

Macro and Micro-Array

Calibration & Software

Microarray Scanner Calibration Slides

FluoProbes provides three sets of microarray calibration slides - CyTM3 Dilution Series Slides, CyTM5 Dilution Series Slides, and Arrayed Slides. Specifically designed for checking and calibrating array scanner performance, these products let you monitor the daily performance of your scanner. They're also ideal for matching results from multiple scanners and for normalizing your array results.

- ◆ Calibrate array scanner performance
- ◆ Assess the stability of your array scanner's sensitivity
- ◆ Compare laser power and sensitivities of multiple scanners
- ◆ Normalize microarray results

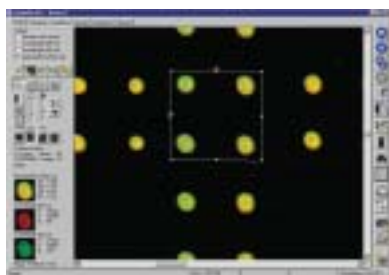
CyTM3 & CyTM5 Dilution Series Slides

With CyTM3 & CyTM5 Dilution Series Slides, you can define the dynamic range of Cy dye fluorescence for your particular scanner. You can also determine the sensitivity detection limit of your scanner, and assess the stability of your scanner's sensitivity over time.

Dilution Series Slides are printed with either CyTM3 or CyTM5 dye in two-fold serial dilutions, from 6 200 fluor./ μm^2 to approximately 0.01 dye molecules/ μm^2 . The 20 serial dilutions cover five orders of concentration magnitude, and each dilution series is printed 10 times in a row. At the end of each dilution series, two rows of blank controls (solvent only) are included.

Arrayed Slides for Calibration

These ultra-flat glass slides are essential for calibrating your array scanner i.e., determining alignment and cross channel detection. Each slide is arrayed with spots containing a mixture of CyTM3 and CyTM5 dyes (256 blocks/16 rows and 4 columns); the ratio variation between red and green channel intensities does not exceed 2:1.



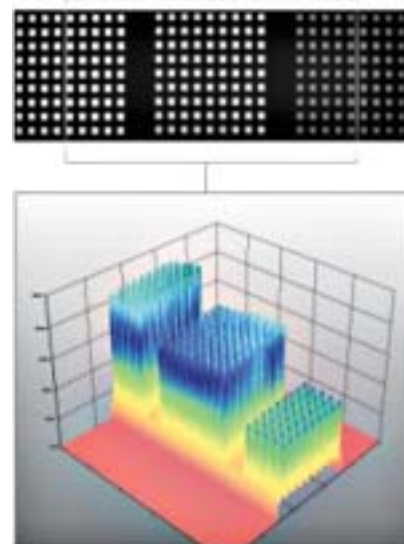
Description	Cat.#	Qty
Cy TM 3 Dilution Series Slides	AW3870	3 slides
Cy TM 5 Dilution Series Slides	AW3880	3 slides
Arrayed Slides	AW3900	3 slides

FluorIS fluorescence image standard

FluorIS is our array imaging standardization tool. Whether you want to compare data over a long period of time or exchange data between different labs, FluorIS makes data matchable and reliable.

An array of almost non bleaching fluorescent spots defined in shape and intensity is provided for calibration and normalization purposes. It allows the direct comparison of array images generated by different fluorescence reader systems or a single detection system at different time intervals. Thus detector variances are omitted.

- ◆ Due to the characteristic intensity patterns of the FluorIS the sensitivity of the particular system is determined.
- ◆ The lateral resolution of the system can be analyzed due to the fluorescent resolution test pattern on the surface.
- ◆ Calibration of various detection platforms is feasible.
- ◆ Array experiments performed on different sites are now comparable.
- ◆ Automated data normalization is performed by application of special IconoClust scripts.



Upper image : fluorescence image of FluorIS 32 μm features.

Lower image : false color image of fluorescence intensity of FluorIS 32 μm features, three intensity values (analyzed by IconoClust, 3D spot view).

Applied in array image acquisition the principle bears the potential to establish a physical fluorescence standard on the arraying standard. This will enable single dye labeling techniques to overcome existing bottlenecks.

Description	Cat.#	Qty
FluorIS, Fluorescence Standard for MicroArray Fluorescence standard for array images. The FluorIS chip is mounted in a microscope slide sized frame provided with a barcode. It is shipped in a slide box sealed under inert gas in a light protective foil.	AZ8830	1 each
FluorIS Calibration Kit (Standard + images analysis software) Kit including one FluorIS fluorescence standard and the current version of IconoClust-F software (including the personal license key) for fast and automated analysis of FluorIS applications.	AZ8840	1 each

IconoClust®- Powerful array image analysis

IconoClust is a powerful imaging software for the analysis of array images of multiple formats. It is designed to meet the needs of highly demanding imaging software while ensuring a high level of data integrity. IconoClust is based on transparent analysis methods. Open program platform features and scripts guarantee easy adaptation to user specific needs and requirements. The software is suited both for beginners in microarray technology and professionals looking for a new array imaging platform.

Description	Cat.#	Qty
IconoClust-F Imaging Software Personal license key to activate the unlimited use of IconoClust-F array imaging software.	AZ8880	1 license

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The MicroArray life cycle.



