

Databases

- Repositories of array and NGS data
 - Mainly expression data
- Share the data and reproduce analysis
- More common
 - Gene Expression Omnibus (GEO) NCBI
 - ArrayExpress (EBI)
 - Gene Expression Atlas (GXA) NCBI

GEO

NCBI Resources ▾ How To ▾

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[Documentation ▾](#)

[Query & Browse ▾](#)

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Gene Expression Omnibus

GEO is a public functional genomics data repository supporting MIAME-compliant data submissions. Array- and sequence-based data are accepted. Tools are provided to help users query and download experiments and curated gene expression profiles.



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Getting Started

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[About GEO Profiles](#)

[About GEO2R Analysis](#)

[How to Construct a Query](#)

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Tools

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Browse Content

[Repository Browser](#)

DataSets: 4348

Series: 110381

Platforms: 19480

Samples: 2936278

Information for Submitters

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GEO

- A public repository for the archiving and distribution of gene expression data submitted by the scientific community.
- **Curated**, online resource for gene expression data browsing, query, analysis and retrieval.
- Convenient for deposition of gene expression data, as required by funding agencies and journals

GEO architecture

- GEO has four kinds of data records
 - **Platform** (GPL) = the technology used and the features detected
 - **Sample** (GSM) = preparation and description of the sample
 - **Series** (GSE) defines a set of samples and how they are related
 - **DataSets** (GDS) sample data collections assembled by GEO staff

GEO architecture

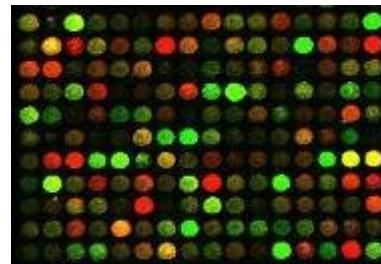
*Submitted by
Manufacturer*

GPL
Platform
descriptions



*Submitted by
Experimentalists*

GSM
Raw/processed
spot intensities
from a single
slide/chip

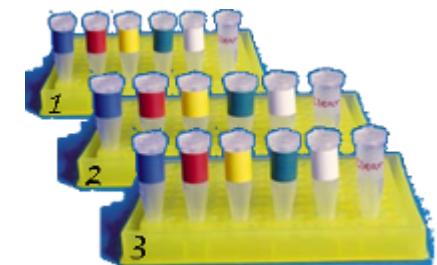


GSE
Grouping of
slide/chip data
“a single experiment”



*Curated by
NCBI*

GDS
Grouping of
experiments



GEO repository browser

Public holdings

Series Platforms Samples Organisms History

[See full list of organisms](#)

Organism	Series	Platforms	Samples
<i>Homo sapiens</i>	46,623	5,425	1,588,653
<i>Mus musculus</i>	32,603	2,361	695,974
<i>Rattus norvegicus</i>	3,630	581	89,643
<i>Drosophila melanogaster</i>	3,417	366	59,509
<i>Arabidopsis thaliana</i>	3,787	380	54,618
<i>Saccharomyces cerevisiae</i>	2,641	601	55,080
<i>Caenorhabditis elegans</i>	1,586	203	15,693
<i>Sus scrofa</i>	718	138	16,231
<i>Bos taurus</i>	793	190	14,295
<i>Oryza sativa</i>	747	193	11,582
<i>Macaca mulatta</i>	433	67	11,233
<i>Zea mays</i>	405	114	11,104
<i>Gallus gallus</i>	670	137	10,229
<i>Escherichia coli</i>	710	155	7,123
<i>Glycine max</i>	259	53	7,357
<i>Xenopus laevis</i>	193	36	2,142

