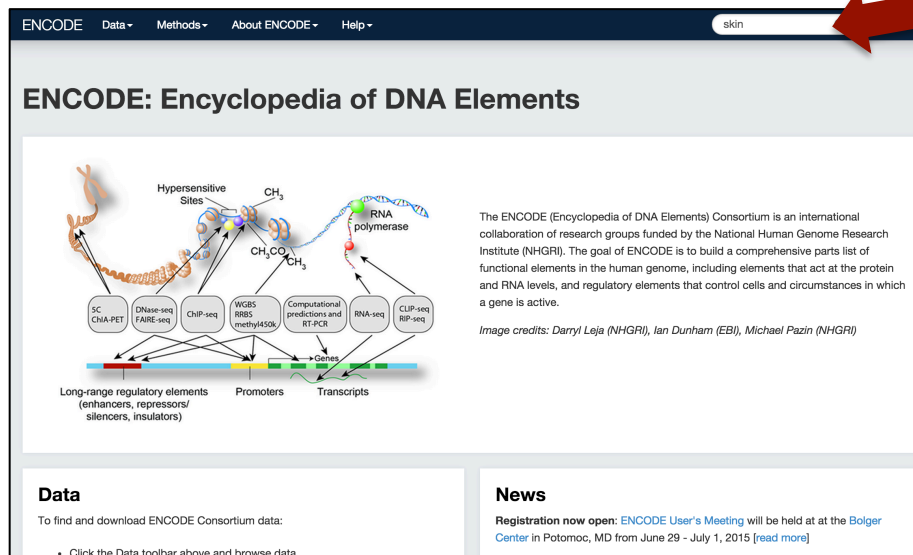


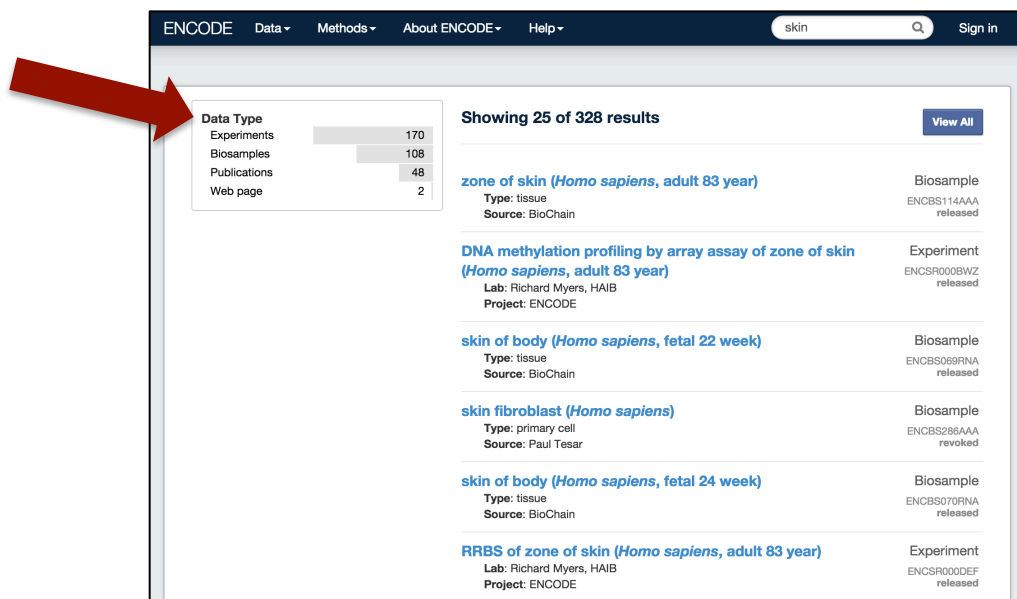
Demo 1: Free text search of ENCODE data

1. Go to <https://www.encodeproject.org>
2. Enter “skin” into the search box on the upper right hand corner



The screenshot shows the ENCODE website homepage. The search bar in the top right corner contains the word "skin". A red arrow points to the search bar. The main content area features a diagram of DNA with various annotations: Hypersensitive Sites, CH₃, CH₃CO, RNA polymerase, SC ChA-PET, DNase-seq, FAIRE-seq, ChIP-seq, WGBS, RRBS, methyl450k, Computational predictions and RT-PCR, RNA-seq, and CLIP-seq, RIP-seq. Below the diagram are labels for Long-range regulatory elements (enhancers, repressors/silencers, insulators), Promoters, and Transcripts. Text on the right explains the ENCODE Consortium's goal. A "Data" section at the bottom left provides a link to find and download data. A "News" section at the bottom right mentions an upcoming meeting.

3. All matches on the website will be shown
4. Select “Experiments”



The screenshot shows the search results page for "skin". A red arrow points to the "Data Type" filter on the left, where "Experiments" is selected. The main content area displays "Showing 25 of 328 results" and a list of results. Each result includes a title, type, and source.

Title	Type	Source
zone of skin (<i>Homo sapiens</i> , adult 83 year)	Biosample	BioChain
DNA methylation profiling by array assay of zone of skin (<i>Homo sapiens</i> , adult 83 year)	Experiment	BioChain
skin of body (<i>Homo sapiens</i> , fetal 22 week)	Biosample	BioChain
skin fibroblast (<i>Homo sapiens</i>)	Biosample	BioChain
skin of body (<i>Homo sapiens</i> , fetal 24 week)	Biosample	BioChain
RRBS of zone of skin (<i>Homo sapiens</i> , adult 83 year)	Experiment	BioChain

5. View all ENCODE assays that contain a match to “skin”

The screenshot shows the ENCODE Data Portal interface. At the top, there are navigation tabs for 'Data', 'Methods', 'About ENCODE', and 'Help'. A search bar contains the term 'skin' and a 'Sign in' button is on the right. The main content area is divided into a left sidebar and a right main panel.

