

The manual for

# **ChIP-Atlas: Dataset Search**

---

1. Search by keyword
2. Search from papers
3. Tips

# Access to ChIP-Atlas Dataset Search

 Peak Browser  Enrichment Analysis  Diff Analysis  Target Genes  Colocalization  Publications  Docs

Find By ID    Search

## ChIP-Atlas

A data-mining suite for exploring epigenomic landscapes by fully integrating 376,000 ChIP-seq, ATAC-seq and Bisulfite-seq experiments.



Peak Browser

[ChIP](#) [ATAC](#) [Bisulfite](#)



Enrichment Analysis

[ChIP](#) [ATAC](#) [Bisulfite](#)



Diff Analysis

[ChIP](#) [ATAC](#)

Dataset Search



Target Genes

[ChIP](#)



Colocalization

[ChIP](#)



Dataset Search

[ChIP](#) [ATAC](#) [Bisulfite](#)

### What's new

- Added **Annotation tracks** to Peak Browser, together with UI improvement (2023/10/25)
- Launched **Diff Analysis** tool enabling to detect differential peaks or differentially methylated regions (2023/10/25)
- **New publication** on the NAR web server issue! <https://doi.org/10.1093/nar/gkac199> (2022/03/24)
- Added **ATAC-Seq and Bisulfite-Seq**, together with UI improvement including 'peak' icon! (2021/10/04)

Access ChIP-Atlas home page (<https://chip-atlas.org>) and click on the “Dataset Search” panel.

# Access to ChIP-Atlas Dataset Search

## ChIP-Atlas: Dataset Search

Tutorial

Find experiments by keywords

Simple search

Detailed search

Show 

10

 entries

Search:

Showing 1 to 10 of 375,698 entries

Copy

TSV

SRX ID	SRA ID	GEO ID	Genome	Antigen class	Antigen	Cell type class	Cell type
<a href="#">SRX019491</a>	SRA012529	<a href="#">GSM534464</a>	hg19, hg38	Input control	Input control	Adipocyte	Adipose stromal cell
<a href="#">SRX019492</a>	SRA012529	<a href="#">GSM534465</a>	hg19, hg38	Histone	H3K4me3	Adipocyte	Adipose stromal cell
<a href="#">SRX019493</a>	SRA012529	<a href="#">GSM534466</a>	hg19, hg38	Histone	H3K4me2	Adipocyte	Adipose stromal cell
<a href="#">SRX019494</a>	SRA012529	<a href="#">GSM534467</a>	hg19, hg38	Histone	H3K4me1	Adipocyte	Adipose stromal cell
<a href="#">SRX019495</a>	SRA012529	<a href="#">GSM534468</a>	hg19, hg38	Histone	H3K27ac	Adipocyte	Adipose stromal cell
<a href="#">SRX019496</a>	SRA012529	<a href="#">GSM534469</a>	hg19, hg38	Histone	H3K27me3	Adipocyte	Adipose stromal cell
<a href="#">SRX019497</a>	SRA012529	<a href="#">GSM534470</a>	hg19, hg38	Histone	H3K36me3	Adipocyte	Adipose stromal cell
<a href="#">SRX019498</a>	SRA012529	<a href="#">GSM534471</a>	hg19, hg38	TFs and others	CTCF	Adipocyte	Adipose stromal cell
<a href="#">SRX019499</a>	SRA012529	<a href="#">GSM534472</a>	hg19, hg38	Histone	H3K4me3	Adipocyte	Adipose stromal cell
<a href="#">SRX019500</a>	SRA012529	<a href="#">GSM534473</a>	hg19, hg38	Histone	H3K4me2	Adipocyte	Adipose stromal cell

A table is displayed showing the sample metadata of the ChIP-seq, ATAC-seq, DNase-seq, and Bisulfite-seq experiments that are archived in ChIP-Atlas. For example, the highlighted line indicates the H3K27ac ChIP-seq data in adipose stromal cells analyzed with human genome assemblies (hg19 and hg38).

# Keyword search

[Peak Browser](#)[Enrichment Analysis](#)[Diff Analysis](#)[Target Genes](#)[Colocalization](#)[Publications](#)[Docs](#)[Find By ID](#)[Go](#)[Search](#)

## ChIP-Atlas: Dataset Search

Find experiments by keywords

[Simple search](#)[Detailed search](#)

Show  entries

Showing 1 to 10 of 57 entries (filtered from 375,698 total entries)

[Copy](#)[TSV](#)

Search:

Pou5f1  
iPS

[? Tutorial](#)

SRX ID	SRA ID	GEO ID	Genome	Antigen class	Antigen	Cell type class	Cell type
<a href="#">SRX1813578</a>	SRA430376	<a href="#">GSM2183773</a>	hg19, hg38	TFs and others	POU5F1	Pluripotent stem cell	iPS cells
<a href="#">SRX1813579</a>	SRA430376	<a href="#">GSM2183774</a>	hg19, hg38	TFs and others	POU5F1	Pluripotent stem cell	iPS cells
<a href="#">SRX2630422</a>	SRA544063	<a href="#">GSM2527650</a>	hg19, hg38	TFs and others	POU5F1	Pluripotent stem cell	iPS cells
<a href="#">SRX2630423</a>	SRA544063	<a href="#">GSM2527651</a>	hg19, hg38	TFs and others	POU5F1	Pluripotent stem cell	iPS cells
<a href="#">SRX12369</a>	SRA156563	<a href="#">GSM1364025</a>	hg19, hg38	TFs and others	POU5F1	Pluripotent stem cell	iPS cells
<a href="#">SRX3038010</a>	SRA592182	<a href="#">GSM2718346</a>	mm9, mm10	TFs and others	Pou5f1	Pluripotent stem cell	iPS cells
<a href="#">SRX3038011</a>	SRA592182	<a href="#">GSM2718347</a>	mm9, mm10	TFs and others	Pou5f1	Pluripotent stem cell	iPS cells
<a href="#">SRX3038012</a>	SRA592182	<a href="#">GSM2718348</a>	mm9, mm10	TFs and others	Pou5f1	Pluripotent stem cell	iPS cells
<a href="#">SRX3038013</a>	SRA592182	<a href="#">GSM2718349</a>	mm9, mm10	TFs and others	Pou5f1	Pluripotent stem cell	iPS cells

SRX ID =  
SRX2630422

Enter any keyword(s) in the search box. For example, entering “Pou5f1 iPS” will filter POU5F1 ChIP-seq data in iPS cells. Click on an experiment ID (= SRX ID; e.g., SRX2630422).