GEO repository browser

Series	Samples	Platforms	DataSets	Summary	Advanced search	
				Search	110,383 series	Export
Accession	Title				Series type(s)	Organism(s)
GSE111800	Small RNA-mediated genomic silencing promotes telomere stability in the absence of telomerase				Non-coding RNA profiling by high throughput sequencing	 Caenorhabditis elegans
GSE111971	Mast cell cytonemes as a defense mechanism against Coxiella burnetii				Expression profiling by array	 Homo sapiens
GSE112551	Molecular mapping of nuclear lamina interactions in the mammalian embryo reveals de novo establishment of nuclear architecture				Genome binding/occupancy profiling by high throughput sequencing	 Mus musculus
GSE122828	Comparison of NK cells and ILC1 in lean versus obese mouse livers by RNASeq				Expression profiling by high throughput sequencing	 Mus musculus
GSE124579	RNA-seq analysis of hPSC-derived brain pericyte-like cells, hPSC-derived neural crest stem cells, and primary human brain pericytes				Expression profiling by high throughput sequencing	 Homo sapiens
GSE128174	Next Generation Sequencing (RNA-Sequencing) for the analysis of RUNX3 targets in H460, H460-ERT2-RUNX3 WT and H460-ERT2-RUNX3 MT(K94/171R mutation)				Expression profiling by high throughput sequencing	 Homo sapiens
GSE128187	Phosphosugar stress in Bacillus subtilis: Intracellular accumulation of mannose 6-phosphate derepresses the glcR-phoC operon from repression by GlcR				Expression profiling by array	 Bacillus subtilis
GSE128188	Candidate Genes for Atrial Fibrillation Identified using Differential Gene Expression from Paired Human Left and Right Atrial Appendages.				Expression profiling by high throughput sequencing	 Homo sapiens
GSE128190	p63 regulated epithelial-to-mesenchymal transition state heterogeneity drives collective invasion.				Expression profiling by array	 Homo sapiens

GEO repository browser

Series	Samples	Platforms	DataSets	Summary	Advanced search	
				Search	2,936,302 samples	Export
Accession	Title			Sample type	Organism(s)	
GSM3039928	wild-type_1			SRA	 Caenorhabditis elegans	
GSM3039929	wild-type_2			SRA	 Caenorhabditis elegans	
GSM3039930	trt-1_1			SRA	 Caenorhabditis elegans	
GSM3039931	trt-1_2			SRA	 Caenorhabditis elegans	
GSM3039932	trt-1_dcr-1_1			SRA	 Caenorhabditis elegans	
GSM3039933	trt-1_dcr-1_2			SRA	 Caenorhabditis elegans	
GSM3045806	HMC-1.2_US_1			RNA	 Homo sapiens	
GSM3045807	HMC-1.2_US_2			RNA	 Homo sapiens	
GSM3045808	HMC-1.2_US_3			RNA	 Homo sapiens	
GSM3045809	HMC-1.2_US_4			RNA	 Homo sapiens	
GSM3045810	HMC-1.2_NM1_1			RNA	 Homo sapiens	
GSM3045811	HMC-1.2_NM1_2			RNA	 Homo sapiens	
GSM3045812	HMC-1.2_NM1_3			DNA	 ...	

GEO series

Series GSE112158

Query DataSets for GSE112158

Status	Public on Mar 11, 2019
Title	Gene expression profiles in GSK-3alpha Ser21Ala knock-in mouse heart
Organism	Mus musculus
Experiment type	Expression profiling by array
Summary	GSK-3 is a serine-threonine protein kinase and consists of two isoforms, GSK-3alpha and GSK-3beta. GSK-3alpha and GSK-3beta are inactivated by phosphorylation at Ser21 and Ser9, respectively. GSK-3alpha Ser21Ala and GSK-3beta Ser9Ala phosphorylation-resistant knock-in mice have constitutively active form of GSK-3.
Overall design	Gene expression in GSK-3alpha Ser21Ala knock-in, GSK-3beta Ser9Ala knock-in, or wild-type mouse hearts were analyzed at baseline. Please note that the wildtype samples were normalized twice for a separate analysis of GSK-3alpha vs wildtype and GSK-3beta vs wildtype. The wildtype samples are included on both series but are the same samples with identical CEL files.
Contributor(s)	Matsuda T , Nakamura M , Zablocki D , Sadoshima J
Citation missing	<i>Has this study been published? Please login to update or notify GEO.</i>
Submission date	Mar 21, 2018
Last update date	Mar 11, 2019
Contact name	Michinari Nakamura
E-mail	nakamumi@njms.rutgers.edu
Organization name	Rutgers New Jersey Medical School
Department	Cell Biology and Molecular Medicine
Lab	Sadoshima Lab
Street address	185 South Orange Ave MSB-I543
City	Newark
State/province	NJ
ZIP/Postal code	07103
Country	USA

GEO series

Platforms (1) [GPL1261 \[Mouse430_2\] Affymetrix Mouse Genome 430 2.0 Array](#)

Samples (4) [GSM3059004 Wild-type1_control_for_alpha](#)

[≡ Less...](#)

[GSM3059005 Wild-type2_control_for_alpha](#)

