# ExprTargetDB Documentation

http://www.scandb.org/apps/microrna/

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# 1. Getting started with ExprTargetDB

## 1.1 Citing ExprTargetDB

If you use ExprTargetDB in any published work, please cite both the database as an electronic resource (http://www.scandb.org/apps/microrna/) and the manuscript describing the methods.

> Gamazon ER, Im H-K, Duan S, Lussier YA, Cox NJ, Dolan ME and Zhang W. ExprTarget: An integrative approach to predicting human microRNA targets. PLoS ONE. 2010

## 1.2 Reporting problems, bugs and questions

If you have any technical problems with ExprTargetDB or would like to report a bug, please notify us by going to the following URL:

> http://www.scandb.org/apps/microrna/contactus.html

If you would like to request a reprint of the published paper, please send your email request to:

> Dr. Wei Zhang, weizhan1@uic.edu or
>
> Dr. M. Eileen Dolan, edolan@medicine.bsd.uchicago.edu

## 1.3 Related online resources

ExprTargetDB is linked to SCAN (http://www.scandb.org/) for enhanced annotations. SCAN (SNP and CNV Annotation Database) is a large-scale database of genetics and genomics data associated to a web-interface and a set of methods and algorithms that can be used for mining the data in it. For more information about SCAN, you may refer to:

> Gamazon ER, Zhang W, Konkashbaev A, Duan S, Kistner EO, Nicolae D, Dolan ME and Cox NJ. SCAN: SNP and Copy number Annotation. Bioinformatics. 2010; 26(2): 259-62.

We expect to publish association results between microRNAs and drug response in PACdb (http://www.pacdb.org/). PACdb (pharmacogenetics and cell-line database) is a central repository of pharmacology-related phenotypes that integrates genotypic, gene expression, and pharmacological data obtained via lymphoblastoid cell lines (LCLs). For more information about PACdb, you may refer to:

Gamazon ER, Duan S, Zhang W, Huang RS, Dolan ME and Cox NJ. PACdb: a database for cell-based pharmacogenomics. Pharmacogenetics and Genomics. 2010; 20(4): 269-73.

ExprTargetDB is supported by the Pharmacogenetics of Anticancer Agents Research (PAAR) Group (http://www.paarpharmacogenomics.org/).

We expect to integrate ExprTargetDB with other existing internet resources of pharmacogenomics such as PharmGKB (http://www.pharmgkb.org/).

## 1.4 More reading

For more background information on the use of LCL model and microRNAs in pharmacogenomic studies, you may refer to:

Zhang W and Dolan ME. Emerging role of microRNAs in drug response. Current Opinion in Molecular Therapeutics. 2010; 12(6).

Welsh M, Mangravite L, Medina MW, Tantisira K, Zhang W, Huang RS, McLeod H and Dolan ME. Pharmacogenomic discovery using cell-based models. Pharmacological Reviews. 2009; 61(4): 413-29.

Zhang W and Dolan ME. Use of cell lines in the investigation of pharmacogenetic loci. Current Pharmaceutical Design. 2009; 15(32): 3782-95.

Zhang W, Ratain MJ and Dolan ME. The HapMap resource is providing new insights into ourselves and its application to pharmacogenomics. Bioinformatics and Biology Insights. 2008; 2: 15-23.

# 2. How to use ExprTargetDB

## 2.1 Organization of the user interface

The user interface of ExprTargetDB is organized as the following tabs.

1. "**Home**": a brief introduction to ExprTarget and ExprTargetDB;

2. "**Search**": this tab provides the major function of ExprTargetDB; either microRNA-centric or gene target-centric queries can be submitted through this tab; a sample input is also provided;

3. "**Download**": users can download the complete dataset of predicted microRNA gene targets through this tab;

4. "**Help**": a link to this "ExprTargetDB Documentation"; and

5. "**Contact Us**": emails of the contributors.

## 2.2 Search ExprTargetDB

The major function of ExprTargetDB can be accessed from the "**Search**" tab. Either microRNA-centric ("**Enter microRNAs**") or gene target-centric ("**Enter possible target genes**") queries can be submitted at ExprTargetDB.

### 2.1.1 Input format for microRNA-centric queries

ExprTargetDB can be used to search for predicted gene targets for a particular microRNA or a list of microRNAs. For microRNA-centric queries, a full symbol (e.g., "**`hsa-miR-138`**") can be used to search for gene targets. Multiple symbols separated by space can be entered for a batch query.