Left Sidebar (Filters):

- Assay:** ChIP-seq (53), RNA-seq (26), DNase-seq (25), RNA profiling by array assay (24), CAGE (9). [+ See more...](#)
- Experiment status:** released (169), revoked (1)
- Genome assembly (visualization):** hg19 (147), mm9 (2)
- Organism:** *Homo sapiens* (167), *Mus musculus* (2)
- Target of assay:** histone (31), histone modification (29), transcription factor (13), control (9)
- Biosample type:** primary cell (163), tissue (5), stem cell (2)

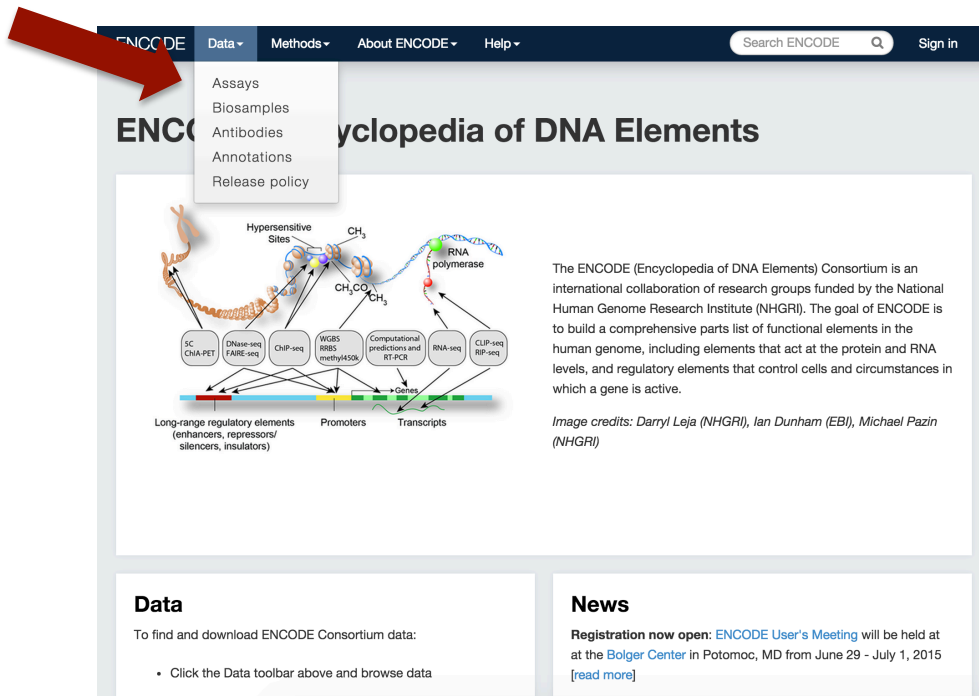
Right Main Panel:

Showing 25 of 170 experiments. Buttons: [Visualize](#), [Download](#), [View All](#)

- RAMPAGE of skin of body (*Homo sapiens*, fetal)** Experiment
Lab: Thomas Gingeras, CSHL
Project: ENCODE
ENCSR000AGU released
- RNA-seq of skin of body (*Homo sapiens*, fetal)** Experiment
Lab: Thomas Gingeras, CSHL
Project: ENCODE
ENCSR000AGA released
- RNA-seq of melanocyte of skin (*Homo sapiens*, adult)** Experiment
Lab: Thomas Gingeras, CSHL
Project: ENCODE
ENCSR000CUR released
- RNA-seq of skin of body (*Homo sapiens*, fetal)** Experiment
Lab: Thomas Gingeras, CSHL
Project: ENCODE
ENCSR000AFG released
- DNA methylation profiling by array assay of zone of skin (*Homo sapiens*, adult 83 year)** Experiment
Lab: Richard Myers, HAIB
Project: ENCODE
ENCSR000BWZ released
- CAGE of melanocyte of skin (*Homo sapiens*, child)** Experiment
Lab: Piero Carninci, RIKEN
Project: ENCODE
ENCSR000CKY released
- CAGE of melanocyte of skin (*Homo sapiens*, adult)** Experiment

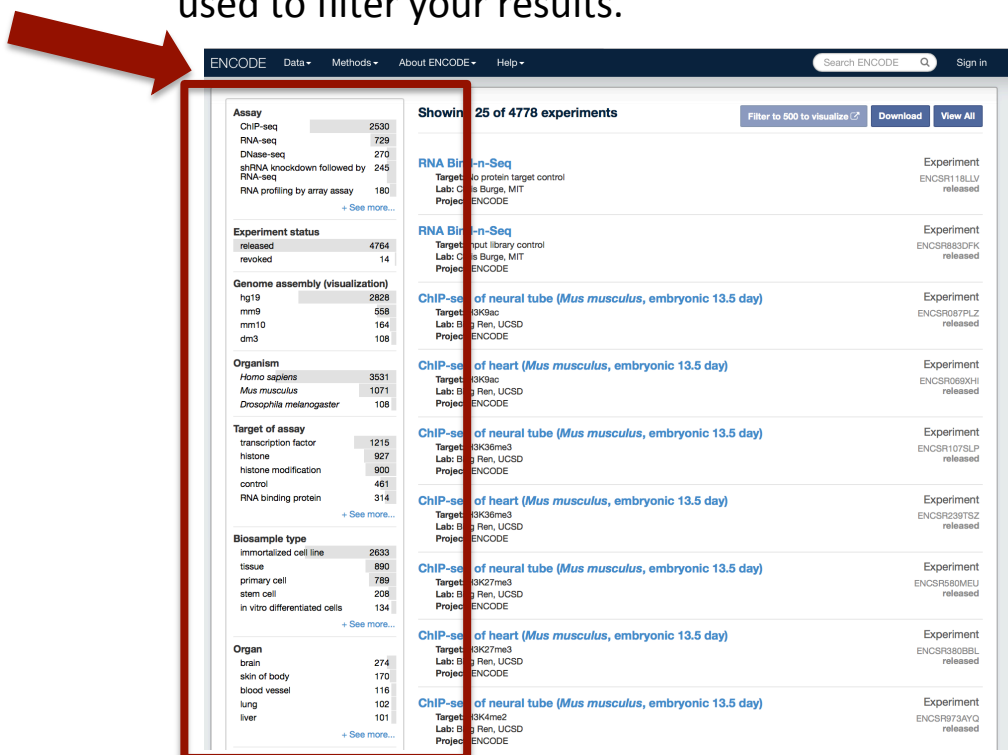
Demo 2: Browsing and filtering of ENCODE data

