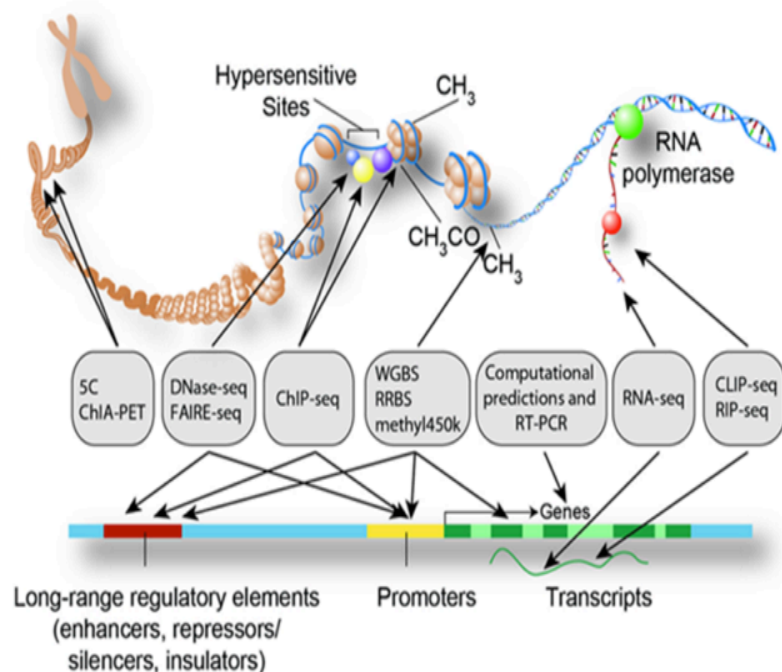


Introduction to the ENCODE Portal



Cricket Alicia Sloan
Data Wrangler Manager
ENCODE DCC
Cherry Lab
Department of Genetics
Stanford School of Medicine

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

<https://www.encodeproject.org>

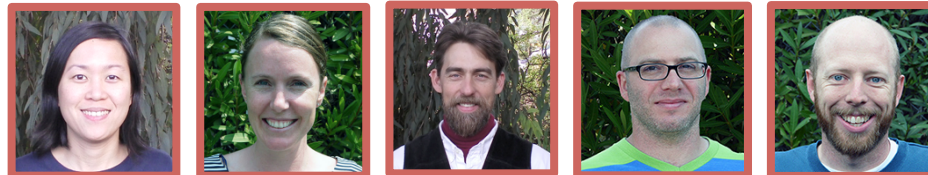


Acknowledgments



Mike Cherry (PI), Ben Hitz, Cricket Sloan

Data Wranglers



Esther Chan, Jean Davidson, J. Seth Strattan, Idan Gabdank, Jason Hilton

Software Engineers



Forrest Tanaka, Tim Dreszer, Bek Baymuradov, Christopher Thomas

Systems Administration, Biocuration Assistants



Stuart Miyasato, Matt Simison, Marcus Ho, Aditi Narayanan, Kathrina Onate

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Cricket A Sloan ENCODE DCC



Reference Materials

slides: <http://bit.ly/24xgJZT>

demos: <http://bit.ly/1tfyamF>

<https://www.encodeproject.org>



ENCODE Portal: Workshop Goals

1

2

3

4

5

What's a
DCC?

