

Leadership

The management team at Compendia Bioscience is comprised of true leaders. Each person brings a unique perspective to the table, from the entrepreneur to the scientist. They are forward-thinking, lead by example, ask thoughtful questions, debate issues with vigor, and embrace ideas from the team.

They unite for the company's mission — to cure cancer with genomic data.

the management team

Daniel R. Rhodes, Ph.D. Co-Founder & CEO

Dr. Rhodes has a 10-year track record in cancer genomics and informatics with more than 30 papers published in peer-reviewed journals. He received a Ph.D. in Bioinformatics from the University of Michigan, contributing to several important advances in the field, including the seminal discovery of recurrent gene fusions in prostate cancer. Dr. Rhodes led the original development of OncoPrint™ and the OncoPrint Concepts Map in addition to several novel bioinformatics methods, including Meta-analysis of Microarrays and Cancer Outlier Profile Analysis (COPA). He has received several awards for his work including the Harold Weintraub Award and the Team Science Award from the AACR. Dr. Rhodes also maintains a part-time faculty research position at the University of Michigan Center for Translational Pathology.

Arul Chinnaiyan, M.D., Ph.D. Co-Founder

Dr. Chinnaiyan is a Professor in the Department of Pathology and Urology at the University of Michigan Medical School. Dr. Chinnaiyan is the Director of Cancer Bioinformatics and the co-Director of the Division of Pathology Informatics. Dr. Chinnaiyan is recognized as a world leader in cancer genomics and has authored more than 100 peer-reviewed publications including in high-impact journals such as Nature, Science, Cell, JAMA and the New England Journal of Medicine. He holds the distinguished S.P. Hicks Endowed Professorship of Pathology and has received numerous awards for his work including the Amgen Outstanding Investigator Award and the Pew Biomedical Scholar Award.

Matt Anstett, MSc VP Scientific Applications

Matt Anstett has ten years of experience in molecular biology, molecular diagnostics and assay development supporting patient diagnostics and drug discovery. Additionally, during his six years with Spotfire, he made significant contributions through partner collaborations, marketing, customer loyalty, software development and achievement of revenue goals that helped position the company as a leading Life Science informatics company. Mr. Anstett has contributed to a number of journals, industry publications and books on Microarray Analysis and High Content Screening.

John Freshley Chief Business Officer

John Freshley is an experienced life-sciences entrepreneur having recently served as President and CEO of Genetics Squared, Inc., an oncology therapeutic development company. In this role, Mr. Freshley led the closure of the Series A financing, recruited a world-class management team with more than 35 years of pharmaceutical industry experience and an industry-leading oncology-focused Scientific Advisory Board. Prior to his term at Genetics Squared, Mr. Freshley served as Director of Corporate Development and Marketing for STATPROBE, a clinical research company. Earlier in his career, Mr. Freshley served in a variety of management roles with operational and business development responsibilities, including Director of Business Development for a start-up cancer discovery and development company and as a founding employee and Director of Marketing for an enterprise software company, Grapevine Technologies, that was sold to Sun Microsystems in 1999.



Chris Gates Manager, Product Informatics

Chris Gates coordinates the design and development of operational software and informatic solutions at Compendia. His background spans several IT roles across many business domains including genomics, pharmaceutical drug-discovery, publishing, electronic medical record systems, and social-science research. Mr. Gates brings to Compendia an enthusiasm for bioinformatics, a mature understanding of the software development lifecycle, and the ability to align visions and build consensus. Since joining Compendia in 2007, he has worked to establish a scalable, efficient software delivery model, enabling the development of Oncomine 4 as well as many internal software/informatic solutions. Around Compendia, he has been recognized for his proclivity for metaphors, occasionally dropping an esoteric word into quotidian conversations, enforcing the "no more than two meanings per word" rule, and also popularizing the phrase, "That's a very good question." Mr. Gates is currently enrolled as a part-time student in the bioinformatics graduate program at the University of Michigan.