[GSM3059006 GSK-3alpha S21A knock-in1](#)

[GSM3059007 GSK-3alpha S21A knock-in2](#)

This SubSeries is part of SuperSeries:

[GSE112160 Gene expression profiles in GSK-3alpha Ser21Ala or GSK-3beta Ser9Ala knock-in mouse heart](#)

Relations

BioProject [PRJNA442502](#)

Analyze with GEO2R

Download family

[SOFT formatted family file\(s\)](#)

[MINiML formatted family file\(s\)](#)

[Series Matrix File\(s\)](#)

Format

[SOFT](#) [?](#)

[MINiML](#) [?](#)

[TXT](#) [?](#)

Supplementary data files not provided

Raw data provided as supplementary file

Processed data included within Sample table

GEO samples

Sample GSM3059005		Query DataSets for GSM3059005
Status	Public on Mar 11, 2019	
Title	Wild-type2_control_for_alpha	
Sample type	RNA	
Source name	wildtype_heart	
Organism	Mus musculus	
Characteristics	strain: C57B6 genotype: wildtype age: 3.6 month tissue: Heart	
Treatment protocol	Baseline	
Extracted molecule	total RNA	
Extraction protocol	Trizol extraction of total RNA was performed according to the manufacturer's instructions.	
Label	biotin	
Label protocol	Biotinylated cRNA were prepared according to the standard Affymetrix protocol	
Hybridization protocol	Hybridization and processing of Affymetrix arrays were performed according to Affymetrix standard protocol.	
Scan protocol	Affymetrix GeneChip arrays were scanned using the Affymetrix GeneArray scanner.	
Description	The CEL file for this sample is identical to the CEL file of GSM3059009 but the processed data were normalized only with GSK-3alpha knockin samples.	
Data processing	Intensity values of all probe sets were normalized by the Robust Multichip Analysis (RMA) method using the Affymetrix Expression Console Software.	
Submission date	Mar 21, 2018	
Last update date	Mar 11, 2019	
Contact name	Michinari Nakamura	
E-mail	nakamumi@njms.rutgers.edu	
Organization name	Rutgers New Jersey Medical School	
Department	Cell Biology and Molecular Medicine	
Lab	Sadoshima Lab	
Street address	185 South Orange Ave MSB-I543	
City	Newark	
State/province	NJ	
ZIP/Postal code	07103	
Country	USA	

Platform ID	GPL1261
Series (2)	GSE112158 Gene expression profiles in GSK-3alpha Ser21Ala knock-in mouse heart GSE112160 Gene expression profiles in GSK-3alpha Ser21Ala or GSK-3beta Ser9Ala knock-in mouse heart
Relations	
Reanalyzed by	GSM3059009

Data table header descriptions

ID_REF	VALUE
	RMA Signal Intensity

Data table

ID_REF	VALUE
1415670_at	8.78463788
1415671_at	10.07098221
1415672_at	11.13134217
1415673_at	6.876071653
1415674_a_at	10.28287666
1415675_at	9.092604973
1415676_a_at	12.50939479
1415677_at	9.49874243
1415678_at	11.56569402
1415679_at	11.49926461
1415680_at	9.380554401
1415681_at	11.03408925
1415682_at	8.635512008
1415683_at	11.48238333
1415684_at	9.177241477
1415685_at	9.085002998
1415686_at	10.39055471
1415687_a_at	13.31039038
1415688_at	11.786736
1415689_s_at	9.587576921

Total number of rows: **45101**

Table truncated, full table size **1026 Kbytes**.

[View full table...](#)

Supplementary file	Size	Download	File type/resource
GSM3059005_DZAB_430-2_WT881_020508.CEL.gz	3.7 Mb	(ftp)(http)	CEL

Raw data (BioProject)

Gene expression profiles in GSK-3alpha Ser21Ala knock-in mouse heart (house mouse)

Accession: PRJNA442502 ID: 442502

GSK-3 is a serine-threonine protein kinase and consists of two isoforms, GSK-3alpha and GSK-3beta. [More...](#)

See Genome Information for *Mus musculus*

Accession	PRJNA442502; GEO: GSE112158
Data Type	Transcriptome or Gene expression
Scope	Multiisolate
Organism	Mus musculus [Taxonomy ID: 10090] Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus; Mus musculus
Submission	Registration date: 21-Mar-2018 Sadoshima Lab, Cell Biology and Molecular Medicine, Rutgers New Jersey Medical School
Relevance	Model Organism

[NAVIGATE UP](#)

This project is a component of the Gene expression profiles in GSK-3alpha Ser21Ala or GSK-3beta Ser9Ala knock-in mouse heart

[NAVIGATE ACROSS](#)

1 additional project is a component of the Gene expression profiles in GSK-3alpha Ser21Ala or GSK-3beta Ser9Ala knock-in mouse heart.

