


# Projekty

E5728

Jaro 2023

# GEO databáze

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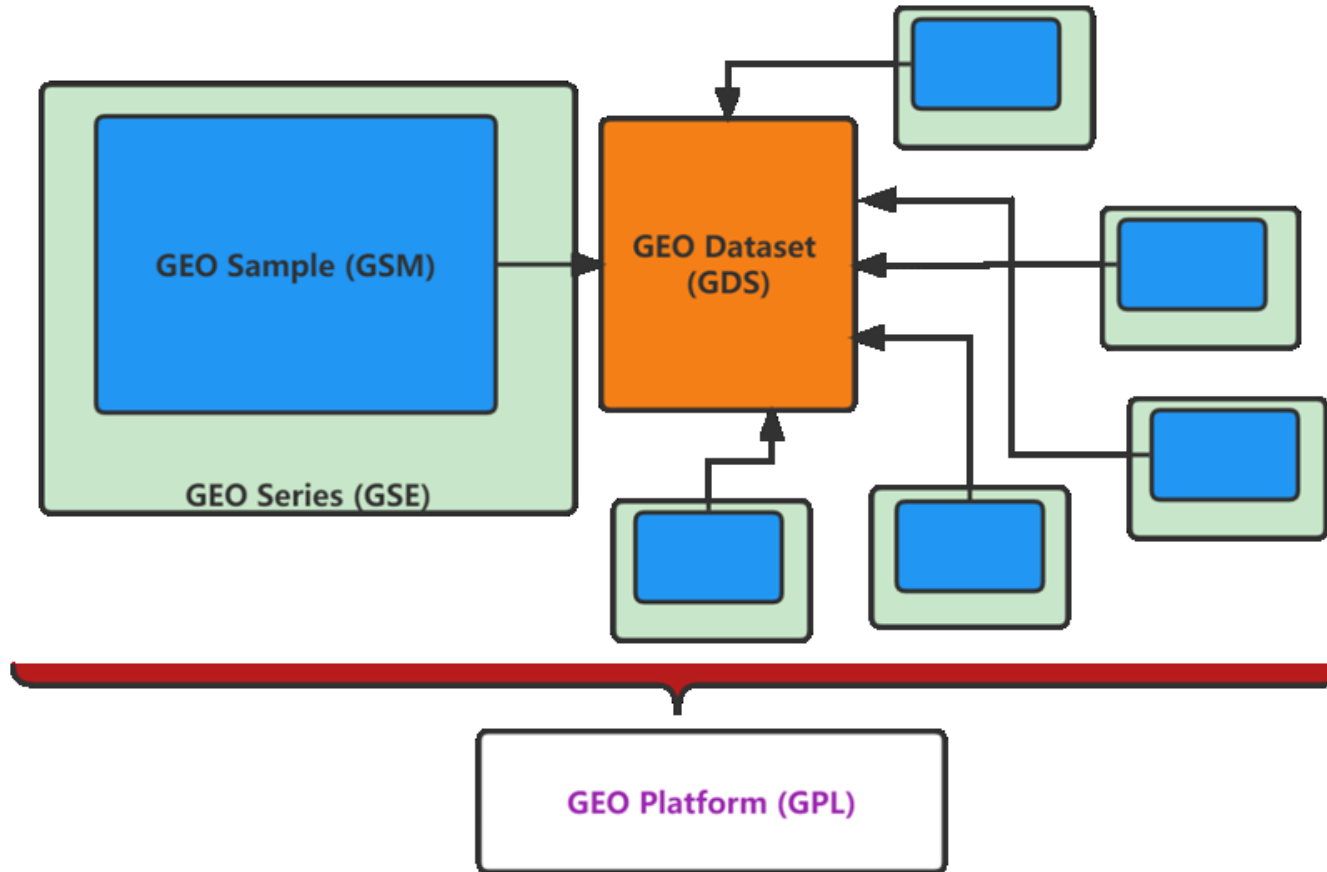
### GEO DataSets Advanced Search Builder

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**Builder**

<input type="text" value="Platform Technology T"/>	
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# GEO databáze

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Entry type  
DataSets (140)  
Series (2,131)  
Samples (35,490)  
Platforms (24)

Organism  
Customize ...