Colleen Kincaid-Beal Chief Operating Officer

Colleen Kincaid-Beal is the Chief Operating Officer with responsibility for project management, quality management, and customer support and vendor management. Ms. Kincaid-Beal oversees internal project teams to ensure progress towards project milestones with appropriate budget and resource management. Ms. Kincaid-Beal's professional experience includes 10 years with a leading clinical data CRO, i3 Statprobe. She served i3 in a variety of roles as clinical data manager, biostatistician and most recently as Sr. Director of Data Management Programming where she held line and project management responsibility for as many as 30 staff working on 70 projects. Included in her portfolio of projects was her leadership role in the development, testing, and support of a secure web-based clinical trial management portal that allowed clinical trial sponsors to review data and data processes and conduct real-time online data analysis.

Seth Sadis Director of Services

Dr. Sadis's background includes academic training in molecular and cell biology including a post-doctoral fellowship at Harvard Medical School where he studied cell cycle regulation via ubiquitin-dependent proteolysis. Following these studies, Dr. Sadis joined Proscript and later Millennium Pharmaceuticals where he supported the Velcade (bortezomib) program and led oncology drug discovery teams prosecuting targets upstream of the proteasome. Dr. Sadis then moved to Pfizer where he held several positions of increasing responsibility in oncology translational medicine and inflammation clinical development ultimately culminating in the position of Clinical Director.

At Compendia, Dr. Sadis oversees the execution and delivery of genomic biomarker projects, including OncoPredictor, to support personalized medicine objectives for the biopharmaceutical industry.

Becky Steck Manager, Scientific Content

Becky Steck is the Manager of Scientific Content, overseeing the collection, curation, and management of incoming data at Compendia Bioscience. Ms. Steck's professional experience includes four years with a leading clinical CRO, i3 Statprobe, where she held positions within clinical data management and project management. While at i3 Statprobe, she specialized in maintaining clinical trial data with the use of third-party electronic data capture software, as well as Oracle and SAS systems. Since coming to Compendia Bioscience in 2007, Ms. Steck has directed the collection, annotation, and quality control of microarray data supporting Oncomine. She also led the development of a controlled vocabulary to facilitate automated organization and analysis of sample metadata covering various genomic data types, including gene expression, DNA copy number, mutation, RNAi, and microRNA.

Peter Wyngaard Chief Technology Officer

Peter Wyngaard is responsible for overseeing software development, personnel, and contractors. Mr. Wyngaard is responsible for overseeing and guiding software, database, and system design, implementation, integration, and testing. Mr. Wyngaard has extensive experience implementing large-scale, commercial, database-driven web applications. As founder and CEO of a web application development firm, InterConnect, he oversaw a team of 14 developers working on several projects simultaneously. As a software architect and developer, Mr. Wyngaard has experience creating searching and browsing interfaces to multi-terabyte academic research databases, and experience designing and implementing content management systems.



A strong foundation

Compendia Bioscience was founded by Arul Chinnaiyan and Dan Rhodes in February 2006 with the goal of building a commercial version of OncoPrint that would have a greater ability to impact drug development and clinical practice.



core values

- None of us is smarter than all of us.
- We will nurture, mentor and challenge each other.
- Our environment will be open and will foster innovation, professionalism and fun.
- We will be driven by science.

partners

Compendia Bioscience focuses on developing partnerships based on the needs of our customers and leading bioinformatics initiatives, identifying a limited number of partnerships that provide value.

AltheaDx

AltheaDx is a diagnostic development and testing company with a mission to translate biomarker discoveries into clinical use. The business has deep capabilities in genetic analysis and PCR technologies specifically.

Ricerca Biosciences

Ricerca Biosciences' OncoPanel™ service provides high content screening of up to 240 cancer cell lines to assess the cytotoxicity and chemotherapeutic potential of specific cancer drugs and drug combinations.

Spotfire

TIBCO Software Inc. is a leading provider of enterprise analytics software for next generation business intelligence. TIBCO Spotfire products offer a visual and interactive experience that helps professionals quickly discover new and actionable insights in information.

products & services



OncoPrint Platform
Data
Application
User model

OncoPrint Power Tools

Tumor Segregation Panels



OncoPredictor

Custom Scientific Services

Driven by science

At Compendia Bioscience we are focused on the development of high quality products and services that drive novel discovery and contribute to improving human health.