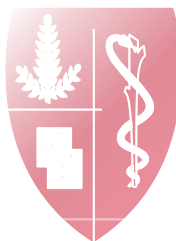
Site
Navigation

Browse and
Search

Visualize and
Download

REST API

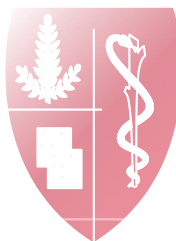
<https://www.encodeproject.org>



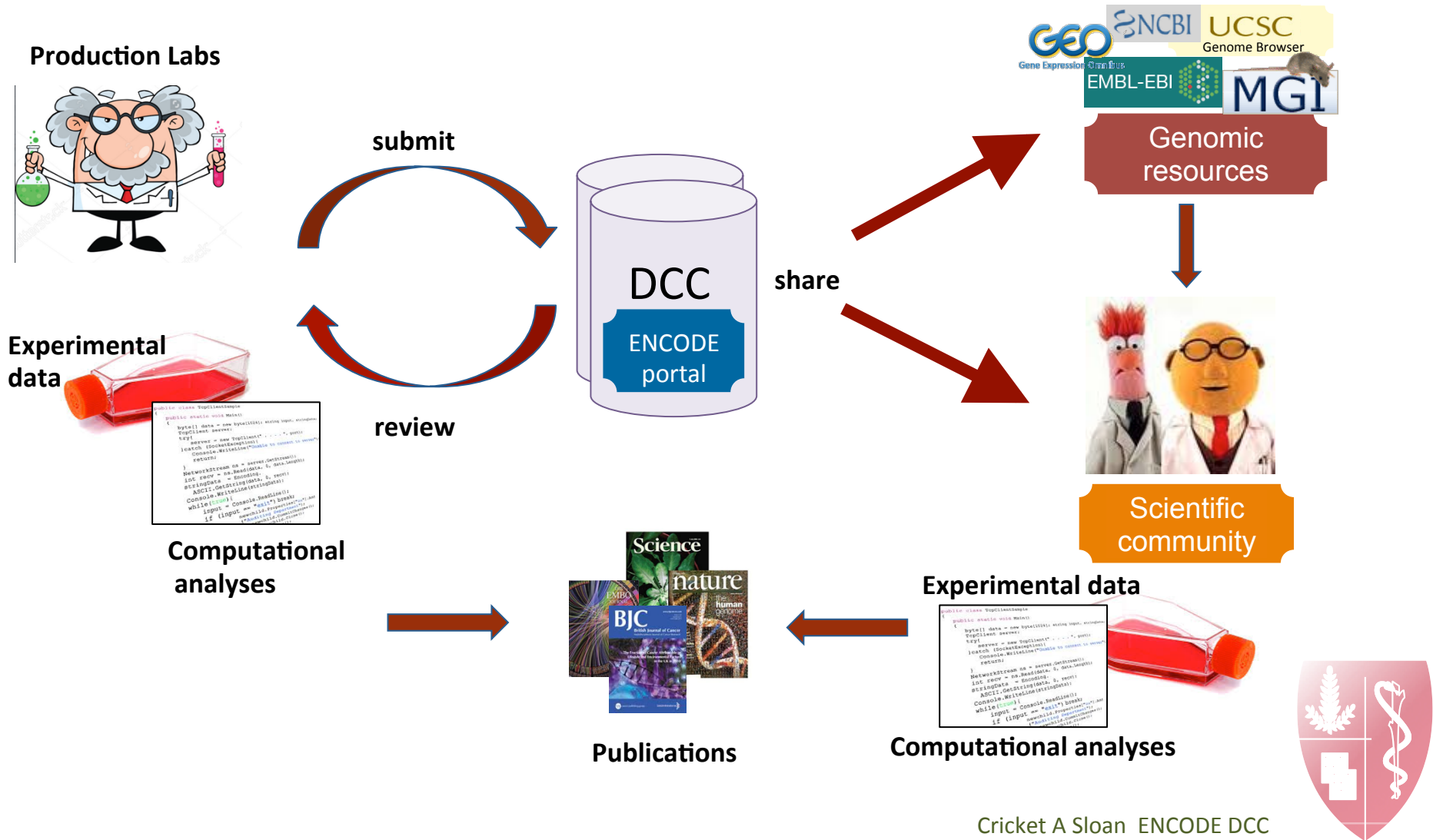
ENCODE Portal: Workshop Goals



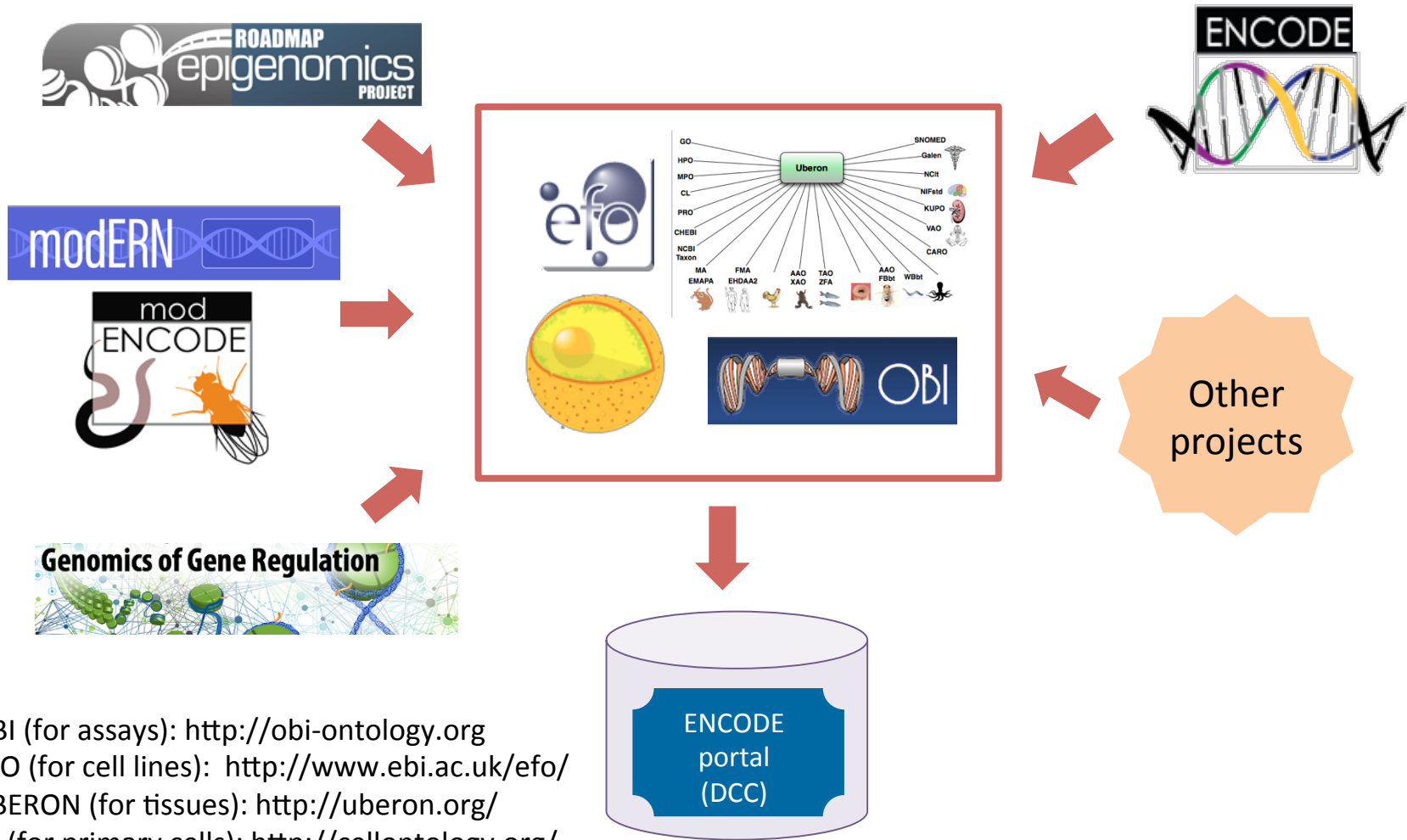
<https://www.encodeproject.org>



Role of a DCC



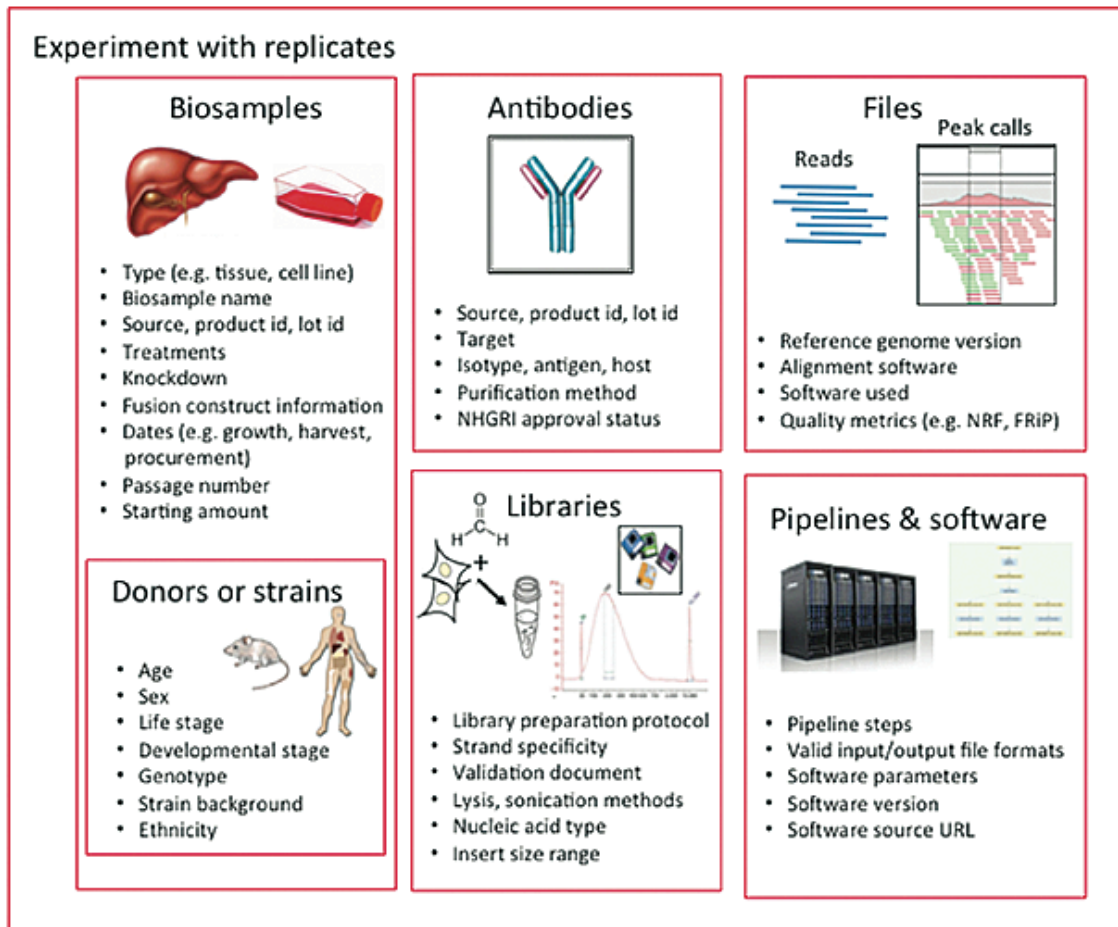
Metadata integration using ontologies



OBI (for assays): <http://obi-ontology.org>
EFO (for cell lines): <http://www.ebi.ac.uk/efo/>
UBERON (for tissues): <http://uberon.org/>
CL (for primary cells): <http://cellontology.org/>
ChEBI (for treatments): <https://www.ebi.ac.uk/chebi/>



Collecting Rich Metadata

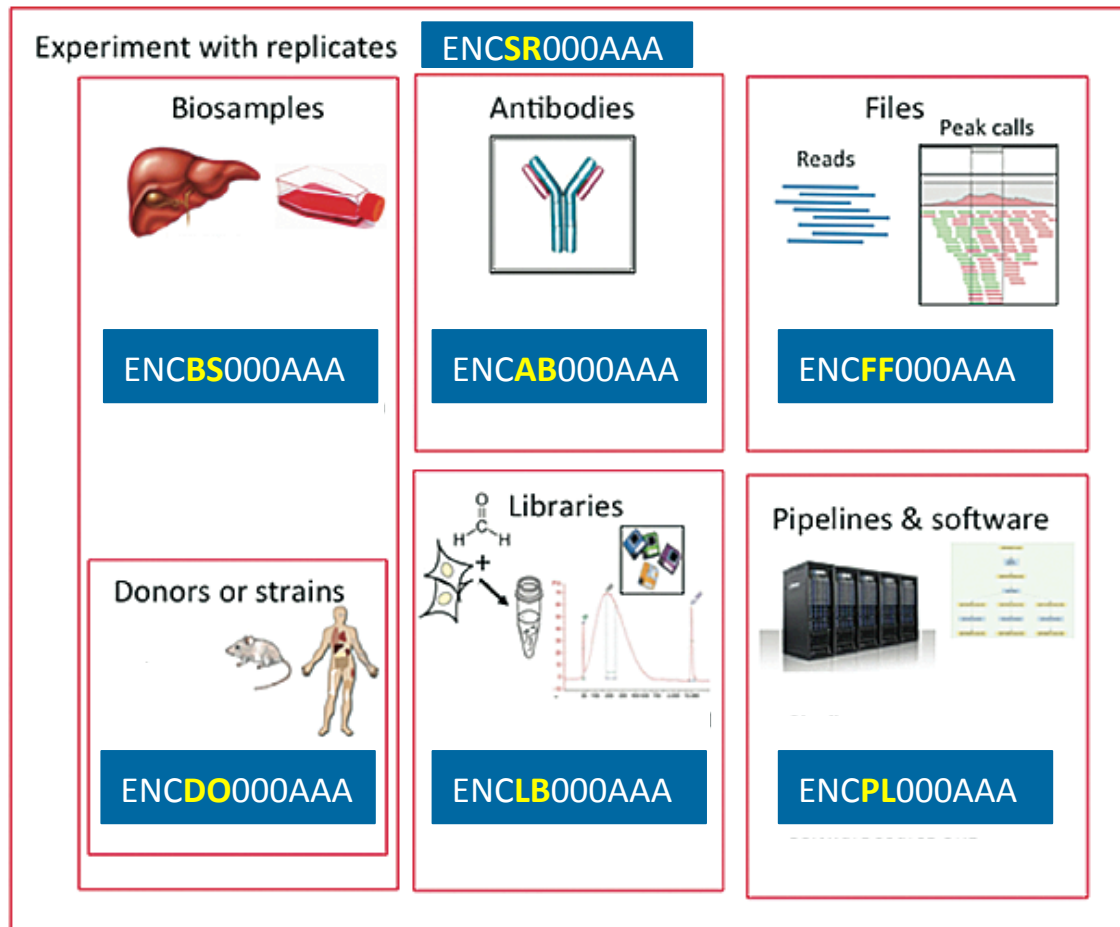


(selected subset of all metadata)

Figure 1, Hong, Eurie L., et al. "Principles of metadata organization at the ENCODE data coordination center." *Database* 2016 (2016): baw001.



Identifying reusable resources

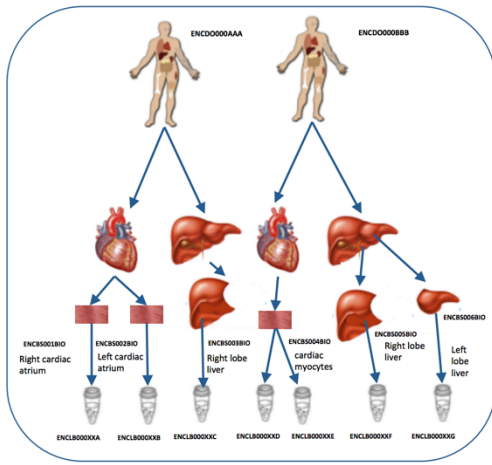


(selected subset of all metadata)

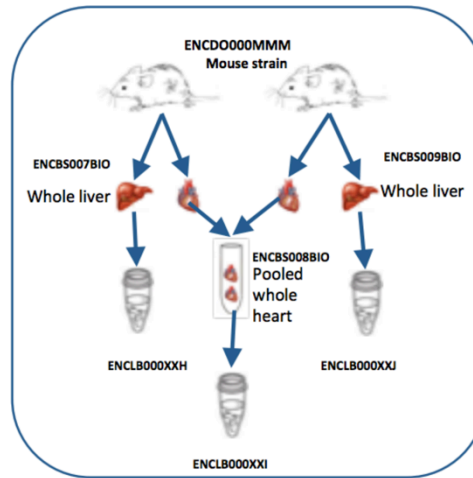
Figure 1, Hong, Eurie L., et al.
"Principles of metadata organization
at the ENCODE data coordination
center." *Database* 2016 (2016):
baw001.



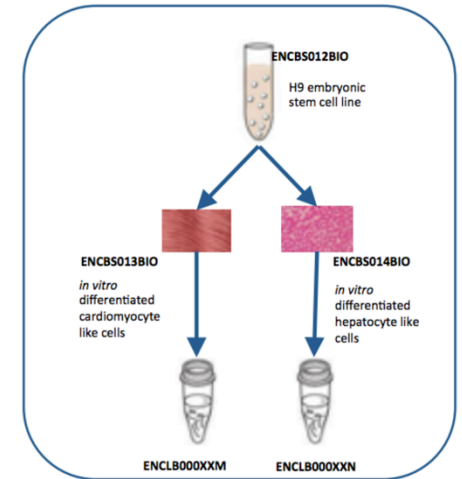
Identifying Biosamples



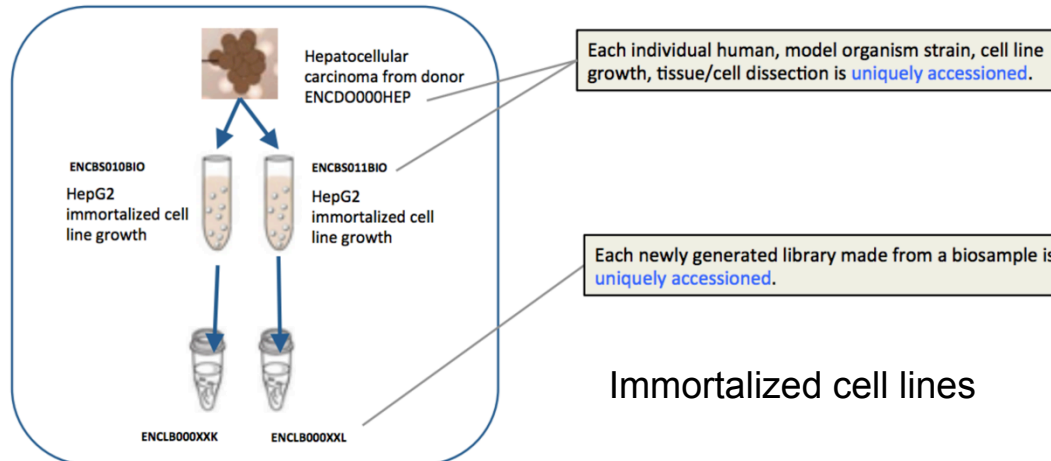
Tissue and primary cell dissections



Model organisms



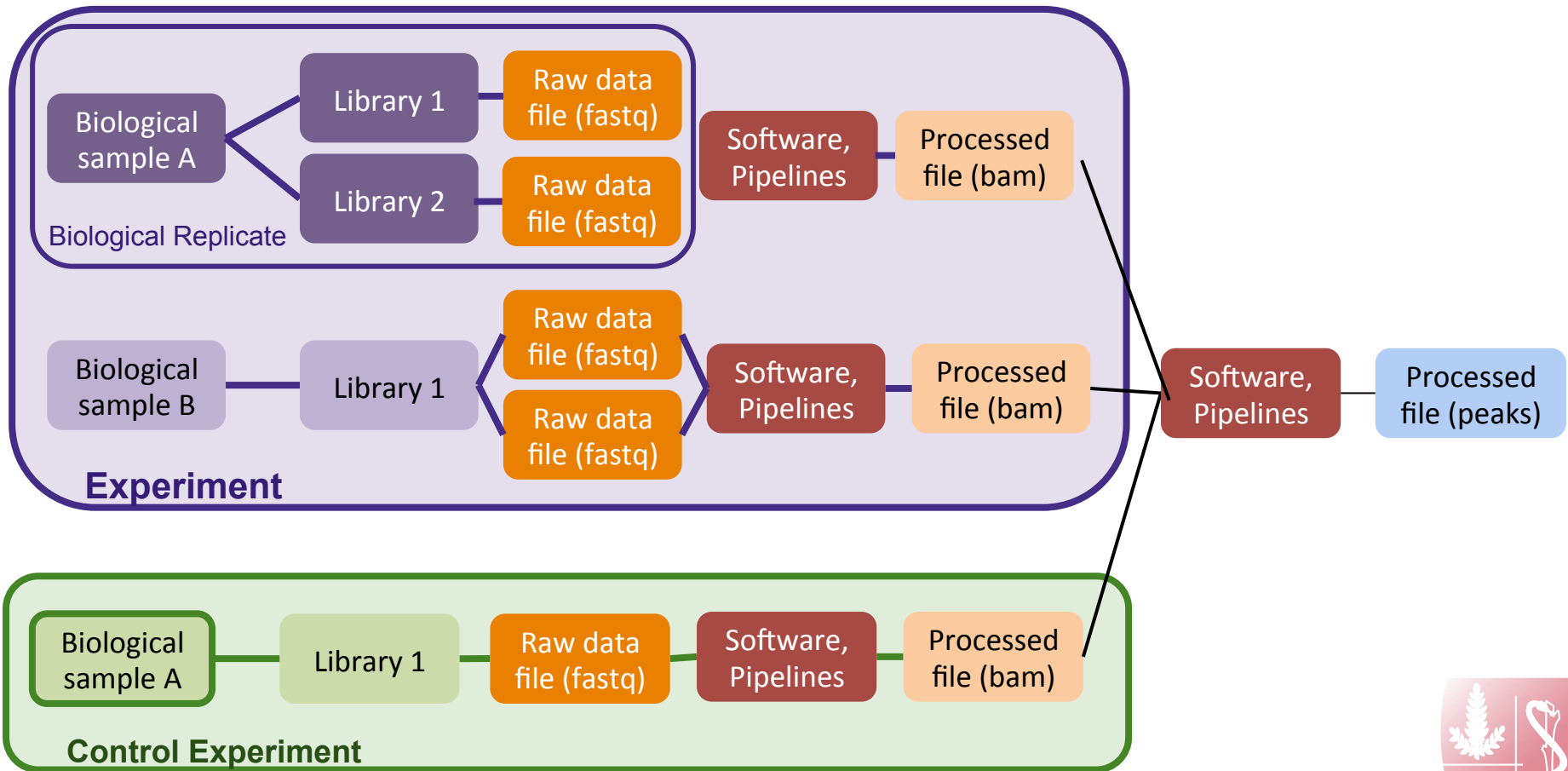
Stem cell derivation



Immortalized cell lines



Data Model to Track Provenance



ENCSR000FCH has sequencing runs,

<https://www.encodeproject.org/experiments/ENCSR768LHG/> has 2 libraries

Cricket A Sloan ENCODE DCC



What can a DCC Provide?

