

Welcome to AMLdb: A database for Acute Myeloid Leukemia!

Acute myeloid leukemia (AML) is a rare cancer usually detected at an advanced stage. It's a disease of immature blood cells. Instead of developing into mature blood cells with finite lifespan, cells with compromised DNA or compromised regulation of DNA continue to divide. Eventually, these diseased cells take over and cause devastating effects on the body. Most patients survive just a few weeks or months after diagnosis. Understanding how AML occurs is difficult because the disease develops silently for many years before patients suddenly have severe symptoms. Therefore, studying AML is challenging.

Taking these challenges into account, we developed AMLdb as a one-stop resource for anyone seeking information on AML. Our database provides comprehensive information on transcriptional and epigenetic dynamics in AML with special emphasis on mutations and drug sensitivity that can help to understand the etiology of the disease, identify and validate biomarkers, classify patients and predict personalized treatment regimens and outcomes. The data has been collected and curated manually from literature as well as repositories and databases like GEO, DepMap, cBioPortal, GDSC and COSMIC.

DATABASE CONTENT

The diagram illustrates the flow of genetic information: DNA is transcribed into mRNA, which is then translated into Protein. Methylation is shown as a modification of DNA. CRISPR-screen & Achilles data are shown as a separate pathway. A box labeled 'REPOSITORIES' contains icons for GEO, DepMap, cBioPortal, and GDSC.

Expression profiling data

See details

Methylation profiling data

See details

CRISPR-Cas9 screens

Achilles data

Dataset gives you the following dropdown options



Acute Myeloid Leukemia Database

HOME

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Welcome to AMLdb: A database for

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GEO data:

Query Search

Profiling Technique

CRISPR-Cas9 screens:

DepMap

Project Achilles

GDSC data:

Drug Search

Upon clicking the query search, the query submission form appears



Query Search

Understanding the genetic and epigenetic factors like gene expression and methylation play a crucial role in early detection of cancer. This page has been designed to allow the user to browse and retrieve information on expression and methylation datasets of AML. User can browse these information using the options provided below. For detailed assistance visit the [HELP](#) section!

Search your keyword using any of the options given below

Query submission form

Choose the fields to be queried :

PubMed ID (eg. 29654265)

Dataset ID (eg. GSE111678)

Profiling Technique (eg. Illumina)

Processing package (eg. Oligo)

Sample source (eg. Blood)


Type of data (eg. Methylation profiling)










Select any of the provided options and click on to search

Table related to the search would appear

Table can be downloaded by clicking on the download button

Search results for Illumina

Download table here 

GSE ID	Pubmed ID	Platform	No of Samples	Profiling Techniques	No of genes	No of probes	Package used for data pre-processing	Source of samples	Values of matrix	Type of data	Download
GSE199452	35618837	Illumina HiSeq 2000 (Homo sapiens)	111	Illumina	52115	NA	NA	Mononuclear cells	TPM	Expression profiling	
GSE199451	35618837	Illumina HiSeq 2000 (Homo sapiens)	22	Illumina	56609	NA	NA	Blood	TPM	Expression profiling	
GSE129094	31076446	Illumina HiSeq 2000 (Homo sapiens)	20	Illumina	60554	NA	NA	Blood	TPM	Expression profiling	
GSE157633	NA	Illumina NextSeq 500 (Homo sapiens)	10	Illumina	54771	NA	NA	Blood	TPM	Expression profiling	
GSE165430	33683341	Illumina HiSeq 4000 (Homo sapiens)	268	Illumina	56376	NA	NA	Blood	TPM	Expression profiling	
GSE106291	29242298	Illumina HiSeq 1500 (Homo sapiens)	250	Illumina	19673	NA	NA	Bone marrow and blood	TPM	Expression profiling	
GSE86506	28123069	Illumina HiSeq 2000 (Homo sapiens)	28	Illumina	50919	NA	NA	AML Blast	TPM	Expression profiling	
GSE84359	28516957	Illumina HiSeq 2500 (Homo sapiens)	16	Illumina	22347	NA	NA	Bone marrow and blood	TPM	Expression profiling	
GSE71800	27780967	Illumina HiSeq 2000 (Homo sapiens)	18	Illumina	21865	NA	NA	Cord blood/bone	TPM	Expression	