We celebrate the achievements of others especially where we had a role to play in the research



in the news

08 DEC 2010

Compendia Bioscience and Althea Diagnostics Develop Breast Cancer Segregation Panel Assay as a Platform for Companion Diagnostic Development

...announced a new strategic partnership with Althea Diagnostics and the immediate availability of the partnership's first joint product and service offerings — the Breast Cancer Segregation Panel™ Assay and Analysis Service.

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17 NOV 2010

Personalized medicine: Tumor analysis reveals new opportunities for existing cancer drugs

Targeted cancer therapies such as trastuzumab (Herceptin), gefitinib (Iressa) and erlotinib (Tarceva) could be used to treat a wider range of cancers than previously thought, according to new research presented today (Wednesday) at the 22nd EORTC-NCI-AACR [1] Symposium on Molecular Targets and Cancer Therapeutics in Berlin.

publications

A gene expression signature associated with "K-Ras addiction" reveals regulators of EMT and tumor cell survival.

Singh A, Greninger P, Rhodes D, Koopman L, Violette S, Bardeesy N, Settleman J. Cancer Cell. 2009 Jun 2;15(6):489-500.

AGTR1 overexpression defines a subset of breast cancer and confers sensitivity to losartan, an AGTR1 antagonist.

Rhodes DR, Ateeq B, Cao Q, Tomlins SA, Mehra R, Laxman B, Kalyana-Sundaram S, Lonigro RJ, Helgeson BE, Bhojani MS, Rehemtulla A, Kleer CG, Hayes DF, Lucas PC, Varambally S, Chinnaiyan AM. Proc Natl Acad Sci U S A. 2009 Jun 1.

Exploring clinical associations using '-omics' based enrichment analyses.

Hanauer DA, Rhodes DR, Chinnaiyan AM. PLoS ONE. 2009;4(4):e5203. Epub 2009 Apr 13.

Coactivator Function Defines the Active Estrogen Receptor- α Cistrome.

Lupien M, Eeckhoutte J, Meyer CA, Krum SA, Rhodes DR, Liu XS, Brown M. Mol Cell Biol. 2009 Apr 13.

events

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Molecular Medicine Tri-Conference

San Francisco, CA
Corporate Sponsor
Booth #301

23 FEB 2011 | 12:40 pm

DRUG DISCOVERY AND DEVELOPMENT CHANNEL
Tumor Segregation Panels: FFPE RT-PCR Assays for Molecular Sub-Typing and Rapid Companion Diagnostic Development

presented by Dr. Dan Rhodes

25 FEB 2011 | 10:05 am

DRUG DISCOVERY AND DEVELOPMENT CHANNEL
OncoPredictor: A System for Identifying Clinically Relevant Biomarkers from Large Scale Cell Line Profiling

presented by Dr. Dan Rhodes

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2-6 APR 2011

AACR Annual Meeting

Orlando, FL
Booth #1265

05 APR 2011 | 8:00 am – 12:00 pm

POSTER: OncoPredictor: A systematic approach for predicting responsive cancer populations from large scale cell line screening

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3-7 JUN 2011

ASCO Annual Meeting

Chicago, IL
Booth #19147



discover

*Discover Oncomine.
Discover more.*

The Potential.

Genomic technology advances have created unprecedented potential—potential for discovery, potential for advances in drug development, but also potential for confusion and misdirection.

The Need.

There is a critical need for solutions that allow cancer researchers to simply and effectively navigate genomics data to make new discoveries, to validate these discoveries, and to apply new discoveries to patients most likely to benefit.

The Solution.

Oncomine accelerates your cancer research by providing simple and powerful ways to navigate and interpret the world's largest collection of cancer genomic data to answer your critical research questions.



ONCOMINE OVERVIEW

Oncomine content

With 534 datasets and 43,000+ samples, Oncomine is the world's largest collection of curated cancer genomics data. More than 601,000 sample facts across 43,000+ samples have been individually reviewed and terms categorized according to The Compendia Ontology.