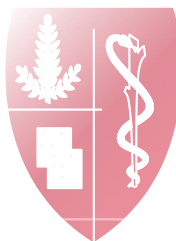
- curation
- integration
- standardization
- resource identification
- provenance and context
- reproducibility
- data sharing



ENCODE Portal: Workshop Goals



<https://www.encodeproject.org>



ENCODE Portal Organization

<https://www.encodeproject.org>

The screenshot shows the ENCODE Portal interface with several callout boxes highlighting key features:

- ENCODER: Encyclopedia of DNA Elements** (Main title)
- Navigation Menu:** ENCODE, Data, Encyclopedia, Materials & Methods, Help
- Search:** Search... (with a magnifying glass icon)
- Find data:** Matrix, Search, Search by region, Publications
- Encyclopedia:** About, Matrix, Search
- Project information, software, pipelines:** Antibodies, Biosamples, Standards and guidelines, Ontologies, File formats, Software tools, Pipelines, Release policy, Data access
- Get started:** Getting started, REST API, Project overview, Tutorials, News, Acknowledgements, Contact
- Quick help:** Quick Start (To find and download ENCODE Consortium data: Click the Data toolbar above and browse data)
- Recent news:** News Follow @EncodeDCC
 - May 13th, 2016: The first ENCODE Hi-C data is released. [read more]
 - May 10th, 2016: We are pleased to announce the release of modern data. [read more]

The background image shows a genomic track with various annotations like SC ChIA-PET, FISH-seq, methyl450k, and Compu predict RT, along with labels for Long-range regulatory elements (enhancers, repressors/silencers, insulators) and Promoters.



Help and Resources

The screenshot shows the ENCODE website navigation bar with 'Materials & Methods' and 'Help' highlighted in red. A search bar is located in the top right. The main heading is 'ENCODE: Encyclopedia of DNA Elements'. Below this is a diagram of DNA with various elements labeled: 'Hypersensitive Sites', 'CH₃', 'CH₃CO', 'CH₃', 'RBS', 'Compu', 'prediction', 'Long-range regulatory elements (enhancers, repressors/silencers, insulators)', 'Promoters', and 'Transcripts'. A blue callout box labeled 'Release Policy' points to the 'Release policy' link in the 'Materials & Methods' menu. Another blue callout box labeled 'Tutorial' points to the 'Tutorials' link in the 'Help' menu. A third blue callout box labeled 'Information on phases and other projects' points to the 'Project overview' link in the 'Help' menu. A fourth blue callout box contains contact information: 'Twitter: @encodedcc, Help desk: encode-help@lists.stanford.edu, Email list for news and announcements: https://mailman.stanford.edu/mailman/listinfo/encode-announce'. At the bottom left, there is a 'Quick Start' section with instructions on how to find and download data. At the bottom right, there is a red shield logo with a white caduceus and a white square.

ENCODE Data Encyclopedia **Materials & Methods** **Help** Search...

ENCODE: Encyclopedia of DNA Elements

Antibodies
Biosamples
Standards and guidelines
Ontologies
File formats
Software tools
Pipelines
Release policy
Data access

Getting started
REST API
Project overview
Tutorials
News
Acknowledgements
Contact

Information on phases and other projects

Tutorial

Release Policy

Twitter: @encodedcc,
Help desk: encode-help@lists.stanford.edu,
Email list for news and announcements:
https://mailman.stanford.edu/mailman/
listinfo/encode-announce

Quick Start

To find and download ENCODE Consortium data:

- Click the Data toolbar above and browse data
- By assay

Cricket A Sloan ENCODE DCC

ENCODE Project Documentation

The screenshot shows the ENCODE Project website interface. At the top, there is a navigation bar with the following menu items: ENCODE, Data, Encyclopedia, Materials & Methods, and Help. A search bar is located on the right side of the navigation bar.

The main content area features a large heading: "ENCODE: Encyclopedia of DNA Elements". Below this heading, there is a diagram illustrating the ENCODE project's focus on understanding the genome. The diagram shows a DNA double helix with various epigenetic marks (CH₃, CH₃CO, CH₃) and associated processes (SC ChIA-PET, DNase-seq FAIRE-seq, ChIP-seq, WGBS RRBS methyl450k, Computational prediction). Below the diagram, there are labels for "Long-range regulatory elements (enhancers, repressors/silencers, insulators)", "Promoters", and "Transcripts".

Callout boxes highlight specific features:

- Publications**: A box containing "Matrix", "Search", "Search by region", and "Publications".
- Experimental standards**: A box containing "Antibodies", "Biosamples", "Standards and guidelines", "Ontologies", "File formats", "Software tools", "Pipelines", "Release policy", and "Data access".
- Tutorial**: A box containing "Getting started", "REST API", "Project overview", "Tutorials", "News", "Acknowledgements", and "Contact".

At the bottom of the page, there are sections for "Quick Start" and "News".

Quick Start
To find and download ENCODE Consortium data:

- Click the Data toolbar above and browse data
- By assay

News Follow @EncodeDCC
May 13th, 2016: The first ENCODE Hi-C data is released. [read more]
May 10th, 2016: We are pleased to announce the release of modern data. [read more]



Publications and Related Datasets

<https://www.encodeproject.org/search/?type=Publication>

Clear Filters

Showing 3 of 3 results

Publication status
published 3

Category

- basic biology 675
- human disease 594
- production 560
- software tool 265
- technology development 166
- model organism biology 165
- pilot phase publication 141
- data standard 6
- database 3
- genomic annotations 3

Available supplemental data
connectivity 1

Genome-wide map of regulatory interactions in the human genome.

Heidari N, Phanstiel DH, He C, et al. *Genome research*. 2014 Dec;24(12):1905-17. PMID:25228660

Available supplemental data: connectivity
Data summary: We generated a genome-wide interaction map of regulatory elements in GM12878 cells using ChIP-seq and RNA-seq. See more

RFECs: random-forest based algorithm for identifying enhancers from chromatin state

DATASETS / FILESET / PUBLICATION DATA

Summary for publication file set ENCSR727WCB

Status: released

Summary	Attribution
Assay(s): ChIA-PET	Lab: Michael Snyder, Stanford
Accession: ENCSR727WCB	External resources: GEO:GSE59395
Description: Supplemental data for Heidari et al., Genome-wide map of regulatory interactions in the human genome.	Publications: PMID:25228660
Biosample term name: K562, GM12878	
Biosample type: immortalized cell line	

Raw data

Accession	File type	Biological replicate	Library	Run type	Read	Lab	Date added
ENCFF002ACL	fastq	1		PE 100nt	R2	Michael Snyder, Stanford	2014-03
ENCFF002ABS	fastq	1		PE 100nt	R2	Michael Snyder, Stanford	2014-03
ENCFF002ACR	fastq	1		PE 100nt	R2	Michael Snyder, Stanford	2014-03
ENCFF002ABR	fastq	1		PE 100nt	R1	Michael Snyder, Stanford	2014-03
ENCFF002ENX	fastq	1		PE 100nt	R2	Michael Snyder, Stanford	2014-07
ENCFF002ENW	fastq	1		PE 100nt	R1	Michael Snyder, Stanford	2014-07

ENCODE data files used in the publication's analysis

PUBLICATIONS / GENOMIC ANNOTATIONS

Genome-wide map of regulatory interactions in the human genome.

Heidari N, Phanstiel DH, He C, Grubert F, Jahanbani F, Kasowski M, Zhang MQ, Snyder M. *Genome research*. 2014 Dec;24(12):1905-17.

Abstract: Increasing evidence suggests that interactions between regulatory elements affect gene expression. We generated a genome-wide interaction map of regulatory elements in GM12878 cells using Chromatin Interaction Analysis by Paired-End Tag Sequencing (ChIA-PET) and RNA-seq. Bound regions including 99.7% of TSS and 98% of enhancers. Correlating this map with ChIP-seq and RNA-seq revealed that key components of three-dimensional chromatin structure affects gene transcription. Comparison of interactions with housekeeping functions, while distal interactions interact with housekeeping functions, while distal interactions interact with housekeeping functions, while distal interactions interact with housekeeping functions. This study reveals new mechanisms of gene regulation in the nucleus.

Datasets: [ENCSR727WCB](#)

References: [PMID:25228660](#)

Related data

Available data: connectivity

Data summary: We generated a genome-wide interaction map of regulatory elements in GM12878 cells using Chromatin Interaction Analysis by Paired-End Tag Sequencing (ChIA-PET) and RNA-seq. Bound regions covered 80% of DNase-seq signal and 98% of enhancers. Correlating this map with ChIP-seq and RNA-seq revealed that key components of three-dimensional (3D) chromatin structure affects gene transcription.

Biosamples

<https://www.encodeproject.org/search/?type=Biosample>

The screenshot displays the ENCODE project search interface. On the left, a 'Filter by feature' sidebar shows various filters such as Organism (Homo sapiens), Biosample status (released), Biosample type (immortalized cell line, in vitro differentiated cells, stem cell), Sex (female), Life stage (adult, embryonic), Transfection type (transient, stable), Transfection method (transduction, electroporation), and Source (ATCC, Alex Meissner, WiCell, Lab: Brenton Graveley, UConn, Bradley Bernstein, Broad). The main area shows 'Showing 25 of 59 results' for 'neuroepithelial stem cell (Homo sapiens, embryonic 5 day)'. A callout box points to the first result, stating 'Every sample has a unique accession'. A second callout box points to the 'Construct details' section of the detailed view, and a third callout box points to the 'Donor information' section. A fourth callout box points to the 'Experiments using this biosample' section. A fifth callout box points to the 'Lab attribution and biosample description' section. The detailed view for 'ENCBS562NPI / in vitro differentiated cells' includes a summary, attribution (Lab: Bradley Bernstein, Broad; Award PI: Bradley Bernstein, Broad; Submitted by: Noam Shorosh; Source: Alex Meissner; Project: ENCODE; Aliases: bradley-bernstein:BioSam 2311), construct details (Target: HES5-human; Construct Type: fusion protein; Description: HES5 promoter fused with GFP cloned by BAC transgenesis; Tag: eGFP (Location: C-terminal)), donor information (Accession: ENC0222AAA; Aliases: encode:donor of H9, roadmap-epigenomics:113; Species: Homo sapiens; Life stage: Embryonic; Age: 5 day; Sex: Female; Health status: Healthy; Ethnicity: Unknown; External resources: GEO:SAMN04284546), and experiments using this biosample (Accession: ENCSP862PLB, Assay: ChIP-seq, Biosample term name: neuroepithelial stem cell, Target: HDK6me3, Lab: Bradley Bernstein, Broad; Accession: ENCSP842NQG, Assay: ChIP-seq, Biosample term name: neuroepithelial stem cell, Target: H3K27ac, Lab: Bradley Bernstein, Broad).

Filter by feature

Lab attribution and biosample description

Every sample has a unique accession

Construct details

Donor information

Experiments that use this biosample

https://v43rc3-master.demo.encodeproject.org/search/?type=Biosample&transfection_method=electroporation

Antibodies

<https://www.encodeproject.org/search/?type=AntibodyLot>

ENCODE Data Encyclopedia Materials & Methods Help Search...

