ONCOMINE: Cancer Microarray Database



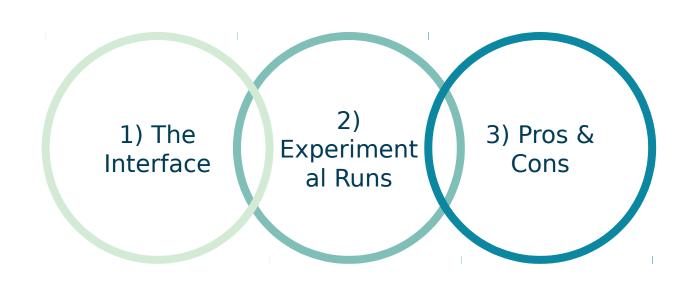
leading cause of death worldwide.

9.6 million deaths in 2018

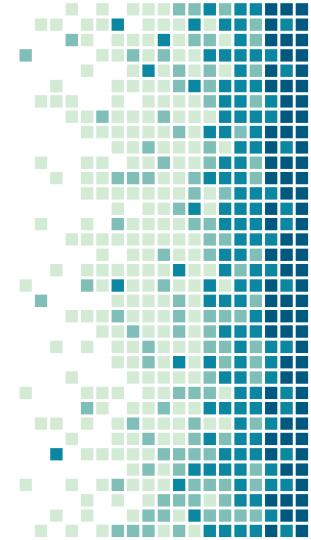
to *us* to make a difference!



- Overvie W



1. The Interface









login

USFR ID:

apredtechenskis@udallas.edu

PASSWORD:

.........

- · Forgot password?
- · Not a user? Register now!



news

Visit our newsroom to find out about the latest developments at Thermo Fisher Scientific.

Did you know that you can include the fee for Oncomine Research Premium Edition in US federal grant applications? Contact us for more information.

events

Whether it's a conference, trade show, or

Oncomine™ Research Edition: 715 datasets and 86,733 samples

Design better experiments. Gain more insights. Prepare to publish faster.

With Oncomine™ Research Premium Edition, you can:

Design better experiments... Answer more questions with fewer experiments, select the most promising gene or cell line, and test your hypothesis.

Gain more biological insights...Discover novel targets for therapeutic development. interrogate gene expression profiles, and identify drug and biological interactions.

Prepare to publish faster...Validate your results faster, visualize data easier and make connections to clinical significance.

iontorrent

by Thermo Fisher Scientific

The Origin of the Oncomine Platform

The Oncomine Platform was conceived by physicians. scientists, and software engineers at the University of Michigan. It was commercialized by Arul Chinnaivan and Dan Rhodes in February 2006 with the goal of building a version that would have a greater ability to impact drug development and clinical practice

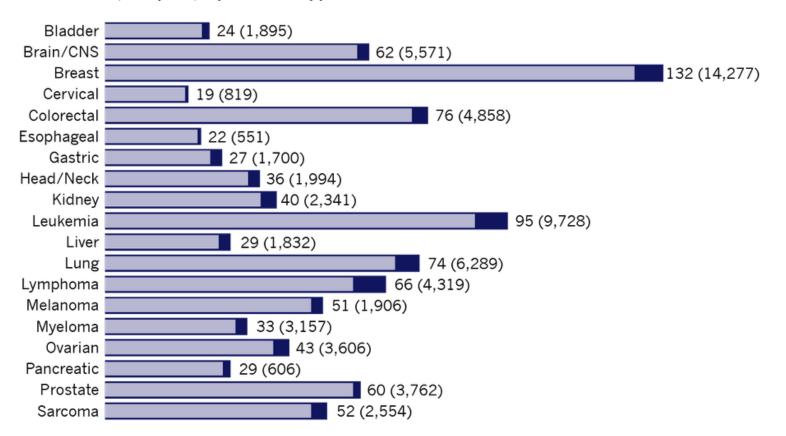
Oncomine Important Features

- By Thermo Fischer Scientific
- Created by Chinnaiyan& Rhodes in 2006

GOAL: to provide "greater ability to impact drug development & clinical practice"