[\[?\] Tips: Experiment ID](#)

# Metadata of the selected experiment

[Browser](#) [Enrichment Analysis](#) [Diff Analysis](#) [Target Genes](#) [Colocalization](#) [Publications](#) [Docs](#) [Find By ID](#)   [Search](#)

Experiment ID

SRX2630422

GSM2527650: ChIP-seq from induced pluripotent s (AG); Homo sapiens; ChIP-Seq

Visualize

Analyze

Download

Link Out

Curated metadata

Sample information curated by ChIP-Atlas

Antigen

Antigen Class

TFs and others

Antigen

POU5F1

Cell type

Cell type Class

Pluripotent stem cell

Cell type

iPS cells

NA

NA

Original metadata

Attributes by original data submitter

Sample

age

53 year

donor ID

ENCDO336AAA

dev stage

adult

sample type

induced pluripotent stem cell line

sex

male

cell line

induced pluripotent stem cell

lab

Thomas Gingeras, CSHL

This is the webpage for **the** experiment ID SRX2630422, displaying the sample metadata curated by ChIP-Atlas staff and described by the original data submitter.

# Metadata of the selected experiment

[Peak Browser](#)[Enrichment Analysis](#)[Diff Analysis](#)[Target Genes](#)[Colocalization](#)[Publications](#)[Docs](#)[Find By ID](#)[Go](#)[Search](#)

**cell line** induced pluripotent stem  
**lab** Thomas Gingeras, CS

Sequence  
library

## Sequenced DNA Library

**library\_strategy** ChIP-Seq  
**library\_source** GENOMIC  
**library\_selection** ChIP  
**library\_construction\_...** general protocol: [https://www.encodeproject.org/documents/6ecd8240-a351-479b-9de6-f09ca3702ac3/@download/attachment/ChIP-seq\\_Protocol\\_v011014.pdf](https://www.encodeproject.org/documents/6ecd8240-a351-479b-9de6-f09ca3702ac3/@download/attachment/ChIP-seq_Protocol_v011014.pdf) general protocol: [https://www.encodeproject.org/documents/6ecd8240-a351-479b-9de6-f09ca3702ac3/@download/attachment/ChIP-seq\\_Protocol\\_v011014.pdf](https://www.encodeproject.org/documents/6ecd8240-a351-479b-9de6-f09ca3702ac3/@download/attachment/ChIP-seq_Protocol_v011014.pdf)

## Sequencing Platform

**instrument\_model** Illumina HiSeq 2000

Process  
log

## Read processing pipeline log

[Where can I get the processing logs?](#)

### hg38

**Number of total reads** 21944406  
**Reads aligned (%)** 96.4  
**Duplicates removed (%)** 2.7  
**Number of peaks** 5454 (qval < 1E-05)

### hg19

**Number of total reads** 21944406  
**Reads aligned (%)** 96.1  
**Duplicates removed (%)** 3.1  
**Number of peaks** 5421 (qval < 1E-05)

The library information and the process log are shown.

# Browsing the data

The screenshot shows the ChIP-Atlas web interface for sample SRX2630422. The top navigation bar includes links for Peak Browser, Enrichment Analysis, Diff Analysis, Publications, Docs, Find By ID, and a search bar. The sample information section displays details about the antigen (POU5F1) and cell type (Pluripotent stem cell). A dropdown menu for the 'Visualize' button is open, showing options for hg38 and hg19, including BigWig and Peak-call (q < 1E-05, 1E-10, 1E-20). An IGV window is also visible at the bottom, showing a genomic track for Human (GRCh38/hg38).