Level of characterization

Additional filters

Showing 25 of 3167 results

View All

Eligibility status

- awaiting lab characterization 1487
- not pursued 1054
- not eligible for new data 394
- eligible for new data 292
- eligible for new data (via exemption) 47

+ See more...

Target Organism

- Homo sapiens 2785
- Drosophila melanogaster 207
- Caenorhabditis elegans 133
- Mus musculus 117
- Aequorea victoria 5

+ See more...

Target of antibody

- transcription factor 1980
- RNA binding protein 1019
- histone 297
- histone modification 292
- chromatin remodeller 145

+ See more...

Characterization method

- immunoprecipitation 1726
- immunoblot 680
- knockdown or knockout 243
- immunoprecipitation followed by mass spectrometry 162
- ChIP-seq comparison 152

+ See more...

Source

- Bethyl Labs 714
- GeneTex 404
- Sigma 404
- Santa Cruz Biotech 273
- Abcam 229

+ See more...

CTCF (*Homo sapiens*) ●
Source: Millipore
Product ID / Lot ID: 07-729 / 2599305

ZMYM3 (*Homo sapiens*) ●
Source: CDI
Product ID / Lot ID: JH39.2.2F10 / HAIB-001

NFE2L2 (*Homo sapiens*) ●●
Source: Santa Cruz Biotech
Product ID / Lot ID: sc-13032x / A1711/I1311

ETS1 (*Homo sapiens*) ●●
Source: Novus
Product ID / Lot ID: NB100-92169 / 360987.0

TBL1XR1 (*Homo sapiens*) ●
Source: Abcam
Product ID / Lot ID: ab24550 / GR80423-1

eGFP (*Aequorea victoria*) ●
Source: Abcam
Product ID / Lot ID: ab290 / GR158277-1

ZHX1 (*Homo sapiens*) ●●
Source: Novus
Product ID / Lot ID: NB600-244A / A1

HNRNPL (*Homo sapiens*) ●
Source: Abcam
Product ID / Lot ID: ab6106 / GR30383-24

KDM5B (*Homo sapiens*) ●
Source: Novus

Antibody
ENCAB830JLB

Antibody
ENCAB426WVA

Antibody
ENCAB408SGF

Antibody
ENCAB032TLC

Antibody
ENCAB596WIK

Antibody
ENCAB976SGG

Antibody
ENCAB064UOI

Antibody
ENCAB734ADP

Antibody
ENCAB888JKB

Every lot has a unique accession



Antibody characterizations

<https://www.encodeproject.org/antibodies/ENCAB000BFX/>

ENCODE Data Encyclopedia Materials & Methods Help Search...

ENCAB000BFX

Antibody against *Homo sapiens* PCBP1

Homo sapiens K562 Eligible for new data

Source (vendor): [MBLI](#)
Product ID: [RN024P](#)
Lot ID: 001
Targets: [PCBP1 \(*Homo sapiens*\)](#)

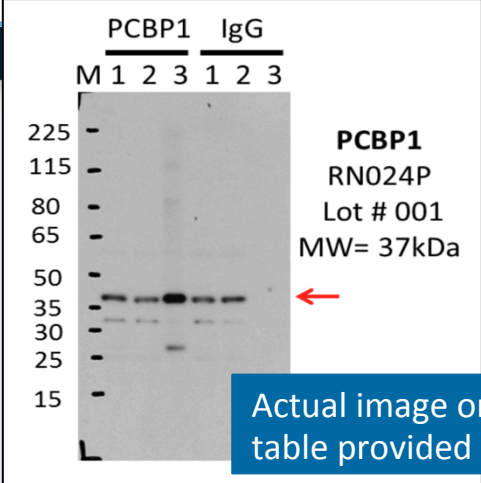
Host: Rabbit
Clonality: Polyclonal
Purification: Affinity
Antigen description: KLH conjugated synthetic peptide, corresponding to internal region of human PCBP1
Aliases: xiang-dong-fu:PCBP1

Characterizations

PCBP1 (<i>Homo sapiens</i>)	PCBP1 (<i>Homo sapiens</i>)
Method: immunoprecipitation	Method: knockdown or knockout
compliant	compliant

Lot information and hyperlinks

Characterizations provided by labs



PCBP1 (*Homo sapiens*)
Method: immunoprecipitation

compliant

Caption:
IP-Western blot analysis of K562 whole cell lysate using PCBP1 specific antibody. Lane 1 is 2.5% of 0.5mg input lysate, lane 2 is 2.5% of supernatant after immunoprecipitation and Lane 3 is 50% of IP enrichment using rabbit polyclonal Anti-PCBP1 antibody. The last three lanes are the same pattern, but with IgG control instead of PCBP1 antibody.

Submitted by: Balaji Sundararaman
Lab: Gene Yeo, UCSD
Grant: U54HG007005
Download: [MBLI_RN024P_001_PCBP1.png](#)
Documents: [ENCODE:Antibody_Characterization_ENCODE3_February2014.pdf](#)

Details of the characterization



Encyclopedia Access

<https://www.encodeproject.org/data/annotations/>

ENCODE Data **Encyclopedia** Materials & Methods Help Search...

ENCODE: Encyclopedia of DNA Annotations

About Matrix Search

chr19 26,844,000 | 26,846,000 | 26,848,000 |

Enhancer-like Regions
DNase Signal
H3K27ac Signal
VISTA Enhancer
PhastCons Conservation

459 results

BIOSAMPLE	TYPE	enhancer-like regions	enhancer prediction	promoter-like regions	chromatin state overlap	DNase master peaks	binding sites	encyclopedia
tissue								
small intestine	4	1						
brain	3	1						
stomach	4							
heart	2	1						
thymus	2	1						
...and 23 more								
primary cell								
fibroblast of lung	4	2	1					
endothelial cell of umbilical vein	2	1	2	1				
foreskin fibroblast	5	1						
keratinocyte	2	1	1	1				
mammary epithelial cell	3	1	1					
...and 56 more								
immortalized cell line								
GM12878	2	1	3	1				
HepG2	2	1	3	1				

Quick Start
To find and download ENCODE Consortium data:

- Click the Data toolbar above and browse data
- By assay



ENCODE Portal: Workshop Goals



<https://www.encodeproject.org>



Find ENCODE Data: Views



SEARCH

REPORT

**MATRI
X**



ENCODE Data Search View

<https://www.encodeproject.org/search/?type=Experiment>

Filters

Assay category

DNA binding	5566
Transcription	2770
DNA accessibility	856
DNA methylation	680
RNA binding	490

+ See more...

Assay

ChIP-seq	5566
DNase-seq	807
polyA mRNA RNA-seq	705
RNA-seq	503
shRNA RNA-seq	445

+ See more...

Project

ENCODE	6451
Roadmap	3127
modENCODE	883
modERN	198
GGR	24

RFA

Roadmap	3127
ENCODE3	3103
ENCODE2	2756
modENCODE	883
ENCODE2-Mouse	557

+ See more...

Experiment status



released	10646
revoked	35
archived	2

Genome assembly (visualization)

hg19	3644
GRCh38	961
mm10-minimal	728
mm9	568
ce10	200

+ See more...

Showing 25 of 10683 results

  [View All](#) [Download](#) [Filter to 100 to visualize](#)

Action buttons

ChIP-seq of HepG2 Experiment
Homo sapiens, child 15 year ENCSR195ZCD released
Target: Control
Lab: Michael Snyder, Stanford
Project: ENCODE

Hi-C of SK-N-DZ Experiment
Homo sapiens, child 2 year ENCSR105KFX released
Lab: Job Dekker, UMass
Project: ENCODE

ChIP-seq of esophagogastric junction Experiment
Homo sapiens, adult 51 year ENCSR211EXK released
Target: Control
Lab: Michael Snyder, Stanford
Project: ENCODE

ChIP-seq of esophagogastric junction Experiment
Homo sapiens, adult 53 year ENCSR361LSG released
Target: Control
Lab: Michael Snyder, Stanford
Project: ENCODE

ChIP-seq of suprapubic skin Experiment
Homo sapiens, adult 51 year ENCSR827FNU released
Target: Control
Lab: Michael Snyder, Stanford
Project: ENCODE

ChIP-seq of suprapubic skin Experiment
Homo sapiens, adult 53 year ENCSR308RWM released
Target: Control
Lab: Michael Snyder, Stanford
Project: ENCODE

Summary per experiment



ENCODE Data Report View

<https://www.encodeproject.org/report/?type=Experiment>

Assay category

- DNA binding 5566
- Transcription 2770
- DNA accessibility 856
- DNA methylation 680
- RNA binding 490

[+ See more...](#)

Assay

- ChIP-seq 5566
- DNase-seq 807
- polyA mRNA RNA-seq 705
- RNA-seq 503
- shRNA RNA-seq 445

[+ See more...](#)

Project

- ENCODE 6451
- Roadmap 3127
- modENCODE 883
- modERN 198
- GGR 24

RFA

- Roadmap 3127
- ENCODE3 3103
- ENCODE2 2756
- modENCODE 883
- ENCODE2-Mouse 557

[+ See more...](#)

Showing results 1 to 25 of 10683

Columns
Download TSV

Can adjust columns and download the TSV

ID	Accession	Assay Type	Assay Nickname	Target	Biosample	Description	Lab	Project
ENCSR195ZCD	ENCSR195ZCD	ChIP-seq	ChIP-seq	Control	HepG2	ChIP-seq on human HepG2		
ENCSR105KFX	ENCSR105KFX	HIC	Hi-C		SK-N-DZ	HIC experiment done on SK-N-DZ	Job Dekker, UMass	ENCODE
ENCSR211EXK	ENCSR211EXK	ChIP-seq	ChIP-seq	Control	esophagogastric junction	ChIP-seq on human esophagogastric junction	Michael Snyder, Stanford	ENCODE
ENCSR361LSG	ENCSR361LSG	ChIP-seq	ChIP-seq	Control	esophagogastric junction	ChIP-seq on human esophagogastric junction	Michael Snyder, Stanford	ENCODE
ENCSR827FNU	ENCSR827FNU	ChIP-seq	ChIP-seq	Control	suprapubic skin	ChIP-seq on human suprapubic skin	Michael Snyder, Stanford	ENCODE
ENCSR308RWM	ENCSR308RWM	ChIP-seq	ChIP-seq	Control	suprapubic skin	ChIP-seq on human suprapubic skin	Michael Snyder, Stanford	ENCODE

Tabular format

Can sort by column



ENCODE Data Matrix View

<https://www.encodeproject.org/matrix/?type=Experiment>

Filter by keyword

Filters

Organized by assay

ENCODE Data Encyclopedia Materials & Methods Help

Experiment Matrix

Click or enter search terms to filter the experiments included in the matrix.

Assay
 ChIP-seq 5567
 DNase-seq 806
 polyA mRNA RNA-seq 705
 RNA-seq 502
 shRNA RNA-seq 445
 + See more...

Assay category
 DNA binding 5567
 Transcription 2771
 DNA accessibility 855
 DNA methylation 680
 RNA binding 490
 + See more...

Target of assay
 histone 2854
 histone modification 2854
 transcription factor 1637
 broad histone mark 1572
 control 1431
 + See more...

Date released
 October, 2015 3161
 May, 2016 605
 February, 2016 521
 October, 2011 457
 January, 2016 448
 + See more...

Available data
 fastq 6914
 bam 5697
 bigWig 4968
 bed narrowPeak 2268
 bigBed narrowPeak 2197
 + See more...

Organism
 Homo sapiens 7883
 Mus musculus 1609
 Caenorhabditis elegans 566
 Drosophila melanogaster 490
 Drosophila pseudoobscura 10
 + See more...

Biosample type
 immortalized cell line 3739
 tissue 3046
 primary cell 1810
 whole organisms 747
 stem cell 576
 + See more...

Organ
 brain 655
 skin of body 293
 kidney 246
 lung 244
 muscle organ 239
 + See more...