1. Go to <https://www.encodeproject.org>
2. Under the “Data” menu bar, select “Assays”



The screenshot shows the ENCODE website interface. The top navigation bar includes 'Data', 'Methods', 'About ENCODE', and 'Help'. A search bar and 'Sign in' link are on the right. The 'Data' menu is open, showing options: 'Assays', 'Biosamples', 'Antibodies', 'Annotations', and 'Release policy'. A red arrow points to the 'Assays' option. Below the menu is a large graphic titled 'ENCODE Encyclopedia of DNA Elements' showing a DNA strand with various elements like 'Hypersensitive Sites', 'CH₃', 'CH₃CO', 'RNA polymerase', 'SC ChIA-PET', 'DNase-seq', 'FARE-seq', 'ChIP-seq', 'WGBS', 'RBS', 'methyl450k', 'Computational predictions and RT-PCR', 'RNA-seq', and 'CLIP-seq'. Below the graphic are sections for 'Data' and 'News'.

3. All publicly available assays are shown. The categories on the left are metadata describing the assays. They can be used to filter your results.



The screenshot shows the ENCODE website interface displaying a list of 25 of 4778 experiments. A red arrow points to the left sidebar containing metadata filters for assays, experiment status, genome assembly, organism, target of assay, biosample type, and organ. The main content area shows a list of experiments with columns for Target, Lab, and Project.

Assay	Count
ChIP-seq	2530
RNA-seq	729
DNase-seq	270
shRNA knockdown followed by RNA-seq	245
RNA profiling by array assay	180

Experiment status	Count
released	4764
revoked	14

Genome assembly (visualization)	Count
hg19	2828
mm9	558
mm10	164
dm3	108

Organism	Count
Homo sapiens	3531
Mus musculus	1071
Drosophila melanogaster	108

Target of assay	Count
transcription factor	1215
histone	927
histone modification	900
control	461
RNA binding protein	314

Biosample type	Count
immortalized cell line	2633
tissue	890
primary cell	789
stem cell	208
in vitro differentiated cells	134

Organ	Count
brain	274
skin of body	170
blood vessel	116
lung	102
liver	101

Experiment	Target	Lab	Project
Experiment ENCSR118LLV released	RNA binding protein target control	is Burge, MIT	ENCODE
Experiment ENCSR883DFK released	input library control	is Burge, MIT	ENCODE
Experiment ENCSR087PLZ released	ChIP-seq of neural tube (<i>Mus musculus</i> , embryonic 13.5 day)	IK9ac, Ren, UCSD	ENCODE
Experiment ENCSR0590H released	ChIP-seq of heart (<i>Mus musculus</i> , embryonic 13.5 day)	IK9ac, Ren, UCSD	ENCODE
Experiment ENCSR107SLP released	ChIP-seq of neural tube (<i>Mus musculus</i> , embryonic 13.5 day)	IK36me3, Ren, UCSD	ENCODE
Experiment ENCSR239TSSZ released	ChIP-seq of heart (<i>Mus musculus</i> , embryonic 13.5 day)	IK36me3, Ren, UCSD	ENCODE
Experiment ENCSR80MEU released	ChIP-seq of neural tube (<i>Mus musculus</i> , embryonic 13.5 day)	IK27me3, Ren, UCSD	ENCODE
Experiment ENCSR302BBL released	ChIP-seq of heart (<i>Mus musculus</i> , embryonic 13.5 day)	IK27me3, Ren, UCSD	ENCODE
Experiment ENCSR073AYG released	ChIP-seq of neural tube (<i>Mus musculus</i> , embryonic 13.5 day)	IK4me2, Ren, UCSD	ENCODE

5. View all ENCODE assays that are filtered by selecting “skin of body”. Note that the results are not straight text matches. For example, “fibroblast of arm”, and “keratinocytes” are included in the results list.

The screenshot shows the ENCODE website interface. On the left, a sidebar contains various filter categories with counts. A red box highlights the 'Organ' section, where 'skin of body' is selected and highlighted in blue. A red arrow points from the left towards the 'skin of body' selection. The main content area displays a list of 25 experiments, all filtered by the selected criteria. The experiments listed include:

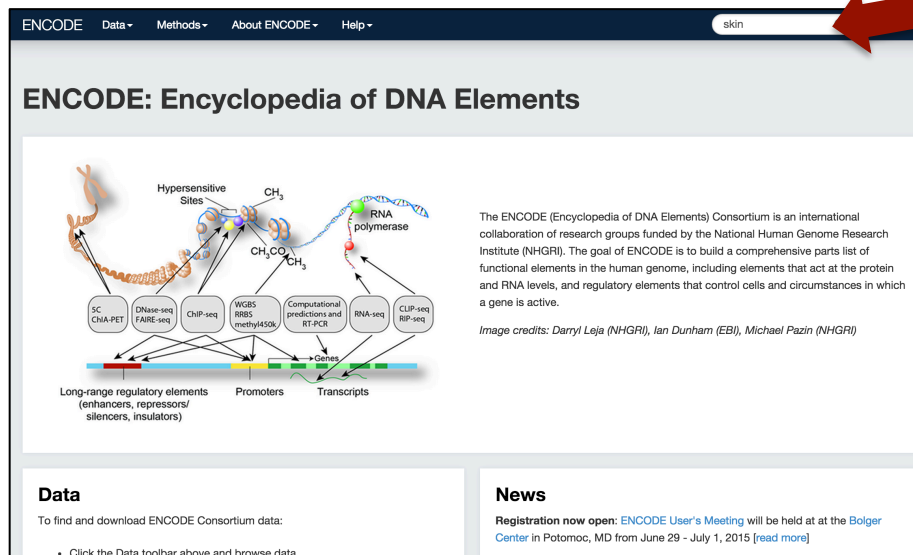
- DNase-seq of fibroblast of arm (*Homo sapiens*, adult 53 year)
- RNA-seq of fibroblast of arm (*Homo sapiens*, adult 53 year)
- RAMPAGE of fibroblast of arm (*Homo sapiens*, adult 53 year)
- RNA-seq of fibroblast of arm (*Homo sapiens*, adult 53 year)
- RNA-seq of melanocyte of skin (*Homo sapiens*, adult)
- RNA-seq of melanocyte of skin (*Homo sapiens*, child)
- RNA-seq of hair follicle dermal papilla cell (*Homo sapiens*, adult)
- RNA-seq of fibroblast of dermis (*Homo sapiens*, adult)
- RNA profiling by array assay of keratinocyte (*Homo sapiens*)
- RNA profiling by array assay of keratinocyte (*Homo sapiens*)