Oncomine is a collection of more than 2,800+ pre-computed differential analyses of the data utilizing our standardized sample facts and consistent analysis methods across each dataset.

Oncomine solution

Even with these impressive numbers, the real value of Oncomine becomes apparent when you can quickly and easily discover or validate a target; when you can identify activated pathways, processes and clinical phenotypes correlated to drug response; when you can identify patient populations where your target is amplified or over expressed.

With a suite of web applications tailored to user and organization needs, Oncomine is a simple and powerful tool to harness the potential of cancer genomics data.



Oncomine expertise

Beyond Oncomine, Compendia Bioscience is a team of cancer genomics experts with deep experience at leveraging the Oncomine platform to focus on your burning questions.

applications

The Oncomine applications are tailored to fit the needs of users, labs and companies across the cancer research community. Each edition features convenient, web-based access from any computer, regardless of where your organization is based.

- Oncomine Concepts Edition has an integrated interface with smart search and an easy to navigate filter tree so you can quickly get to the information you are seeking.
- Oncomine Enterprise Edition allows for integration of proprietary data in a secure environment. Analyze your data against the Oncomine database to see it in a whole new light.

services

Compendia's team of experts has intimate knowledge of the Oncomine database and can help answer most questions using advanced techniques.

- Oncomine Project Edition leverages both Oncomine Concepts Edition and Compendia Bioscience's scientific expertise to scope and deliver a focused "Oncomine-enabled" research project such as target discovery and validation, patient population identification, discovery of sensitivity and resistance biomarkers, and identification of molecular subtypes of disease.
- OncoPredictor™ is a joint service offering from Compendia Bioscience and Ricerca Biosciences focused specifically on helping pharmaceutical and biotech companies develop sensitive and resistance biomarkers for drug development.

platform

The Oncomine platform is comprised of four essential and integrated parts—data, curation, ontology, and analysis. This combination enables the researcher, biologist, or bioinformatics scientist to easily navigate the Oncomine database to answer essential cancer research questions.

The Oncomine platform also supports our service offerings by allowing Compendia scientists flexible access to the Oncomine database in order to address questions not easily answered through the web applications.



platform

Building science on a strong foundation

The Oncomine platform is the foundation upon which novel cancer discoveries are made. With more than 445 peer reviewed journal articles referencing Oncomine and ground-breaking discoveries, it has become an industry standard tool.

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

- ~ its scalability with 534 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

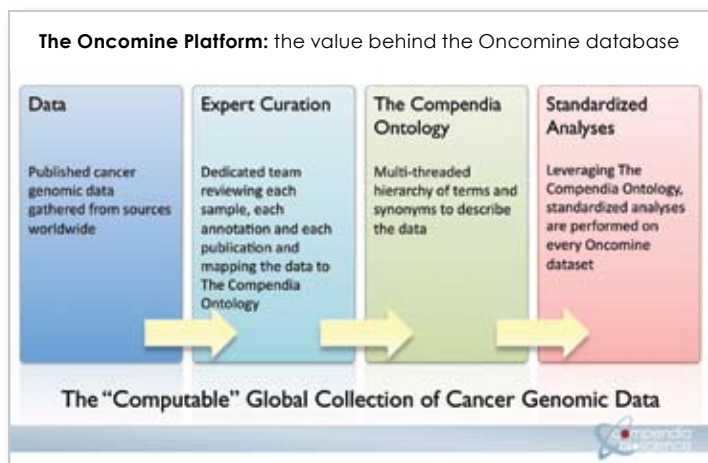
Good science has always been built on the foundation of good science that came before. In the genomic era the opportunity for scientific advancement has never been greater, but neither has the challenge of assembling the full breadth of earlier advancements into a coherent whole from which new discoveries 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 four essential and integrated layers that together provide a strong foundation:

