**Patented Technology**
Phenotype MicroArrays™ and their use are covered by U.S. Patent Nos. 5,627,045, 6,046,021, 6,387,651, 6,436,631, 6,472,201, 6,686,173, 6,696,239, and 6,727,076, as well as pending applications, all owned by Biolog, Inc. and the OmniLog® instrument is covered by U.S. Patent No. 6,271,022, owned by Biolog, Inc.

The purchase price paid for the Phenotype MicroArray™ technology by end users grants them a non-transferable, non-exclusive license to use Phenotype MicroArrays™ for internal research only. Internal research only means that the Phenotype MicroArray™ technology is excluded from resale or use for the making or selling, either directly or indirectly of any commercial product or service. A separate commercial license is available from Biolog, Inc. for commercial uses or applications.

**Proprietary Trademarks**
OmniLog is a registered trademark and Phenotype MicroArray is a trademark of Biolog, Inc. Microsoft and Windows are registered trademarks of Microsoft Corporation.

---

**Ordering Information:**

For customer service, contact us at:

**Phone:** 800-284-4949

**Address:**
21124 Cabot Boulevard
Hayward, CA 94545
U.S.A.

**Email:** csorders@biolog.com
Table of Contents

Product Description ________________________________________________ 1

OmniLog® Systems _______________________________________________ 4

Phenotype MicroArray™ (PM) Panels and Accessories – Mammalian Cells 4

Dye Mixes and Inoculating Fluids for PM Mammalian Panels____________ 4

Phenotype MicroArray™ Panels and Accessories – Microbial Cells_______ 5

Biolog Prepared Plated Media _________________________________________ 5

Other Prepared Plated Media _________________________________________ 5

Dye Mixes and Inoculating Fluids for PM Microbial Panels _____________ 6

Phenotype MicroArray™ Services____________________________________ 6

Disposable Hardware ______________________________________________ 6

Ordering Information_______________________________________________ 7

Terms & Conditions________________________________________________ 7

Service Contract Options __________________________________________ 7
Product Description

The Phenotype MicroArray™ (PM) system and software were developed by the same experts at Biolog that pioneered modern phenotypic identification of bacteria and fungi. Using much of what was learned from our identification work we expanded the technology to provide extremely detailed phenotypic testing of cells for genomics, drug development, toxicology, cell fingerprinting, and other research applications.

Phenotype MicroArray™ panels of up to 1,920 phenotypic tests have been developed for:

- Gram negative bacteria
- Gram positive bacteria
- Yeast and filamentous fungi
- Mammalian cells

The OmniLog® PM System
Generates a kinetic response curve for all assays simultaneously and monitors, either directly or indirectly, most known aspects of cell function.

The range of phenotypes analyzed includes:

1) Nutrient uptake and transport functions
2) Catabolism of carbon, nitrogen, phosphorus, and sulfur
3) Biosynthesis of small molecules
4) Biosynthesis of polymeric macromolecules
5) Formation of cellular structures
6) Cellular respiratory functions
7) Stress and repair functions
8) Other cellular properties

Phenotype MicroArrays™ allow researchers, for the first time, to analyze hundreds to thousands of cellular phenotypes simultaneously in an efficient and standardized format. The OmniLog PM System analyzes, in vitro, a cell’s response to a drug or genetic change by comprehensively scanning cellular phenotypes and detecting changes.

This new capability of measuring the complete system-wide response of a living cell to a drug or genetic alteration can be an important complement to data obtained from molecular methods such as DNA microarrays and proteomic analyses.

The PM technology is covered by many patents. Commercial and non-commercial licenses are granted when these products are purchased (see page ii for details).
OmniLog® PM

Suite of Programs

OmniLog PM software contains a suite of algorithms that work in conjunction with the OmniLog reader and Biolog’s PM panels. These programs allow you to display kinetic PM panel data recorded by the OmniLog reader, manage and analyze the data, export it in a variety of raw and processed forms, and generate reports.

Software Functions

- Drives the OmniLog reader
- Guides loading and reading PM panels
- Creates a kinetic data file for each PM panel for use in the other program modules

File Management/Kinetic Analysis

- Assembles PM panel data files into data lists
- Displays kinetic plots of the data

Parametric Analysis

- Extracts data lists from the File Management/Kinetic Analysis module
- Calculates parameters from the PM kinetic data.
- Allows comparison of two data lists
- Allows exporting of data to bioinformatics programs for further analysis.
OmniLog® PM

The PM suite of software will process the data gathered for each strain or cell line analyzed in the OmniLog System. The software can automatically compare two or more cell lines over hundreds to thousands of phenotypes.

Comparison of cell lines and their phenotypic responses provides very useful information. Where there are similar phenotypic responses in both cell lines the kinetic curve is yellow, unique phenotypic responses expressed by only one of the cell lines is identified by a unique color assigned to that cell line. This allows the user to rapidly review the graphic output and visually identify changes between two cell lines.

Where significant differences are found between cell lines, the software automatically highlights the difference and a report is generated listing and characterizing the phenotypic differences found.

Sample Report: Differences in Phenotypes in the PM panels discovered between two cell lines

PM Report:
EcoL_Sd_30 versus EcoL_Sd_35

Phenotypes Gained:
PM02 D03 63 Proflavine antibacterial, flavone
PM14 C05 26 1-Ascorbylate DNA intercalator
PM16B C07 120 Protamine sulfate membrane, ATPase
PM17 C13 51 Lys-Pro N-source
PM12B H05,H06,H07 554 Kanamycin protein synthesis, aminoglycoside
PM12B I02,I03,I04 544 Paromomycin protein synthesis, aminoglycoside
PM12B I03 296 Neomycin protein synthesis, aminoglycoside
PM12B H04 144 Osaxydamycin protein synthesis, macrolide
PM16A H07/H08 441 Chloramphenicol wall
PM16A D03 186 Cefuroxime wall, cephalosporin second generation
PM16A A04 224 Ampicillin wall, lactam
PM16A H10 291 Ofloxacin wall, lactam
PM12B D07,D08 -214 Iodoacetate oxidation, sulfhydryl
PM13A G06 -62 Cefamandole wall, cephalosporin
PM14A D01 -62 Iodoacetate oxidation, sulfhydryl
PM17A G06 -62 Chloramphenicol wall, lactam

Phenotypes Lost:
PM11B E10,E11,E12 -547 Nalidixic acid DNA gyrase (GN), DNA topoisomerase (GP)
PM20 D05,D06,D07,D08 -498 Ciprofloxacin DNA gyrase (GN), DNA topoisomerase (GP)
PM11B E05,E06,E07 -486 Enoxacin DNA gyrase (GN), DNA topoisomerase (GP)
PM10A B11,B12 -444 Oxolinic acid DNA gyrase (GN), DNA topoisomerase (GP)
PM11B B11,B12 -438 Lomefloxacin DNA gyrase (GN), DNA topoisomerase (GP)
PM11B H10,H11 -291 Ofloxacin DNA gyrase (GN), DNA topoisomerase (GP)
PM12B D12 -214 Cefuroxime wall, cephalosporin
PM14A D01 -214 Iodoacetate oxidation, sulfhydryl
PM17A G06 -214 Chloramphenicol wall, lactam

Appendix:
Carbon and Nutrient Max Read Hour: 024
Nitrogen, Phosphorus, Sulfur Max Read Hour: 048
Sensitivity Max Read Hour: 024

The software also allows for export of the phenotypic data so that additional analysis can be performed – for example, clustering the phenotypic data from a number of strains or drugs.