biodot.
- The "Proof of Concept" has been completed by demonstrating that we can move plates around between the Biomek and Biodot and initiate Biodot methods.

Objectives outstanding:

- Validate the HDR can transfer into 1,536-well plates using custom pins. The initial test results are very promising!
- Validate the accuracy and precision of the Biodot with the HDR for a standard enzyme assay in 384- and 1,536-well plates.
- Minor modifications to the Biodot hardware and software.

INTEGRATED ROBOTICS SYSTEMS

Beckman/SAGIAN offers 'core' molecular biology solutions

John Hicks ◆ SAGIAN division of Beckman
Christian Oste, Ph.D. ◆ Beckman Instruments

Since Beckman Instruments and SAGIAN joined forces in 1996, the combination of automated liquid handling (Biomek® 2000 Laboratory Automated Workstation), labware management (ORCA® linear arm) and scheduling software (SAMI®) has facilitated the full automation of a variety of standard assay procedures. The approach, referred to as "core" systems, assembles a number of different devices on the worksurface, each designed for a specific task, and all under the control of the scheduling software. Although core systems can be tailored to narrowly defined applications, they will most likely include automated liquid handling, linear robotic movement and scheduling software.

Three major types of biochemical assays have been addressed: ELISA, cell-based and binding assays. In each case, a basic system architecture is proposed, with a menu of peripheral devices from which to choose in order to optimize the final system configuration according to user-specific requirements.

Defining the list of components necessary to perform molecular biology applications can be more challenging, due to the diversity and complexity of routine protocols, such as template preparation and reaction setup (e.g., cycle sequencing, etc.). Therefore, the architecture of a molecular biology core system will forcibly have to be more open. This requirement may lead to several configurations featuring increasing levels of automation.

As the throughput needs of a given laboratory increase, the need for automating part or all of a process will increase as well. The first attempt at integrating thermal cycling and automated liquid handling capabilities lead to positioning an MJ Research PTC-200 in the place of the Biomek 2000 left extension module, allowing for direct pipetting into a microplate or array of microtubes set in the PTC's block. This configuration addresses the needs of a low-throughput laboratory, particularly in cycle sequencing applications.

Next in increasing complexity is a proposed hybrid system, dedicated to non-gel-based characterization of amplified nucleic acids (i.e., hybridization). The majority of components are shared with the binding assay core system, namely carousel, plate sealing, lidding, incubator,

detector and an MJ Research Tetrad (i.e., four independent blocks) unit. Alternatively, if magnetic beads are used in the procedure, a magnetic bead separation station (currently under development at SAGIAN) could take the place of the plate washing unit or be added to the system.

The advantage of such a strategy is that the user could initially acquire an "off-the-shelf" binding assay system, and add to it an MJ Tetrad and possibly even a magnetic beads station, without at any point diminishing the capabilities of the system in binding assay applications. The MJ Tetrad would fit on an additional optical table set on the opposite side of the ORCA rail. This approach will contribute to expanding the versatility of the system, while improving productivity by increasing the number of hours in operation.

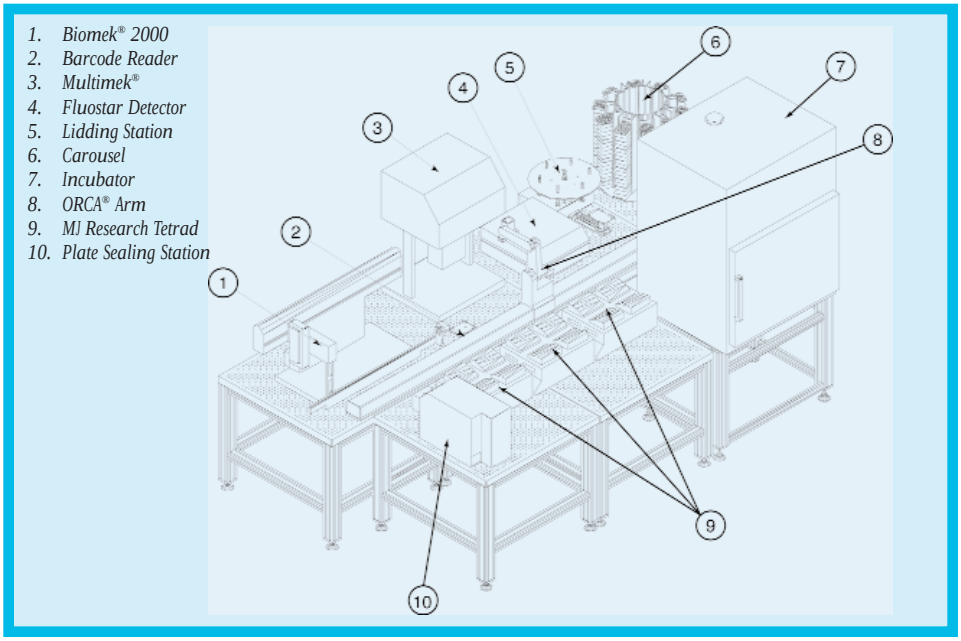

Figure 4. Example of high-throughput cycle sequencing configuration.