Click here to go the GEO website for the particular GSEID

Click here to go the PubMed page for literature

Download the final matrix of the GSEID here

Click the second option "Profiling Technique" to view the proportion of the datasets from different platforms like Affymetrix, Illumina and Agilent



Acute Myeloid Leukemia Database

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Welcome to AMLdb: A database for

Acute myeloid leukemia (AML) is a rare cancer usually detected at an advanced stage. It's a disease of immature blood cells that have not fully developed and are still in the process of maturing. Instead of developing into mature blood cells with finite lifespan, cells with compromised DNA or compromised regulation of DNA continue to divide. Eventually, these diseased cells crowd out normal blood cells, leading to various symptoms. Understanding how AML occurs is difficult because the disease develops silently and is often asymptomatic. Taking these challenges into account, we developed AMLdb as a one-stop resource for anyone seeking information on epigenetic dynamics in AML with special emphasis on mutations and drug sensitivity that can help to understand personalized treatment regimens and outcomes. The data has been collected and curated manually from various public repositories and databases like GEO, DepMap, cBioPortal, GDSC and COSMIC.

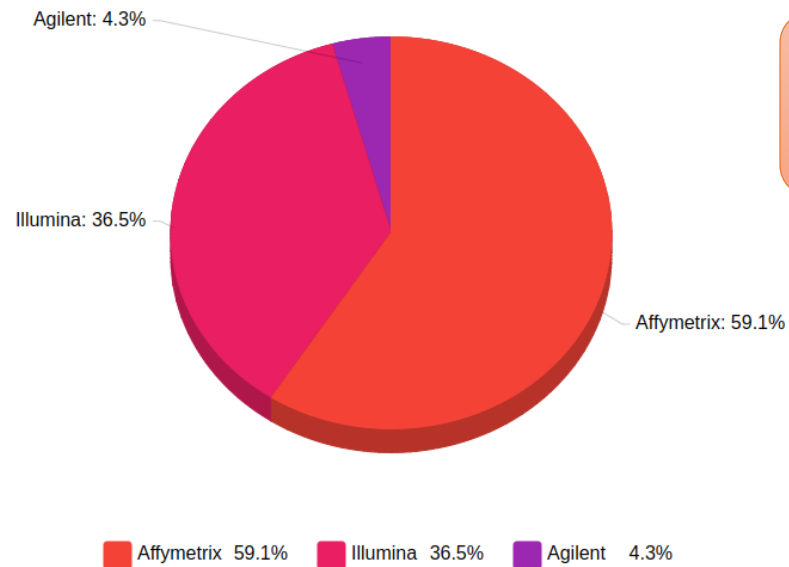
Acute Myeloid Leukemia!

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- DATASET** ▾
- GEO data:
 - Query Search
- Profiling Technique
- CRISPR-Cas9 screens:
 - DepMap
 - Project Achilles
- GDSC data:
 - Drug Search

Profiling Techniques

Various profiling techniques have been employed to decipher the events that leads to the progression of a normal tissue into a cancerous one. Here individual datasets from GEO portal, belonging to different platforms were collected and curated manually to study the expression of genes. User can click on to any of the below provided links to access the data associated with the respective platform. For detailed assistance visit the [HELP](#) section!



A Pie chart would appear showing the proportion datasets from all three platforms that has been included in the database.

The Pie chart is linked to the respective pages from where the information can be downloaded as shown in the above images

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Upon clicking the DepMap option a search box would appear

DepMap data

The CRISPR-Cas9 technology has permitted accurate identification of the crucial genes essential for the survival and proliferation of cancer cells through Cas-9 mediated gene cleavage. Here a total of 26 AML cells lines and 17387 genes along with their corresponding gene effect scores have been uploaded from DepMap database to pick out the essential genes of AML that can be used to decipher the drug targets. The user can enter a gene in the search box given below to visualize the data in tabular and graphical form. For detailed assistance visit [Help](#) section!