The sidebar filters include:

- Assay:** ChIP-seq (53), RNA-seq (26), DNase-seq (25), RNA profiling by array assay (24), CAGE (9)
- Experiment status:** released (169), revoked (1)
- Genome assembly (visualization):** hg19 (150), mm9 (2)
- Organism:** *Homo sapiens* (167), *Mus musculus* (2)
- Target of assay:** histone (31), histone modification (29), transcription factor (13), control (9)
- Biosample type:** primary cell (163), tissue (5), stem cell (2)
- Organ:** brain (274), **skin of body (170)**, blood vessel (116), lung (102), liver (101)
- Life stage:** unknown (71), adult (60), child (13), postnatal (13), fetal (12)

Demo: Combine search & filter of ENCODE data

1. Go to <https://www.encodeproject.org>
2. Enter “skin” into the search box on the upper right hand corner



ENCODE: Encyclopedia of DNA Elements

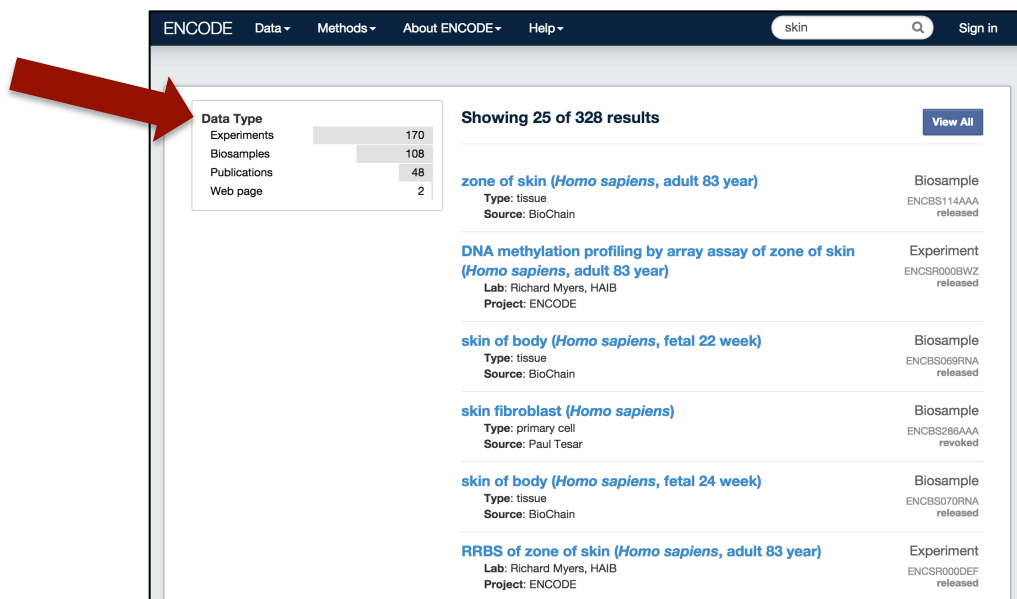
The ENCODE (Encyclopedia of DNA Elements) Consortium is an international collaboration of research groups funded by the National Human Genome Research Institute (NHGRI). The goal of ENCODE is to build a comprehensive parts list of functional elements in the human genome, including elements that act at the protein and RNA levels, and regulatory elements that control cells and circumstances in which a gene is active.

Image credits: Darryl Leja (NHGRI), Ian Dunham (EBI), Michael Pazin (NHGRI)

Data
To find and download ENCODE Consortium data:
Click the Data toolbar above and browse data

News
Registration now open: ENCODE User's Meeting will be held at the Bolger Center in Potomac, MD from June 29 - July 1, 2015 [read more]

3. All matches on the website will be shown
4. Select “Experiments”



ENCODE Data Methods About ENCODE Help skin Sign in

Showing 25 of 328 results [View All](#)

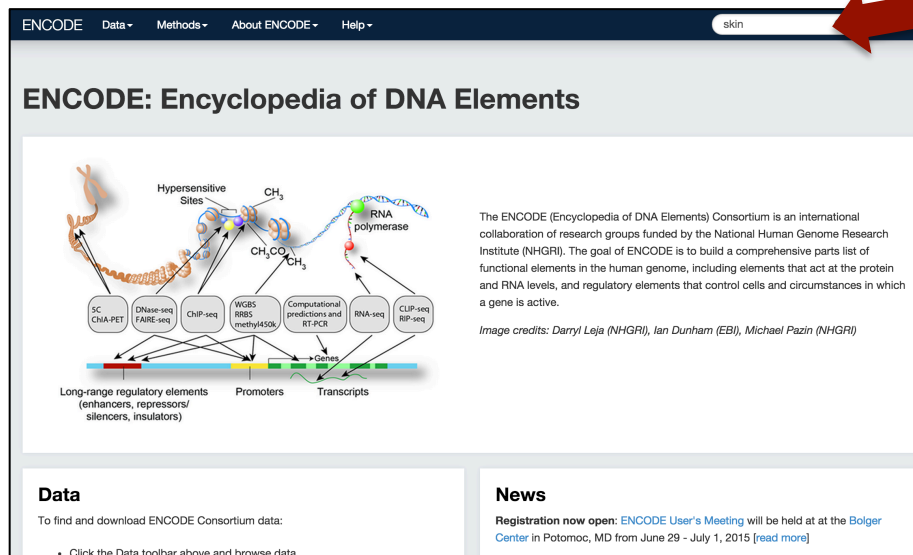
Result Title	Type
zone of skin (<i>Homo sapiens</i>, adult 83 year)	Biosample
DNA methylation profiling by array assay of zone of skin (<i>Homo sapiens</i>, adult 83 year)	Experiment
skin of body (<i>Homo sapiens</i>, fetal 22 week)	Biosample
skin fibroblast (<i>Homo sapiens</i>)	Biosample
skin of body (<i>Homo sapiens</i>, fetal 24 week)	Biosample
RRBS of zone of skin (<i>Homo sapiens</i>, adult 83 year)	Experiment

