

ABOUT THE GENOMICS CORE LABORATORIES

The Genomics Core Laboratories represent a cooperative effort of UCSF and Gladstone scientists. The cores provide support to investigators using DNA microarray technology. Participating cores include the UCSF Sandler Asthma Basic REsearch Center (SABRE) Functional Genomics Core Facility and the J. David Gladstone Institutes Genomics Core Laboratory. While each core puts a high priority on projects most closely related to the goals of its main sponsor, the cores also support other projects. The cores utilize recharge mechanisms and in some cases costs associated with high-priority projects are subsidized. The cores are able to provide training and consultation in laboratory procedures and data analysis and to provide access to equipment and supplies for approved projects.

MICROARRAY TECHNOLOGIES

The Core Laboratories support both spotted array and Affymetrix GeneChip technologies.

Spotted array technology. The cores produce spotted long oligonucleotide arrays for both human and mouse genomes. These arrays are available for sale to approved projects. We do not produce spotted *cDNA* arrays, but we may be able to assist investigators wishing to use spotted *cDNA* arrays produced elsewhere. Spotted array procedures (including sample labeling, hybridization, and scanning) can be performed by project personnel. Training, consultation, and access to specialized equipment are available through the cores. In some cases, core personnel may be available to perform some or all of these steps if project investigators prefer this approach. This may be a more practical approach for inexperienced investigators pursuing pilot projects or other studies involving small numbers of arrays. Spotted array experiments are generally much less costly than Affymetrix GeneChip experiments.

Affymetrix GeneChips. GeneChips for many species are produced and sold by Affymetrix. The cores have equipment for hybridization, staining, and scanning of GeneChips. The equipment is operated by core staff, who can perform these procedures for approved users who have purchased GeneChips. In most cases, users prepare samples for hybridization (i.e., synthesize cRNA from RNA). Training and consultation are available through the cores.

APPLICATION PROCESS

Investigators wishing to work with any of the Genomics Core Laboratories should submit an application. To simplify this process, we have developed a single application form. If you have questions about how to complete this form, please contact Andrea Barczak (andrea.barczak@ucsf.edu, 415-514-4373), Chris Barker (cbarker@gladstone.ucsf.edu, 415-734-2521), or David Erle (david.erle@ucsf.edu, 415-514-4370). Please complete as much of the form as you can and submit it electronically to Andrea Barczak (abarczak@medSFGH.ucsf.edu). Representatives of each of the cores review all submitted applications to identify the most appropriate way to support each project. Following this initial review, we will contact the project PI to arrange a planning meeting with core personnel who will be involved in the work. The initial application can be revised as necessary following that meeting.

DETAILED INSTRUCTIONS

The first two pages should be completed by entering requested information into text fields and check boxes. Pressing the TAB key selects the next field or check box. Check boxes can be checked or unchecked by clicking on the box, or by selecting the box and pressing the x key. The third page should be completed by typing (or pasting) text below the headings.

PAGE 1

PROJECT TITLE, PI INFORMATION

Self-explanatory.

CO-INVESTIGATOR(S) AND OTHER PERSONNEL

Please list all project investigators who will be directly involved so that we can invite them to the planning meeting and will know how to contact them during the course of the project.

SUPPORTED BY



THE UCSF SANDLER CENTER FOR
BASIC RESEARCH IN ASTHMA



THE J. DAVID GLADSTONE INSTITUTES
AT THE UNIVERSITY OF CALIFORNIA SAN FRANCISCO



PROJECT SUPPORT

Required in order to document eligibility for support by several mechanisms. Recommended for all applications, as this information will help the cores work with you to budget appropriately for your next grant application.

REQUESTS FOR SUPPORT FROM CORE LABORATORY SPONSORS

This information will be used to determine whether projects qualify for support from one or more of our sponsors. This is important, since sponsored projects receive high priority and may be eligible for subsidized services.

➤ [UCSF Sandler Asthma Basic REsearch Center \(SABRE\)](#)

The Sandler Center provides support for microarray studies related to the basic biology of asthma. Priority will be given to UCSF investigators studying asthma-related biology and to investigators supported by the Sandler Program in Asthma Research (SPAR).

➤ [The J. David Gladstone Institutes](#)

Gladstone investigators are eligible for support from the Gladstone Genomics Core Laboratory.

