



Proteomic Technologies Reagents Resource Workshop

December 12-13, 2005

# Clinical Proteomic Technologies Initiative for Cancer

*<http://proteomics.cancer.gov>*

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# Clinical Proteomic Technologies Initiative



## **Objective:**

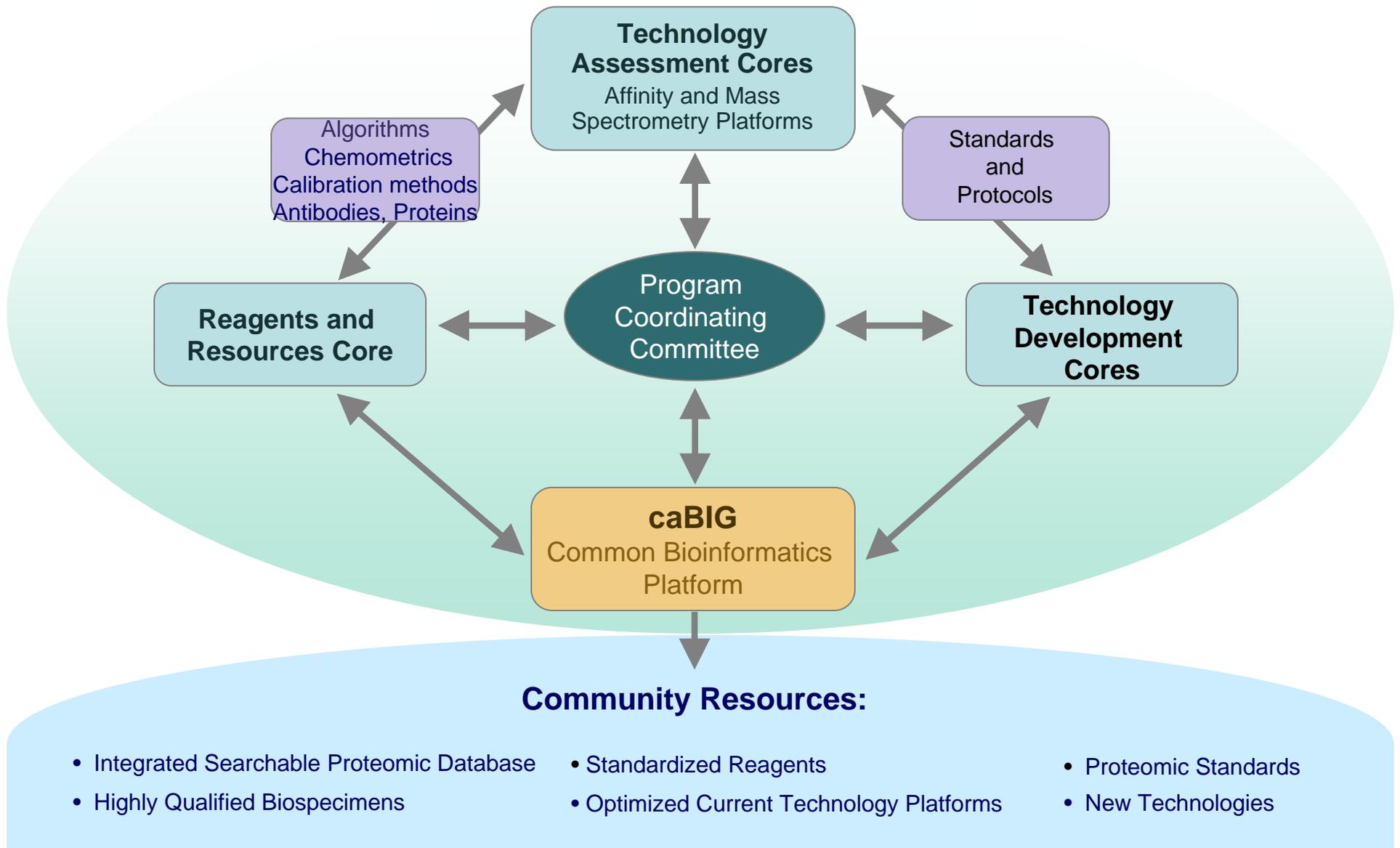
- Integrated approach to develop and enhance proteomic technology measurement capabilities

## **Expected Results:**

- Creation of public resources
  - Reference sets, reagents, protocols, algorithms, and databases
- Accelerated protein-related discovery research and applications
- Enhanced knowledge base to support discovery and translational research
  - Validated identification of 1500 features of interest in cancer biology
  - Well characterized and documented candidate-based approaches for peptide/protein identification



# Clinical Proteomic Technologies Initiative Strategy



# Clinical Proteomics: Technology Development, Advancement, and Standardization



- Clinical Proteomic Technology Assessment Consortia (CPTACs)
- Advanced Proteomic Platforms, Analytical Methods, and Computational Sciences
  - Sample Preparation and Labeling Technologies
  - Sample Fractionation Technologies
  - Mass Spectrometry
  - Protein Capture and Microarray Technologies
  - Data Analysis
  - Microsimulation
  - Validation

# Clinical Proteomic Reagents Resource



## **Role:**

To serve the investigator community as a central public resource for well characterized proteomic reagents and resources.