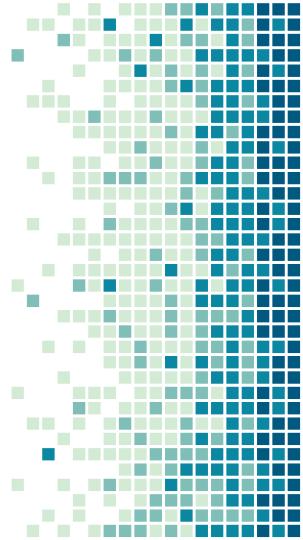
- Oncomine Research Edition
- Oncomine Research
 Premium Edition
- Scalability
- High quality
- Standardized analysis

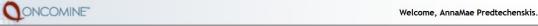
Datasets (Samples) by Cancer Types*



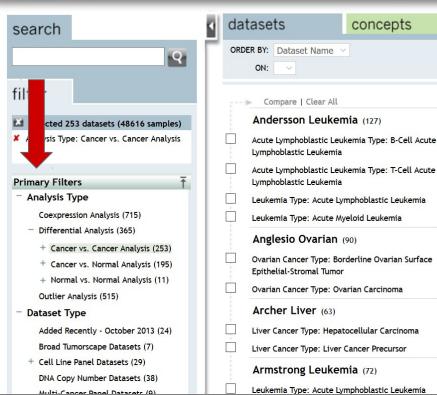
^{*}This bar chart represents datasets. The darker color denotes an increase in datasets (samples) over the last data release. Some samples are represented in multiple cancer types. The Oncomine database also has 12,764 normal samples.