In this example, the following assumptions are made:

- The typical template to be sequenced would be either M13 or plasmid.
- The protocol for isolation/cleanup of the template involves the use of magnetic beads.
- The template concentration is normalized prior to setting up the cycle sequencing reaction.

Typically, a Multimek™ 96-channel pipetting device is used in conjunction with a magnetic beads station to isolate and clean up the templates. Next, a fluorescence plate reader is used to measure the template concentration, after adding a fluorescent intercalator to an aliquot of template solution. The Biomek 2000 "cherry-picking" routine normalizes the concentrations of the templates, possibly disregarding those whose concentration would fall below a predetermined threshold. Thereafter, the Biomek reorganizes the normalized selected templates in fresh 96-well plates and sets up the cycle sequencing reactions.

The core system approach for automating basic molecular biology protocols allows us to take the first step toward the complete automation of entire processes. Those steps that are particularly robust — such as setting up cycle sequencing reactions — would be the first ones to consider for hands-off operation. Sometimes, simply automating "modules" or discrete sets of steps may make more sense, and can result in a higher level of overall reliability than attempting to automate the entire process from start to finish.

Looking Ahead

Plug-and-play future is in sight

Jeff Chapman ◆ Beckman Instruments

Automation, with the development of integrated laboratory robotic systems, has played a significant role in the evolution of drug discovery strategies. Of course, processes of synthesis have been greatly advanced with the use of combinatorial chemistry, creating even greater demands for simplified high-throughput screening and automated analytical characterization.

Essentially, once ideal compounds have been synthesized, screened, identified and consolidated, a bottleneck generates in their subsequent re-handling for characterization. An important step in process improvement becomes the development of a common format that can be used from synthesis to final analysis.

The gap between synthesis, handling, screening and analysis is bridged with the use of the 96-well plate, an industry standard in automation. This need for automation drives Beckman's product development and is considered key in the design of all the company's new analytical systems. The most recent example of the "integration of analytical tools" approach is seen with the release of the P/ACE™ System MDQ.

Figure 5. The P/ACE™ System MDQ.

The P/ACE System MDQ is a capillary electrophoresis (CE) system developed with the 96-well plate at the center of its design. The P/ACE System MDQ is a pharmaceutical CE developed to assist in drug discovery, and is the only CE system designed from the ground up to streamline methods development, methods validation and methods transfer to QC.

CE has come a long way in the last nine years and is now enjoyed as a very robust and reproducible technology used extensively for analysis of highly polar compounds.

Figure 6. ORCA® arm moves 96-well plates from the Biomek® to the P/ACE System MDQ.

CE has excelled in the analysis and characterization of proteins, including those that are glycosylated; in the separation and quantitation of nucleic acids; and the analysis of highly polar compounds such as ions and those notoriously difficult basic pharmaceuticals. Additionally, the free-solution approach of CE has been ideal for creating a milieu of chirality and represents the best analytical tool for the resolution of chiral enantiomers.

In summary, the P/ACE System MDQ utilizes the 96-well plate as a common sampling platform, allowing an easy transition from screening and consolidation to analyte characterization. Although this sampling format is currently off-line from our integrated laboratory robotics, our goal is to integrate these analytical tools as plug-and-play modules, enhancing greatly the degree of laboratory automation.

EVENTS

SBS conference forum for discourse on high-throughput screening

Lauren Eckert ◆ SAGIAN division of Beckman

With its emphasis on colleague networking and providing a forum for sharing emerging technologies, the Society for Biomolecular Screening (SBS) conference has become the premier forum for scientists, users and suppliers involved in high-throughput screening.

The third annual SBS conference, held in San Diego in September, showcased 78 booths and exhibits and provided energizing speaker conferences and product introductions from around the world. Nearly 520 attendees and 170 exhibit personnel attended, well over the expected total of 500.