### 2.2.2 Input format for gene target-centric queries

ExprTargetDB can be used to search if a particular gene or a list of genes are the targets of microRNAs. For gene target-centric queries, a symbol (e.g., "**`PAPDS`**") can be used. Multiple symbols separated by space can be entered for a batch query.

### 2.2.3 Select prediction algorithm

The following prediction algorithms can be selected: 1) TarBase; 2) miRanda miRBase; 3) TargetScan; 4) PicTar; 5) Expression Microarray in LCLs; 6) miRanda + LCL Expression; and 7) ExprTarget.

### 2.2.4 Select p-value or score cutoff

Users can specify the p-value or score cutoff for the chosen prediction algorithm. The supported ranges of scores or p values are as follows:

1) TarBase: experimentally supported;
2 ) miRanda: p-value can be set between [0,1];
3) TargetScan: p-value can be set between [0,1];
4) PicTar: score can bet set between [0,1000];
5) Expression Microarray in LCLs: p-value can be set between [0,1];
6) miRanda + LCL expression: p-value can be set between [0,1];
7) ExprTarget: score can be set between [0,10000]

## 2.3 An Example

a. Search for "**hsa-miR-138**" and set a score cutoff of "**100**" for "**ExprTarget**" (Figure 1).

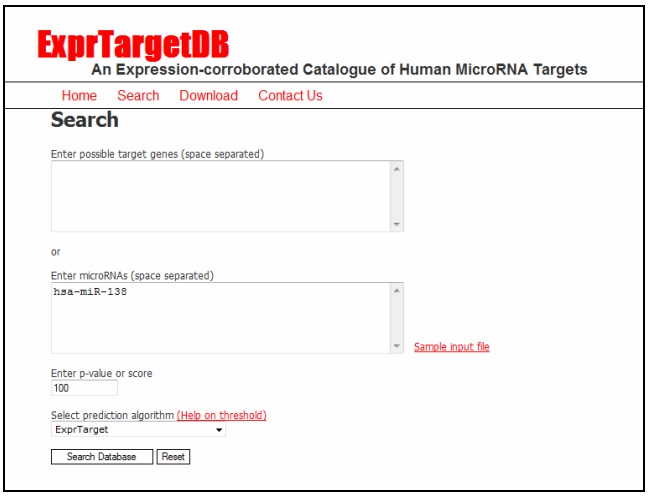


Figure 1. Search for "hsa-miR-138".

b. The output for the example (Figure 2) (e.g., "**SUFU**").

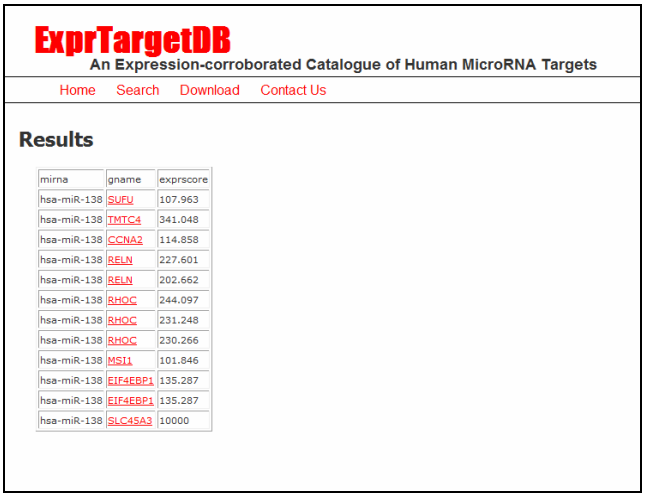


Figure 2. Gene targets for "hsa-miR-138".

c. Search for "**SUFU**" and set a score cutoff of "**100**" for "**ExprTarget**" (Figure 3).