## **Key Features:**

- Develop standard reagents (antibodies, proteins, and peptides)
- Perform characterization and QA/QC
- Provide an interactive resource “catalog” through caBIG
- Expedite acquisition and distribution of reagents and data on reagent performance

# The Cancer Genome Anatomy Project



## The Cancer Genome Anatomy Project

CGAP HOW TO | **Genes** | Chromosomes | Tissues | SAGE Genie | RNAi | Pathways | Tools

### CGAP Info

- [Educational Resources](#)
- [Slide Tour](#)
- [Team Members](#)
- [References](#)

### CGAP Data

- [Download](#)

### Quick Links:

- [ICG](#)
- [NCI Home](#)
- [NCICB Home](#)
- [NCBI Home](#)
- [OCG](#)



## The **C**ANCER **G**ENOME **A**NATOMY **P**ROJECT

The goal of the NCI's Cancer Genome Anatomy Project is to determine the gene expression profiles of normal, precancer, and cancer cells, leading eventually to improved detection, diagnosis, and treatment for the patient. By collaborating with scientists worldwide, CGAP seeks to increase its scientific expertise and expand its databases for the benefit of all cancer researchers.

### The CGAP Web Site

Interconnected modules provide access to all CGAP data, bioinformatic analysis tools, and biological resources allowing the user to find "in silico" answers to biological questions in a fraction of the time it once took in the laboratory.

 <b>Genes</b> Gene information, clone resources, SNP500Cancer, GAI, and transcriptome analysis <b>NEW!</b>	 <b>Chromosomes</b> FISH-mapped BAC clones, SNP500Cancer, and the Mitelman database of chromosome aberrations
 <b>Tissues</b> cDNA library information, methods, and EST-based gene expression analysis	 <b>SAGE Genie</b> Analysis of gene expression using <b>long NEW!</b> and <b>short</b> SAGE tag data for both <b>human</b> and <b>mouse NEW!</b>
 <b>Pathways</b> Diagrams of biological pathways and protein complexes, with links to genetic resources for each known protein	 <b>Tools</b> Direct access to all analytic and data mining tools developed for the project
 <b>RNAi <b>NEW!</b></b> RNA-interference constructs, targeted specifically against cancer relevant genes.	

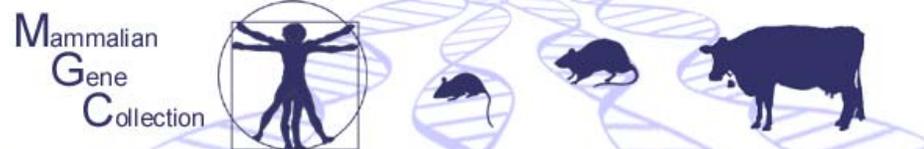
**cgap.nci.nih.gov**

### New Initiatives

- The NCI supports the [Initiative for Chemical Genetics](#) (ICG), which is developing a systematic approach for harnessing synthetic chemistry to discover molecular mechanisms in basic cell biology. This approach aims to emulate the success of classical genetics as a discovery platform using chemicals that alter the function of specific proteins in place of mutations. These results will be incorporated into the Gene Info pages of the relevant genes.
- The OCG/NCI and NHGRI recently convened a workshop to assess the value of a project to catalogue all of the DNA sequence changes that occur in tumorigenesis. A summary of the workshop and its recommendations are available at [Exploring Cancer through Genomic Sequence Comparisons](#). Follow-up information will be posted on the CGAP web site as it becomes available.



# Mammalian Gene Collection



[MGC Home](#)

## Clone Info

- ◆ [Where to Buy](#)
- ◆ [Vectors & Method Overviews](#)

## Sequencing Info

- ◆ [Candidate Clones for Genes](#)
- ◆ [MGC ESTs](#)

## MGC Info

- ◆ [Project Summary](#)
- ◆ [Project Teams](#)
- ◆ [NIH Institutes](#)
- ◆ [References](#)

## Other Species Collections

- ◆ [Danio \(ZGC\)](#)
- ◆ [Xenopus \(XGC\)](#)

## MAMMALIAN GENE COLLECTION

05-Dec-05	Human	Mouse	Rat	Cow
Total MGC full ORF clones	21,466	16,721	5,168	2,124
Non-redundant genes	13,385	12,216	4,876	1,554
Candidate clones for full-length sequencing	3,026	906	456	1,879

## About the MGC

The goal of the Mammalian Gene Collection (MGC), a trans-NIH initiative, is to provide full-length open reading frame (FL-ORF) clones for human, mouse, and rat genes. In 2005, the project added the selection and tracking of cow cDNAs generated by Genome Canada. Initially, cDNA libraries provided the source of the clones. Recently, alternative methods based on gene-specific amplification have been developed to target the recovery of human and mouse genes absent from the MGC collection. (See [References](#) 1, 2, 3)

All MGC sequences are deposited in GenBank and the clones can be purchased from [distributors](#) of the [IMAGE](#) consortium. For background information about the MGC, please read the [Project Summary](#).