- data—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
- curation—genomic data curation and management principles guided by clinical data quality standards and organized by The Compendia Ontology
- ontology—a comprehensive way to characterize Oncomine data, metadata and analyses that also drives consistent downstream analyses
- analyses—consistent application of robust, peer-reviewed analysis methods across the entire compendium of Oncomine data



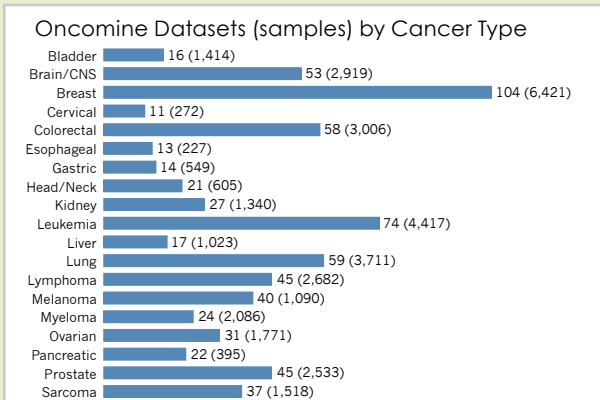
Stronger over time

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 your burning research questions.

data

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

534 datasets • 43,000+ samples • 601,000+ 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 standardized.

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 comprehensive way to characterize Oncomine data, metadata and analyses, which evolves as the database grows. 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

Find your target

Oncomine web applications enable researchers to discover more and accelerate drug development. Whether your focus is target discovery or finding patient profiles for your drug, Oncomine provides access to the world's largest collection of expertly curated cancer research data.

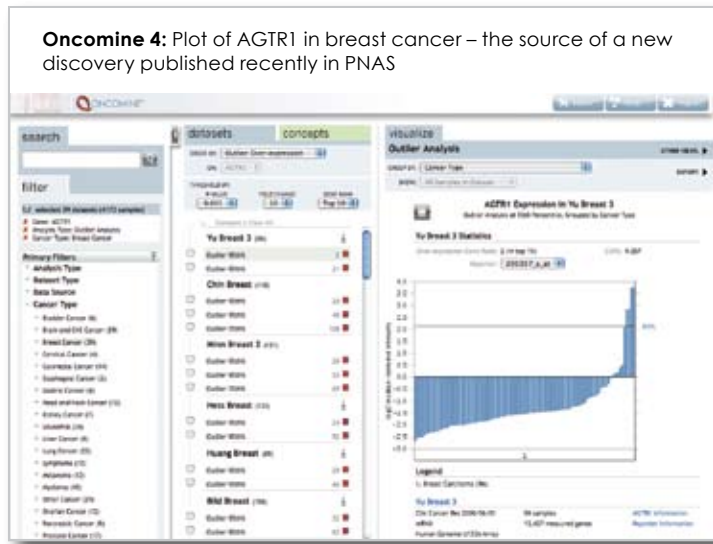
The Oncomine web applications reveal a vast amount of research data through standardized vocabulary, analyses and visualizations. And the streamlined interface makes sharing your findings with colleagues easy.

Each Oncomine edition is tailored for the specific research needs of companies, both large and small.

PROFESSIONAL APPLICATIONS

Find your target

Oncomine'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 key cancer research questions about your target or your drug.



Oncomine Concepts 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, subtypes, and experiments can be assessed online, in seconds. Additionally, it allows users to search the Oncomine database for enrichment of user-defined gene signatures. These analyses provide valuable insight into biology, regulation, pathways, drug response, and patient populations.

Oncomine Enterprise Edition provides the ability to securely share user-defined signatures across an organization as well as add proprietary gene expression datasets to the Oncomine database. Your data go through the same rigorous curation process as all other Oncomine data, assimilating it to the entire Oncomine database for more powerful meta-analysis.

Enabling research

From the smallest start-up to the biggest multinational company, Compendia Bioscience has options that can meet both their needs and their budget.