Study type  
Expression profiling by array  
Methylation profiling by array  
Customize ...

Author  
Customize ...

Attribute name  
tissue (19,306)  
strain (341)  
Customize ...

Publication dates  
30 days  
1 year  
Custom range...

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**Search results**  
Items: 1 to 20 of 37785 << First < Prev Page 1 of 1890 Next > Last >>

[Expression data for Vanderbilt triple-negative breast cancer subtype classification](#)

1. (Submitter supplied) This study developed a triple-negative **breast cancer** (TNBC) surrogate subtype classification that represents TNBC subtypes based on the Vanderbilt subtype classification The web-based subtyping tool TNBCtype was used to classify the TNBC cohort into Vanderbilt subtypes  
Organism: Homo sapiens  
Type: Expression profiling by array  
Platform: GPL16686 147 Samples  
Download data: CEL  
GDS: [GDS300000](#) ID: [GDS300000](#)

**Top Organisms** [\[Tree\]](#)  
Homo sapiens (36765)  
Mus musculus (921)  
Rattus norvegicus (65)  
synthetic construct (55)  
Mus (972)  
More...

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3. [responses to the HDAC6 inhibitor ricolinostat \[array\]](#)  
(Submitter supplied) Despite the anticancer activity of pan-histone deacetylase (HDAC) inhibitors, their clinical use has been limited due to toxicity. However, the development of more specific inhibitors that selectively inhibit individual HDACs is emerging as a novel and well-tolerated alternative. Here, we present the results of the first clinical trial evaluating the activity of ricolinostat (the leading HDAC6 inhibitor) in **breast cancer** (BC)

Jak vybrat projekt:

- Téma, kterému rozumíte (jasný dizajn)
- Maximálně 20 vzorků (z výpočetních důvodů)
- Vhodná platforma (viz níže)
- Nejlépe porovnání skupin (a v každé skupině min. 3 biologické – ne technické – replikáty)

# Informace o projektu

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE202536>

Co si všítat dál v popisu projektu:

Existující publikace - pomůže Vám porovnat výsledky

Typ platformy

Má základní data!

NCBI GEO Accession Display

Scope: Self Format: HTML Amount: Quick GEO accession: GSE202536

**Series GSE202536** Query DataSets for GSE202536

Status: Public on Feb 27, 2023  
Title: Doxorubicin response in a triple negative breast cancer cell model: long-term resistance versus short-term stress  
Organism: [Homo sapiens](#)  
Experiment type: Expression profiling by array  
Summary: We have used a cell model for triple negative breast cancer, CAL51 cells, to study the transcriptional profiling of chemotherapy drug response. A doxorubicin resistant derivative has been generated, named CALDOX, which is able to proliferate in the continuous presence of 0.4 micro molar doxorubicin in the culture medium. In addition, both naive CAL51 and drug resistant CALDOX cells, the short-term response to doxorubicin treatment has been studied.

Overall design: CAL51 cells were treated with 0.4 micro M doxorubicin until they were able to survive and proliferate in the presence of drug (these drug resistant cells are termed CALDOX). Short-term effects of doxorubicin were studied in CAL51 cells (with treatments for 24 and 48 h with 0.4 micro M doxorubicin) and CALDOX cells (with treatment for 24 h with 4 micro M doxorubicin). For the array experiment, RNA isolated from three independent cultures were used for each condition.

Contributor(s): [Yague E, Kumar U](#)  
Citation missing: *Has this study been published? Please [login](#) to update or [notify](#) GEO.*  
Submission date: May 09, 2022  
Last update date: Mar 01, 2023  
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Organization name: University of Nottingham  
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Country: United Kingdom

Platforms (1): [GPL570](#) [HG-U133\_Plus\_2] Affymetrix Human Genome U133 Plus 2.0 Array

Samples (15): [GSM6123775](#) CAL - 1  
[GSM6123776](#) CAL - 2  
[GSM6123777](#) CAL - 3

Relations: BioProject: [PRJNA836497](#)

Analyze with GEO2R

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<a href="#">MINIML formatted family file(s)</a>	<a href="#">MINIML</a>
<a href="#">Series Matrix File(s)</a>	<a href="#">TXT</a>