Data Type

Experiments	170
Biosamples	108
Publications	48
Web page	2

Demo 3: Combine search & filter of ENCODE data

1. Go to <https://www.encodeproject.org>
2. Enter “skin” into the search box on the upper right hand corner



ENCODE: Encyclopedia of DNA Elements

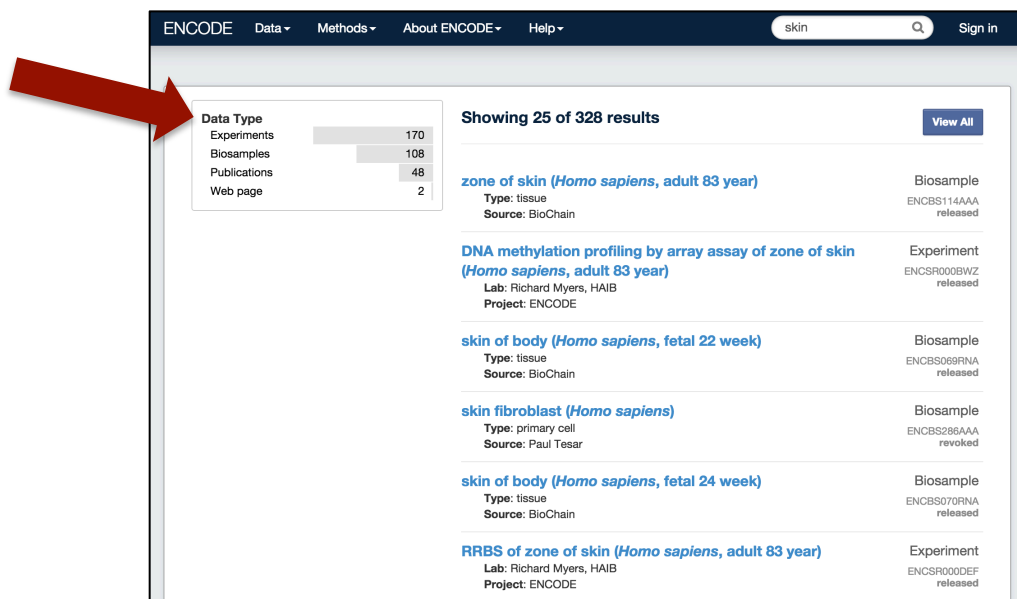
The ENCODE (Encyclopedia of DNA Elements) Consortium is an international collaboration of research groups funded by the National Human Genome Research Institute (NHGRI). The goal of ENCODE is to build a comprehensive parts list of functional elements in the human genome, including elements that act at the protein and RNA levels, and regulatory elements that control cells and circumstances in which a gene is active.

Image credits: Darryl Leja (NHGRI), Ian Dunham (EBI), Michael Pazin (NHGRI)

Data
To find and download ENCODE Consortium data:
Click the Data toolbar above and browse data

News
Registration now open: ENCODE User's Meeting will be held at the Bolger Center in Potomac, MD from June 29 - July 1, 2015 [read more]

3. All matches on the website will be shown
4. Select “Experiments”



ENCODE Data Methods About ENCODE Help skin Sign in

Showing 25 of 328 results [View All](#)

Data Type

Experiments	170
Biosamples	108
Publications	48
Web page	2

zone of skin (*Homo sapiens*, adult 83 year) Biosample
Type: tissue
Source: BioChain
ENCBS114AAA released

DNA methylation profiling by array assay of zone of skin (*Homo sapiens*, adult 83 year) Experiment
Lab: Richard Myers, HAIB
Project: ENCODE
ENCBSR000BWZ released

skin of body (*Homo sapiens*, fetal 22 week) Biosample
Type: tissue
Source: BioChain
ENCBS069RNA released

skin fibroblast (*Homo sapiens*) Biosample
Type: primary cell
Source: Paul Tesar
ENCBS286AAA revoked

skin of body (*Homo sapiens*, fetal 24 week) Biosample
Type: tissue
Source: BioChain
ENCBS070RNA released

RRBS of zone of skin (*Homo sapiens*, adult 83 year) Experiment
Lab: Richard Myers, HAIB
Project: ENCODE
ENCBSR000DEF released

5. View all ENCODE assays that contain a match to “skin”

The screenshot shows the ENCODE Data Browser interface with a search for 'skin'. The left sidebar contains filters for Assay, Experiment status, Genome assembly, Organism, Target of assay, and Biosample type. The main content area shows 25 of 170 experiments. The search results are as follows:

Assay	Count
ChIP-seq	53
RNA-seq	26
DNase-seq	25
RNA profiling by array assay	24
CAGE	9

Experiment status	Count
released	169
revoked	1

Genome assembly (visualization)	Count
hg19	147
mm9	2

Organism	Count
<i>Homo sapiens</i>	167
<i>Mus musculus</i>	2

Target of assay	Count
histone	31
histone modification	29
transcription factor	13
control	9