Examples:

*This applies for both DepMap and Project Achilles data

Any gene can be searched by entering the name in the search box

Click here to view the bar graph

This table showing gene effect values of the selected gene across the AML cell lines would appear along with clinical characteristics

Download the table here



Acute Myeloid Leukemia Database

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Your search results:

The following table shows the dependency scores of gene CSF3 in AML cell lines: [Download table here](#)

Click to view the [Plot](#)

DepMap ID	ACH-000004	ACH-000005	ACH-000045	ACH-000113	ACH-000146	ACH-000168	ACH-000195	ACH-000200
Cell line	HEL	HEL9217	MV411	OCIAML2	THP1	NOMO1	SET2	SET3
Sample collection site	haematopoietic_and_lymphoid_tissue	bone_marrow	haematopoietic_and_lymphoid_tissue	haematopoietic_and_lymphoid_tissue	haematopoietic_and_lymphoid_tissue	bone_marrow	haematopoietic_and_lymphoid_tissue	haematopoietic_and_lymphoid_tissue
Primary/Metastasis	NA	NA	Primary	Primary	Primary	Primary	NA	NA
Lineage	blood	blood	blood	blood	blood	blood	blood	blood
Sex	Male	Male	Male	Male	Male	Female	Female	Female
Age	30	30	10	65	1	31	71	71
CSF3	-0.1496834	-0.4235607	-0.3548392	-0.2998907	-0.3131698	-0.4168453	-0.2995105	-0.2995105

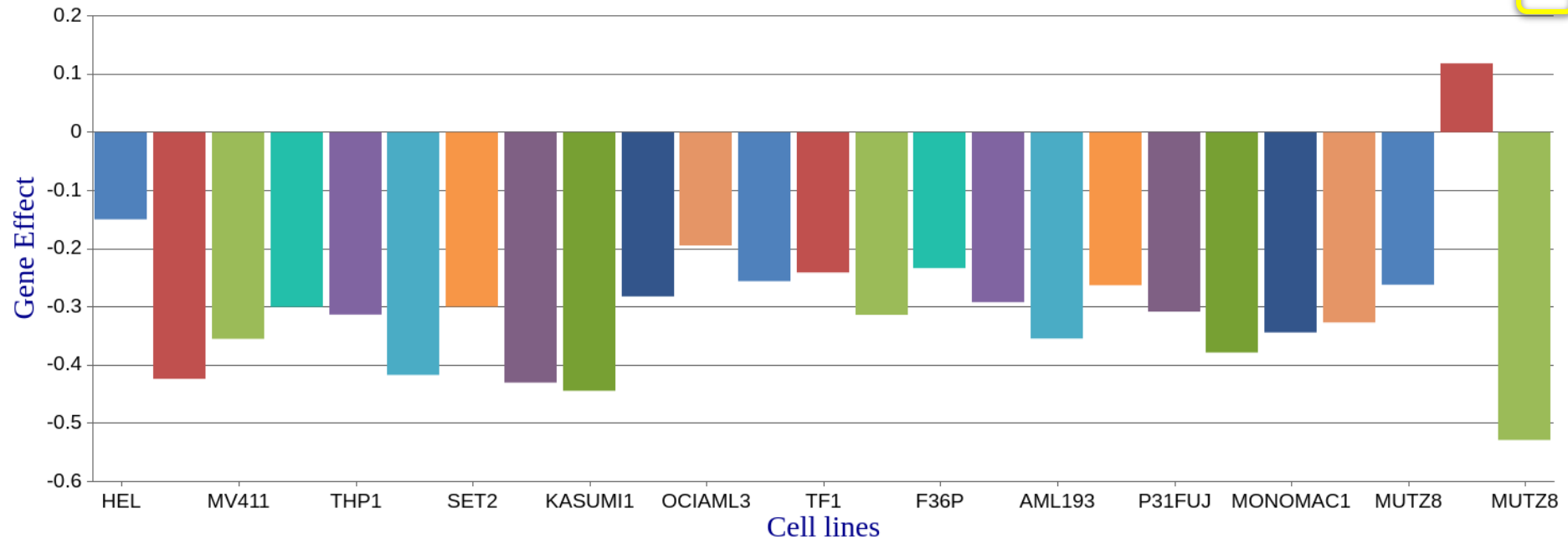
Scroll to see the entire table

Bar graph of Gene effect v/s Cell lines

Graphical visualization for the gene: CSF3

This plot marks the essentiality scores of the gene CSF3 against 26 different cell lines of AML. Lower score implies loss of its function compromises the viability of cancer cells. This explains the vulnerability of cancer cells that can expedite therapeutic discovery.