Visualize

hg38

BigWig

Peak

IGV

Sample information curated by ChIP-Atlas

Antigen	
Antigen Class	TFs and others
Antigen	POU5F1

Cell type	
Cell type Class	Pluripotent stem cell
Cell type	iPS cells
NA	NA

Attributes by original data submitter

Sample
age
donor ID
dev stage
sample type
sex
cell line
lab

Sequenced DNA Libr

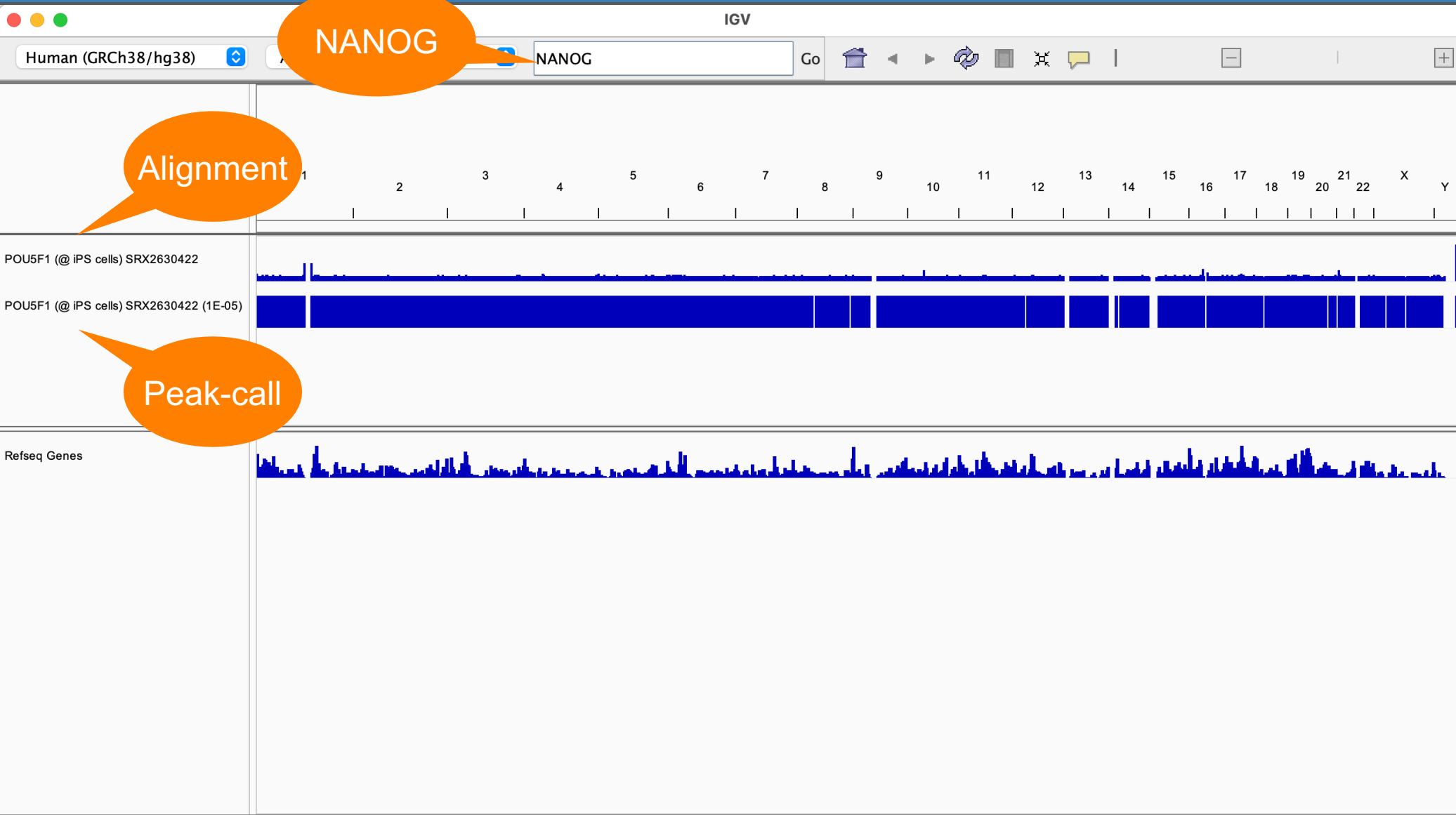
Human (GRCh38/hg38) All Go

1 2 3 4 5 6 7 8 9 10 11

To view the alignment and peak-call data on genome browser IGV, make sure that IGV has been launched before clicking on “Visualize”, “BigWig”, and “Peak-call”.

[🔗 Tips: Installation of IGV](#)