Biosample type	Count
primary cell	163
tissue	5
stem cell	2

Showing 25 of 170 experiments	Buttons
Visualize Download View All	

Experiment Title	Experiment ID
RAMPAGE of skin of body (<i>Homo sapiens</i>, fetal)	ENCSR000AGU released
RNA-seq of skin of body (<i>Homo sapiens</i>, fetal)	ENCSR000AGA released
RNA-seq of melanocyte of skin (<i>Homo sapiens</i>, adult)	ENCSR000CUR released
RNA-seq of skin of body (<i>Homo sapiens</i>, fetal)	ENCSR000AFG released
DNA methylation profiling by array assay of zone of skin (<i>Homo sapiens</i>, adult 83 year)	ENCSR000BWZ released
CAGE of melanocyte of skin (<i>Homo sapiens</i>, child)	ENCSR000CKY released
CAGE of melanocyte of skin (<i>Homo sapiens</i>, adult)	Experiment

6. If looking for RNA-seq data from adult samples, select “RNA-seq” under Assay and “adult” under Life Stage.

The screenshot shows the ENCODE Data Browser interface with the search results filtered to show 10 of 10 experiments. Two red arrows point to the 'RNA-seq' filter in the Assay section and the 'adult' filter in the Life stage section. The search results are as follows:

Assay	Count
ChIP-seq	20
RNA-seq	10
DNase-seq	9
RNA profiling by array assay	6
DNA methylation profiling by array assay	5

Experiment status	Count
released	10

Genome assembly (visualization)	Count
hg19	6

Organism	Count
<i>Homo sapiens</i>	10

Biosample type	Count
primary cell	10

Organ	Count
skin of body	10
lymphatic vessel	2

Life stage	Count
unknown	11
adult	10
child	4
fetal	2

Showing 10 of 10 experiments	Buttons
Visualize Download	

Experiment Title	Experiment ID
RNA-seq of melanocyte of skin (<i>Homo sapiens</i>, adult)	ENCSR000CUR released
RNA-seq of melanocyte of skin (<i>Homo sapiens</i>, adult)	ENCSR000CVM released
RNA-seq of hair follicle dermal papilla cell (<i>Homo sapiens</i>, adult)	ENCSR000CUB released
RNA-seq of fibroblast of arm (<i>Homo sapiens</i>, adult 53 year)	ENCSR489KNQ released
RNA-seq of fibroblast of arm (<i>Homo sapiens</i>, adult 53 year)	ENCSR797BPP released
RNA-seq of fibroblast of dermis (<i>Homo sapiens</i>, adult)	ENCSR000CUI released

Demo 4: Visualize data

Details of how to configure tracks will be presented during the UCSC Genome Browser workshop. This demo just shows what to expect as you are connected to the browser.

1. Get the list of assays illustrated in Demo 3.
2. Select “Visualize” button on the upper right corner. This will automatically create a trackhub to visualize the results

The screenshot shows the ENCODE Data Hub interface. On the left, there are filters for Assay, Experiment status, Genome assembly, Organism, Biosample type, Organ, and Life stage. The main area displays a list of 10 experiments, all related to RNA-seq of melanocyte of skin and fibroblast of arm. A red arrow points to the 'Visualize' button in the top right corner of the experiment list.

3. An intermediate page listing the reference genome is shown. Trackhubs can be made with different reference

The screenshot shows a 'Hub Connect Successful' message. It states: 'You will be automatically redirected to the gateway page for this hub's default database (hg19) in 3 seconds.' It also provides contact information for the ENCODE Data Coordination Center Data Hub and the reference genome (hg19).

4. The trackhub will be connected. Enter a gene name or enter submit. Details of how to configure tracks will be presented during the UCSC Genome Browser workshop.

The screenshot shows the 'Human (Homo sapiens) Genome Browser Gateway' page. It includes a search bar with fields for group (Mammal), genome (Human), assembly (Feb. 2009 (GRCh37/hg19)), position (chr21:33,031,597-33,041,570), and search term. A red arrow points to the 'submit' button. Below the search bar, there are links for 'track search', 'add custom tracks', 'track hubs', and 'configure tracks and display'.

5. The track hub is listed as “Hub (search)”

UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

chr21:33031597-33041570 9,974 bp. enter position, gene symbol or search terms go [More on-site workshops available!](#)

Scale chr21: 33,833,000 | 33,834,000 | 33,835,000 | 2 kb | 33,836,000 | 33,837,000 | 33,838,000 | 33,839,000 | 33,840,000 | 33,841,000

RNA-seq of fibroblast of dermis - ENCSR000CUH
 RNA-seq of fibroblast of dermis - ENCSR000CUY
 RNA-seq of hair follicle dermal papilla cell - ENCSR000CUB
 RNA-seq of melanocyte of skin - ENCSR000CUR
 RNA-seq of melanocyte of skin - ENCSR000CVM

move start Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag side bars or labels up or down to reorder tracks. Drag tracks left or right to new position. move end

collapse all expand all

Hub (search) refresh

RNA-seq of fibroblast of dermis - ENCSR000CUH	RNA-seq of fibroblast of dermis - ENCSR000CUY	RNA-seq of hair follicle dermal papilla cell - ENCSR000CUB	RNA-seq of hair follicle dermal papilla cell - ENCSR000CVC	RNA-seq of melanocyte of skin - ENCSR000CUR	RNA-seq of melanocyte of skin - ENCSR000CVM
---	---	--	--	---	---

6. Hover over tracks to view file-related metadata.

RNA-seq of melanocyte of skin - ENCSR000CVM - ENCF000KDT plus strand signal rep 1 drag to reorder

UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)

RefSeq Genes

Publications: Sequences in Scientific Articles

Human mRNAs from GenBank

Human ESTs That Have Been Spliced

H3K27Ac Mark (Often Found Near Active Regulatory Elements) on 7 cell lines from ENCODE

7. Click on left hand grouping to configure tracks and view more metadata, including file download links and links back to the ENCODE Portal.

