

OFFICE of CANCER GENOMICS

MISSION

The National Cancer Institute's (NCI) **Office of Cancer Genomics (OCG)** aims to advance the understanding of cancer at the molecular level with the ultimate goal of improving clinical outcomes. Through its various innovative and collaborative research programs, OCG fosters cancer genomics research (the systematic analysis of changes in the genomes of tumors) and the rapid translation of the resulting molecular insights into the clinic.

GOALS

- Support, guide, manage, and maintain major cancer genomics research programs
- Support research that translates the growing amount of genomics information into therapeutic strategies for individual patients (i.e. precision medicine)
- Provide genomics information, technology, methods, informatics tools and material resources to its program researchers and the larger cancer research community

PROGRAMS

In its programs, OCG applies genome-based technologies in order to expand the knowledge base of and resources to cancer researchers in their pursuit of an increased understanding of cancer biology for improved treatment strategies. OCG programs are highly collaborative endeavors, as they interconnect with a number of other research projects. Data and resource tools generated from OCG programs are made publicly available online.

Visit <http://ocg.cancer.gov> for more information.

Cancer Genome Anatomy Project (CGAP)/Cancer Genome Characterization Initiative (CGCI)

CGAP is a user-friendly online resource for the research community designed to provide access to biological tissue characterization data. CGAP has a wide range of genomic data that includes gene expression profiles of normal, precancerous, and cancerous cells, single nucleotide polymorphism analysis of cancer-related genes, and the Mitelman database of chromosomal aberrations in cancer.

CGCI supports research that comprehensively examines the alterations in cancer genomes to gain insight into the underlying mechanisms of those cancers. CGCI pushes the limits of cutting-edge genomic sequencing methods to provide the cancer research community superior genomic data on selected cancer types such as medulloblastoma, non-Hodgkin lymphoma, and HIV-associated cancers.

The HIV+ Tumor Molecular Characterization Project (HTMCP), one recently launched CGCI research project, will use full genomic and transcriptomic sequencing to uncover distinct features of the same tumor types from HIV+ and HIV- patients. To date, HTMCP is accruing three tumor types: diffuse large B-cell lymphomas, lung, and cervical carcinomas. A limited number of Burkitt lymphoma and anal carcinoma cases are also being accrued to examine the applicability of the genomic sequencing technologies to these two cancers.

To learn more about CGAP and CGCI, visit <http://ocg.cancer.gov/programs/cgap.asp>.

Cancer Target Discovery and Development (CTD²) Network

The goal of the CTD² Network is to develop new scientific approaches to accelerate the translation of genomic discoveries into novel treatments. To accomplish this, the CTD² Network emphasizes interaction of laboratories with complementary and unique technical expertise in areas such as bioinformatics, genome-wide loss-of-function *in vitro* and *ex vivo* screening, and small molecule high-throughput screening.

To learn more about CTD², visit <http://ocg.cancer.gov/programs/ctdd.asp>.

Therapeutically Applicable Research to Generate Effective Treatments (TARGET)

TARGET is a comprehensive molecular characterization initiative that utilizes state-of-the-art genomics tools to identify molecular changes that drive the most prevalent childhood cancers: acute lymphoblastic leukemia, acute myeloid leukemia, neuroblastoma, osteosarcoma, and Wilms Tumor. Emphasis is placed on finding the alterations that can be targeted using novel therapies. TARGET is organized into a collaborative network of disease-specific project teams that leverage the strengths and resources of various NCI programs, including the Children's Oncology Group (COG), Cancer Therapy Evaluation Program (CTEP) and Office of Cancer Genomics, to fulfill its mission. This cooperative approach allows for efficient discovery and translation of scientific insights so that more effective, less toxic treatments can be developed faster, thus, reducing the devastating burden of cancer for children and their families.

To learn more about TARGET, visit <http://target.cancer.gov>.

RESOURCES FOR THE RESEARCH COMMUNITY

OCG has worked to advance cancer research through collaborative efforts and the establishment of various initiatives that have since evolved into successful research programs and valuable resources.

Cancer Genetic Markers of Susceptibility (CGEMS)

CGEMS is a robust research program that uses highly collaborative genome-wide association studies (GWAS) to identify common genetic variants that affect individual risk of developing cancer. CGEMS began as a three-year pilot study in 2005 by OCG and NCI's Division of Cancer Epidemiology (DCEG) and is now entirely managed by DCEG. The raw data from CGEMS projects is available for download upon approval.

To learn more about CGEMS, visit <http://cgems.cancer.gov>.

The ORFeome Collaboration (OC)

The goal of the OC, an informal volunteer multi-institutional collaboration, is to provide the research community a library of human cDNA clones with at least one validated, full open reading frame (ORF) from each of the currently defined human genes. The ORF clones do not include 5' and 3' UTRs and can be easily sub-cloned into virtually any type of expression vector. These clones are available to researchers worldwide through multiple commercial distributors.

To learn more about the OC, visit <http://www.orfeomecollaboration.org>.

Mammalian Gene Collection (MGC)

Completed in 2009, the MGC created a bank of "expression-ready" clones for the great majority of protein-coding human and mouse genes. The clones are available to the research community for a wide range of studies. A trans-NIH initiative, the MGC is a resource for full-length open reading frame (FL-ORF) clones for human, mouse, cow, and rat genes. In total, 73,000 FL-ORFs are available. The MGC infrastructure and protocols were applied to two other publicly accessible gene collection projects: *Xenopus laevis* and *Xenopus tropicalis* (frog) and *Danio rerio* (zebrafish), XGC and ZGC respectively.

To learn more about MGC, visit <http://mgc.nci.nih.gov>.

EDUCATIONAL RESOURCES – Coming Soon!

OCG plans to start populating its website with clear and engaging educational materials by the end of 2012. These materials will touch on a handful of topics, including cancer genomics and genomic sequencing, and will be directed towards a broader audience.

DATA SHARING

All data and publications generated by OCG initiatives are shared with the research community through data portals. Genomic profiles for a variety of tumor types (including clinical, molecular characterization, and processed sequence data) are easily accessible through a user-friendly Data Matrix specific to each OCG initiative. The program -specific data matrices are maintained by the Data Coordinating Center (DCC) at the NCI Center for Bioinformatics and Information Technology (CBIT), which manages and stores all data generated for OCG. Through the DCC, the research community can access up to four levels of data (from raw/trace files through cumulative data) for each chip-based and sequencing platform employed. Raw sequence data is stored at the NCBI Sequence Read Archive (SRA) and accessible through the NCBI database for Genotypes and Phenotypes (dbGaP). Data generated by OCG programs is also compatible with caBIG® analytical tools, which enables researchers to explore the data for their own research efforts.

To access a program-specific data matrix, visit <http://ocg.cancer.gov/data/portals.asp>.

dbGAP website: <http://www.ncbi.nlm.nih.gov/gap>

caBIG website: <https://cabig.nci.nih.gov>

OCG e-News

Everyone is invited to check out the **OCG e-News**, a quarterly online newsletter that strives to keep the community abreast of OCG projects as well as related research and resources.

Sign up to receive the **OCG e-News** at http://ocg.cancer.gov/email_signup.asp.

Contact OCG

Office of Cancer Genomics
National Cancer Institute
Building 31, Room 10A07
31 Center Drive, MSC 2580
Bethesda, Maryland 20892-2580

Phone: (301) 451-8027

Fax: (301) 480-4368

E-mail: ocg@mail.nih.gov

Website: <http://ocg.cancer.gov>