**Note:** Please check the GenBank record of each MGC full-length clone for detailed sequence annotation. Some MGC sequences have nucleotide differences that are not supported by other experimental data.

## Search for Full-length MGC Clones by Gene Symbol or Keyword

Select  Human or  Mouse or  Rat or  Cow

Enter Gene Symbol	<input type="text"/>	<input type="button" value="Search"/>	<input type="button" value="Help"/>
Enter Gene Keyword	<input type="text"/>	<input type="button" value="Search"/>	<input type="button" value="Help"/>

# SAGE Anatomic Viewer Result for ERBB2

NORMAL		CANCER	
		<a href="#">Brain</a>	
		Retina	No Data
		Thyroid	
		Lung	
		Heart	Not Applicable
		Breast <a href="#">Breast cell subtypes</a>	
		Stomach	
		Pancreas	
		Liver	
		Kidney	
		Colon	
		Peritoneum	

Tags per 200,000

- < 2
- 2 to 3
- 4 to 7
- 8 to 15
- 16 to 31
- 32 to 63
- 64 to 127
- 128 to 255
- 256 to 512
- > 512

	Spinal Cord	No Data
	Ovary	
	Placenta	Not Applicable
	Prostate	
	Bone Marrow	No Data
No Data	Cartilage	
	Muscle	No Data
	Skin	
	Lymph Node	No Data
	White Blood Cells	No Data
	<a href="#">Embryonic Stem Cell</a>	No Data
	Vascular	No Data



## RESEARCH PLATFORMS

### HIGHLIGHTS

12.08.05  
RFA-CA-07-005: Advanced Proteomic Platforms and Computational Sciences issued. Receipt Date: April 11, 2006 [\[more\]](#)

06.28.05  
BSA Approves Proteomics Initiative NCI Cancer Bulletin [\[more\]](#)

Sign Up for Updates from [proteomics.cancer.gov](http://proteomics.cancer.gov)

[\[submit\]](#)

### NCI PROTEOMICS INITIATIVE

#### Clinical Proteomic Technologies Initiative for Cancer

In a major effort to accelerate advances in the prevention, diagnosis and treatment of cancer, the National Cancer Institute (NCI) has launched the Clinical Proteomic Technologies Initiative for Cancer. The 5-year, \$104 million program is aimed at optimizing current proteomic technologies and developing the new technologies, reagents, systems, and working consortia needed to significantly advance the field of cancer proteomics research.

Read the Clinical Proteomic Technologies Initiative for Cancer [Executive Summary](#) and [Mission and Goals](#) for additional information.

### SPOTLIGHT



#### Message From the NCI Director

One of the most potentially fruitful areas of cancer research is the exploration of the human proteome. Over the years, NCI's programs in proteomics have produced compelling data indicating that proteins will likely define the changes that constitute the cancer process. [\[more\]](#)

### FUNDING NOTICES

[Advanced Proteomic Platforms and Computational Sciences](#)  
Notice Number: RFA-CA-07-005

[Clinical Proteomic Technology Assessment Consortia](#)  
Notice Number: NOT-CA-05-029

# NCI Proteomics and Biomarker Discovery

- Clinically relevant, cancer-specific peptides and proteins will assist in the early detection and treatment of cancer patients
- Multidisciplinary approaches and coordinated programs are necessary to identifying and validating biomarkers
  - Mouse Proteomic Technology Consortia
  - Clinical Proteomic Technologies Initiative (CPTI)
  - Cancer Bioinformatics Grid (caBIG)
  - Biospecimen Coordinating Committee (BCC)
  - Interagency Oncology Task Force
- Outcomes of the CPTI
  - Well characterized procedures to identify and validate peptides and proteins within the dynamic ranges of putative cancer proteins in human plasma or serum
  - Publicly available protocols, reagents, resources, and analytical platforms
- CPTI
  - <http://proteomics.cancer.gov>
  - Advanced Proteomic Technologies
    - <http://grants1.nih.gov/grants/guide/rfa-files/RFA-CA-07-005.html>
  - Clinical Proteomic Technology Assessment Consortia (CPTAC)
    - <http://grants.nih.gov/grants/guide/notice-files/NOT-CA-05-029.html>
  - Protein Structure Initiative (PSI) Materials Repository
    - <http://grants1.nih.gov/grants/guide/rfa-files/RFA-GM-06-003.html>



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