Supplementary file	Size	Download	File type/resource
<a href="#">GSE202536_RAW.tar</a>	80.6 Mb	<a href="#">(http)(custom)</a>	<a href="#">TAR</a> (of <a href="#">CEL</a> )

Raw data provided as supplementary file  
Processed data included within Sample table

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# Informace o platformě:

## Affymetrix Human Genome U133 Plus 2.0 Array

NCBI > GEO > Accession Display Not log

Scope: Self Format: HTML Amount: Quick GEO accession: GPL570 GO

**Platform GPL570** [Query DataSets for GPL570](#)

Status Public on Nov 07, 2003

Title [HG-U133\_Plus\_2] Affymetrix Human Genome U133 Plus 2.0 Array

Technology type in situ oligonucleotide

Distribution commercial

Organism [Homo sapiens](#)

Manufacturer Affymetrix

Manufacture protocol see manufacturer's web site

Complete coverage of the Human Genome U133 Set plus 6,500 additional genes for analysis of over 47,000 transcripts  
All probe sets represented on the GeneChip Human Genome U133 Set are identically replicated on the GeneChip Human Genome U133 Plus 2.0 Array. The sequences from which these probe sets were derived were selected from GenBank®, dbEST, and RefSeq. The sequence clusters were created from the UniGene database (Build 133, April 20, 2001) and then refined by analysis and comparison with a number of other publicly available databases, including the Washington University EST trace repository and the University of California, Santa Cruz Golden-Path human genome database (April 2001 release).  
In addition, there are 9,921 new probe sets representing approximately 6,500 new genes. These gene sequences were selected from GenBank, dbEST, and RefSeq. Sequence clusters were created from the UniGene database (Build 159, January 25, 2003) and refined by analysis and comparison with a number of other publicly available databases, including the Washington University EST trace repository and the NCBI human genome assembly (Build 31).

Description Affymetrix submissions are typically submitted to GEO using the GEO submission method described at [http://www.ncbi.nlm.nih.gov/projects/geo/info/geo\\_affy.html](http://www.ncbi.nlm.nih.gov/projects/geo/info/geo_affy.html)  
June 03, 2009: annotation table updated with netaffx build 28  
June 06, 2012: annotation table updated with netaffx build 32  
June 23, 2016: annotation table updated with netaffx build 35

Web link <http://www.affymetrix.com/support/technical/byproduct.affx?product=hg-u1>  
<http://www.affymetrix.com/analysis/index.affx>

Submission date Nov 07, 2003

Last update date Dec 14, 2020

Organization Affymetrix, Inc.

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Street address  
City Santa Clara  
State/province CA  
ZIP/Postal code 95051  
Country USA

Samples (167954) [GSM18422](#), [GSM18423](#), [GSM18424](#), [GSM18425](#), [GSM18426](#), [GSM18427](#) [More...](#)

Series (5578) [GSE1145](#) changes in cardiac transcription profiles brought about by heart failure

## Jak vybrat platformu?

- Nejlépe Affymetrix nebo cDNA
- Nejlépe zavedenou (již je tady několik let) - viz status – pak již existují standardní metody analýzy a balíky pro zpracování
- Ale musí být pravidelne udržována (viz description a pravidelné update)
- Nejlépe s hodně vzorky a datovými soubory (samples and series)

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL570>

# Doporučené parametry

1. Projekt na lidech nebo myších
2. Platforma Affymetrix nebo cDNA - čím více projektů je na platformě, tím lépe (nevybírat extra vzácné nebo extra nové platformy)
3. Expresní data transkriptom
4. Maximálně 20 vzorků, pokud více, nutno vybrat podskupinu vzorků – pak ale problém s bodem 4
5. Jasný a pochopitelný dizajn (něco, čemu rozumíte)
6. Existující publikace (pomůže Vám v analýze, můžete porovnat výsledky)
7. Má základní (raw) data a klinické informace

# Jak stáhnout data

## 1. Přímo z webu

## 2. S pomocí Bioconductoru

```
if (!require("BiocManager", quietly = TRUE))
  install.packages("BiocManager")

BiocManager::install("GEOquery")
```

Call

```
library(GEOquery) #directlycall
eSet <- getGEO("GSE21933",
  destdir = '.',
  getGPL = F)
```