Plot of Gene Effect v/s Cell lines



Welcome to AMLdb: A database for

Acute myeloid leukemia (AML) is a rare cancer usually detected at an advanced stage. It's a disease of immature blood cells that have not fully developed into mature blood cells with finite lifespan, cells with genetic defects that are not responding to normal regulatory signals, and cells that are not maturing properly. These cells are accumulating and crowding out the normal blood cells, leading to various effects on the body. Most patients survive just a few weeks or months after diagnosis. Understanding how AML occurs is difficult because the disease develops silently and is often challenging to treat. Taking these challenges into account, we developed AMLdb as a one-stop resource for anyone seeking information on epigenetic dynamics in AML with special emphasis on mutations and drug sensitivity that can help to understand personalized treatment regimens and outcomes. The data has been collected and curated manually from various public repositories and databases like GEO, DepMap, cBioPortal, GDSC and COSMIC.


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Leukemia!

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Keyword search for Drugs against AML cell lines

This page is designed to retrieve information on the different drugs used against AML cell lines. User can browse these information using the options provided below. For detailed assistance visit the [HELP](#) section!

Select the drug name 

--Select--
--Select--
5-azacytidine
5-Fluorouracil
A-366
ABT737
Afatinib
Afuresertib
AGI-5198
AGI-6780
AGK2
Alistertib
Alpelisib
alpha-lipoic acid
AMG-319

Submit

Drug search option will take you to a page where you can select the drug name from the dropdown menu

Click here to visit PubChem website for the drug

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Acute Myeloid Leukemia Database

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Search results for **5-azacytidine** [Download table here](#)

Click to view the [Plot](#)

Cell Line Name	CESS	GDM-1	HL-60	KG-1	KMOE-2	ME-1	ML-2	MOLM-13	MONO-MAC-6	NKM-1	NOMO-1	OCI-AML2	OCI-AML3	OCI-AML5
logIC50 (μm)	2.9190	0.9696	0.9171	1.6323	1.9511	1.7563	1.1985	0.2405	-0.0267	2.1990	1.5132	0.6170	1.3280	2.0463

Upon clicking plot option the bar graph of logIC50 v/s Cell lines appears

AMLdb
Acute Myeloid Leukemia Database

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Graphical visualization for the drug: 5-azacytidine

This plot gives the logIC50 values of drug 5-azacytidine against different cell lines of AML. Lower logIC50 value implies more potent is the drug

Plot of Cell Lines v/s logIC50

Cell Line	logIC50 (μm)
CESS	2.9190
GDM-1	0.9696
HEL	0.9171
HL-60	1.6323
KASUMI-1	1.9511
KG-1	1.7563
KMOE-2	1.1985
ME-1	0.2405
ML-2	-0.0267
MOLM-13	2.1990
MOLM-16	1.5132
MONO-MAC-6	0.6170
NKM-1	1.3280
NOMO-1	2.0463
OCI-AML2	
OCI-AML3	
OCI-AML5	
P31-FUJ	
PL-21	
QIMR-WIL	
THP-1	

