

The Cancer Molecular Analysis Portal (CMA)

The Cancer Molecular Analysis (CMA) portal (<https://cma.nci.nih.gov/cma/>), a component of the caBIG® (cancer Biomedical Informatics Grid®) program, provides a single web interface to a collection of analytical tools that help users explore, visualize and integrate genomic data with corresponding clinical information. The CMA helps researchers find novel correlations between data and observations that would be difficult or impossible to find using conventional analytical tools and methods.

The CMA was developed to facilitate integrated analysis of data from translational research studies such as TCGA (The **C**ancer **G**enome **A**tlas), REMBRANDT (**R**epository of **M**olecular **B**RAin **N**eoplasia **D**a**T**a) and TARGET (Therapeutically **A**pplicable **R**esearch to **G**enerate **E**ffective **T**reatments). These ongoing programs have already identified novel candidate biomarkers in several types of cancer.

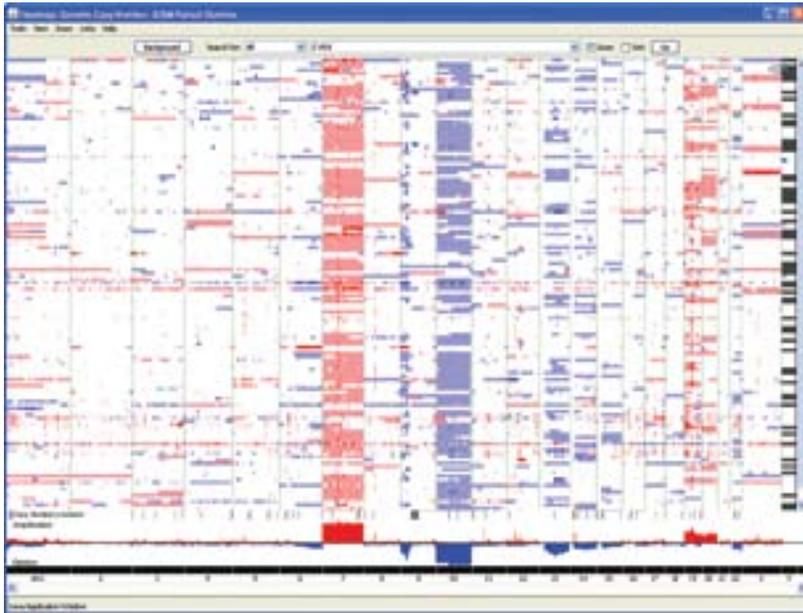
The CMA portal provides an easy-to-use web interface to tools for the analysis and visualization of genomic information such as gene expression, gene copy number, mutation and methylation data, as well as clinical information including treatment history, pathology status, tumor site and surgical history. Additional analytical functionality and access to additional data sets will be available as portal development continues. User feedback is encouraged to help direct future portal development.



Features of the CMA portal include

- **Gene View**
View expression, copy number and mutation information on a gene-by-gene or pathway basis
- **Genome View**
View chromosomal information including amplification, deletion, mutation and expression with the ability to zoom in for details
- **Clinical View**
Query clinical information and identify correlations between genomic and clinical data, including Kaplan-Meier survival plots
- **Analysis tools**
Select subsets of data for analysis using GenePattern and Principle Component Analysis

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Accessing the CMA Portal

The CMA portal (<https://cma.nci.nih.gov/cma/>) is accessible using Internet Explorer, Mozilla, or Firefox.

Resources

caBIG® Community Website

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

caBIG® Tool Inventory

<https://cabig.nci.nih.gov/inventory>

NCI Center for Bioinformatics Applications Support

<mailto:ncicb@pop.nci.nih.gov>

About caBIG®

The caBIG® (cancer Biomedical Informatics Grid®) initiative, overseen by the National Cancer Institute Center for Biomedical Informatics and Information Technology (NCI CBIIT), was conceived to connect the cancer research and clinical communities through open, interoperable technology that facilitates data sharing and collaboration, speeding the translation of discoveries from research to clinical care. Since its inception, caBIG® has successfully launched innovative tools, infrastructure, and policy resources that enable individuals and organizations in the cancer community and beyond to move further down the path to realizing Personalized Medicine.



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