28858 additional projects are related by organism.

Project Data:

Resource Name	Number of Links
GEO DataSets	1
▼ GEO Data Details	
Parameter	Value
Data volume, Spots	180404
Data volume, Processed Mbytes	5
Data volume, Supplementary Mbytes	15

Raw data (SRA)

[SRX4404498](#): GSM3290910: Bin67_K785R_RNA-Seq_Rep2; Homo sapiens; RNA-Seq

1 ILLUMINA (NextSeq 500) run: 32.1M spots, 2.4G bases, 911.3Mb downloads

Submitted by: NCBI (GEO)

Study: The mSWI/SNF ATPase module mediates subcomplex identity and non-catalytic targeting in SCCOHT [RNA-seq]

[PRJNA481742](#) • [SRP154344](#) • [All experiments](#) • [All runs](#)

[show Abstract](#)

Sample: Bin67_K785R_RNA-Seq_Rep2

[SAMN09689616](#) • [SRS3558908](#) • [All experiments](#) • [All runs](#)

Organism: [Homo sapiens](#)

Library:

Instrument: NextSeq 500

Strategy: RNA-Seq

Source: TRANSCRIPTOMIC

Selection: cDNA

Layout: SINGLE

Construction protocol: One million cells of each condition were harvested using Qiagen RNeasy kit and 1 ug was DNase treated and used in Illumina TruSeq Stranded mRNA library prep kit All library prep and sequencing were 75bp single end on Illuminia Nextseq 500

Experiment attributes:

GEO Accession: [GSM3290910](#)

Links:

Runs: 1 run, 32.1M spots, 2.4G bases, [911.3Mb](#)

Run	# of Spots	# of Bases	Size	Published
<u>SRR7536933</u>	32,079,217	2.4G	911.3Mb	2019-03-12

GEO search engines

- GEO data can be queried as:
 - Datasets: **experiment-centric** view using Entrez **GEO DataSets**
 - Gene profiles: **gene-centric** view using Entrez **GEO Profiles**
- Selecting either takes you to a similar Entrez introduction page

GEO datasets

GEO DataSets GEO DataSets ▾ prostate cancer
Create alert Advanced

Entry type Summary ▾ 20 per page ▾ Sort by Default order ▾ Send to: ▾

DataSets (79)
Series (1,637)
Samples (24,051)
Platforms (39)

Organism
Customize ...

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

Author
Customize ...

Attribute name
tissue (8,821)
strain (745)
Customize ...

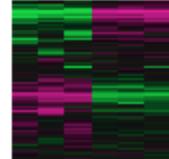
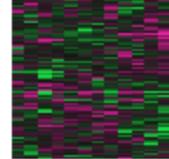
Publication dates
30 days
1 year
Custom range...

[Clear all](#)
[Show additional filters](#)

Search results
Items: 1 to 20 of 25806 << First < Prev Page of 1291 Next > Last >>

[MicroRNA-135b overexpression effect on prostate cancer cell line: time course](#)
1. Analysis of LNCaP **prostate cancer** (PCa) cells overexpressing miRNA-135b for up to 36 hours. LNCaP cells express the androgen receptor (AR). MiRNA-135b overexpression in AR+ PCa cells results in slower growth compared to AR knockdown. Results provide insight into the basis of this slower growth.
Organism: Homo sapiens
Type: Expression profiling by array, transformed count, 2 protocol, 3 time sets
Platform: [GPL10558](#) Series: [GSE57820](#) 12 Samples
Download data
DataSet Accession: GDS6100 ID: 6100
[PubMed](#) [Full text in PMC](#) [Similar studies](#) [GEO Profiles](#) [Analyze DataSet](#)