➤ [UCSF Cancer Center](#)

The Cancer Center has provided support to the Gladstone Genomics Core for support of Affymetrix based studies.

PAGE 2

SAMPLES

Please provide basic information about the source of your RNA (e.g., “cell lines,” “sorted human leukocytes,” or “mouse lungs.”) Tell us how many samples you expect to analyze and approximately how much RNA you expect to obtain from each sample. We generally use total RNA (and not polyA RNA) for array analyses. Even rough estimates will help us to anticipate supply, labor, and equipment needs and to determine which methods may be most useful.

MICROARRAY TYPES

Please see “Microarray Technologies” section, above.

CORE LAB SERVICES REQUESTED

We work with project investigators to determine the appropriate division of labor between project and core lab personnel for each project. In general, project investigators perform RNA extractions, however the Gladstone Core can provide RNA isolation services for nonhuman solid tissue or cell pellet samples, but not whole blood. If RNA isolation services are needed we can sometimes refer you to another facility at UCSF. The cores provide support for a number of commercial array platforms including Affymetrix, Agilent, Exiqon and Nimblegen arrays. The cores can provide training and consultation to allow investigators to perform most or all array experimental procedures themselves. Alternatively, depending upon resource availability, some or all of these procedures can be performed by core personnel. Please check all of the answers that apply to your project. Appropriate analysis of the array data generated by the cores is essential, please be sure to indicate if you expect to need help in this area.

STATUS AND TIMETABLE

The cores depend upon project investigators to provide information that helps us schedule our activities. We need to know when you expect to have RNA samples available for analysis. In some cases, all RNAs should be extracted and analyzed before beginning array experiments. In other cases, array experiments can begin when only some RNAs are available. If you do not yet have RNA samples available and can make a reasonable estimate of when samples will be available, please do so. In most cases, project investigators will be involved directly in carrying out array experiments, and the cores need to know when these investigators will be ready to begin. Please understand that this usually demands a substantial time commitment.

PAGE 3

Please provide us with some basic information about the objectives and design of your project. In general, this section should be *no longer than 1-1.5 pages*.

HYPOTHESIS(ES)/SPECIFIC AIMS

Briefly summarize your hypothesis(es) and/or explain what you hope to learn from these experiments. A hypothesis is not required, since some microarray studies are primarily exploratory rather than hypothesis-driven.

BACKGROUND AND SIGNIFICANCE

For studies requesting support from the Sandler Center, please include an explanation of the relevance to asthma.

PRELIMINARY STUDIES

This section is optional. If you do not wish to present preliminary studies, simply delete the section including its title in its entirety.

EXPERIMENTAL DESIGN

Briefly describe the nature of the samples to be studied. Indicate how many different groups and how many replicates you expect to include. Do not give details of your experimental system. Note that in most cases you should plan to run a minimum of 3 independent biological (not technical) replicates for each experimental condition.

ANALYSIS

Specifically list all comparisons that you plan to perform using the new data set. If there is existing preliminary data to be compared please specify and provide as much detail as possible. Please be aware that when comparing different data sets it is critical to prepare the new samples using methods that most closely match those used to generate the older data.

APPLICATION SUBMISSION

Please use "Save As..." to save the file and include the PI's name in the filename (e.g., jane_doe_application.doc). Submit the application (in Microsoft Word format) by e-mail to Chris Barker (cbarker@gladstone.ucsf.edu) and Andrea Barczak (abarczak@medSFGH.ucsf.edu).

PROJECTS INVOLVING SAMPLES FROM HUMAN SUBJECTS

Project investigators are responsible for obtaining approval or certification of exempt status from the appropriate Institutional Review Board (e.g., the UCSF CHR) whenever human subjects are involved. All samples submitted to the cores must be coded in order to ensure that the cores are not given any information that might be used to identify human subjects.

ACKNOWLEDGING CORE LAB SUPPORT

Our success and continued funding is dependent upon you. Please help us by acknowledging support from core lab(s), and by providing us with a copy of all publications resulting from this work. Suggested language for acknowledgements in publications:

Sandler Asthma	<i>Microarray studies were supported by the UCSF Sandler Center for Basic Research in Asthma Functional Genomics Core Facility and by the Sandler Family Foundation.</i>
Gladstone	<i>Microarray studies were supported by the J. David Gladstone Institutes Core Genomics Laboratory.</i>