



# platform

*Building science on a strong foundation*

The Oncomine platform is the foundation upon which novel cancer discoveries are made. With more than 250 peer reviewed journals referencing Oncomine and ground-breaking discoveries, it has become an industry standard tool.

Supporting both our web applications and our scientific services capabilities, the Oncomine platform is unique for:

- ~ its scalability with more than 500 independent datasets
- ~ its high-quality, expertly curated data
- ~ its rich, extensive, and controlled ontology of terms
- ~ its standardized analysis conventions to assure clear and consistent interpretation of results

# THE ONCOMINE PLATFORM

## A strong foundation

Good science has always been built on the foundation of good science that came before. In the genomic era the opportunity for scientific advancement has never been greater, but neither has the challenge of assembling the full breadth of earlier advancements into a coherent whole from which new discoveries can be made.

With a clear focus on cancer, Compendia Bioscience has uniquely assembled the world's most important cancer genomics data from high impact, peer-reviewed publications into the standardized and computable form called The Oncomine Platform.

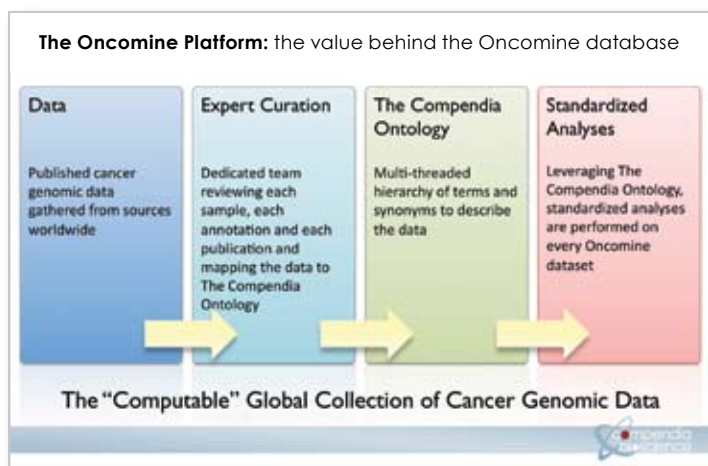
## Layers of strength

The Oncomine Platform is built on three separate and essential layers that bind together to provide the strength of our foundation:

- proactive data collection processes, including direct correspondence with study authors to gather all of the available sample facts, often beyond those presented in the original publication
- genomic data curation and management principles guided by clinical data quality standards and organized by The Compendia Ontology
- consistent application of robust, peer-reviewed analysis methods across the entire compendium of Oncomine data

## Stronger over time

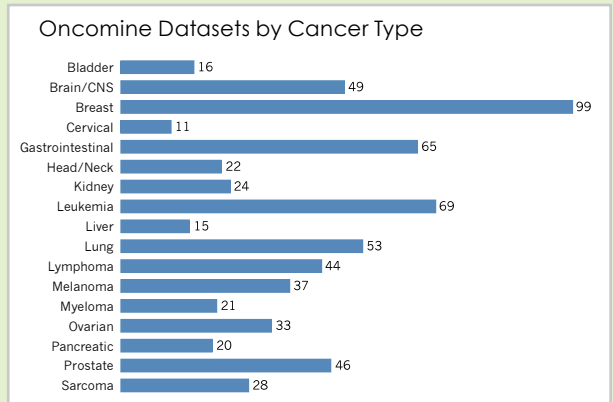
Oncomine is unique in the cancer genomic field in that Compendia continually invests in and improves The Oncomine Platform to provide more data, more metadata, more types of genomic and molecular data, more analyses, and more powerful visualizations for cancer researchers to answer their burning research questions.



## data

Our team is dedicated to collecting, analyzing, and integrating the latest data expediently and with acute attention to detail.

500+ datasets • 39,000+ samples • 500,000+ sample facts



## curation & ontology

As part of the Oncomine 4 project, 500,000+ sample facts across 39,000+ samples have been individually reviewed and terms normalized.

The data team works directly with study authors to gather all available sample facts and regularly includes data not found in other sources.

The Compendia Ontology is a new and comprehensive way to characterize Oncomine data, metadata and analyses. It is visually represented to application users in the search and browse interface, revealing the contents of the database. It also drives consistent downstream analyses through a set of standardized rules.

## analyses

Oncomine is enhanced by a powerful set of analysis functions that compute gene expression signatures, clusters, and gene set modules, automatically extracting biological insights from the data.



# applications

## *Answers revealed*

OncoPrint web applications enable researchers to discover more. Whether your focus is a gene or pathway, OncoPrint serves up access to the world's largest collection of expertly curated cancer research data.

The OncoPrint web applications reveal a vast amount of research data through standardized vocabulary, analyses and visualizations. And the streamlined interface makes sharing your findings with other users easy.

Each OncoPrint edition is tailored for the specific research needs of researchers, labs and institutions across the cancer research community.

# ACADEMIC APPLICATIONS

## Find your target

OncoPrint's carefully curated data and analyses are served up to users through a unified web interface designed by scientists for scientists. This interface is inspired by users to reflect workflows that easily answer research questions about your gene or pathway.

**OncoPrint Research Edition** is a powerful web application that integrates and unifies high-throughput cancer profiling data so that target expression across a large volume of cancer types, and experiments can be accessed online, in seconds. This edition features annual data updates and basic analysis types such as cancer vs. normal, multi-cancer and coexpression.

**OncoPrint Research Premium Edition** is a subscription version that allows users with advanced research needs to take advantage of additional features and analyses. This edition features quarterly data updates and both basic and advanced analyses such as clinical outcome, patient treatment response, and cell line perturbations. Plus users have the ability to search for multiple genes at one time, export and share results, upload custom concepts, and access enhanced support.

Funding for OncoPrint Research Premium Edition can be applied for directly in federal grant applications under ADP/Computer Services. For a more detailed description that may be useful in the budget justification portion of the proposal, please visit [www.oncoPrint.org](http://www.oncoPrint.org).



## Product licensing

OncoPrint Research Edition is available under a no-fee license. Visit [www.oncoPrint.org](http://www.oncoPrint.org) to register.

OncoPrint Research Premium Edition is available for purchase in 2-user and 5-user packages. Visit [www.compendiobio.com/products/upgrade.html](http://www.compendiobio.com/products/upgrade.html).

Institutional site licenses for OncoPrint Research Premium Edition are available. Please contact [orpesales@compendiobio.com](mailto:orpesales@compendiobio.com) for more information.

## solutions

- Easily compare gene expression profiles between normal and cancer samples
- Compare gene expression between different molecular, pathological, and clinical subtypes of cancer
- Investigate expression of genes in pathways and networks associated with cancer
- Identify pathways, processes, chromosomal regions, and regulatory motifs activated in cancer
- Search for genes that distinguish disease subtypes, as well as genes that predict cancer types and subtypes

## features

### OncoPrint Research Edition features:

- Improved user interface with smart search
- Gene and concept summaries
- Outlier analysis, meta-analysis, and meta-COPA

### OncoPrint Research Premium Edition features:

- Advanced search features, including multi-gene searching, allow you to visualize your data faster and easier
- Quarterly data updates help make your research more robust by viewing it in context of the latest cancer studies
- My Concepts is a custom concept upload that makes your workflows more efficient by allowing you to quickly run an analysis on your specific concept
- Export results to Excel and PowerPoint to perform additional analyses and easily share your findings
- Sophisticated built-in analyses allow you to answer critical research questions about your data
  - Cancer subtype analyses
  - Clinical outcome analyses
  - Patient treatment response analyses
  - Perturbation analyses
  - Drug sensitivity analyses
- Enhanced support