[Peptidyl-prolyl cis/trans isomerase Pin1 deficiency effect on prostate cancer cells](#)
2. Analysis of **prostate cancer** (PC) cell lines LNCap (androgen-dependent) and DU145 (androgen-independent) following siRNA-mediated knockdown of Peptidyl-prolyl cis/trans isomerase Pin1. Results provide insight into molecular mechanisms underlying Pin1 modulation of both PC two cell lines.
Organism: Homo sapiens
Type: Expression profiling by array, transformed count, 2 cell line, 3 protocol sets
Platform: [GPL6244](#) Series: [GSE67457](#) 6 Samples
Download data: CEL
DataSet Accession: GDS5805 ID: 5805
[PubMed](#) [Full text in PMC](#) [Similar studies](#) [GEO Profiles](#) [Analyze DataSet](#)



GEO profiles

GEO Profiles GEO Profiles ▾ NKX3-1
Create alert Advanced

Gene symbol Summary ▾ 20 per page ▾ Sort by Subgroup effect ▾
Customize ... Send to: ▾

Gene keyword Search results
Customize ...

Organism Items: 1 to 20 of 5476
Customize ...

Gene ontology << First < Prev Page 1 of 274 Next > Last >>
Customize ...

Differential expression

Up/down genes

DataSet keyword

Customize ...

GEO accession

Customize ...

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[Nkx3-1 - Lupus susceptibility locus Sle1a.1 in murine model of lupus: CD4+ T cells](#)
Annotation: Nkx3-1, NK-3 transcription factor, locus 1 (Drosophila)
Organism: Mus musculus
Reporter: GPL1261, 1449998_at (ID_REF), GDS4050, 18095 (Gene ID), NM_010921
DataSet type: Expression profiling by array, transformed count, 8 samples
ID: 77241293
[GEO DataSets](#) [Gene](#) [UniGene](#) [Profile neighbors](#) [Chromosome neighbors](#) [Homologene neighbors](#)

[Nkx3-1 - Model for inflammatory signaling in prostate epithelium based on expression of a constitutively active version of IκB kinase 2 \(IKK2ca\)](#)
Annotation: Nkx3-1, NK-3 transcription factor, locus 1 (Drosophila)
Organism: Mus musculus
Reporter: GPL6246, 10416195 (ID_REF), GDS4119, NM_010921, BC132401, BC132427, U73460, U88542, chr14:69190692-69194661 (SPOT ID)
DataSet type: Expression profiling by array, transformed count, 6 samples
ID: 79450254
[GEO DataSets](#) [Gene](#) [UniGene](#) [Profile neighbors](#) [Chromosome neighbors](#) [Homologene neighbors](#)