Project
 ENCODE 6452
 Roadmap 3127
 modENCODE 883
 modERN 198
 GGR 24

Genome assembly (visualization)
 hg19 3644
 GRCh38 961
 mm10-minimal 728
 mm9 568
 ce10 200

10684 results

ASSAY: ChIP-seq, DNase-seq, polyA mRNA RNA-seq, RNA-seq, shRNA RNA-seq, RNA microarray, eCLIP, WGBS, RRBS, small RNA-seq, CAGE, single cell RNA-seq, RNA Biol-n-Seq, DNase-seq, Replic-seq, genotyping array, RPPAGE, RIP-seq, microRNA counts, MRE-seq, ...and 22 more

Category	Assay	Count	Assay	Count	Assay	Count	Assay	Count	Assay	Count	Assay	Count	Assay	Count	Assay	Count	Assay	Count		
immortalized cell line	K562	374	21	18	13	227	12	156	1	1	8	9	2	6	1	1	29	1	2	
	HepG2	150	3	11	6	218	7	112	1	2	3	6	2	6	1	1	1	1	1	
	GM12878	174	2	10	5	8	2	2	6	6	13	2	6	1	1	14	1	2	2	
	A549	110	14	21	2	2	1	9	3	1	1	1	1	1	1	1	1	1	1	
	HeLa-S3	103	4	5	4	1	3	6	1	6	1	1	1	1	1	1	1	1	1	
tissue	liver	131	5	14	11	10	1	1	2	1	3	2	6	3						
	heart	93	20	8	10	10	8	1	1	1	1	1	2	6						
	lung	80	15	8	5	10	7	3	1	2	1	4								
	stomach	69	18	11	5	8	1	4												
	kidney	69	16	9	4	2	4	4					2	1	1	4				
primary cell	common myeloid progenitor, CD34-positive	67	15	1	13	1	9													
	CD4-positive helper T cell	77	8	3	1	1	3								1				3	
	trophoblast cell	58	6	4	1	2														
	endothelial cell of umbilical vein	35	2	5	2	2	1	5			1	6	1						1	
	Purkinje cell				1						61									
whole organisms	multi-cellular organism	571	73	50				15												
	carcass	12	4					4												
stem cell	H1-hESC	186	3	12	3	1	4	6	3	4	2	2							1	4
	H9	66	2	2		1	2	1							1					1
	neuronal stem cell	32	1																	
	ES-E14	25	1	1																
	HUES64	16	2			2	1													
in vitro differentiated cells	mesenchymal stem cell	64	2	4				2	2											
	mesoderm	43	2	4				2												
	chondrocyte	32							3											
	neuronal stem cell	20	4					3	1											
	neural cell	22	1							3										1
induced pluripotent stem cell line	induced pluripotent stem cell	9	5	2	4			1	1											1

Collapsed by biosample term



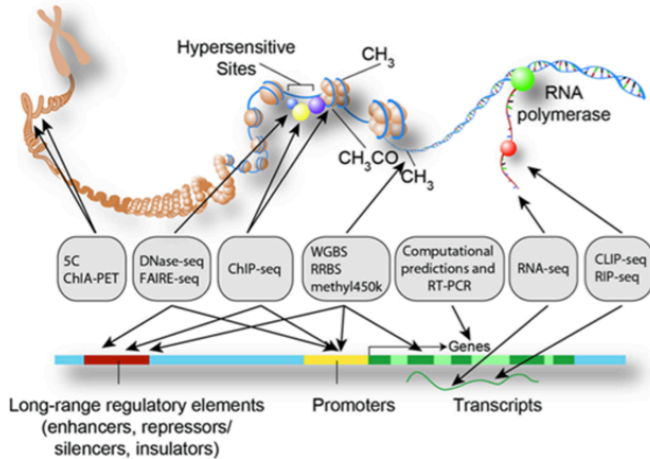
Browse

Find ENCODE data

Search



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)

Quick Start

To find and download ENCODE Consortium data:

- Click the Data toolbar above and browse data
- [By assay](#)

News [Follow @EncodeDCC](#)

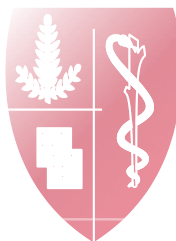
May 13th, 2016: The first ENCODE [Hi-C data](#) is released. [\[read more\]](#)

May 10th, 2016: We are pleased to announce the release of modERN data. [\[read more\]](#)



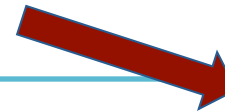
Search ENCODE data

Demo 1: Free text search of ENCODE data



Search ENCODE data

Enter "skin" into search box



ENCODE Data Encyclopedia Materials & Methods Help Search...

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)

Quick Start

To find and download ENCODE Consortium data:

- Click the Data toolbar above and browse data

News [Follow @EncodeDCC](#)

May 13th, 2016: The first ENCODE [Hi-C data](#) is released. [[read more](#)]

May 10th, 2016: We are pleased to announce the release of modERN data. [[read more](#)]



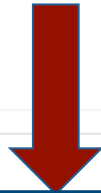
Search ENCODE data

skin



Data Type	Count
Dataset	367
Experiment	346
Biosample	173
Publication	59
Series	16

[+ See more...](#)



Showing 25 of 602 results

[View All](#)

lower leg skin (*Homo sapiens*, adult 54 year)

Type: tissue
Summary: Homo sapiens lower leg skin tissue male adult (54 years)
Source: Kristin Ardlie

Biosample
ENCBS089CWO
released

Project

ENCODE	194
Roadmap	151
modENCODE	1

RFA

ENCODE2	158
ENCODE3	34
ENCODE	2

Experiment status

released	192
revoked	2

Genome assembly (visualization)

hg19	157
GRCh38	31
mm9	2

Organism

<i>Homo sapiens</i>	191
<i>Mus musculus</i>	2

Target of assay

histone	37
histone modification	37
broad histone mark	19
narrow histone mark	18
control	14

[+ See more...](#)

Biosample type

primary cell	177
tissue	15
stem cell	2

Lab: Michael Snyder, Stanford
Project: ENCODE

ChIP-seq of suprapubic skin

Homo sapiens, adult 37 year

Target: Control
Lab: Michael Snyder, Stanford
Project: ENCODE

Experiment
ENCSSR607EOD
released

ChIP-seq of suprapubic skin

Homo sapiens, adult 54 year

Target: Control
Lab: Michael Snyder, Stanford
Project: ENCODE

Experiment
ENCSSR277LNZ
released

small RNA-seq of skin of body

Homo sapiens, fetal

Lab: Thomas Gingeras, CSHL
Project: ENCODE

Experiment
ENCSSR000AGA
released

RAMPAGE of skin of body

Homo sapiens, fetal

Lab: Thomas Gingeras, CSHL
Project: ENCODE

Experiment
ENCSSR000AGU
released

RNA-seq of melanocyte of skin

Homo sapiens, adult

Lab: Thomas Gingeras, CSHL
Project: ENCODE

Experiment
ENCSSR000CUR
released

ChIP-seq of fibroblast of dermis

Homo sapiens, adult

Target: H3K36me3
Lab: Bradley Bernstein, Broad
Project: ENCODE

Experiment
ENCSSR000APP
released

skin is an ontological search, not just text match



Browse ENCODE data

Demo 2: Browsing and filtering of ENCODE data



Browse ENCODE data

The screenshot shows the ENCODE project website interface. At the top, there is a navigation bar with 'ENCODE', 'Data', 'Encyclopedia', 'Materials & Methods', and 'Help'. A search bar is located on the right. Below the navigation bar, a dropdown menu is open under 'Encyclopedia', with 'Search' highlighted. A red arrow points from the 'Search' option to the main content area. The main content area is titled 'ENCODE Encyclopedia of DNA Elements' and displays search results for 'ChIP-seq of HepG2'. On the left, there is a diagram of a DNA molecule with various elements labeled: 'Hypersensitive Sites', 'SC ChIA-PET', 'DNase-seq FAIRE-seq', 'ChIP-seq', 'WGBS RRBS methyl', 'Long-range regulatory elements (enhancers, repressors/silencers, insulators)', and 'Promoter'. Below the diagram is a 'Quick Start' section with instructions on how to find and download ENCODE Consortium data. The search results are displayed in a grid format, showing 25 of 10683 results. The first result is 'ChIP-seq of HepG2' for 'Homo sapiens, child 15 year', with a target of 'Control', lab of 'Michael Snyder, Stanford', and project of 'ENCODE'. The second result is 'Hi-C of SK-N-DZ' for 'Homo sapiens, child 2 year', with a lab of 'Job Dekker, UMass' and project of 'ENCODE'. The third result is 'ChIP-seq of esophagogastric junction' for 'Homo sapiens, adult 51 year', with a target of 'Control', lab of 'Michael Snyder, Stanford', and project of 'ENCODE'. The fourth result is 'ChIP-seq of esophagogastric junction' for 'Homo sapiens, adult 53 year', with a target of 'Control', lab of 'Michael Snyder, Stanford', and project of 'ENCODE'. The search results are organized into several categories: Assay category, Assay, Project, and RFA. Each category has a horizontal bar chart showing the number of results for each sub-category. For example, in the 'Assay category' section, 'DNA binding' has 5565 results, 'Transcription' has 2772, 'DNA accessibility' has 855, 'DNA methylation' has 680, and 'RNA binding' has 490. In the 'Assay' section, 'ChIP-seq' has 5565 results, 'DNase-seq' has 806, 'polyA mRNA RNA-seq' has 705, 'RNA-seq' has 503, and 'shRNA RNA-seq' has 445. In the 'Project' section, 'ENCODE' has 6451 results, 'Roadmap' has 3127, 'modENCODE' has 883, 'modERN' has 198, and 'GGR' has 24. In the 'RFA' section, 'Roadmap' has 3127 results, 'ENCODE3' has 3103, 'ENCODE2' has 2756, and 'modENCODE' has 883. The search results are also filtered by 'Showing 25 of 10683 results' and include buttons for 'View All', 'Download', and 'Filter to 100 to visualize'.

ENCODE Encyclopedia of DNA Elements

Assay category

DNA binding	5565
Transcription	2772
DNA accessibility	855
DNA methylation	680
RNA binding	490

[+ See more...](#)

Assay

ChIP-seq	5565
DNase-seq	806
polyA mRNA RNA-seq	705
RNA-seq	503
shRNA RNA-seq	445

[+ See more...](#)

Project

ENCODE	6451
Roadmap	3127
modENCODE	883
modERN	198
GGR	24

RFA

Roadmap	3127
ENCODE3	3103
ENCODE2	2756
modENCODE	883

Showing 25 of 10683 results

[View All](#) [Download](#) [Filter to 100 to visualize](#)

ChIP-seq of HepG2 Experiment
Homo sapiens, child 15 year
ENCSTR195ZCD released
Target: Control
Lab: Michael Snyder, Stanford
Project: ENCODE

Hi-C of SK-N-DZ Experiment
Homo sapiens, child 2 year
ENCSTR105KFX released
Lab: Job Dekker, UMass
Project: ENCODE

ChIP-seq of esophagogastric junction Experiment
Homo sapiens, adult 51 year
ENCSTR211EXK released
Target: Control
Lab: Michael Snyder, Stanford
Project: ENCODE

ChIP-seq of esophagogastric junction Experiment
Homo sapiens, adult 53 year
ENCSTR361LSG released
Target: Control
Lab: Michael Snyder, Stanford

Quick Start

To find and download ENCODE Consortium data:

- Click the Data toolbar above and browse by:
 - By assay
 - By biosample
 - By genomic annotations

Filter all ENCODE data using metadata

- Categories on the left are metadata describing assays and files
- Selecting an option in the category narrows results
- Choosing more than one option in a category acts as an “OR”
- Choosing more than one category acts as an “AND”
- Select “skin” under the “Organ” category

<https://www.encodeproject.org>

The screenshot shows the ENCODE project website interface. The top navigation bar includes 'ENCODE', 'Data', 'Encyclopedia', 'Materials & Methods', and 'Help', along with a search bar. The left sidebar contains several filter categories with horizontal bar charts and counts:

- Assay category**: DNA binding (5565), Transcription (2772), DNA accessibility (855), DNA methylation (680), RNA binding (490). + See more...
- Assay**: ChIP-seq (5565), DNase-seq (806), polyA mRNA RNA-seq (705), RNA-seq (503), shRNA RNA-seq (445). + See more...
- Project**: ENCODE (6451), Roadmap (3127), modENCODE (883), modERN (198), GGR (24).
- RFA**: Roadmap (3127), ENCODE3 (3103), ENCODE2 (2756), modENCODE (883), ENCODE2-Mouse (557). + See more...
- Experiment status**: released (10646), revoked (35), archived (2).