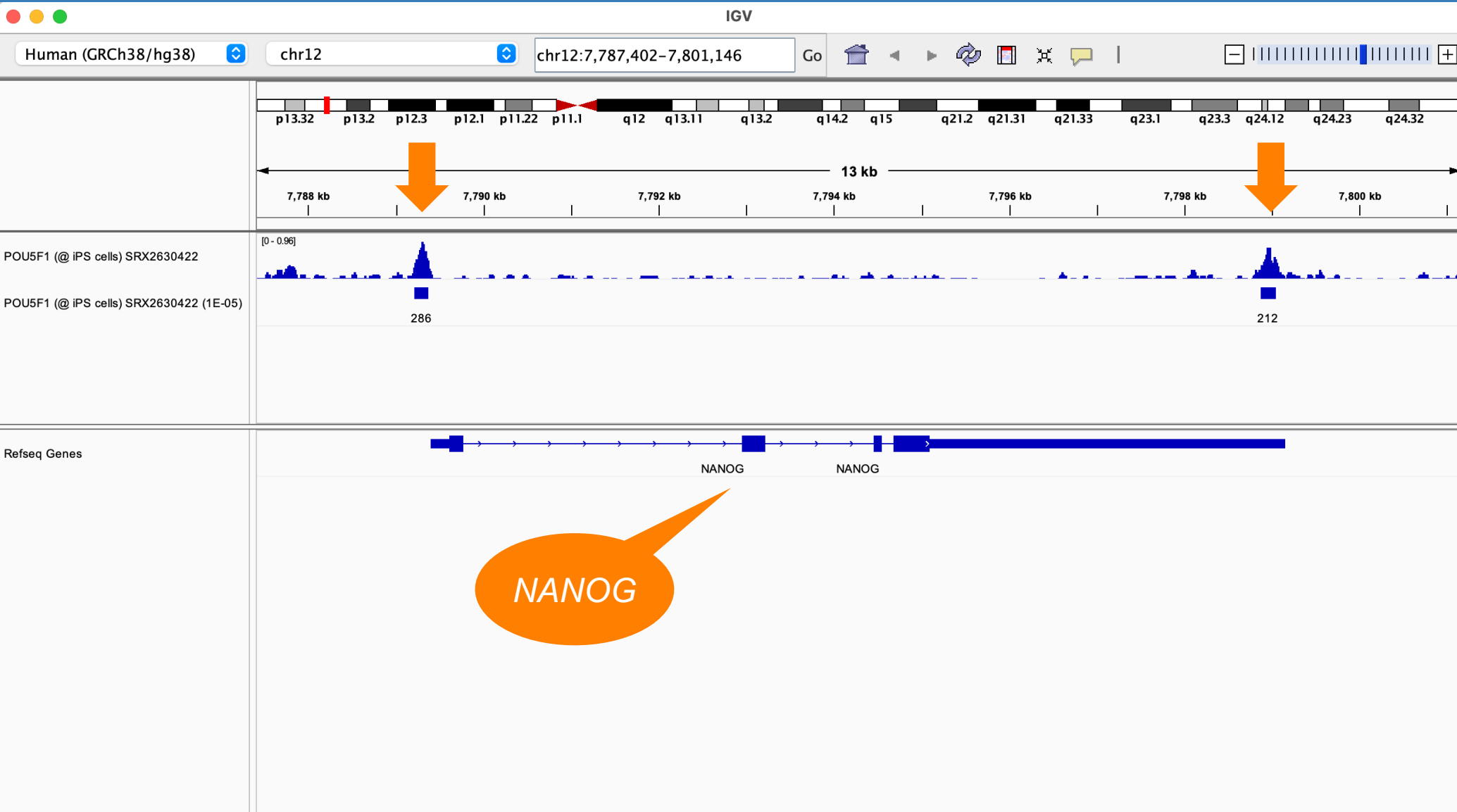
# Browsing the data



The alignment and peak-call data are loaded into IGV. Enter a gene name of interest (e.g., *NANOG*)



# Browsing the data



POU5F1 binding is evident around the *NANOG* gene locus.

# Downloading the data

Peak Browser

Enrichment Analysis

Diff Analysis

Target Genes

Colocalization

cs

Find By ID

GSM469863

Go

Search

Download

SRX2630422

GSM2527650: ChIP-seq from induced pluripotent stem cell (ENCLB429KAG); Homo sapiens; ChIP-seq

Visualize

Analyze

Download

Link Out

Sample information curated by ChIP-Atlas

Antigen

Antigen Class

TFs and others

Antigen

POU5F1

Cell type

Cell type Class

Pluripotent stem cell

Cell type

iPS cells

NA

NA

Attributes by original data submitter

Sample

age

53 year

donor ID

ENCDO336AAA

dev stage

adult

sample type

induced pluripotent stem cell line

sex

male

cell line

induced pluripotent stem cell

lab

Thomas Gingeras, CSHL

- For hg38
- BigWig
- Peak-call (q < 1E-05)
- Peak-call (q < 1E-10)
- Peak-call (q < 1E-20)
- For hg19
- BigWig
- Peak-call (q < 1E-05)
- Peak-call (q < 1E-10)
- Peak-call (q < 1E-20)

You can download the alignment data and peak-call data by clicking on the “Download” button.

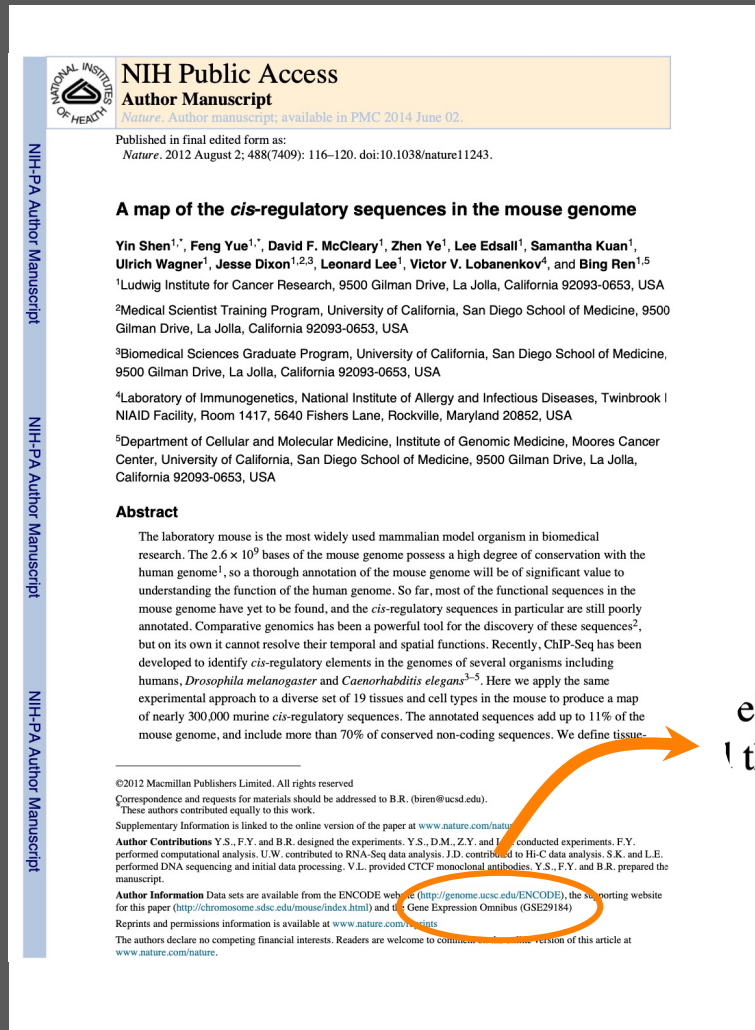
The manual for

# **ChIP-Atlas: Dataset Search**

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1. Search by keyword
2. Search from papers
3. Tips

# Search from papers



Shen, et al., 2012 Nature

website (<http://genome.ucsc.edu/ENCODE>), the s  
the Gene Expression Omnibus (GSE29184)

preprints

Most papers presenting high-throughput sequencing data describe a Gene Expression Omnibus (GEO) ID beginning with “GSE”.

NCBI

Resources

How To

GEO Home

Documentation

Query & Browse

Email GEO

Sign in to NCBI

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.

GSE29184

GSE29184

Search

Getting Started

Overview

FAQ

About GEO DataSets

About GEO Profiles

About GEO2R Analysis

How to Construct a Query

How to Download Data

Tools

Search for Studies at GEO DataSets

Search for Gene Expression at GEO Profiles

Search GEO Documentation

Analyze a Study with GEO2R

Studies with Genome Data Viewer Tracks

Programmatic Access

FTP Site

ENCODE Data Listings and Tracks

Browse Content

Repository Browser

DataSets:4348

Series:217620

Platforms:25749

Samples:6988915

Information for Submitters

Login to Submit

Submission Guidelines



Update Guidelines

MIAME Standards



Citing and Linking to GEO

Guidelines for Reviewers

GEO Publications

  
Gene Expression Omnibus

HOMESEARCHSITE MAPGEO PublicationsFAQMIAMEEmail GEO

NCBI > GEO > **Accession Display** Not logged in | [Login](#) 

mouse over screen elements for information.