Direct inquiries to sales@compendiabio.com.

the big picture

gene expression and cancer

- Easily compare gene expression profiles between cancer and normal samples
- Compare gene expression between different molecular, pathological, and clinical cancer subtypes
- Search for genes that distinguish and predict cancer types and subtypes

identify and validate

- Identify potential drug targets by filtering for “druggable” gene families such as kinases and membrane-bound proteins
- Validate target gene expression in normal tissues, benign conditions, hematological malignancies and solid tumors
- Investigate expression of genes in pathways and networks associated with cancer
- Identify pathways, processes, chromosomal regions, and regulatory motifs activated in cancer

drug and biology interaction

- Associate diseases with the gene signature of a compound
- Identify pathways regulated by a compound
- Use a compound's gene signature from animal studies to identify like compounds and potential toxicological associations with it

features

Oncomine is a database-driven web application providing users with the ability to navigate, analyze, and visualize gene expression and copy number data and molecular concepts.

- Smart search with auto-complete
- Multi-gene and multi-term search
- Meta-analysis and Meta-COPA
- Rapid navigation and visualization of results
- Oncomine support community
- Export results to Excel, PowerPoint and SVG
- Proprietary concept upload and association concepts



services

Uncomplicated solutions

Cancer research is full of complicated questions.

The professionals at Compendia Bioscience can leverage years of experience and OncoPrint-enabled research capabilities to help answer your burning research questions.

- ~ Target discovery and validation
- ~ Patient population identification
- ~ Discovery of genomic biomarkers
- ~ Identification of molecular subtypes of disease

ONCOMINE-RELATED SERVICES

Uncomplicated solutions

Cancer research is full of complicated questions. The role that cancer genomics data plays in answering those questions is not always clear.

Compendia Bioscience's well-published scientists have unique experience and expertise in the application of genomics data and genomics tools to address key cancer research questions and provide uncomplicated solutions that combine:

- the power of The OncoPrint Platform
- industry leading third-party partnerships
- tailored scientific service projects delivered by our scientists

Compendia has worked with both large and small companies to perform services such as:

Target validation Compendia will investigate potential cancer targets in OncoPrint and evaluate your target's expression in both normal and cancer tissues. We will identify specific histological or pathological subtypes with unique expression of your target and investigate outlier status of your target across all disease types. We will also identify cell lines that share similar expression to your primary tumor population of interest.

Discover molecular subtypes of disease Using the enormous breadth and diversity of the OncoPrint database, Compendia has developed a systematic approach for the identification and application of molecular subtypes of specific cancers. Compendia can work with you to refine these subtypes and identify specific molecular markers that may be useful in your drug discovery or development programs.



Patient population identification Compendia has developed several different and complementary approaches to identify patient populations most likely to benefit from a specific cancer therapy or combination. These approaches include:

- utilizing Compendia's molecular subtyping system to discover companion diagnostics
- utilizing OncoPredictor (see sidebar) to generate genomic biomarkers of sensitivity and resistance
- utilizing partners specializing in human tumor grafts and in vivo services

experts

An additional advantage of working with Compendia Bioscience on a professional services basis is that our scientists have direct access to the OncoPrint data platform and can perform analyses and answer questions that cannot be addressed directly through the OncoPrint web applications.

solutions

OncoPrint Project Edition

OncoPrint Project Edition combines the power of OncoPrint and the hands-on experience of Compendia Bioscience to answer your key questions.

Compendia scientists work directly with you to apply OncoPrint to your research question within the framework of a professional services project.

Included in the project is an OncoPrint Project Edition license with direct links to OncoPrint analysis results as project deliverables wherever possible. After Compendia scientists have done the heavy lifting and provided key sets of results, you and your colleagues can pick up the research from that point in order to ask and answer additional follow-up questions related to your research project.



ONCOPREDICTOR™

OncoPredictor™

OncoPredictor combines cell line profiling services, OncoPanel 240, from Ricerca Biosciences with OncoPrint and Compendia's scientific services to identify genomic biomarkers of drug sensitivity and resistance and patient populations most enriched for those biomarkers.

Human Tumor Xenograft discovery and validation

Compendia works with partners who specialize in human tumor grafts and other in vivo services helping your program to prioritize lead compounds, narrow down possible disease indications, and identify biomarkers to stratify patient populations in clinical trials.