The main content area shows 'Showing 25 of 10683 results' with buttons for 'View All', 'Download', and 'Filter to 100 to visualize'. The results list includes:

- ChIP-seq of HepG2**: *Homo sapiens*, child 15 year. Target: Control. Lab: Michael Snyder, Stanford. Project: ENCODE. Experiment: ENCSR195ZCD released.
- Hi-C of SK-N-DZ**: *Homo sapiens*, child 2 year. Lab: Job Dekker, UMass. Project: ENCODE. Experiment: ENCSR105KFX released.
- ChIP-seq of esophagogastric junction**: *Homo sapiens*, adult 51 year. Target: Control. Lab: Michael Snyder, Stanford. Project: ENCODE. Experiment: ENCSR211EXK released.
- ChIP-seq of esophagogastric junction**: *Homo sapiens*, adult 53 year. Target: Control. Lab: Michael Snyder, Stanford. Project: ENCODE. Experiment: ENCSR361LSG released.
- ChIP-seq of suprapubic skin**: *Homo sapiens*, adult 51 year. Target: Control. Lab: Michael Snyder, Stanford. Project: ENCODE. Experiment: ENCSR827FNU released.

Search & Filter ENCODE data

Demo 3: Combine search & filter of ENCODE data



Combine Search and Filtering

ENCODE Data Encyclopedia Materials & Methods Help Search...

Showing 25 of 602 results

Data Type

- Dataset 367
- Experiment 346
- Biosample 173
- Publication 59
- Series 16

View All

Showing 25 of 346 results

Assay category

- DNA binding 123
- Transcription 106
- DNA accessibility 58
- DNA methylation 41
- Genotyping 10

View All Download Filter to 100 to visualize

ChIP-seq of suprapubic skin

Experiment ENCSR827FNU released

Experiment ENCSR277LNZ released

Experiment ENCSR308RWM released

Experiment ENCSR607EOD released

Showing 14 of 14 results

Assay category Transcription 14

Assay

- CHIP-seq 30
- RNA-seq 14
- DNase-seq 9
- RNA microarray 6
- DNase array 5

Project ENCODE 14

RFA ENCODE3 11 ENCODE2 3

Experiment status released 14

Genome assembly (visualization) GRCh38 14 hg19 7

Organism Homo sapiens 14

Biosample type primary cell 8 tissue 6

Organ skin of body 10 lymphatic vessel 2

Life stage adult 14 newborn 11 child 3

RNA-seq of melanocyte of skin Experiment ENCSR000CUR released Lab: Thomas Gingeras, CSHL Project: ENCODE

RNA-seq of suprapubic skin Experiment ENCSR862RGX released Lab: Thomas Gingeras, CSHL Project: ENCODE

RNA-seq of suprapubic skin Experiment ENCSR108MAU released Lab: Thomas Gingeras, CSHL Project: ENCODE

RNA-seq of suprapubic skin Experiment ENCSR480SLD released Lab: Thomas Gingeras, CSHL Project: ENCODE

RNA-seq of lower leg skin Experiment ENCSR460YCS released Lab: Thomas Gingeras, CSHL Project: ENCODE

https://www.encodeproject.org/search/?searchTerm=skin&type=Experiment&assay_title=RNA-seq&replicates.library.biosample.life_stage=adult

Cricket A Sloan ENCODE DCC



Experimental Details Page (continued)

<https://www.encodeproject.org/experiments/ENCSR000CUR/>

Displaying 20 of 62 files

Raw data

Accession	File type	Anisogenic replicate	Library	Run type	Read	Lab	Date added	File size
ENCF000HZ	fastq	1	ENCLB555APG	PE 101nt	R2	Thomas Gingeras, CSHL	2011-07-13	9.52 GB
ENCF000HY	fastq	1	ENCLB555APG	PE 101nt	R1	Thomas Gingeras, CSHL	2011-07-13	9.32 GB
ENCF000HV	fastq	2	ENCLB555AMU	PE 101nt	R2	Thomas Gingeras, CSHL	2011-07-13	11 GB
ENCF000HC	fastq	2	ENCLB555AMU	PE 101nt	R1	Thomas Gingeras, CSHL	2011-07-13	10.8 GB

Processed data GRCh38 V24

Accession	File type	Output type	Anisogenic replicate	Mapping assembly	Genome annotation	Lab	Date added	File size
ENCF187GIO	tsv	gene quantifications	1	GRCh38	V24	ENCODE Processing Pipeline	2016-03-01	9.45 MB
ENCF230TKY	tsv	transcript quantifications	1	GRCh38	V24	ENCODE Processing Pipeline	2016-03-01	29.5 MB
ENCF708XMO	bigWig	plus strand signal of all reads	1	GRCh38	V24	ENCODE Processing Pipeline	2016-03-01	223 MB
ENCF580VXJ	bigWig	minus strand signal of unique reads	1	GRCh38	V24	ENCODE Processing Pipeline	2016-03-01	204 MB
ENCF538OCD	bigWig	minus strand signal of all reads	1	GRCh38	V24	ENCODE Processing Pipeline	2016-03-01	217 MB
ENCF786JJB	bigWig	plus strand signal of unique reads	1	GRCh38	V24	ENCODE Processing Pipeline	2016-03-01	210 MB
ENCF944WOQ	bam	transcriptome alignments	1	GRCh38	V24	ENCODE Processing Pipeline	2016-02-	18.4
ENCF751ARF	bigWig	minus strand signal of unique reads	2	GRCh38	V24	ENCODE Processing Pipeline	2016-03-01	143 MB
ENCF455XJY	bam	alignments	2	GRCh38	V24	ENCODE Processing Pipeline	2016-03-01	25.2 GB
ENCF438HIO	bam	transcriptome alignments	2	GRCh38	V24	ENCODE Processing Pipeline	2016-03-01	22.7 GB

Experiments with ENCSR000CUR as a control:

Accession	Assay	Biosample term name	Target	Description	Lab
ENCSR000KZ	CAGE	melanocyte of skin	CAGE on human NHEM-M2 cellular long (b-200 nt) polyadenylated RNA	Piero Carninci, RIKEN	

Displaying 1 of 1

Documents

General protocol
Description: Specific protocol for library ENCLB555AMU
LID47259.pdf

General protocol
Description: Specific protocol for library ENCLB555APG
LID47258.pdf

Certificate of analysis
Description: PromoCell certificate of analysis
NHEM27011001_2_Gingeras_protocol.pdf

Certificate of analysis
Description: PromoCell certificate of analysis
NHEM27012303_Gingeras_protocol.pdf

ENCODE | SANTA CRUZ | Stanford University
Contact | Terms of Use | Submitter sign-in
©2016 Stanford University.

Table showing details for all files. A drop down menu allows you to filter the files mapped to the assembly of your choice.

Experiments controlled by this experiment

Protocol documents



Curated datasets for context

<https://www.encodeproject.org/experiments/ENCSR061DPP/>

ENCODE Data Methods About Help Search...

EXPERIMENTS / CHIP-SEQ / MUS MUSCULUS / EMBRYONIC FACIAL PROMINENCE

Experiment summary for ENCSR061DPP

Status: released Validation: pending

Summary	Attribution
Assay: ChIP-seq	Lab: Bing Ren, UCSD
Target: H3K27me3	Award PI: Bing Ren, UCSD
Biosample summary: embryonic facial prominence (<i>Mus musculus</i> , embryonic 15.5 day mixed)	Project: ENCODE
Biosample Type: tissue	Aliases: bing-ren:e15.5_embryonic_facial_prominence_H3K27me3
Replication type: isogenic	Date released: 2015-11-03
Description: H3K27me3 ChIP-seq on embryonic 15.5 day mouse embryonic facial prominence	Related datasets: ENCSR899FPM ⓘ
Nucleic acid type: DNA	Reference Epigenome for mouse embryonic facial prominence (15.5 day).
Size range: 300-500	
Lysis method: SDS	
Fragmentation method: sonication (generi	
Size selection method: gel	

Experiments in reference epigenome series ENCSR899FPM

Accession	Assay	Target	Description	Lab
ENCSR061DPP	ChIP-seq	H3K27me3	H3K27me3 ChIP-seq on embryonic 15.5 day mouse embryonic facial prominence	Bing Ren, UCSD
ENCSR091WNX	ChIP-seq	H3K4me1	H3K4me1 ChIP-seq on embryonic 15.5 day mouse embryonic facial prominence	Bing Ren, UCSD
ENCSR137NUN	ChIP-seq	H3K9me3	H3K9me3 ChIP-seq on embryonic 15.5 day mouse embryonic facial prominence	Bing Ren, UCSD
ENCSR193AEW	ChIP-seq	H3K4me2	H3K4me2 ChIP-seq on embryonic 15.5 day mouse embryonic facial prominence	Bing Ren, UCSD
ENCSR382DRK	ChIP-seq	H3K27ac	H3K27ac ChIP-seq on embryonic 15.5 day mouse embryonic facial prominence	Bing Ren, UCSD
ENCSR461SRF	microRNA-seq		miRNA-seq on embryonic 15.5 day mouse embryonic facial prominence	Ali Mortazavi, UCI
ENCSR606AJV	ChIP-seq	H3K36me3	H3K36me3 ChIP-seq on embryonic 15.5 day mouse embryonic facial prominence	Bing Ren, UCSD

Search & Filter ENCODE data

Demo 4: Region Search



Region Search Version 1

<https://www.encodeproject.org/region-search/>

ENCODE Data Encyclopedia Materials & Methods Help Search...

Matrix
Search
Search by region
Publications

ENCODE Encyclopedia of DNA Elements

Hypersensitive Sites CH₃ RNA polymerase

The ENCODE (Encyclopedia of DNA Elements) Consortium is an international collaboration of research groups funded by the National Human Genome Research Institute of the U.S. Department of Health and Human Services. The goal of the ENCODE project is to identify all functional elements in the human genome, including genes, promoters, enhancers, and other regulatory elements. The project is a major component of the International Human Genome Consortium (IHGC).

ENCODE Data Encyclopedia Materials & Methods Help Search...

Region search

Enter any one of human Gene name, Symbol, Synonyms, Gene ID, HGNC ID, coordinates, rsid, Ensemble ID

Please enter valid coordinates

Long-range regulatory elements (enhancers, repressors/silencers, insulators) Promoters Transcripts



Region Search Version 1

<https://www.encodeproject.org/region-search/>

Input:

Gene ID, HGNC Symbol, coordinate range, RSID, Ensembl

Converts:

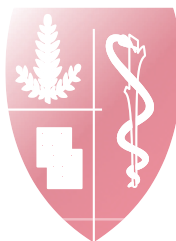
The identifier to genomic coordinates of specific assembly
(Version 1 is only hg19)

Intersects:

This range with coordinates of all bed files.
(Version 1 is TF ChIP and DNAase-seq only)

Returns:

The list of experiments with intersecting files



Region Search Version 1

<https://www.encodeproject.org/region-search/>

The screenshot displays the ENCODE Region Search interface. At the top, there is a navigation bar with links for ENCODE, Data, Encyclopedia, Materials & Methods, and Help, along with a search bar. The main heading is "Region search". Below this, a search input field contains the text "rs4686483 chr3:188118225-188118225".

On the left side, there are several filter categories:

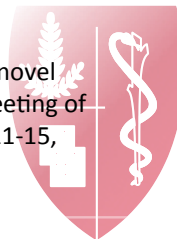
- Assay:** DNase-seq (9)
- Biosample term:** T-helper 2 cell (2), Mel-2183 (1), inferior parietal cortex (1), limb (1), naive B cell (1). A "+ See more..." link is present.
- Organism:** Homo sapiens (9)
- Organ:** brain (2), large intestine (1)
- Genome assembly:** hg19 (9)
- Available data:** bam (9), bed narrowPeak (9), bigWig (9), fastq (8), bigBed narrowPeak (5)

The main content area shows "Showing 9 of 9" results. There are two buttons: "Download Elements" and "Visualize". The results are listed as follows:

Assay	Experiment
DNase-seq of naive B cell <i>Homo sapiens</i> Lab: Gregory Crawford, Duke Project: ENCODE	Experiment ENCSR000ELG released
DNase-seq of Mel-2183 <i>Homo sapiens</i> Lab: Gregory Crawford, Duke Project: ENCODE	Experiment ENCSR000ELC released
DNase-seq of sigmoid colon <i>Homo sapiens, adult 53 year</i> Lab: John Stamatoyannopoulos, UW Project: ENCODE	Experiment ENCSR907VOR released
DNase-seq of limb <i>Homo sapiens, fetal</i> Lab: John Stamatoyannopoulos, UW Project: ENCODE	Experiment ENCSR532CRI released

Example (narcolepsy SNP)¹:
chr3:188118225(rs4686483)

1. Ollila HM et al. Genome-wide association study identifies novel genetic loci in narcolepsy. [abstract]. In: 30th Anniversary Meeting of the Associated Professional Sleep Societies, LLC; 2016 June 11-15, Denver, CO. Abstract 0006.