SAGIAN and Beckman co-hosted a customer-focused booth featuring the Biomek® 2000, ORCA® Generations, a series of expandable, modular workstations including the 1-meter ORCA robot, Multimek® 96 Automated 96-Channel Pipettor, Plate Sealer, Carousel, and new Microplate Bar Code Print and Apply station. Systems were operational, allowing those stopping by our booth the opportunity to appraise stations firsthand and get their questions answered. Traffic was brisk and the feedback exceptional.

Since returning from the show, Beckman and SAGIAN R&D and engineering teams have been putting the final touches on new equipment releases in addition to groundbreaking product software. Look for these new technologies to be unveiled in January at Lab Automation '98 in San Diego, and this March at Pittcon '98 in New Orleans.

To learn more about the Society for Biomolecular Screening, call up the SBS website at www.sbsonline.org., or e-mail membership questions to sbsemail@aol.com.

Beckman, SAGIAN and Wallac Oy host customer appreciation night

Lauren Eckert ◆ SAGIAN division of Beckman

An evening spent watching a spectacular sunset over the Pacific while listening to jazz and sipping a glass of Merlot at the Stephen Birch Aquarium in La Jolla was the perfect way to end an intense day of exhibits, conferences and sessions, Sept. 23, after the Society for Biomolecular Screening conference. Participating in the fun were members of Club Biomek, and customers of Beckman, SAGIAN and Wallac Oy.

The aquarium was open for self-guided tours, which included a room-size tank, home to a 20-foot forest of swaying kelp, and hundreds of smaller tanks teeming with fascinating and unusual sea life. The 250-plus crowd strolled from the renowned aquatic displays to the aromatic dining stations spilling over with shrimp, sushi, grilled ahi, smoked turkey, Caesar salad, and other mouthwatering dishes. The mood was relaxed, and the food, live music and wine excellent. Conversation ranged from the best after-hours haunts in Old Towne to new-product buzz and shared insights from the trade show.

The evening was topped off with chocolate-covered strawberries and champagne, a fitting ending to a rich evening.

ANNOUNCEMENTS

Drug Discovery Today article looks at core system model

David W. Brandt, Ph.D. ◆ Beckman Instruments

In an upcoming issue of *Drug Discovery Today* is an article describing the theoretical principles on which Beckman and SAGIAN base the development of core systems. This article was prepared by myself with extensive input by Tim Bruemmer and Carl Murray from SAGIAN.

Laboratory automation is an evolving technology that has grown in complexity and sophistication over the past decade. High-throughput screening is the discipline that has driven the automation technology to the point where principles can be stated about how much and what is appropriate to automate in an HTS laboratory.

The Drug Discovery Today article discusses the principles that are central to a successful and productive HTS system. Furthermore, we describe an approach to designing and programming HTS systems to achieve a higher degree of reliability than what has been experienced in the past.

Learn about TCL at Lab Automation '98

As mentioned earlier, our new BioScript™ Pro advanced development software is based on Tool Command Language (TCL). If you are interested in learning more about TCL and how to develop custom user interfaces to laboratory automation equipment, there is a TCL class scheduled during Lab Automation '98, to be held Jan. 17-21 in San Diego, Calif.

Petar Stojadinovic of Chiron Corp., who is very experienced at developing custom applications on the Biomek® 2000 and Multimek™ 96, will teach the class.

For more information about class registration, call up the Association for Laboratory Automation (ALA) web page at http\\labautomation.org or send an e-mail to Petar at peters@chiron.com.

BIOMEK® 2000 INTERNET ADDRESSES

Michael W. Clark, Ph.D ◆ Beckman Instruments

T^3 Update strives to communicate all available Biomek 2000 methods, whether constructed by Beckman or other Biomek users. Listed here are a few internet sites that use the Biomek 2000 in their pursuits and have made their methods available. In addition, you can do a keyword search for "Biomek" and view ALL sites referencing the Biomek system.