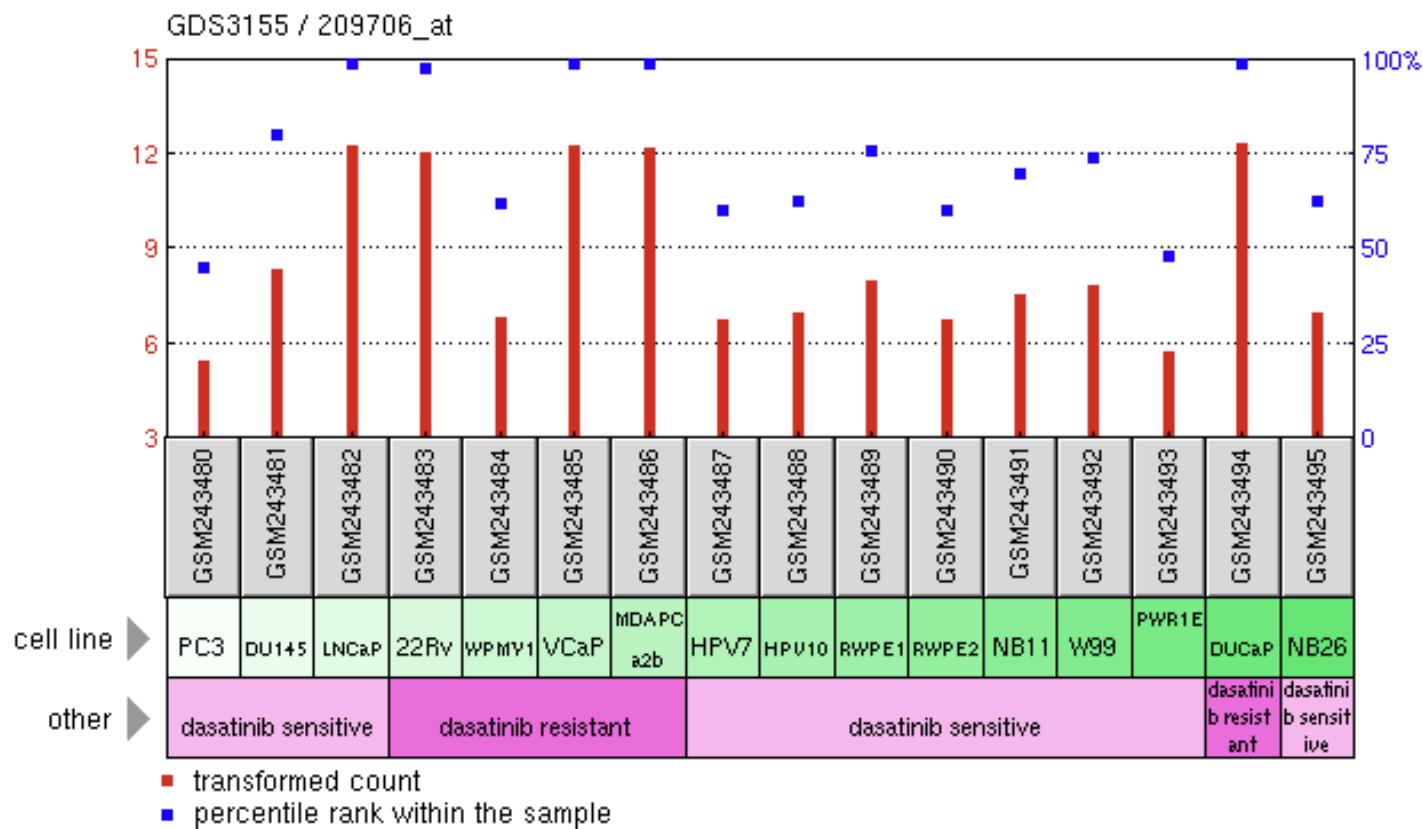
[NKX3-1 - Androgen sensitive and insensitive prostate cancer cell lines: expression profiles](#)
Annotation: NKX3-1, NK3 homeobox 1
Organism: Homo sapiens
Reporter: GPL3341, 33937 (ID_REF), GDS1699, AA442287
DataSet type: Expression profiling by array, log2 ratio, 8 samples
ID: 18277063
[GEO DataSets](#) [Gene](#) [UniGene](#) [Profile neighbors](#) [Chromosome neighbors](#) [Homologene neighbors](#)

GEO profiles

Profile GDS3155 / 209706_at

Title Dasatinib resistant and sensitive prostatic cancer cell lines

Organism Homo sapiens



Gene Expression Atlas (GXA)

- <https://www.ebi.ac.uk/gxa>
- Provides information on gene expression patterns
- Gene expression data are re-analyzed with common pipelines

GXA

[Home](#) | [Browse experiments](#) | [Download](#) | [Release notes](#) | [FAQ](#) | [Help](#) | [Licence](#) | [About](#) | [Feedback](#)

Baseline expression Differential expression NKX3-1 information

Baseline expression Differential expression

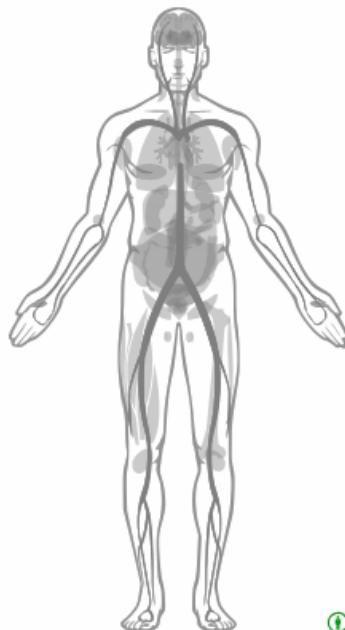
NKX3-1 information

Show anatomograms

Filter your results

Homo sapiens

- Organism part
 - Cell line
 - Cell type
 - Developmental stage
 - Disease
 - Individual
 - Sex



Organism part

Showing 25 experiments:

This figure is a horizontal stacked bar chart illustrating gene expression patterns across various tissues and brain regions. The y-axis on the left lists genes: Ex, lab, lap, (ab), map, ann, 22, 21, and 18. The x-axis at the top lists tissue/regions: adipose tissue, atrium auricular region, brain, Brodmann (1909) area 9, cerebellar hemisphere, choroid plexus, diencephalon, ectocervix, esophagogastric junction, fallopian tube, frontal lobe, heart left v., and R. Each bar represents a gene, and its total length corresponds to the expression level of that gene in a specific tissue or region. The bars are composed of blue and grey segments, likely representing different transcript variants or isoforms.