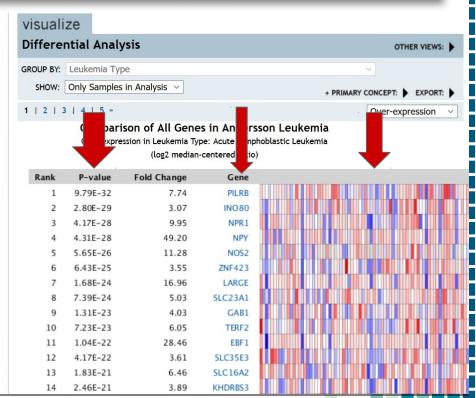
2. Experimental Runs

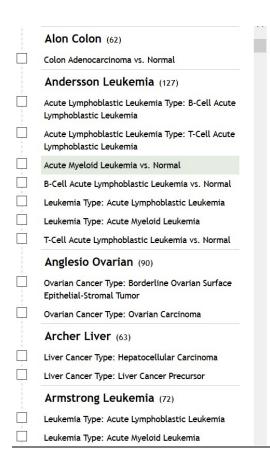








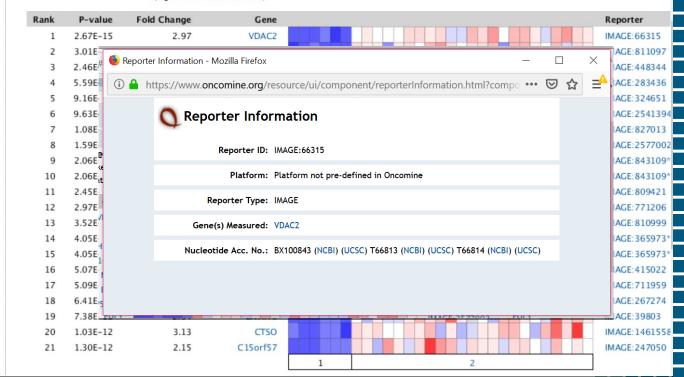




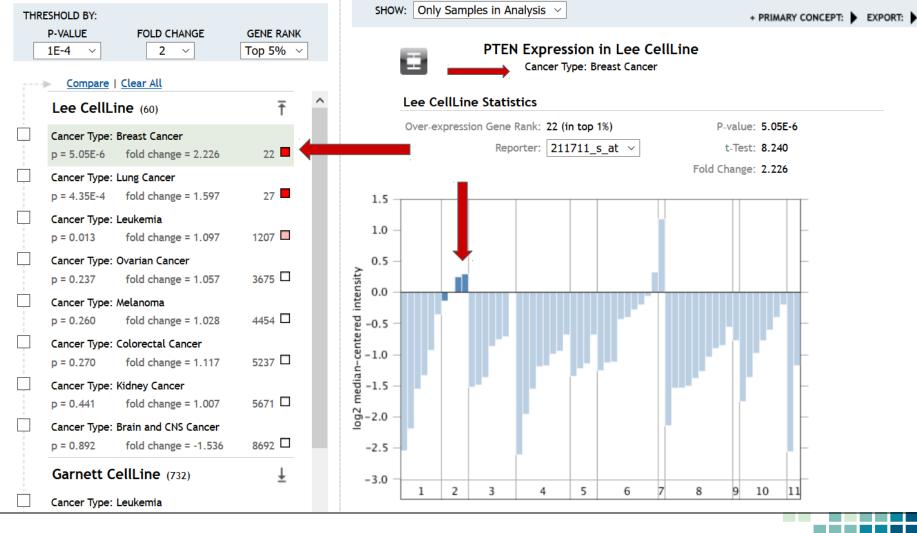
Comparison of All Genes in Andersson Leukemia

Over-expression in Acute Myeloid Leukemia vs. Normal

(log2 median-centered ratio)



1		Companison of All Genes Across Z Analyses							
i	Cancer Type: Bladder Cancer			Over-express	sion				
	Cancer Type: Brain and CNS Cancer	Median Rank	p-Value	Gene		1			
	Cancer Type: Breast Cancer	56.5	3.23E-12	TCF4					
	Cancer Type: Colorectal Cancer	69.0	8.17E-18	LIX1L				444	
	Cancer Type: Esophageal Cancer	74.5	5.81E-11	IFFO1					-
	Cancer Type: Gastric Cancer	94.0	4.88E-11	BCAT1					
1		123.5	2.39E-11	ZNF655					
i	Cancer Type: Head and Neck Cancer	191.0	2.13E-8	LDHB					
i	Cancer Type: Kidney Cancer	314.0	3.13E-9	ZEB1		LDHB Rank: 359			4
	Cancer Type: Leukemia	358.5	2.35E-12	MSN		p-Value: 4.26E-8			
	Cancer Type: Liver Cancer	377.5	6.83E-12	MTMR9					
	Cancer Type: Lung Cancer	405.5	6.51E-10	TGFB1					
1		491.0	2.48E-6	EBF1					
Y	Cancer Type: Lymphoma	507.5	4.64E-8	GIT2					
	Cancer Type: Melanoma	544.5	5.45E-6	ATG2B					-
	Cancer Type: Myeloma	560.0	2.50E-9	SMAD4					
	Cancer Type: Ovarian Cancer	572.0	1.03E-7	FGFR1OP2					
	Cancer Type: Pancreatic Cancer	575.5	2.51E-7	DNAJC8					
		598.5	1.81E-5	RPL27A					
	Cancer Type: Prostate Cancer	600.0	4.11E-9	AP1M1					
~	Cancer Type: Sarcoma	620.0	2.42E-10	CCDC88A					
	DNA Barretina CellLine 2 (947)	662.5	8.02E-7	PTAFR					
					1 2				
Щ	Cancer Type: Bladder Cancer	Logond				_			
	Cancer Type: Brain and CNS Cancer		Legend						
	Cancer Type: Breast Cancer		1. Cancer Type: Lymphoma Barretina CellLine, Nature, 2012						
	Cancer Type: Colorectal Cancer	2. Cancer Type	Cancer Type: Sarcoma Barretina CellLine, Nature, 2012						
	Carlos 1,po. Colorectal Carlos	Barretina C							