GSE29184

self

Format: HTML

Amount: Quick

GEO accession: GSE29184

GO

**Series GSE29184**

[Query DataSets for GSE29184](#)

Status	Public on Jul 01, 2012
Title	A draft map of cis-regulatory sequences in the mouse genome
Organism	<a href="#">Mus musculus</a>
Experiment type	Genome binding/occupancy profiling by high throughput sequencing Expression profiling by high throughput sequencing Genome variation profiling by high throughput sequencing
Summary	The laboratory mouse is the most widely used mammalian model organism in biomedical research. The 2.6 billion bases of the mouse genome share a high degree of conservation with the human genome, so a thorough annotation of the mouse genome will be of significant value to understanding the function of the human genome. To date, most of the functional sequences in the mouse genome have yet to be found, and the cis-regulatory sequences in particular are still poorly annotated. Comparative genomics has been a powerful tool for

This is a GEO Web site of the GSE29184 series.

# Looking for an experiment ID

Street address	9500 Gilman Drive
City	La Jolla
State/province	CA
ZIP/Postal code	92093
Country	USA

Samples

(3) [GPL9250](#) Illumina Genome Analyzer II (Mus musculus)  
[GPL11002](#) Illumina Genome Analyzer IIx (Mus musculus)  
[GPL13112](#) Illumina HiSeq 2000 (Mus musculus)

Samples (143)  
[More...](#)

[GSM722631](#) RenLab-CTCF-cortex  
[GSM722632](#) RenLab-H3K4me1-cortex  
[GSM722633](#) RenLab-H3K4me3-cortex

Click

SuperSeries is composed of the following SubSeries:  
[GSE29218](#) A draft map of cis-regulatory sequences in the mouse genome [ChIP-Seq]  
[GSE29278](#) A draft map of cis-regulatory sequences in the mouse genome [RNA-Seq]  
[GSE34587](#) A draft map of cis-regulatory sequences in the mouse genome [HiC]

## Relations

BioProject [PRJNA139991](#)

[See on Genome Data Viewer](#)

Scroll down

Scroll down to see the list of samples of the GSE29184 series. Click on “More” to see all samples.


# Looking for an experiment ID

Street address	9500 Gilman Drive
City	La Jolla
State/province	CA
ZIP/Postal code	92093
Country	USA

Platforms (3)

- [GPL9250](#) Illumina Genome Analyzer II (Mus musculus)
- [GPL11002](#) Illumina Genome Analyzer IIx (Mus musculus)
- [GPL13112](#) Illumina HiSeq 2000 (Mus musculus)

Samples (143)

 [Less...](#)

- [GSM722631](#) RenLab-CTCF-cortex
- [GSM722632](#) RenLab-H3K4me1-cortex
- [GSM722633](#) RenLab-H3K4me3-cortex
- [GSM722634](#) RenLab-Pol2-cortex
- [GSM722635](#) RenLab-Input-cortex
- [GSM722636](#) RenLab-CTCF-bone-marrow
- [GSM722637](#) RenLab-H3K4me1-bone-marrow
- [GSM722638](#) RenLab-H3K4me3-bone-marrow
- [GSM722639](#) RenLab-Pol2-bone-marrow
- [GSM722640](#) RenLab-Input-bone-marrow
- [GSM722663](#) RenLab-CTCF-cerebellum

ID


The sample names are displayed with experiment IDs beginning with “GSM”, which is used to browse the data with ChIP-Atlas. For example, GSM722631 is the ID of a CTCF ChIP-seq experiment in the brain





# Access to ChIP-Atlas Dataset Search


## ChIP-Atlas


A data-mining suite for exploring epigenomic landscapes by fully integrating 376,000 ChIP-seq, ATAC-seq and Bisulfite-seq experiments.


**Peak Browser**  
[ChIP](#) [ATAC](#) [Bisulfite](#)

**Enrichment Analysis**  
[ChIP](#) [ATAC](#) [Bisulfite](#)

**Diff Analysis**  
[ChIP](#) [ATAC](#) [Bisulfite](#)

**Target Genes**  
[ChIP](#)

**Colocalization**  
[ChIP](#)

**Dataset Search**  
[ChIP](#) [ATAC](#) [Bisulfite](#)

Dataset Search

### What's new

- Added **Annotation tracks** to Peak Browser, together with UI improvement (2023/)
- Launched **Diff Analysis** tool enabling to detect differential peaks or differentially n
- New publication** on the NAR web server issue! <https://doi.org/10.1093/nar/gkac1>
- Added **ATAC-Seq and Bisulfite-Seq**, together with UI improvement including 'pe

## ChIP-Atlas: Dataset Search

Find experiments by keywords

[Simple search](#) [Detailed search](#)

**Show**  **entries** Search:

Showing 1 to 10 of 375,698 entries

[Copy](#) [TSV](#)

