

INSTITUTE FOR  
Personalized  
Medicine

FOX CHASE  
CANCER CENTER

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Decades of experience and research in cancer care tells us that no two cancers are alike: some

respond well to a particular therapy, while others, seemingly identical, do not respond at all. One reason for this discrepancy is that tumors, especially solid tumors, accumulate particular sets of mutations in many genes, and that these gene sets differ among individual patients. However, we now have the ability to determine genetic information in such tumors, and to act on this information when considering therapies. In this way, we hope to make the “one-size-fits-all” approach to cancer therapy a thing of the past.

In an effort to improve treatment of patients with cancer, Fox Chase Cancer Center has initiated a new program in which we aim to determine the genetic lesions that characterize tumors in living patients.

**The immediate objective** of the Institute is to sequence the entire cancer exome to find mutations in genes that impact key, targetable, signaling pathways in patients with metastatic disease.

#### HIGH-THROUGHPUT SEQUENCING

Fox Chase has recently established high-throughput DNA sequencing for translational cancer genomics at our Institute for Personalized Medicine. We prepare genomic and exome-enriched libraries from frozen and laser-capture-microdissection generated cancer samples. Illumina sequencing technology is used to sequence these libraries, enabling the comprehensive characterization of mutations in individual cancer samples.

#### BIOSAMPLE REPOSITORY

Fox Chase Cancer Center established the Biosample Repository to coordinate the ethical collection, storage, annotation, and distribution of tissue and peripheral blood samples to support translational research. This center-wide activity is directed by Andrew K. Godwin, Ph.D. The Biosample Repository is a CAP accredited and CLIA-approved facility and functions to identify participants, administers informed consent, collects tissue, blood, and/or urine samples from selected populations, and obtains information on personal and family histories of cancer, clinical intervention, and lifestyle factors for use in research.

Working in collaboration with pathologists, medical oncologists, surgeons and other hospital personnel, specially trained staff obtains patient consent, collects samples and assembles comprehensive clinical information about each donor and the corresponding samples. As part of this banking the Biosample Repository provides i) outstanding diagnostic pathology support; ii) a comprehensive informed consent process for the use of tissue, blood, urine, and/or bone marrow from patients and participants for research; iii) a specialized biospecimen bank devoted to the collection and distribution of specimens to support research; and iv) extensive supporting data from the clinical record and self-reported health history of each participant.

All specimens are linked to comprehensive clinical databases. The Biosample Repository has banked over 10,000 fresh-frozen tissue samples (tumor and normal tissue) and over 16,000 blood samples (e.g., whole blood, plasma, serum, leukocytes, erythrocytes, lymphoblastoid cell lines, and DNA isolated from leukocytes) and obtained cancer history data to be utilized in genetic-, epigenetic-, and proteomic-related research. The Biosample Repository houses over 700,000 sample vials including plasma, serum, viable leukocytes and DNA and has access to >100,000 surgical pathology cases.

<http://www.fccc.edu/research>

The Fox Chase Biosample Repository is a core asset that distinguishes our personalized medicine efforts from similar initiatives being contemplated elsewhere.

### CLINICAL STRENGTHS

Fox Chase has a well-established and highly productive clinical trials program that enrolls >200 patients/year onto a diverse menu of phase I clinical trials. The program has a dedicated Protocol Support Laboratory for the acquisition, processing, storing, shipping, and analysis of biosamples procured before and after treatment on selected drugs.

Genomic sequencing will allow us to describe, characterize and visualize our patient populations according to the actual genetic abnormalities in their tumors. Patients will be entered onto appropriate clinical trials not only of targeted therapies but also of cytotoxic therapies provided they have the correct genetic signature that optimizes the benefit:risk ratio for receiving the drug(s).

### QUANTITATIVE STRENGTHS

The Biostatistics and Bioinformatics Facility and the Population Studies Facility are institutional resources that support data management and analysis in multiple Fox Chase efforts, including high-throughput sequencing, the Biosample Repository and the clinical trials program. The facilities have substantial expertise in high-throughput data analyses, functional genomics, clinical trial design and analysis, data mining via machine learning, mathematical modeling, and advanced sequence analysis. This expertise allows for the development of models that provide improved estimates of an individual patient's outcome under a number of different potential treatments, thus enabling more informed treatment choice based on individualized risk.

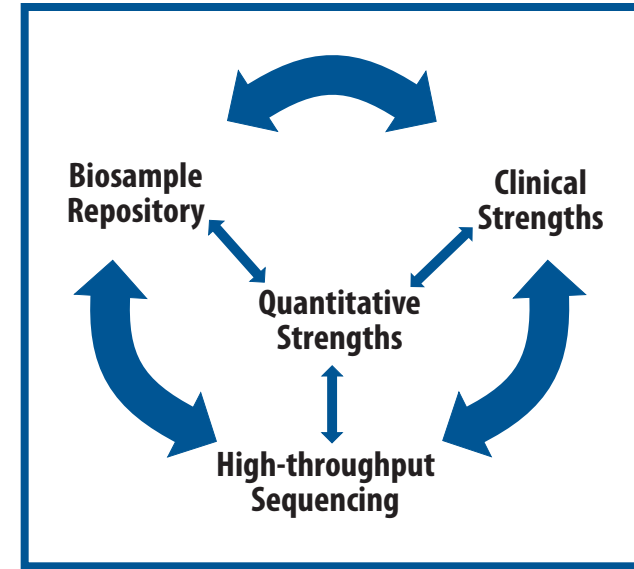
### INDUSTRY PARTNERSHIPS

Fox Chase has a rich history of forming strategic partnerships with industry to more quickly bring projects forward by integrating its strengths with those of its partners.

We welcome industry partnerships as we embark on this endeavor to use genetics and molecular biology to allow for better disease diagnoses, prediction of disease course, and selection of the most appropriate treatment options. The Institute for Personalized Medicine will complement the needs of industry and the healthcare community while furthering our mission to accelerate the integration of emerging technologies into team-based science to reduce the burden of cancer in all individuals.

### VISION

Our vision is one in which at the time of diagnosis and again at disease progression, a patient's cancer will be sequenced either for selected genes of interest or the entire genome. The resultant information will be housed in a searchable database, thereby allowing patients to be matched to particular drugs based upon mechanism of action, regardless of the phase of clinical trial. Updated eligibility criteria will no longer state the requirement for a given disease but instead, will articulate a far more sophisticated paradigm focusing on pathway activation, gene mutation, or combinations thereof.



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