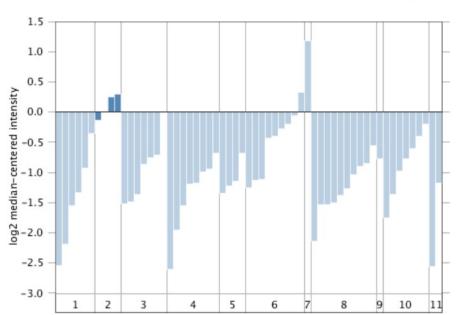
PTEN Expression in Lee CellLine

Cancer Type: Breast Cancer

Lee CellLine Statistics

Over-expression Gene Rank: 22 (in top 1%) P-value: 5.05E-6 Reporter: 211711_s_at ~ t-Test: 8.240

Fold Change: 2.226





PowerPoint

Publication-quality graphic (SVG)

Excel - Analysis Comparison

Excel - Analysis Gene List

Excel - Dataset Detail

Summary

Cancer vs. Cancer & Cancer vs. Normal

Analyzing the complete databases.

Red=overexpression

Blue=under-

expression

Lymphoma vs.
Sarcoma
Expression

Go to specific cell line (Barretina cell line) and compare expression over a smaller gene set.

Compare p-values.

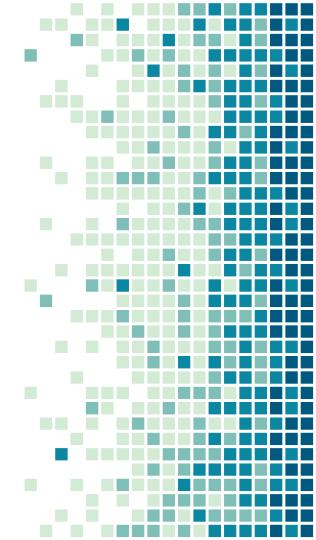
PTEN Gene Expression

Search a specific gene of interest.

View multiple different cancer types and the correlating expression.

Export options.

3. Pros & Cons



Shortcomings

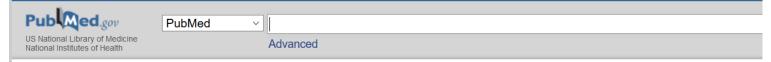
- You need to make an account to get any info.
- While there is a large amount of information with an account, you don't have access to everything unless you pay a subscription fee.
- At first, the interface is not intuitive and clear; it is not user friendly to many outside cancer research.

Strengths

- The user guide is very helpful!
- There is a large compilation of metadata and link-outs.
- It combines statistical analysis with the biological analysis.



Come!



Format: Abstract - Send to -

Neoplasia. 2004 Jan-Feb;6(1):1-6.

ONCOMINE: a cancer microarray database and integrated data-mining platform.

Rhodes DR¹, Yu J, Shanker K, Deshpande N, Varambally R, Ghosh D, Barrette T, Pandey A, Chinnaiyan AM.

Author information

Abstract

DNA microarray technology has led to an explosion of oncogenomic analyses, generating a wealth of data and uncovering the complex gene expression patterns of cancer. Unfortunately, due to the lack of a unifying bioinformatic resource, the majority of these data sit stagnant and disjointed following publication, massively underutilized by the cancer research community. Here, we present ONCOMINE, a cancer microarray database and web-based data-mining platform aimed at facilitating discovery from genome-wide expression analyses. To date, ONCOMINE contains 65 gene expression datasets comprising nearly 48 million gene expression measurements form over 4700 microarray experiments. Differential expression analyses comparing most major types of cancer with respective normal tissues as well as a variety of cancer subtypes and clinical-based and pathology-based analyses are available for exploration. Data can be queried and visualized for a selected gene across all analyses or for multiple genes in a selected analysis. Furthermore, gene sets can be limited to clinically important annotations including secreted, kinase, membrane, and known gene-drug target pairs to facilitate the discovery of novel biomarkers and therapeutic targets.

The Journey to Difference



Cancer Can Affect Us All...



THANK YOU!

Any questions?