ENCODE Portal: Workshop Goals



<https://www.encodeproject.org>



Visualize ENCODE data

Demo 5: Visualize data



Visualize Button

The image shows a screenshot of the ENCODE project website. On the left, there is a sidebar with filters for Assay category, Assay, Project, RFA, Experiment status, Genome assembly (visualization), Organism, Biosample type, and Life stage. The main content area displays search results for RNA-seq of HepG2 cells. A red arrow points from the 'Visualize' button in the search results to a detailed genomic track visualization in the UCSC Genome Browser.

ENCODE Project Search Results:

- Showing 25 of 39 results
- Assay category: Transcription (39)
- Assay: RNA-seq (39)
- Project: ENCODE (39)
- RFA: ENCODE3 (39)
- Experiment status: released (39)
- Genome assembly (visualization): GRCh38 (39)
- Organism: Homo sapiens (39)
- Biosample type: immortalized cell line (39)
- Life stage: adult (28)

Search Results:

- RNA-seq of HepG2**
Homo sapiens, child 15 year
Lab: Eric Lécuyer, IRCM
Project: ENCODE
- RNA-seq of HepG2**
Homo sapiens, child 15 year
Lab: Eric Lécuyer, IRCM
Project: ENCODE
- RNA-seq of HepG2**
Homo sapiens, child 15 year
Lab: Eric Lécuyer, IRCM
Project: ENCODE
- RNA-seq of K562**
Homo sapiens, adult 53 year
Lab: Eric Lécuyer, IRCM
Project: ENCODE
- RNA-seq of K562**
Homo sapiens, adult 53 year
Lab: Eric Lécuyer, IRCM
Project: ENCODE

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

chr9:133,252,000-133,280,861 28,862 bp.

The visualization shows various tracks including: ENTP4, ENTP4-AS1, ENTP4-AS2, ENTP4-AS3, ENTP4-AS4, ENTP4-AS5, ENTP4-AS6, ENTP4-AS7, ENTP4-AS8, ENTP4-AS9, ENTP4-AS10, ENTP4-AS11, ENTP4-AS12, ENTP4-AS13, ENTP4-AS14, ENTP4-AS15, ENTP4-AS16, ENTP4-AS17, ENTP4-AS18, ENTP4-AS19, ENTP4-AS20, ENTP4-AS21, ENTP4-AS22, ENTP4-AS23, ENTP4-AS24, ENTP4-AS25, ENTP4-AS26, ENTP4-AS27, ENTP4-AS28, ENTP4-AS29, ENTP4-AS30, ENTP4-AS31, ENTP4-AS32, ENTP4-AS33, ENTP4-AS34, ENTP4-AS35, ENTP4-AS36, ENTP4-AS37, ENTP4-AS38, ENTP4-AS39, ENTP4-AS40, ENTP4-AS41, ENTP4-AS42, ENTP4-AS43, ENTP4-AS44, ENTP4-AS45, ENTP4-AS46, ENTP4-AS47, ENTP4-AS48, ENTP4-AS49, ENTP4-AS50, ENTP4-AS51, ENTP4-AS52, ENTP4-AS53, ENTP4-AS54, ENTP4-AS55, ENTP4-AS56, ENTP4-AS57, ENTP4-AS58, ENTP4-AS59, ENTP4-AS60, ENTP4-AS61, ENTP4-AS62, ENTP4-AS63, ENTP4-AS64, ENTP4-AS65, ENTP4-AS66, ENTP4-AS67, ENTP4-AS68, ENTP4-AS69, ENTP4-AS70, ENTP4-AS71, ENTP4-AS72, ENTP4-AS73, ENTP4-AS74, ENTP4-AS75, ENTP4-AS76, ENTP4-AS77, ENTP4-AS78, ENTP4-AS79, ENTP4-AS80, ENTP4-AS81, ENTP4-AS82, ENTP4-AS83, ENTP4-AS84, ENTP4-AS85, ENTP4-AS86, ENTP4-AS87, ENTP4-AS88, ENTP4-AS89, ENTP4-AS90, ENTP4-AS91, ENTP4-AS92, ENTP4-AS93, ENTP4-AS94, ENTP4-AS95, ENTP4-AS96, ENTP4-AS97, ENTP4-AS98, ENTP4-AS99, ENTP4-AS100.

At the UCSC Genome Browser

Genomes Genome Browser Tools Mirrors Downloads My Data View Help About Us

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr9:133,252,000-133,280,861 28,862 bp. go

chr9 (q34.2) 9p23 21.3 21.1 9q12 q13 31.1 32 33.1

Scale chr9: 133,255,000| 133,260,000| 10 kb | 133,265,000| 133,270,000| hg38 133,275,000|

RNA-seq of fibroblast of arm - ENCSR510QZ4
RNA-seq of fibroblast of dermis - ENCSR000CUH

ENCF075U20
ENCF098RRY
ENCF325YXD
ENCF710DYV
ENCF000HMK
ENCF000HMT
ENCF000HNA
ENCF000HNB
ENCF000HNG
ENCF000HWH
ENCF075CXE
ENCF077KSU
ENCF102NVX
ENCF120SYM
ENCF183CHV
ENCF232ZLN
ENCF260VJW
ENCF278HST
ENCF355AYH
ENCF410HOR
ENCF419JDG
ENCF419TBQ
ENCF439ZS0
ENCF549FKJ
ENCF599RMH
ENCF620SNY
ENCF642RLU
ENCF685JCV
ENCF689KGG
ENCF748FWL
ENCF786STS
ENCF790EHG
ENCF877WMB
ENCF883IOU
ENCF000GBC
ENCF000GSL
ENCF000GCU

Hub (search) refresh

DNase-seq of A549 - ENCSR077EYC hide	DNase-seq of A549 - ENCSR128IVG hide	DNase-seq of A549 - ENCSR136DNA(Target - Control) hide	DNase-seq of A549 - ENCSR294XUZ hide	DNase-seq of A549 - ENCSR347CEH hide	DNase-seq of A549 - ENCSR384KCZ full
DNase-seq of A549 - ENCSR406EMB full	DNase-seq of A549 - ENCSR523FJT hide	DNase-seq of A549 - ENCSR565WPR hide	DNase-seq of A549 - ENCSR599WJC hide	DNase-seq of A549 - ENCSR660OQE hide	DNase-seq of A549 - ENCSR837VHE hide
RNA-seq of A549 - ENCSR070IYV hide	RNA-seq of A549 - ENCSR154TDP hide	RNA-seq of A549 - ENCSR224PTG full	RNA-seq of A549 - ENCSR255VBV hide	RNA-seq of A549 - ENCSR326PTW hide	RNA-seq of A549 - ENCSR385TFN hide
RNA-seq of A549 - ENCSR543QRU hide	RNA-seq of A549 - ENCSR546PPG full	RNA-seq of A549 - ENCSR624RID hide	RNA-seq of A549 - ENCSR632DQP(Target - Control) full	RNA-seq of A549 - ENCSR656FIH hide	RNA-seq of A549 - ENCSR924BHE hide

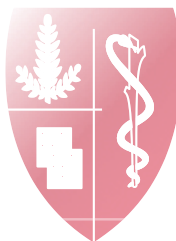


Download ENCODE data

Demo 6: Batch download data

<https://www.encodeproject.org>

Cricket A Sloan ENCODE DCC



Download Button

ENCODE Data Encyclopedia Materials & Methods Help Search...

Showing 25 of 39 results

View All Download Visualize

RNA-seq of HepG2
Homo sapiens, child 15 year
Lab: Eric Lécuyer, IRCM
Project: ENCODE
Experiment ENCSR813BDU released

RNA-seq of HepG2
Homo sapiens, child 15 year
Lab: Eric Lécuyer, IRCM
Project: ENCODE
Experiment released

RNA-seq of HepG2
Homo sapiens, child 15 year
Lab: Eric Lécuyer, IRCM
Project: ENCODE
Experiment released

RNA-seq of HepG2
Homo sapiens, child 15 year
Lab: Eric Lécuyer, IRCM
Project: ENCODE
Experiment released

RNA-seq of K562
Homo sapiens, adult 53 year
Lab: Eric Lécuyer, IRCM
Project: ENCODE
Experiment ENCSR896YIB released

RNA-seq of K562
Homo sapiens, adult 53 year
Lab: Eric Lécuyer, IRCM
Project: ENCODE
Experiment released

Assay category: Transcription (39)

Assay: shRNA RNA-seq (443), RNA-seq (39), polyA mRNA RNA-seq (38), RAMPAGE (27), CRISPR RNA-seq (19)

Project: ENCODE (39)

RFA: ENCODE3 (39)

Experiment status: released (39)

Genome assembly (visualization): dm3 (41), GRCh38 (39), hg19 (34), mm10-minimal (4)

Organism: *Homo sapiens* (39)

Biosample type: tissue (93), primary cell (57), immortalized cell line (39), in vitro differentiated cells (11), induced pluripotent stem cell line (2)

Life stage: adult (28)

Using batch download

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
```

Close Download

files (1).txt



Download Part 1: Metadata

```
files.txt
https://www.encodeproject.org/metadata/searchTerm=skin&type=Experiment&award.project=ENCODE&assay_title=RNA-seq&replicates.library.biosample.life_stage=adult/
metadata.tsv
https://www.encodeproject.org/files/ENCFF627NPY/@download/ENCFF627NPY.fastq.gz
https://www.encodeproject.org/files/ENCFF065GSV/@download/ENCFF065GSV.fastq.gz
https://www.encodeproject.org/files/ENCFF920BRU/@download/ENCFF920BRU.bam
https://www.encodeproject.org/files/ENCFF710DYV/@download/ENCFF710DYV.bigWig
https://www.encodeproject.org/files/ENCFF681LOB/@download/ENCFF681LOB.bam
https://www.encodeproject.org/files/ENCFF656YPD/@download/ENCFF656YPD.bam
https://www.encodeproject.org/files/ENCFF775DYT/@download/ENCFF775DYT.tsv
https://www.encodeproject.org/files/ENCFF192VMT/@download/ENCFF192VMT.tsv
https://www.encodeproject.org/files/ENCFF457XYP/@download/ENCFF457XYP.bam
https://www.encodeproject.org/files/ENCFF341SCS/@download/ENCFF341SCS.tsv
https://www.encodeproject.org/files/ENCFF098RRY/@download/ENCFF098RRY.bigWig
https://www.encodeproject.org/files/ENCFF325YXD/@download/ENCFF325YXD.bigWig
https://www.encodeproject.org/files/ENCFF075UZ0/@download/ENCFF075UZ0.bigWig
https://www.encodeproject.org/files/ENCFF888KTF/@download/ENCFF888KTF.tsv
https://www.encodeproject.org/files/ENCFF001RAX/@download/ENCFF001RAX.fastq.gz
https://www.encodeproject.org/files/ENCFF001RAY/@download/ENCFF001RAY.fastq.gz
https://www.encodeproject.org/files/ENCFF001RBP/@download/ENCFF001RBP.fastq.gz
https://www.encodeproject.org/files/ENCFF001RBQ/@download/ENCFF001RBQ.fastq.gz
https://www.encodeproject.org/files/ENCFF115EFK/@download/ENCFF115EFK.bam
https://www.encodeproject.org/files/ENCFF707ERG/@download/ENCFF707ERG.bam
https://www.encodeproject.org/files/ENCFF364VKV/@download/ENCFF364VKV.bigWig
https://www.encodeproject.org/files/ENCFF837DRS/@download/ENCFF837DRS.bigWig
https://www.encodeproject.org/files/ENCFF370BGJ/@download/ENCFF370BGJ.bigWig
https://www.encodeproject.org/files/ENCFF129VXB/@download/ENCFF129VXB.bigWig
https://www.encodeproject.org/files/ENCFF474PBL/@download/ENCFF474PBL.bigWig
https://www.encodeproject.org/files/ENCFF463VRQ/@download/ENCFF463VRQ.bigWig
https://www.encodeproject.org/files/ENCFF164RKE/@download/ENCFF164RKE.bigWig
https://www.encodeproject.org/files/ENCFF451DHE/@download/ENCFF451DHE.bigWig
https://www.encodeproject.org/files/ENCFF623BWE/@download/ENCFF623BWE.bam
https://www.encodeproject.org/files/ENCFF597WCI/@download/ENCFF597WCI.bam
```



Download Part 2: Files

Using batch download ×

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
```

[Close](#) [Download](#)