The Biomek 2000 Home Page(Check here first)
http://www.beckman.com/biorsrch/prodinfo/biomek/biohome.htm

Listed are Internet postings of Biomek 2000-related information:

Protein Assays and Drug Screening

Using the Biomek 2000 to Automate an EIA for the Quantitation of Polysaccharides; utilizing a Zymark robotic arm.
http://www.islar.com/abstract/charbonn.htm

The MultiScreen Assay System.
http://www.millipore.com/analytical/technote/multiscreen/whatis.html

GSU chemistry resources: departmental equipment/facilities.
http://131.96.145.20/facilities/resources.html

Olfaction: from receptor genes to information processing. I: molecular recognition and transduction.
http://dapsas1.weizmann.ac.il/~bmgraaf/papers/expression/expression.html

DNA Template Preparation

Automated plasmid preparation.
http://www-hgc.lbl.gov/instr/kauer.html

The Swiss Blood-Testing Unit (STU). LabAutomation'97 Abstract

http://lab automation.org/LA/LA98/posterlist98.html

Overview of Roe Laboratory Sequencing Strategy A.

http://www.genome.ou.edu/SeqStrategy.html

Nucleic Acid Detection and Amplification Assays

Biorobotics homepage protocols and a complete Biomek labbook for performing PCR and minipreps.

http://www.tigem.it/TIGEM/BIOMEK/biorobotic.html

An automated oligonucleotide ligation assay using the Biomek.

http://labautomation.org/LA/LA97/papers/piani.html

New applications of high sensitivity nucleic acid stains.

http://www.probes.com/lit/bioprobes25/part09.html

Technical & Application Bulletin Index

The following information is available from Beckman:
Technical(T) and Application(A) Information Bulletins

T-1709	The Automation of Three Clinically Important ELISAs with the GenELISA V2.1 System
T-1710A	A Method for Interfacing the High-Density Replication System with the Biomek® 1000 Side Loader
T-1711	Preparation of High-Density Colony Filters for Screening Cosmid Libraries
T-1713	Hybridoma Screening Using the High-Density Replicating System on the Biomek 1000 Automated Laboratory Workstation
T-1721	Complete ELISA Automation Using the Biomek 1000 SL and SL Incubator
A-1743	Validation of the Biomek 1000 BioRobotics System for LAL Endotoxin Testing Using the BioWhittaker Kinetic-QCL System
A-1749	Complete Automation of Endotoxin Detection Using the Biomek 1000 BioRobotics System for LAL Endpoint Assays
A-1759A	Use of the Biomek Workstation for Ki Determinations
A-1764A	ELISA Automation: A Biomek 1000 to Biomek 2000 Comparison of Clinical ELISAs
A-1765A	Automation of HIV Proteinase Enzyme Assay Using Scintillation Proximity (SPA) Technology
A-1766A	High-Throughput DNA Sequencing Reactions Using the Biomek 2000 BioRobotics System
A-1767B	Contamination-Free PCR Preparation of Multiple Samples Using the Biomek 2000 Laboratory Automation Workstation
A-1802A	Radioimmunoassay Automation: Development of a Single-Step Assay Using the Biomek 2000 Laboratory Automation Workstation Integrated with the MicroBeta PLUS 96-Well Scintillation/Luminescence Detector
A-1826A	High Throughput Purification of Plasmid DNA Using the 96-Plasmid Purification Kit on the Biomek 2000 Laboratory Automation Workstation
A-1835A	High Throughput Automated Purification of Plasmid DNA Using the 96-Plasmid Purification Kit With the Gripper Tool on the Biomek 2000 Laboratory Automation Workstation
BA96-3145	Biomek 2000 Laboratory Automation Workstation: Modifying Pipetting Tool Specifications in BioWorks Software
BA96-3146	Biomek 2000 Laboratory Automation Workstation: Introducing New Labware Specifications into BioWorks™ Software
T-1809A	Integration of the Biomek 2000 and Wallac MicroBeta Trilux Microtiter Plate Scintillation/Luminescence Detector
T-1832A	The Gripper Tool: Expanding the Functionality of the Biomek 2000 Laboratory Automation Workstation
T-1833A	Colony Selection with an Automated 384-Pin High-Density Replicating Tool (HDRT)
T-1843A	Bioscript™ Pro: Programming Language for the Biomek 2000
T-1845A	Beckman/Sagian "Core" Molecular Biology Systems

Article Reprints

The following article reprints are available from Beckman:

007-134	A Flexible, Integrated System for Automation of Hybridoma and ELISA Procedures, E.W. Stewart and N.C. Appleby
007-135	Automated Sanger Dideoxy Sequencing Reaction Protocol, J. Zimmerman, H. Voss, C. Schwager, J. Stegemann and W. Ansorge, Federation of European Biochemical Societies, 223: 432-436 (1988)
007-137	Automation of Dideoxynucleotide DNA Sequencing Reactions Using a Robotic Workstation, R. K. Wilson, A.S. Yuen, S.M. Clark, C. Spence, P. Arakelian and L.E. Hood, BioTechniques 6: 776- (1988)
007-138	Automated Methods for Single-Stranded DNA Isolation and Dideoxynucleotide DNA Sequencing Reactions on a Robotic Workstation, E.R. Mardis and B. A. Roe, BioTechniques, 7: 840- (1989)
007-182	Detection and Quantification of Gene Amplification Products by a Nonisotopic Automated System, M. Holodniy, M.A. Winters and T. C. Merigan. BioTechniques 12: 37-39 (1992)
007-320	Pharmaceutical Biotechnology International (1995). Beckman Corporate Profile and High-Throughput Screening Article.

