NATIONAL CANCER INSTITUTE
Center for Cancer Genomics

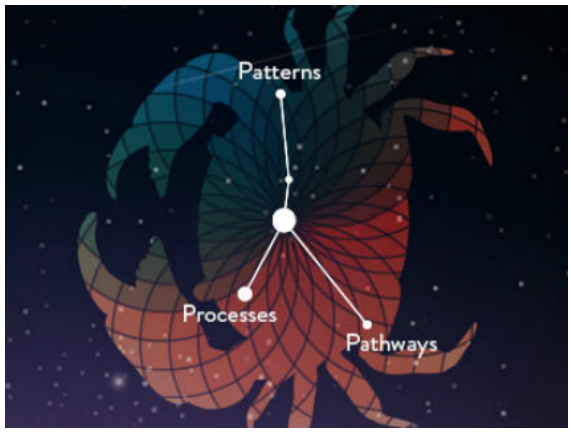
The Cancer Genome Atlas Program (TCGA)

The Cancer Genome Atlas (TCGA), a landmark cancer genomics program, molecularly characterized over 20,000 primary cancer and matched normal samples spanning 33 cancer types. This joint effort between NCI and the National Human Genome Research Institute began in 2006, bringing together researchers from diverse disciplines and multiple institutions.

Over the next dozen years, TCGA generated over 2.5 petabytes of genomic, epigenomic, transcriptomic, and proteomic data. The data, which has already led to improvements in our ability to diagnose, treat, and prevent cancer, will remain publicly available for anyone in the research community to use.

TCGA Outcomes & Impact

TCGA has changed our understanding of cancer, how research is conducted, how the disease is treated in the clinic, and more.



TCGA's Pan-Cancer Atlas

A collection of cross-cancer analyses delving into overarching themes on cancer, including cell-of-origin patterns, oncogenic processes, and signaling pathways. Published in 2018 at the program's close

Access TCGA Data

Access TCGA data through the Genomic Data Commons Data Portal, along with web-based analysis and visualization tools.

TCGA Cancers Selected for Study

An overview of the 33 cancers selected for molecular characterization and the criteria TCGA used to select them.

TCGA Computational Tools

Some of the data processing, visualization, and other computational tools developed by TCGA network researchers and collaborators.

TCGA Molecular Characterization Platforms

Descriptions and supporting materials for each of the sequencing platforms and other technologies used to generate the TCGA data set.

TCGA Timeline and Milestones

The events leading up to TCGA's inception in 2006 and major milestones in the program's history.