SRX ID	SRA ID	GEO ID	Genome	Antigen class	Antigen	Cell type class	Cell type
<a href="#">SRX019491</a>	<a href="#">SRA012529</a>	<a href="#">GSM534464</a>	hg19, hg38	Input control	Input control	Adipocyte	Adipose stromal cell
<a href="#">SRX019492</a>	<a href="#">SRA012529</a>	<a href="#">GSM534465</a>	hg19, hg38	Histone	H3K4me3	Adipocyte	Adipose stromal cell
<a href="#">SRX019493</a>	<a href="#">SRA012529</a>	<a href="#">GSM534466</a>	hg19, hg38	Histone	H3K4me2	Adipocyte	Adipose stromal cell
<a href="#">SRX019494</a>	<a href="#">SRA012529</a>	<a href="#">GSM534467</a>	hg19, hg38	Histone	H3K4me1	Adipocyte	Adipose stromal cell
<a href="#">SRX019495</a>	<a href="#">SRA012529</a>	<a href="#">GSM534468</a>	hg19, hg38	Histone	H3K27ac	Adipocyte	Adipose stromal cell
<a href="#">SRX019496</a>	<a href="#">SRA012529</a>	<a href="#">GSM534469</a>	hg19, hg38	Histone	H3K27me3	Adipocyte	Adipose stromal cell
<a href="#">SRX019497</a>	<a href="#">SRA012529</a>	<a href="#">GSM534470</a>	hg19, hg38	Histone	H3K36me3	Adipocyte	Adipose stromal cell
<a href="#">SRX019498</a>	<a href="#">SRA012529</a>	<a href="#">GSM534471</a>	hg19, hg38	TFs and others	CTCF	Adipocyte	Adipose stromal cell
<a href="#">SRX019499</a>	<a href="#">SRA012529</a>	<a href="#">GSM534472</a>	hg19, hg38	Histone	H3K4me3	Adipocyte	Adipose stromal cell
<a href="#">SRX019500</a>	<a href="#">SRA012529</a>	<a href="#">GSM534473</a>	hg19, hg38	Histone	H3K4me2	Adipocyte	Adipose stromal cell

Previous

1

2

3

4

5

...

37570

Next

Open the webpage of ChIP-Atlas Dataset Search.

# Search with an experiment ID

▲ Peak Browser    📄 Enrichment Analysis    📄 Diff Analysis    📄 Target Genes    📄 Colocalization    📄 Publications    📄 Docs    Find By ID    SRX018625    Go    🔍 Search

## ▲ ChIP-Atlas: Dataset Search

Find experiments by keywords

Simple search    Detailed search

Show 10 entries

Showing 1 to 1 of 1 entries (filtered from 375,698 total entries)

Copy

TSV

Search: GSM722631

SRX ID	SRA ID	GEO ID	Genome	Antigen class	Antigen	Cell type class	Cell type
<a href="#">SRX062939</a>	SRA036615	GSM722631	mm9, mm10	TFs and others	Ctcf	Neural	Brain cortex

Previous

1

Next



THIS WORK IS SUPPORTED BY [NIG SUPERCOMPUTER SYSTEM](#) AND [JST NBDC JPMJND2202](#).

ALL DATA AND ANALYSIS TOOLS PROVIDED BY CHIP-ATLAS ARE LICENSED UNDER [CC-BY 4.0](#). ATTRIBUTION SHOULD BE MADE TO OUR [PUBLICATION](#) WHEN USING THESE RESOURCES.

NEED HELP? CREATE AN ISSUE ON [GITHUB](#) OR [CONTACT US](#)

Enter an experiment ID of interest in the search box (e.g., GSM722631), and click on the SRX ID (SRX062939) to view the data on IGV as shown above.

🔗 [Tips: Experiment ID](#)

# Search with a series ID

## ChIP-Atlas: Dataset Search

Find experiments by keywords

Simple search

Detailed search

SRA ID

entries

Search: SRA036615

10 of 122 entries (filtered from 375,698 total entries)

Copy

TSV

SRX ID	SRA ID	GEO ID	Genome	Antigen class	Antigen	Cell type class	Cell type
SRX062944	SRA036615	GSM722636	mm9, mm10	TFs and others	Ctcf	Blood	Bone Marrow Cells
SRX062945	SRA036615	GSM722637	mm9, mm10	Histone	H3K4me1	Blood	Bone Marrow Cells
SRX062946	SRA036615	GSM722638	mm9, mm10	Histone	H3K4me3	Blood	Bone Marrow Cells
SRX062947	SRA036615	GSM722639	mm9, mm10	RNA polymerase	RNA polymerase II	Blood	Bone Marrow Cells
SRX062948	SRA036615	GSM722640	mm9, mm10	Input control	Input control	Blood	Bone Marrow Cells
SRX112920	SRA036615	GSM851270	mm9, mm10	Histone	H3K27ac	Blood	Bone Marrow Cells
SRX112978	SRA036615	GSM851328	mm9, mm10	Unclassified	Unclassified	Blood	Thymus
SRX112979	SRA036615	GSM851329	mm9, mm10	Histone	H3K4me1	Blood	Thymus
SRX112980	SRA036615	GSM851330	mm9, mm10	Histone	H3K4me3	Blood	Thymus

SRA036615

Searching with an SRA ID (e.g., SRA036615) will filter the data in the same series or project.

# Search with a series ID

## ChIP-Atlas: Dataset Search

Find experiments by keywords

Simple search

Detailed search

SRA ID

entries

Search: SRA036615

10 of 122 entries (filtered from 375,698 total entries)

Copy

TSV

SRX ID	SRA ID	GEO ID	Genome	Antigen class	Antigen	Cell type class	Cell type
SRX062944	SRA036615	GSM722636	mm9, mm10	TFs and others	Ctcf	Blood	Bone Marrow Cells
SRX062945	SRA036615	GSM722637	mm9, mm10	Histone	H3K4me1	Blood	Bone Marrow Cells
SRX062946	SRA036615	GSM722638	mm9, mm10	Histone	H3K4me3	Blood	Bone Marrow Cells
SRX062947	SRA036615	GSM722639	mm9, mm10	RNA polymerase	RNA polymerase II	Blood	Bone Marrow Cells
SRX062948	SRA036615	GSM722640	mm9, mm10	Input control	Input control	Blood	Bone Marrow Cells
SRX112920	SRA036615	GSM851270	mm9, mm10	Histone	H3K27ac	Blood	Bone Marrow Cells
SRX112978	SRA036615	GSM851328	mm9, mm10	Unclassified	Unclassified	Blood	Thymus
SRX112979	SRA036615	GSM851329	mm9, mm10	Histone	H3K4me1	Blood	Thymus
SRX112980	SRA036615	GSM851330	mm9, mm10	Histone	H3K4me3	Blood	Thymus

SRA036615

Searching with an SRA ID (e.g., SRA036615) will filter the data in the same series or project.