ArrayExpress

 ArrayExpress

Search 🔍
Examples: E-MEXP-31, cancer, p53, Geuvadis _advanced search

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Filter search results

Page 1 2 3 4 5 6 .. 2875

Showing 1 - 25 of 71854 experiments

Page size 25 50 100 250 500

Accession	Title	Type	Organism	Assays	Released	Processed	Raw	Views	Atlas
E-MTAB-6425	Expression of DNA repair and cell cycle genes in a cohort of primary and recurrent glioblastoma multiforme patients	transcription profiling by array	Homo sapiens	87	Today			1	-
E-MTAB-7765	RNAseq of the small intestine of mice 6 days after they were transplanted with either wildtype allogeneic T cells or glucocorticoid-resistant allogeneic T cells (mouse model of acute graft-versus-host disease)	RNA-seq of coding RNA	Mus musculus	10	Yesterday			-	-
E-MTAB-7672	An integrated global analysis of compartmentalized HRAS signaling	transcription profiling by array	Homo sapiens	18	Yesterday	-		-	-
E-MTAB-6987	Single-cell RNA sequencing of VE-Cadherin+ cells isolated from mouse E10.5 aorta-gonad-mesonephros region	RNA-seq of coding RNA from single cells	Mus musculus	96	Yesterday	-		-	-
E-MTAB-7747	ChIP-seq for H3K27ac in the GR18 cell line treated for 1.5 h with 1 µM dexamethasone	ChIP-seq	Homo sapiens	1	11/03/2019			-	-
E-MTAB-7746	ATAC-seq in GR18 cell line comparing cells treated for 90 minutes with 1 micro molar dexamethasone with vehicle (ethanol) control-treated cells	ATAC-seq	Homo sapiens	2	11/03/2019			-	-

Bioconductor

All Packages

Bioconductor version 3.8 (Release)

Autocomplete biocViews search:

► StatisticalMethod (572)
▼ Technology (1049)
CRISPR (7)
ddPCR (2)
FlowCytometry (53)
► MassSpectrometry (79)
▼ Microarray (427)
ChipOnChip (7)
GenotypingArray (1)
MethylationArray (25)
MicroRNAArray (1)
mRNAMicroarray (14)
MultiChannel (7)
OneChannel (76)
ProprietaryPlatforms (6)
TissueMicroarray (1)
TwoChannel (63)

Packages found under OneChannel:

Rank based on number of downloads: lower numbers are more frequently downloaded.

Show All ▾ entries

Search table:

Package	Maintainer	Title	Rank
limma	Gordon Smyth	Linear Models for Microarray Data	11
affy	Rafael A. Irizarry	Methods for Affymetrix Oligonucleotide Arrays	30
GEOquery	Sean Davis	Get data from NCBI Gene Expression Omnibus (GEO)	40
vsn	Wolfgang Huber	Variance stabilization and calibration for microarray data	56
aroma.light	Henrik Bengtsson	Light-Weight Methods for Normalization and Visualization of Microarray Data using Only Basic R Data Types	71
gcma	Z. Wu	Background Adjustment Using Sequence Information	86
oligo	Benilton Carvalho	Preprocessing tools for oligonucleotide arrays	87
aftxparser	Kasper Daniel Hansen	Affymetrix File Parsing SDK	89
affyPLM	Ben Bolstad	Methods for fitting probe-level models	100
lumi	Pan Du, Lei Huang, Gang Feng	BeadArray Specific Methods for Illumina Methylation and Expression Microarrays	116
gage	Weijun Luo	Generally Applicable Gene-set Enrichment for Pathway Analysis	117
globaltest	Jelle Goeman	Testing Groups of Covariates/Features for Association with a Response Variable, with Applications to Gene Set Testing	127
simpleaffy	Crispin Miller	Very simple high level analysis of Affymetrix data	134
beadarray	Mark Dunning	Quality assessment and low-level analysis for Illumina BeadArray data	143
DMRcate	Tim Peters	Methylation array and sequencing spatial analysis methods	162
annaffy	Colin A. Smith	Annotation tools for Affymetrix biological metadata	170
ArrayExpress	Suhail Mohammed	Access the ArrayExpress Microarray Database at EBI and build Bioconductor data structures: ExpressionSet, AffyBatch, NChannelSet	179