RNA-seq of melanocyte of skin - ENCSR000CVM - ENCF000KDT plus strand signal rep 1 drag to reorder

UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)

RefSeq Genes

Publications: Sequences in Scientific Articles

Human mRNAs from GenBank

Human ESTs That Have Been Spliced

H3K27Ac Mark (Often Found Near Active Regulatory Elements) on 7 cell lines from ENCODE

8. ENCODE metadata for the track hub

RNA-seq of melanocyte of skin - ENCSR000CVM Track Settings

RNA-seq of melanocyte of skin - ENCSR000CVM

Maximum display mode: [Reset to defaults](#)

Select views ([help](#)):

Peaks Signals

Peaks Configuration

Show only items with score at or above: (range: 0 to 1000)

Signals Configuration [Graph configuration help](#)

Type of graph:

Track height: pixels (range: 8 to 100)

Data view scaling: Always include zero:

Vertical viewing range: min: max: (range: 0 to 127)

Transform function: Transform data points by:

Windowing function: Smoothing window: pixels

Negate values:

Draw y indicator lines: at y = 0.0: at y =

List subtracks: only selected/visible all

Views ¹	Track Name ²
<input checked="" type="checkbox"/> dense	Peaks RNA-seq of melanocyte of skin - ENCSR000CVM - ENCF000KDN bedRnaElements contigs pooled
<input checked="" type="checkbox"/> dense	Signals RNA-seq of melanocyte of skin - ENCSR000CVM - ENCF000KDQ minus strand signal rep 1
<input checked="" type="checkbox"/> dense	Signals RNA-seq of melanocyte of skin - ENCSR000CVM - ENCF000KDR minus strand signal rep 2
<input checked="" type="checkbox"/> dense	Signals RNA-seq of melanocyte of skin - ENCSR000CVM - ENCF000KDT plus strand signal rep 1
<input checked="" type="checkbox"/> dense	Signals RNA-seq of melanocyte of skin - ENCSR000CVM - ENCF000KDU plus strand signal rep 2

RNA-seq on skin melanocytes primary whole cells (NHEM-M2) from rRNA-depleted Total RNA less than 200 nucleotides in size that was pre-treated with TAP prior to cloning.

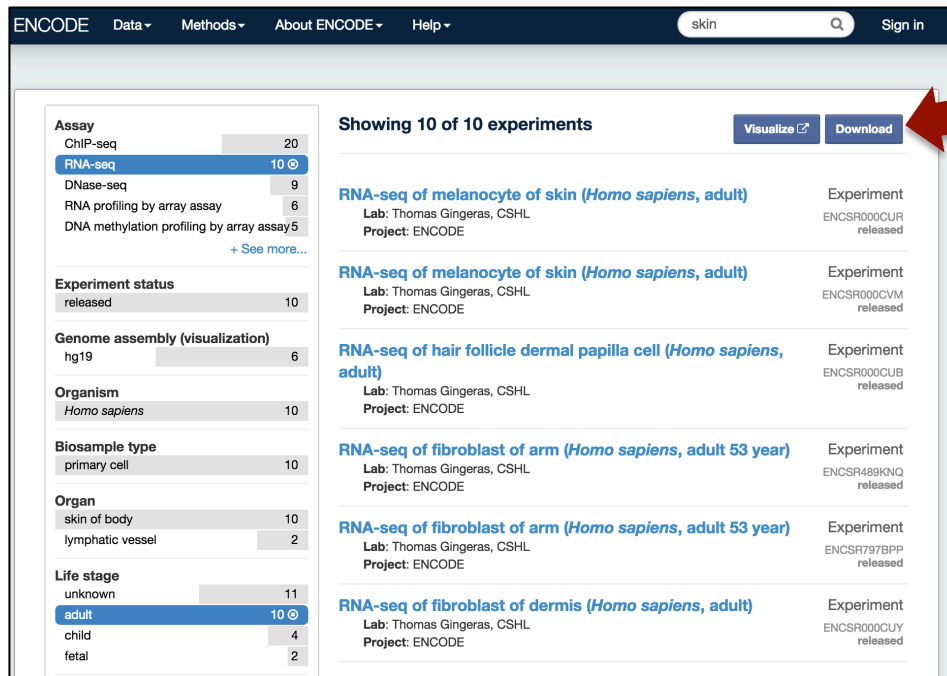
This trackhub was automatically generated from the files and metadata for the experiment - [ENCSR000CVM](#)

Accession	File type	Output type	Biological replicate	Download link
ENCF000KDN	bigBed	bedRnaElements contigs	pooled	Click here
ENCF000KDQ	bigWig	minus strand signal 1		Click here
ENCF000KDR	bigWig	minus strand signal 2		Click here
ENCF000KDT	bigWig	plus strand signal 1		Click here
ENCF000KDU	bigWig	plus strand signal 2		Click here

[ENCODE data use policy](#)