# Search with a series ID

[Peak Browser](#)[Enrichment Analysis](#)[Diff Analysis](#)[Target Genes](#)[Colocalization](#)[Publications](#)[Docs](#)[Find By ID](#)[Go](#)[Search](#)

## ChIP-Atlas: Dataset Search

Find experiments by keywords

[Simple search](#)[Detailed search](#)[? Tutorial](#)

SRA ID

entries

Search:

10 of 122 entries (filtered from 375,698 total entries)

[Copy](#)[TSV](#)

SRX ID	SRA ID	GEO ID	Genome	Antigen class	Antigen	Cell type class	Cell type	Title	Attributes
<a href="#">SRX062944</a>	<a href="#">SRA036615</a>	<a href="#">GSM722636</a>	mm9, mm10	TFs and others	Ctcf	Blood	Bone Marrow Cells	RenLab-CTCF-bone-marrow	<b>source_name:</b> Mouse bone marrow <b>strain:</b> C57BL/6 <b>chip antibody:</b> CTCF <b>chip antibody details:</b> Kim et al., 2007
<a href="#">SRX062945</a>	<a href="#">SRA036615</a>	<a href="#">GSM722637</a>	mm9, mm10	Histone	H3K4me1	Blood	Bone Marrow Cells	RenLab-H3K4me1-bone-marrow	<b>source_name:</b> Mouse bone marrow <b>strain:</b> C57BL/6 <b>chip antibody:</b> H3K4me1 <b>chip antibody details:</b> Abcam, ab8895
<a href="#">SRX062946</a>	<a href="#">SRA036615</a>	<a href="#">GSM722638</a>	mm9, mm10	Histone	H3K4me3	Blood	Bone Marrow Cells	RenLab-H3K4me3-bone-marrow	<b>source_name:</b> Mouse bone marrow <b>strain:</b> C57BL/6 <b>chip antibody:</b> H3K4me3 <b>chip antibody details:</b> Millipore, 05-745
<a href="#">SRX062947</a>	<a href="#">SRA036615</a>	<a href="#">GSM722639</a>	mm9, mm10	RNA polymerase	RNA polymerase II	Blood	Bone Marrow Cells	RenLab-Pol2-bone-marrow	<b>source_name:</b> Mouse bone marrow <b>strain:</b> C57BL/6 <b>chip antibody:</b> Pol2 <b>chip antibody details:</b> Canvance, MMS-126R
<a href="#">SRX062948</a>	<a href="#">SRA036615</a>	<a href="#">GSM722640</a>	mm9, mm10	Input control	Input control	Blood	Bone Marrow Cells	RenLab-Input-bone-marrow	<b>source_name:</b> Mouse bone marrow <b>strain:</b> C57BL/6 <b>chip antibody:</b> none (Input) <b>chip antibody details:</b> None

Searching with an SRA ID (e.g., SRA036615) will filter the data in the same series or project.

[Tips: Series ID](#)

The manual for

# **ChIP-Atlas: Dataset Search**

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1. Search by keyword
2. Search from papers
3. Tips

# Tips: Series ID and Experiment ID

	NCBI GEO	NCBI SRA	EBI ERA	DDBJ DRA
Series ID	GSE29184 = SRA036615		ERA18567000	DRA000484
Experiment ID	GSM851325 = SRX112975 GSM851326 = SRX112976 GSM851327 = SRX112977 GSM851328 = SRX112978 GSM851329 = SRX112979 GSM851330 = SRX112980 GSM851331 = SRX112981 GSM851332 = SRX112982 GSM851333 = SRX112983		ERX9976498 ERX9976499 ERX9976500 ERX9976501 ERX9976502	DRX001135 DRX001136 DRX001137 DRX001138 DRX001139 DRX001140 DRX001141 DRX001142

ChIP-Atlas covers ChIP-seq, ATAC-seq, DNase-seq, and Bisulfite-seq data from the NCBI GEO, NCBI SRA, EBI ERA, and DDBJ DRA databases. NCBI GEO and SRA have the same series and experiments; **however**, the IDs are different. EBI ERA and DDBJ DRA data are not shared with NCBI GEO.

# Tips: Installation of IGV

## Download IGV

Did you know that there is also an **IGV web application** that runs only in a web browser, does not use Java, and requires no downloads? See <https://igv.org/app>. Click on the Help link in the app for more information about using IGV-Web.

### Latest release of IGV Desktop: 2.17.0

#### M1/M2 Mac Users:

Apple's Rosetta software is required to run the IGV MacOS App that includes Java. If you run IGV with your own Java installation, Rosetta may not be required if your version of Java runs natively on M1/M2.

#### Linux users:

The 'IGV for Linux' download includes AdoptOpenJDK (now Eclipse Temurin) version 17 for x64 Linux. See their list of supported platforms [here](#). If your platform is not on the "x64 Linux" list, or the packaged Java does not work on your version of Linux, download the 'Command line IGV for all platforms' and use it with your own Java installation.