BIOMEK FREQUENTLY ASKED QUESTIONS

Questions

1. I have many destination plates with only one source plate. Everything is staying the same except the location of the destination plate. Do I have to rewrite the transfer function for every new destination?

2. My current method uses two rows of tips. If I power down the Biomek and the next day I run the method again, will the instrument start from the beginning of the tip box or will it remember where it left off?

3. How can I transfer 1 µl of pure water?

4. Does Beckman sell sterile 2.0-ml square-well titer plates?

5. Does Beckman sell a lid for the 2.0-ml square-well titer plate?

Answers

1. No. As long as everything is exactly the same, you need to highlight the line BELOW the transfer function, hold down the <ALT> key and, with your mouse, click on the location for the new destination. This will copy the original transfer with the new location for the destination.

2. The Biomek 2000 will remember where the dirty tips are as long as the instrument has stayed powered up. Also, if two methods are run back to back, it will tip track as long as the initial configuration has the same label on the tip box and is in the same location. To answer the question, the method run on day two will start at the beginning because the instrument was powered down. The memory was reset. If the instrument was NOT powered down, the method run on day two would start with the third row of tips.

3. Pure water has a high surface tension. Always pipette into liquid. Use a P20 or MP20 tool with a "to contain with blowout." Adjust the bias and calculate the slope and offset for 1 to 2 µl. Increase the delays from 100 to 500 and prewet the tip.

4. Yes; the part number is 609681 for a case of 24 polypropylene plates.

5. Beckman sells foil lid covers, part number 538619, quantity of 100. These lids are cut in a 96-well format and have adhesive on the back. The cover can be secured by using your hand or by adhering with a rubber roller, part number 538619.

Integrated Robotics Systems Frequently Asked Questions

Adrian Tabion ◆ SAGIAN division of Beckman

Questions

1. After checking or re-teaching the global frame, the ORCA® robot tries to access stations with the fingers pointed toward the tables (-180 Bend in the hand). Why?

2. After a power outage, the IID is not running but there is a "C:\" at the top of the screen.

3. What is the offset rack used for?

4. When I calibrate, I cannot enable the pendant.

5. During a run, I get an error in SAMI-RT which states "Array index out of range."

6. How do I know where my plates come from at the beginning of the run and where they end up at the end of the run (i.e. — what carousel positions)?

7. I have an overabundance of code, log, and method files. What can I delete?

Answers

1. In Frame_GlobalA or B, hit <Calculate> and <Replace>, then save the frame.

2. Type "iidmain" and hit <Enter > on the keyboard. This will restart the IID program.

3. To ensure the accuracy of the "Put" and "Get" motions on a core system, we approach the positions from the same direction to take into account the overshoot in the motors. Since the motors consistently have the same overshoot, the positions, when approached from the same directions, will be accurate.

4. Enable the teach pendant in the window (click on the <Enable Pendant> button) that appears when you click on <Control> and select "Calibrate" from the Robot window.

5. SAMI-RT cannot accept method names, authors, or descriptions with 21 or more characters. Open your method in SAMI, and double-click on the gray circle in your method (the "new method" or "lollipop" node at the top) and check your number of characters and hit "OK" after adjusting the method name, author, or description.

6. After scheduling your method (or clicking on "File," selecting "Open Schedule," and choosing your code file), click on "Setup" and select "View Summary." You should see a listing of the objects' Origins and Destinations.

7. Any code file that you do not need to run in MDS anymore can be deleted along with all of the files with the same name but different extension (there should be nine files including the .cod file).If you have been running without errors, you can delete any log files (*.log in the c:\sami\logfiles directory) that you do not want to keep. Any method that you no longer run can also be deleted (*.mth in the c:\sami\methods directory). If you plan on using the old methods, old log files, or old code files, you can move them to another directory (create one or use an existing one) or to a disk.

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