Download plot form here

Analysis section provides you with the following options

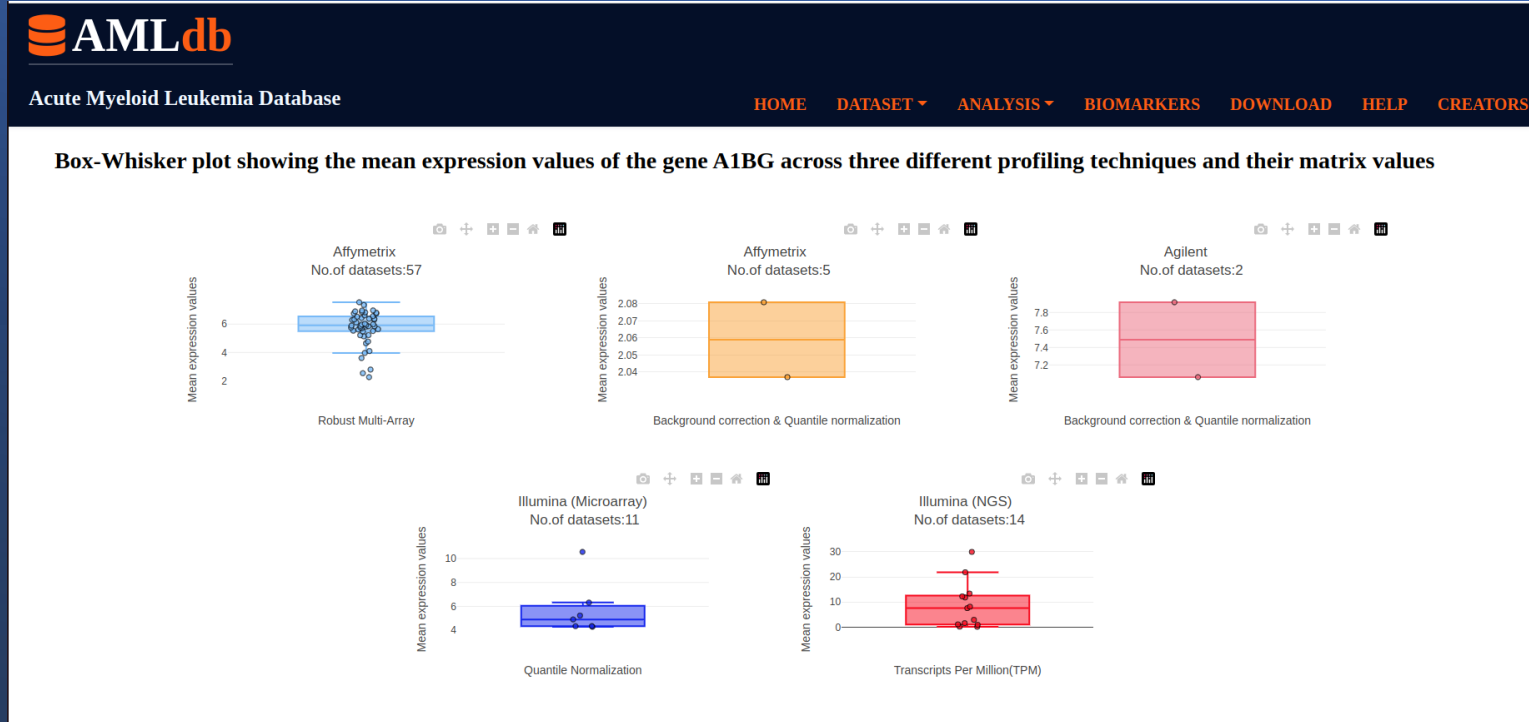
The screenshot shows the AMLdb homepage. The navigation bar includes 'HOME', 'DATASET', 'ANALYSIS', 'BIOMARKERS', 'DOWNLOAD', 'HELP', and 'CREATORS'. The 'ANALYSIS' menu is open, showing options for 'PROFILING:' (Expression, Methylation) and 'DRUG SENSITIVITY' (Mutational analysis). The main content area features a welcome message and a paragraph about AML: 'Acute myeloid leukemia (AML) is a rare cancer usually detected at an advanced stage. It's a disease of immature blood cells with compromised DNA or compromised regulation of DNA continue to divide. Eventually, these diseased cells take over and can lead to death within months after diagnosis. Understanding how AML occurs is difficult because the disease develops silently for many years before it becomes apparent. Taking these challenges into account, we developed AMLdb as a one-stop resource for anyone seeking information on AML. Our database provides comprehensive information on transcriptional and epigenetic dynamics in AML with special emphasis on mutations and drug sensitivity that can help to understand the etiology of the disease, identify and validate biomarkers, classify patients and predict personalized treatment regimens and outcomes. The data has been collected and curated manually from literature as well as repositories and databases like GEO, DepMap, cBioPortal, GDSC and COSMIC.'

