High Throughput and Custom Sequencing of DNA on Microlab® STAR

Pharmaceutical

At GATC Biotech, it was the superior flexibility and accuracy of Microlab® STAR that made it highly suitable for high throughput sequencing and custom sequencing of single samples. High throughput sequencing such as Estimated Sequence Tag (EST) sequencing, Bacterial Artificial Chromosome (BAG) sequencing, or whole genome sequencing requires efficient and quick processing of large numbers of samples. Custom sequencing on the other hand requires flexibility for processing single samples. More than 100 standard or customer specific primers are available for use on the instrument. The single, highly flexible and scalable robotics instrument deck of Microlab® STAR meets these diverse needs. The Microlab® STAR provides viable sample tracing. Each process is controlled by a laboratory information management system (LIMS) developed by GATC Biotech. This LIMS processes all log files from the



different robots involved in the sequencing process, and creates work lists for the robots involved at each step of the process.

With the automation of both, high throughput sequencing and custom sequencing, GATC Biotech eliminated labor-intensive steps. The chances for errors are reduced by bar-coding tubes and microtiterplates and tracking them throughout the process.

Component

Description

Microlab® STAR from HAMILTON 8 channels 300 |xl / autoload P/N 173005

• Pipetting workstation for high throughput and high precision liquid handling. • 8 independent SOOuJ pipetting channels with unique air displacement pipetting principle. • Unique CO-RE technology (Compression-induced 0-Ring Expansion) couples tips or needles on the pipetting head. • Including autoload option for automatically loading/ unloading and barcode identification of used labware.

Microlab® STAR User Software from HAMILTON P/N 911002

 Ultimate control software to manage any specific pipetting and plate handling steps of Microlab® STAR. User-friendly, WIN® NT-based software (Drag and Drop).

Instrument Deck Setup The various procedures require specific setups of the Microlab® STAR instrument deck to cater for different types of microtiterplates.



The 8 independent pipetting channels of the Microlab® STAR allow liquid handling of a wide range of volumes. Volumes from 1u,I to IOOOjil are pipetted accurately. Small amounts of DNA or primer

pipetted from customer tubes and transferred to microtiterplates for further use. Larger volumes are stored in bigger wells on the instrument deck and can easily be transferred as and when required.

Loading and barcode identification of tubes are continuous. The barcode reader of the <u>Microlab® STAR</u> scans horizontally (microtiterplates) as well as vertically (tubes).

Each of the 8 independent pipetting channels is separately controlled, allowing different volumes to be pipetted simultaneously and accurately.



The outstanding features of the independent pipetting channels are, the unique air displacement pipetting principle, and the pipetting channel specific liquid level detection.

Traceability The tube and microtiterplate barcodes are read automatically prior to processing. Microlab® STAR provides log files with complete information about the samples and procedures. This allows management of microtiterplates, reaction tubes and data handling in post processing.

Application software The WIN® NT-based software used to create procedures on the Microlab® STAR is flexible and provides an easy to use graphic interface. Complex processes can be programmed quickly and easily.

An important feature of the software is its ability to process data provided by external sources. This data can be imported and processed while a procedure is running. The log files containing the information about the samples and work lists are also created during processing. They can be exported to the GATC LIMS, for example. This interactive and dynamic system processes work list information and sample information read from the barcode, and so allows seamless integration of the Microlab® STAR into the whole process.

A Typical Procedure

DNA normalization

In order to carry out high throughput sequencing, it is important to have the same DNA concentration in all wells of a microtiterplate. The preparation and purification of DNA often leads to different DNA concentrations (up to a factor of 4). Diluting the DNA sample with varying amounts of water normalizes the concentration, and so simplifies the subsequent steps in the sequencing process.

DNA concentration is determined photometrically at 260 nm using a photometer specially designed for microtiterplates. This

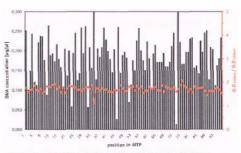
Conclusion The Microlab® STAR developed and produced by Hamilton is a modular and flexible system. It can easily be adapted to various processes and systems, and it can be integrated into a variety of molecular biological applications. At GATC Biotech, the Microlab® STAR simplified the automation of two different and demanding sequencing processes.

information is sent to the LIMS, which creates a work list for the Microlab® STAR.

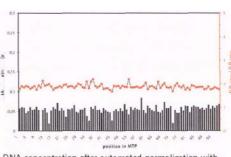
The instrument deck of

the Microlab® STAR is loaded with up to 8 microtiterplates containing samples that need normalizing. The same number of empty microtiterplates is also loaded onto the instrument deck. After checking and verifying the barcodes, 300 u,l disposable tips pipette the j correct amount of

DNA I into



DNA concentration before automated normalization



DNA concentration after automated normalization with Microlab® STAR.

microtiter- i plates, and then a pre- ° calculated amount of water is added to bring the DNA to the desired concentration.

empty

User statement The flexibility and accuracy of the Microlab@STAR allows diverse molecular biological processes to be automated. Having automated several different sequencing processes with the Microlab@STAR, we will continue automating processes in our laboratory by using this system.

J. Schafer, Team Leader Sequencing, GATC Biotech AG,



Features and benefits

- · Increase of the sequencing capacity.
- · Reduced costs.
- · Reduced manual routine work.
- Efficient processing of large numbers of samples, requiring minimal operator intervention.
- · Flexible and easily programmable software.