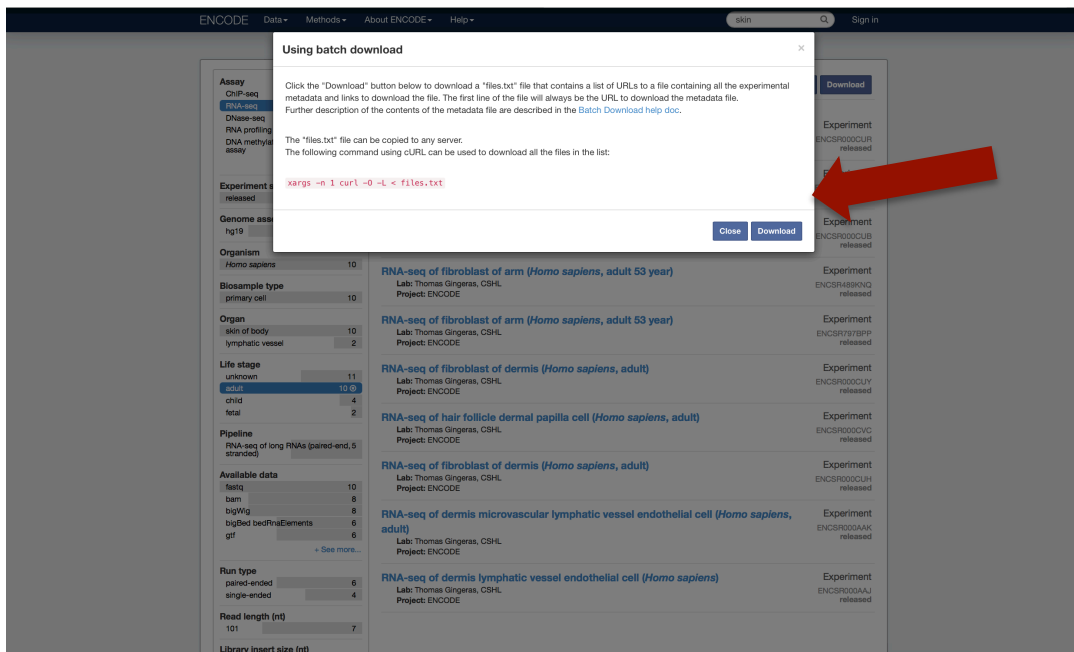
Demo 5: Batch download data

1. Get the list of assays illustrated in Demo 3.
2. Select “Download” button on the upper right corner.



The screenshot shows the ENCODE Data Portal interface. On the left, there are filters for Assay, Experiment status, Genome assembly, Organism, Biosample type, Organ, Life stage, Pipeline, Available data, Run type, and Read length. The main content area displays a list of 10 experiments, all of which are RNA-seq experiments of various cell types and tissues from *Homo sapiens*. A red arrow points to the 'Download' button located in the top right corner of the experiment list.

3. Instructions on the command to batch download files is displayed. Click on ‘Download’ again. This will download a file called ‘files.txt’



The screenshot shows the ENCODE Data Portal interface with a modal dialog box open. The dialog box is titled "Using batch download" and contains the following text:

Click the "Download" button below to download a "files.txt" file that contains a list of URLs to a file containing all the experimental metadata and links to download the file. The first line of the file will always be the URL to download the metadata file. Further description of the contents of the metadata file are described in the [Batch Download help doc](#).

The "files.txt" file can be copied to any server.
The following command using curl can be used to download all the files in the list:

```
xargs -n 1 curl -O -L < files.txt
```

At the bottom of the dialog box, there are "Close" and "Download" buttons. A red arrow points to the "Download" button.

4. Open files.txt. This includes a list of links to all the files for those experiments. The first link contains the metadata. You can select the subset of files by using the 'available data' facet.

```
https://www.encodeproject.org/metadata/searchTerm=skin&type=experiment&assay_term_name=RNA-seq&replicates.library.biosample.life_stage=adult/metadata.tsv
https://www.encodeproject.org/files/ENCF000IGV/@download/ENCF000IGV.bigWig
https://www.encodeproject.org/files/ENCF000IGW/@download/ENCF000IGW.bigWig
https://www.encodeproject.org/files/ENCF000IGY/@download/ENCF000IGY.bam
https://www.encodeproject.org/files/ENCF000IHA/@download/ENCF000IHA.bigWig
https://www.encodeproject.org/files/ENCF000IHB/@download/ENCF000IHB.bigWig
https://www.encodeproject.org/files/ENCF000IHC/@download/ENCF000IHC.fastq.gz
https://www.encodeproject.org/files/ENCF000IHD/@download/ENCF000IHD.bigWig
https://www.encodeproject.org/files/ENCF000IHF/@download/ENCF000IHF.bigBed
https://www.encodeproject.org/files/ENCF000IHG/@download/ENCF000IHG.gtf.gz
https://www.encodeproject.org/files/ENCF000IHI/@download/ENCF000IHI.gtf.gz
https://www.encodeproject.org/files/ENCF000IHK/@download/ENCF000IHK.gtf.gz
https://www.encodeproject.org/files/ENCF000IHM/@download/ENCF000IHM.gtf.gz
https://www.encodeproject.org/files/ENCF000IHO/@download/ENCF000IHO.bigBed
https://www.encodeproject.org/files/ENCF000IHR/@download/ENCF000IHR.gtf.gz
https://www.encodeproject.org/files/ENCF000IHT/@download/ENCF000IHT.gtf.gz
https://www.encodeproject.org/files/ENCF000IHV/@download/ENCF000IHV.fastq.gz
https://www.encodeproject.org/files/ENCF000IHY/@download/ENCF000IHY.fastq.gz
https://www.encodeproject.org/files/ENCF000IHZ/@download/ENCF000IHZ.fastq.gz
https://www.encodeproject.org/files/ENCF536CFG/@download/ENCF536CFG.bigWig
https://www.encodeproject.org/files/ENCF594YIZ/@download/ENCF594YIZ.tsv
https://www.encodeproject.org/files/ENCF594YIZ/@download/ENCF594YIZ.tsv
```

5. Transfer this file to your server and use
xargs -n 1 curl -O -L < files.txt

Exercises using the ENCODE Portal

Exercise 1: CHIP-seq assays

- How many CHIP-seq assays are available against H3K27me3 in mouse
- How many unique antibodies are used?
- Of the antibodies used, which one(s) have been fully characterized to current ENCODE standards?

Exercise 2: Controls

- What is the accession for control experiment for ENCSR778SIU?
- How many assays use this control?

Exercise 3: Recently released data

- What was the total number of assays released in June 2015?
- How many of each kind?

Exercise 4: Files

- What are the accession(s) and md5sum(s) to the fastq files for biological replicate 1 in assay ENCSR000AFI?
- What are the accessions of the alignment (bam) files made from the fastq's ?
- Which software tool and version was used to generate them?

Exercise 5: Protein factors

- Which assays have been performed against IGF2BP1?

REST API exercises using the ENCODE Portal

Pre-requisites: download or install these tools to help you get started

- A JSON pretty-printer plugin for your web browser, such as JSONView (for Chrome or Firefox) or JSON Formatter (for Safari)
- A few python modules
 - pip install requests
 - pip install json
 - pip install jsonschema

Help document: <https://www.encodeproject.org/help/rest-api/>

Sample script: https://github.com/ENCODE-DCC/submission_sample_scripts/blob/master/get.py

Try the exercises listed on the previous page. They can be performed programmatically as well.