*Same for methylation profiling data

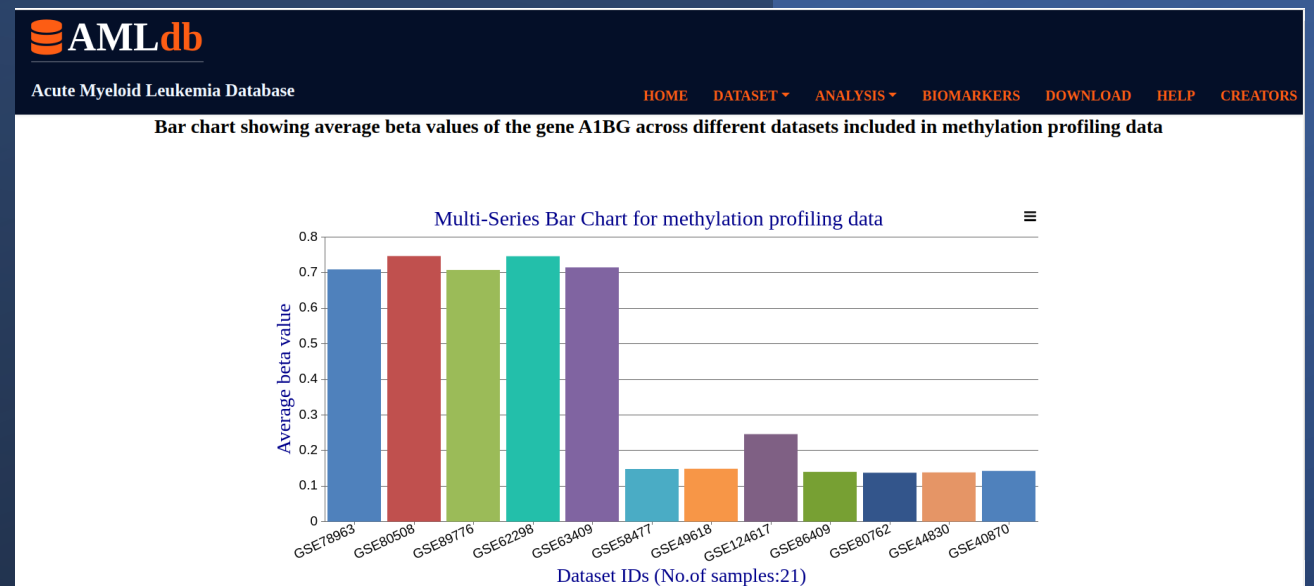
The screenshot shows the 'Expression profiling gene search' page. It features a search box with 'A1BG' entered and a magnifying glass icon. Below the search box are three circular buttons labeled 'A1BG', 'AKT3', and 'A2M' under the heading 'Examples:'. The page text reads: 'This page is designed to retrieve information on the expression profiling analysis for the selected gene. The user can enter a gene in the search box given below to visualize gene expression of queried gene as Box-Whisker's plots. For detailed assistance visit the HELP section!'.

Expression profiling will take you to the search page where name of a gene can be entered in the search box

The search results will give you the Box-Whisker plots showing mean expression values of the gene



The search results will give you the Bar graph showing average beta values of the gene for methylation data



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PROFILING:

Expression

Methylation

DRUG SENSITIVITY


Mutational analysis


Drug sensitivity characterization in AML cell lines



Investigating genetic and epigenetic changes in cancer cells can provide insight into the sensitivity of those cells to certain chemicals, and can also be used as indicators of how the cells may respond to different drugs marking its sensitivity or resistance. This page has been designed to allow the user to browse and retrieve information on 41 different genes that has shown a mutation frequency >5 in 23 AML cell lines. User can browse these information using the options provided below to understand how different cell lines respond to the tested drugs. For detailed assistance visit the [HELP](#) section!