**What's New:** See the [Release Notes](#) for what's new in each IGV release.



IGV MacOS App  
Java included



IGV MacOS App  
Separate Java 17 required



IGV for Windows  
Java included



IGV for Windows  
Separate Java 17 required



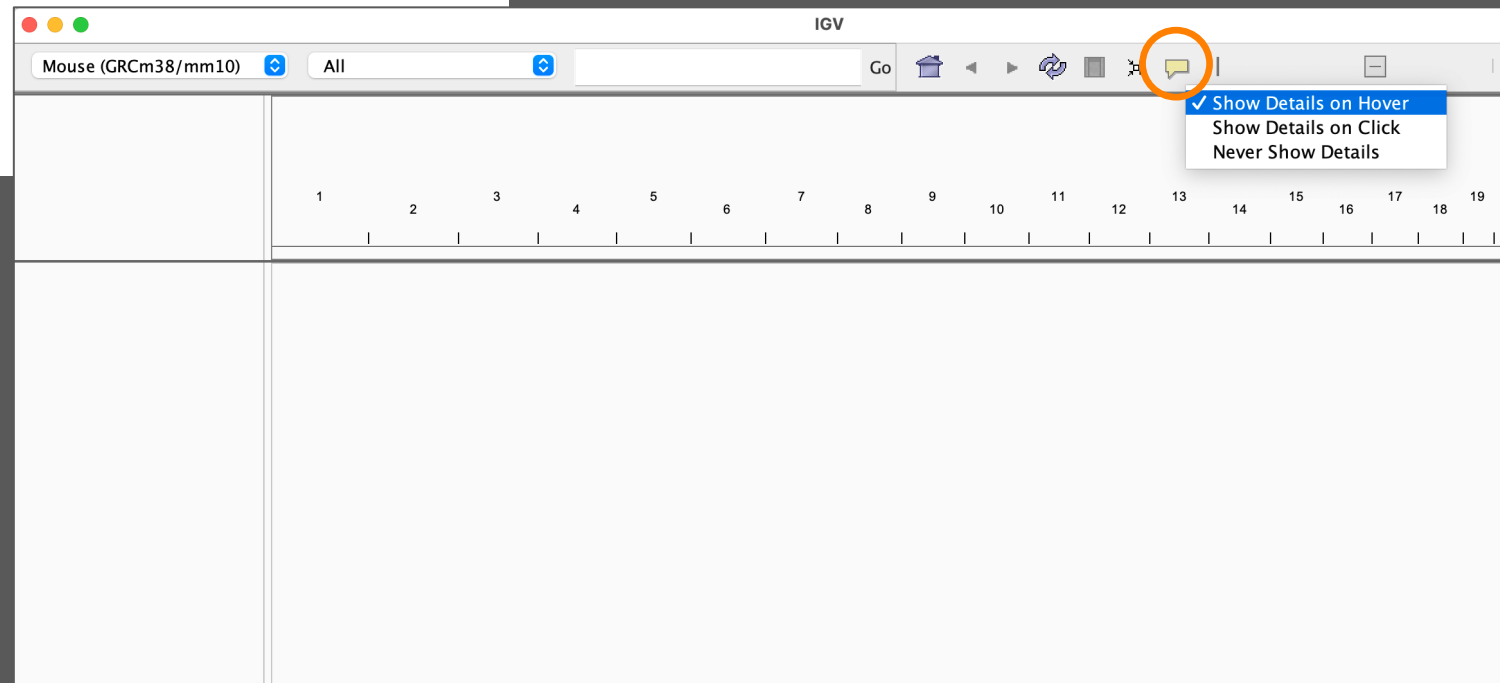
IGV for Linux  
Java included



Command line IGV and igvtools for all platforms  
Separate Java 17 required

← Download IGV  
(<https://igv.org/doc/desktop/#DownloadPage/>)

↓ Launch IGV and check “Show Details on Hover”





# Tips: Detailed search

[Peak Browser](#)[Enrichment Analysis](#)[Diff Analysis](#)[Target Genes](#)[Colocalization](#)[Publications](#)[Docs](#)[Find By ID](#)[Go](#)[Search](#)

## ChIP-Atlas: Data

Detailed  
search

[? Tutorial](#)

Find experiments by keywords

[Simple search](#)[Detailed search](#)

Show  entries

Search:

Showing 1 to 10 of 2,337 entries (filtered from 375,698 total entries)

[Copy](#)[TSV](#)

SRX ID	SRA ID	GEO ID	Genome	Antigen class	Antigen	Cell type class	Cell type	Title	Attributes
<a href="#">SRX3751764</a>	SRA662944	<a href="#">GSM3027215</a>	hg19, hg38	Histone	H3K27ac	Adipocyte	LPS141	LPS141 H3K27ac; Homo sapiens; ChIP-Seq	<b>source_name:</b> LPS141 <b>cell type:</b> liposarcoma cells <b>chip antibody:</b> H3K27ac (Activemotif, #39133)
<a href="#">SRX3751774</a>	SRA662944	<a href="#">GSM3027225</a>	hg19, hg38	Histone	H3K27ac	Adipocyte	402-91	MLS402 H3K27ac; Homo sapiens; ChIP-Seq	<b>source_name:</b> MLS 402-91 <b>cell type:</b> liposarcoma cells <b>chip antibody:</b> H3K27ac (Activemotif, #39133)
<a href="#">SRX3751780</a>	SRA662944	<a href="#">GSM3027231</a>	hg19, hg38	Histone	H3K27ac	Adipocyte	1765-92	MLS1765 H3K27ac; Homo sapiens; ChIP-Seq	<b>source_name:</b> MLS 1765-92 <b>cell type:</b> liposarcoma cells <b>chip antibody:</b> H3K27ac (Activemotif, #39133)
<a href="#">SRX14830576</a>	SRA1402804	<a href="#">GSM6040821</a>	mm9, mm10	Histone	H3K27ac	Adipocyte	Brown adipocytes	1 warm ncd H3K27ac; Mus musculus; ChIP-Seq	<b>source_name:</b> iBAT <b>strain:</b> C57BL/6N <b>tissue:</b> iBAT <b>age_weeks:</b> 20 <b>chip antibody:</b> H3K27ac (Active Motif 39133) <b>diet:</b> chow

The “Detailed search” mode allows to search from the original sample metadata described by the data submitter, such as the catalog number of the antibody used.