Partisan arrayLIMS

The Microarray Laboratory Information Management System

Main Features

- ◆ Management of array experiments and production
- ◆ Multi-user environment
- ◆ Computer system independence
- ◆ Data security
- ◆ Low data redundance
- ◆ Data mining
- ◆ Import and export of array features
- ◆ Protocol and documentation functions
- ◆ Template function
- ◆ Quality management
- ◆ MGED standard compliant

It is designed to manage all pertinent issues in a microarray life cycle, such as array design, array production, biochemical reactions (hybridization), detection (image scanning/acquisition), data analysis and data mining.

The system provides clear management based on objects (organised in object networks), accession rights and user roles.

The Principle

Typical objects of the arrayLIMS are the following : hierarchical projects, experiments, microarrays, microplates, samples, probes, protocols, scanned raw images, imaging results or data mining results. All objects can be divided into classes with specific attributes (e.g. classes of the object substance, gene, oligonucleotide, PCR, fragment, tissue, etc.). Users will receive defined privileges for different actions. PARTISAN arrayLIMS provides an intuitive web interface that enables the user to browse the database like the internet.

PARTISAN arrayLIMS - Ready for HTS ?

PARTISAN is an essential platform for fully automated array-manufacturing and array-analysis processing. PARTISAN supports up-to-date methods and technologies for experiments with high throughput. Combined with our imaging software Iconoclust, PARTISAN can provide service for future advanced procedures, new integrated devices (like the AP microreactor cartridge or the AT Genomics Lab Analysis Platform), new labeling assays, standardization tools (like FluorIS - the Fluorescence Image Standard) and chip technologies.

Description

Partisan arrayLIMS

Cat.#

BA9571

Qty

each

Genorama™ Chip Design Software

Genorama™ Chip Design Software is a complete set of programs required for genotyping chip design. Programs are also available separately.

Program in Genorama™ Chip Design Software

Program	I Program package	II Program package	III Program package
ProbeDesigner™			<input checked="" type="checkbox"/>
PickSNP™		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
BioPrimer™	<input checked="" type="checkbox"/> PCR Primer design	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
GenomeTester™	<input checked="" type="checkbox"/> package – for those who	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
MultiPLX™	<input checked="" type="checkbox"/> do genomic PCR.	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
ChipTester™			<input checked="" type="checkbox"/>

1. PickSNP™ - for SNP selection of large-scale genotyping

The program is particularly optimized for selection of uniformly distributed set of SNPs over large chromosomal regions or over the whole genome. This is often required for haplotype structure determination in certain regions of the chromosome.

Haplotype tag SNPs can be used for SNP selection only in genomic regions where haplotype block structure is known. User-defined number of SNPs can be selected from the human genome from specific chromosomes, particular chromosome regions, and around certain genes. Users can specify additional information such as :

- ◆ Location relative to genes (exonic SNPs or genic SNPs)
- ◆ Maximum distance from the nearest exon (e.g. all SNPs within 3 kb from nearest exon)
- ◆ Minimum distance between two consecutive SNPs
- ◆ Haplotype block structure (select only haplotype tag SNPs)

2. ProbeDesigner™ - for designing APEX primer

The program is dedicated to choose APEX primers that are suitable for SNP genotyping by APEX. APEX primer testing is necessary to avoid false or failed signals due to secondary structure, dimer formation and direct repeats.

3. BioPrimer™ - for PCR primer design

The program automatically selects optimal PCR primers for large datasets of human SNPs. All PCR primers are tested against the human genome sequence to ensure that unique PCR product is amplified (see next paragraph for details).

Template sequence is automatically masked to avoid :

- ◆ Design of PCR primers over known SNPs
- ◆ Design of PCR primers in repeated regions
- ◆ Design of PCR primers that contain short direct repeats.

Our software system can design 100 000 high-quality PCR primers in less than one hour on typical workstation with one Pentium4 processor.

4. GenomeTester™ _ for testing uniqueness of the primers

The program tests quickly user-provided PCR primers against the human genome. This is necessary to find and eliminate primers with excessive number of binding sites (to avoid failed PCR) and to find alternative PCR products (avoid false signals in genotyping experiment). We have written extremely efficient programs GenomeMasker™ and GenomeTester™ for the Genome Test. Our GenomeTester™ is optimized for the human genome, however other completely sequenced genomes can also be used.

5. MultiPLX™ _ grouping of PCR primers according to their compatibility

The program calculates the optimal combinations of primer pairs for PCR primer multiplexing. Primer compatibility is tested against each other as well as against each other's products. Additionally, the Genome Test is performed with all possible PCR primer pairs in each multiplex group. This avoids appearance of unwanted PCR products from multiplexed groups.

6. ChipTester™ _ for testing SNP technological mutual suitability for APEX.

The software controls the technological mutual suitability of different SNPs that are needed to be analyzed on one chip, substitute SNPs which APEX primers can interact with PCR product of another SNP. At the moment it is provided as a service.

The software package can be purchased in different forms

1. One computer from your lab will get access for 6 months to our server to perform calculations on the ASPER server through internet.
2. Software will be installed locally, in your lab. A server with our software can be accessed from any computer in local intranet with web browser.