Search your keyword using any of the options given below

Genes:  ABCA4

Drugs:  --Select--

Submit

- Select--
- Gemcitabine
- GSK1904529A
- Irinotecan
- Olaparib
- Rapamycin
- SN-38
- Veliparib

Mutational analysis will take you to the page where a particular gene and drug could be selected from the dropdown menu

Biomarkers section will display the following table of potential biomarkers of AML

AMLdb
Acute Myeloid Leukemia Database

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Biomarkers of AML

The following table shows some of the biomarkers of AML resourced from the published literatures. Click here to download the table : [Download table here](#)

Biomarker	Biomolecule	Subject	Regulation	Type	Experiment	Significance	Source	PubMedID	Methods	Tools	Cohort
HCK	mRNA	Human	Upregulation	Prognostic	Stromal, immune, and ESTIMATE scores evaluation	p<0.048	TCGA-LAML	35280440	Pathway Enrichment Analysis, Protein-Protein Interaction (PPI) Network, Cox Regression Analysis and Kaplan-Meier Survival Analysis, Gene Set Enrichment Analysis , Go Analysis, Kegg Analysis	ESTIMATE and CIBERSORT algorithms, R package, clusterprofiler package, STRING database, Cytoscape, Spearman's or Pearson's correlation test, heatmap, intersection analysis	200 patients
ITGB2	mRNA	Human	Upregulation	Prognostic	Stromal, immune, and ESTIMATE scores evaluation	p<0.005	TCGA-LAML	35280440	Pathway Enrichment Analysis, Protein-Protein Interaction (PPI) Network, Cox Regression Analysis and Kaplan-Meier Survival Analysis, Gene Set Enrichment Analysis , Go Analysis, Kegg Analysis	ESTIMATE and CIBERSORT algorithms, R package, clusterprofiler package, STRING database, Cytoscape, Spearman's or Pearson's correlation test, heatmap, intersection analysis	201 patients
ITGAM	mRNA	Human	Upregulation	Prognostic	Stromal, immune, and ESTIMATE scores evaluation	p<0.04	TCGA-LAML	35280440	Pathway Enrichment Analysis, Protein-Protein Interaction (PPI) Network, Cox Regression Analysis and Kaplan-Meier Survival Analysis, Gene Set Enrichment Analysis , Go Analysis, Kegg Analysis	ESTIMATE and CIBERSORT algorithms, R package, clusterprofiler package, STRING database, Cytoscape, Spearman's or Pearson's correlation test, heatmap, intersection analysis	202 patients

Table can be downloaded from here

This link will take you to the Genecard webpage where information about the gene can be obtained

Click here to go the PubMed page for literature

Download datasets

In this page user can click on the following options to download the respective datasets. It contains final matrices of expression, methylation, CRISPR-Cas9 screens data uploaded and maintained in this database. For detailed assistance visit the [HELP](#) section!

Expression profiling data

Methylation profiling data

CRISPR-Cas9 screens data

Download option allow you to download individual datasets by clicking on the following options

Expression profiling data download

The database's complete list of gene expression profiling datasets is displayed on this page. Click the download button provided against each of the GSE ID's to download them.

GSE ID	No of Samples	Download
GSE111678	260	↓
GSE110087	41	↓
GSE107465	30	↓
GSE104099	45	↓
GSE84334	45	↓
GSE84881	23	↓
GSE70124	46	↓
GSE26294	16	↓
GSE50928	13	↓
GSE24895	14	↓

To go to individual GSEIDs click here

For example; if "Expression profiling data" is selected, all the GSEIDs corresponding to that would appear along with their sample number

Download final matrix files here

*Same for Methylation profiling data

Download datasets

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Expression profiling data

Methylation profiling data

CRISPR-Cas9 screens data

CRISPR-Cas9 screens download

The database's complete list of CRISPR-Cas9 screens data is displayed on this page. Click the download button provided against DepMap and Project Achilles data to download them.

DepMap data	Gene Effect 	Gene Dependency 
Project Achilles data	Gene Effect 	Gene Dependency 

Upon clicking "CRISPR-Cas9 screens data" the following table appears containing gene effect and gene dependency files from DepMap and Project Achilles data

Download gene effect file from here

Download gene dependency file from here

The Hep section opens a page with six options. Click on the options below to read the hidden content



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Glossary

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