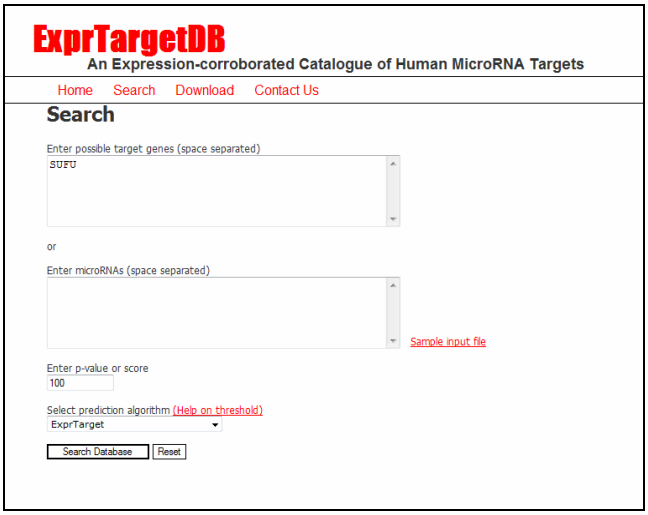


Figure 3. Search for "SUFU".

d. The output for the example (Figure 4) (e.g., "**hsa-miR-138**").

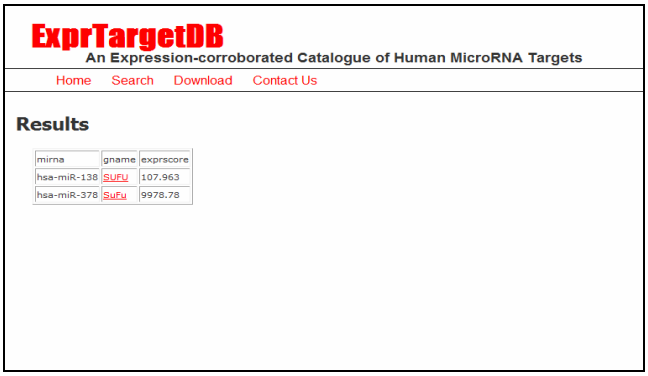


Figure 4. MicroRNA hosts for "SUFU".

# 3. FAQs

## 3.1 What is ExprTargetDB

ExprTargetDB is a public database of human microRNA targets. It implements a novel approach that integrates some of the most frequently used microRNA target predictions as well as microRNA datasets on the HapMap CEU (Caucasians from Utah, USA) and YRI (Yoruba people from Ibadan, Nigeria) samples.

## 3.2 What are the HapMap LCLs?

The Phase 1/2 HapMap samples are Epstein Barr Virus-transformed LCLs derived from apparently healthy individuals of African (YRI), European (CEU) and Asian (CHB, Han Chinese from Beijing, China; and JPT, Japanese from Tokyo, Japan) ancestry. The HapMap LCLs have been used as a model for pharmacogenomic studies as well as other human genetic studies. Extensive genotypic data on >6 million SNPs (single nucleotide polymorphisms) are available for these samples through the International HapMap Project (http://www.hapmap.org/) and the 1000 Genomes Project (http://www.1000genomes.org/). Phenotypic data including gene expression using various microarrays (Affymetrix Human Exon array, Illumina BeadChips), microRNA expression using the Exiqon platform, and cellular toxicities of some anticancer agents are also publicly available.

## 3.3 Where to download the raw microRNA expression data?

We used the Exiqon miRCURRY LNA™ platform (v10.0) to measure microRNA expression in the 58 unrelated CEU samples and 59 unrelated YRI samples. We are actively analyzing

the microRNA expression data. We will upload the raw microRNA expression data to ExprTargetDB and/or PACdb in the future.

### 3.4 Where to download the raw mRNA expression data?

We used our previously published mRNA data in ExprTargetDB. The raw mRNA expression data can be downloaded at the NCBI Gene Expression Omnibus (http://www.ncbi.nlm.nih.gov/geo/). The accession number for the latest version is **GSE9703**. For more information on that dataset, you may refer to:

> Zhang W, Duan S, Bleibel WK, Wisel SA, Huang RS, Wu X, He L, Clark TA, Chen TX, Schweitzer AC, Blume JE, Dolan ME and Cox NJ. Identification of common genetic variants that account for transcript isoform variation between human populations. Human Genetics. 2009; 125(1): 81-93.

## 4. Acknowledgements

ExprTargetDB was funded through the Pharmacogenetics of Anticancer Agents Research Group (http://www.pharmacogenetics.org/) by the National Institutes of Health/National Institute of General Medical Sciences (NIH/NIGMS) grant U01GM61393, National Institutes of Health/National Cancer Institute grants CA139278 and U54 CA121852, NIH/NCI Breast SPORE P50 CA125183, and the University of Chicago Comprehensive Cancer Research Center Pilot Project Program. Data deposits are supported by the NIH/NIGMS grant U01GM61374 (http://www.pharmgkb.org/).