ENCODE Portal: Workshop Goals

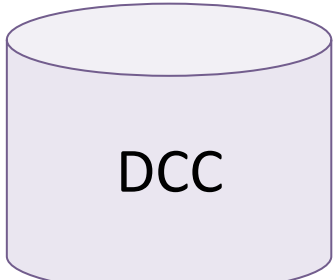


<https://www.encodeproject.org>



Access the ENCODE Portal via REST API

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



```
1 status: "CURRENT",
2 part_of: {},
3 biosample_term_name: "camera-type eye",
4 description: "Human fetal whole eye",
5 age_units: "week",
6 embryo_id_prefix: {},
7 life_stage: "fetal",
8 constructs: [],
9 accession: "ENC006898A",
10 lab:
11 status: "CURRENT",
12 acc: "16-122-109",
13 institute_name: "Cold Spring Harbor Laboratory",
14 phone2: "",
15 address1: "500 Sunnyside Blvd",
16 postal_code: "11797",
17 phone1: "516-437-4105",
18 url: "http://lab.cshlb.org/ncg/ncg2",
19 name: "Thomas Gingeras",
20 title: "Thomas Gingeras, CSHL",
21 schema_version: "1",
22 state: "NY",
23 country: "USA",
24 awards: []
25 termsname: {}
26 awards: []
27 description: "The overall goal of this project is to generate fine-structure RNA maps in human and mouse (C57BL/6J) tissues and primary cell lines using a variety of high-throughput sequencing platforms, to evaluate the biological importance of novel transcripts by determining if evidence of their transcribed products can be identified. From each sample analyzed, we propose to isolate long (200 nucleotides) and short (< 200 nucleotides) RNA in biological duplicate. Illumina-based maps for these samples will initially be generated using (1) RNA sequencing using of total RNA, (2) RNA-seq of tobacco acid pyrophosphatase (TAP) pre-treated short RNA (3) 5' end Cap Analysis of Gene Expression (5' CAGE) of total RNA. Additionally, for a subset of primary cell lines we will generate the above libraries from nuclear and cytoplasmic subcellular fractions. Long RNA-seq data will be distilled down into functional elements consisting of splice junctions, polyadenylation sites and de novo genes and transcripts. The short RNA data will be distilled into contigs representing the 5' ends of short RNAs up to the read length. 5' CAGE data will be analyzed to form clusters representing the 5' ends of transcripts linked to a tag internal to the transcript body. Importantly, each element will be assessed for reproducibility using a nonparametric irreproducible detection rate (pidm) script. Collectively, these data will allow for the detection of novel transcribed regions and supportive information as to the location of promoter regions and subcellular residence of transcripts. In aggregate, these data will be used to generate models of both noncoding and protein coding transcripts and to distinguish isoforms at complex loci necessary to obtain a comprehensive view of mammalian transcription. For a subset of these samples we will simultaneously collect the genome sequence of the human donors to provide a reference map that will be used to map the RNA data against and derive information concerning allele-specific expression and RNA editing. Unannotated transcripts will be tested using Isoseq (v1.0) sequencing. Lastly, proteomic analysis will be done and the results compared against the unannotated transcripts."
41 end_data: {}
42 title: "LANGUAGE OF TRANSCRIPTION IN HUMAN AND MOUSE",
43 url: "http://project.encodeproject.nih.gov/project_info_details.cfm?aid=402436",
44 url2: "http://encode241-0157-4597-b5ef-266a2240a6f",
45 schema_version: "1",
46 type: "item"
47 }
48 }
49 }
50 requests: "ENCODE"
```



ENCODE Antibodies Biosamples Experiments Targets Effort Clon.

Biosamples > Tissue > Human

ENCS006898A / Tissue

Term name: camera-type eye
Term ID: LISBION.000019
Description: Human fetal whole eye
Source: BioChain Tissue Inc [?]
Product ID: B104106-10-002 [?]
Lot ID: B08026
Project: ENCODE5
Submitted By: Carin Davis
Lab: Thomas Gingeras, CSHL
Grant: US45000704
Note: Purchased as total RNA

Donor information
Donor ID: ENC006898A
Age: 20 week fetal
Sex: Female
Strain: N/A
Health status: Normo

Protocols and supporting documents

Data Sheet
BioChain Human fetal whole eye B08026 data sheet
Submitted By: Carin Davis
Lab: Thomas Gingeras, CSHL
Grant: US45000704
Download: B08026.pdf

Metadata viewed as web page

Metadata in JSON format



```
18 SERVER = 'http://184.109.162.173'
19 AUTHID = '802WMD'
20 AUTHPW = '760trnm12lspz5'
21
22 def get_json(url):
23     h = http.client.HTTPConnection(SERVER)
24     r = h.request('GET', url, headers={'content-type': 'application/json'})
25     r_text = r.read()
26     return r_text
27
28 def post_json(url, payload):
29     h = http.client.HTTPConnection(SERVER)
30     r = h.request('POST', url, payload, headers={'content-type': 'application/json'})
31     r_text = r.read()
32     return r_text
33
34 def get_status(url):
35     r = requests.get(url, auth=(AUTHID, AUTHPW))
36     r_text = r.json()
37     return r_text
38
39 def post_status(url, payload):
40     r = requests.post(url, auth=(AUTHID, AUTHPW), data=payload)
41     r_text = r.json()
42     return r_text
43
44 def get_status(url):
45     r = requests.get(url, auth=(AUTHID, AUTHPW))
46     r_text = r.json()
47     return r_text
48
49 def post_status(url, payload):
50     r = requests.post(url, auth=(AUTHID, AUTHPW), data=payload)
51     r_text = r.json()
52     return r_text
```

Query programmatically using the REST API



All Portal Content is in JSON

<https://www.encodeproject.org/targets/PUF60-human/?format=json>

```
{
  label: "PUF60",
  schema_version: "4",
  status: "current",
  @id: "/targets/PUF60-human/",
  aliases: [ ],
  - dbxref: [
    "HGNC:FIR",
    "ENSEMBL:ENSG00000179950",
    "HGNC:SIABBP1",
    "GeneID:22827",
    "HGNC:ROBPI",
    "UniProtKB:Q9UHX1"
  ],
  - investigated_as: [
    "RNA binding protein"
  ],
  @context: "/terms/",
  - actions: [
    - {
      profile: "/profiles/Target.json",
      href: "/targets/PUF60-human/#!edit",
      name: "edit",
      title: "Edit"
    },
    - {
      profile: "/profiles/Target.json",
      href: "/targets/PUF60-human/#!edit-json",
      name: "edit-json",
      title: "Edit JSON"
    }
  ],
  gene_name: "PUF60",
  uuid: "baab397e-1891-4c4d-8421-827650d243c3",
  - @type: [
    "Target",
    "Item"
  ],
  - organism: {
    - @type: [
      "Organism",
      "Item"
    ]
  }
}
```

- All Portal content is accessible via URL's; just add ?format=json
- The database record is returned in JSON format
- JSON can be parsed in your language of choice
- JSON pretty printers:

Firefox:

<https://addons.mozilla.org/en-us/firefox/addon/jsonview/>

Chrome:

<https://chrome.google.com/webstore/detail/jsonview/chklaanhfefbnpoihckbnefhakgolnmc?hl=en>

Safari:

<https://github.com/rfletcher/safari-json-formatter>



Search Queries are in the URL

Assay

ChIP-seq	29
RNA-seq	8
whole-genome shotgun bisulfite sequencing	4
DNase-seq	2

Experiment status

released	10
----------	----

Genome assembly (visualization)

mm10	4
mm9	4

Organism

<i>Homo sapiens</i>	67
<i>Mus musculus</i>	10

Biosample type

tissue	10
--------	----

Organ

lung	10
------	----

Life stage

adult	5
embryonic	4
postnatal	1

Pineline

Showing 10 of 10 experiments

[Visualize](#) [Download](#)

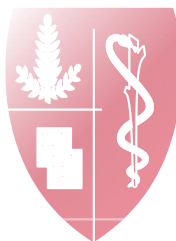
RNA-seq of lung (<i>Mus musculus</i>, embryonic 14.5 day)	Experiment
Lab: Barbara Wold, Caltech Project: ENCODE	ENCSR039ADS released
RNA-seq of lung (<i>Mus musculus</i>, postnatal 0 day)	Experiment
Lab: Barbara Wold, Caltech Project: ENCODE	ENCSR982MRY released
RNA-seq of lung (<i>Mus musculus</i>, adult 8 week)	Experiment
Lab: John Stamatoyannopoulos, UW Project: ENCODE	ENCSR000CMD released
RNA-seq of lung (<i>Mus musculus</i>, adult 10 week)	Experiment
Lab: Michael Snyder, Stanford Project: ENCODE	ENCSR870AQU released
DNase-seq of lung (<i>Mus musculus</i>, adult 8 week)	Experiment
Lab: John Stamatoyannopoulos, UW Project: ENCODE	ENCSR000CNM released
RNA-seq of lung (<i>Mus musculus</i>, adult 8 week)	Experiment
Lab: Thomas Gingeras, CSHL Project: ENCODE	ENCSR000BYT released

https://www.encodeproject.org/search/?searchTerm=lung&type=experiment&assay_term_name=RNA-seq&assay_term_name=DNase-seq&replicates.library.biosample.donor.organism.scientific_name=Mus+musculus



Some example searches

- ENCODE3 data:
[https://www.encodeproject.org/search/?
type=experiment&award.rfa=ENCODE3](https://www.encodeproject.org/search/?type=experiment&award.rfa=ENCODE3)
- All ENCODE data:
[https://www.encodeproject.org/search/?
type=experiment&award.project=ENCODE](https://www.encodeproject.org/search/?type=experiment&award.project=ENCODE)
- All ENCODE3 mouse data:
[https://www.encodeproject.org/search/?
type=experiment&award.rfa=ENCODE3&replicates.library.
biosample.donor.organism.scientific_name=Mus
%20musculus](https://www.encodeproject.org/search/?type=experiment&award.rfa=ENCODE3&replicates.library.biosample.donor.organism.scientific_name=Mus%20musculus)



Programmatic Access to the ENCODE Portal

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

- This JSON data can be retrieved with HTTP Requests
- JSON can be parsed in your language of choice
- Python has a library for HTTP requests

```
GET_object.py *
1  #!/usr/bin/env python
2
3  import requests
4
5  URL = 'https://www.encodeproject.org/experiments/ENCSR236EGS/?format=json'
6
7  response = requests.get(URL)
8
9  experiment = response.json()
10
11  print experiment['accession']
12  print experiment['description']
13
```

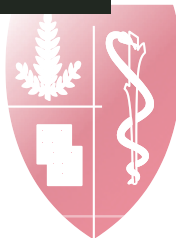
constructed urls

use the response as a dictionary

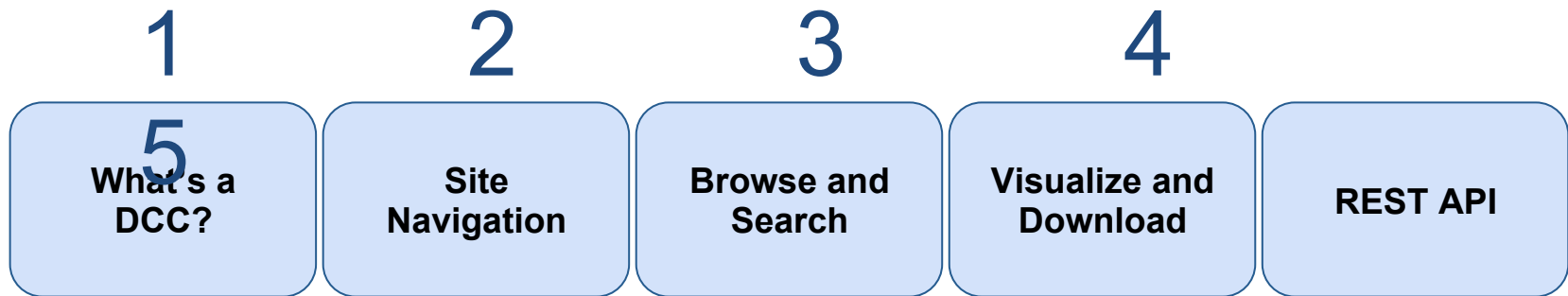


Retrieve Search Results via REST API

```
GET_search.py *
1 #!/usr/bin/env python
2
3 import requests
4
5 URL = ('https://www.encodeproject.org/search/?'
6       'type=experiment&'
7       'assay_term_name=ChIP-seq&'
8       'replicates.library.biosample.donor.organism.scientific_name=Homo sapiens&'
9       'target.investigated_as=transcription factor&'
10      'replicates.library.biosample.biosample_type=in vitro differentiated cells&'
11      'format=json')
12
13 response = requests.get(URL)
14
15 search_result = response.json()['@graph']
16
17 #extract and print the target for each experiment
18 print '\n'.join([experiment['target']['label'] for experiment in search_result])
19
```



ENCODE Portal: Wrapping Up



<https://www.encodeproject.org>



Tomorrow: ENCODE data processing pipelines

Pipeline Workshop Summary

DCC Goals:

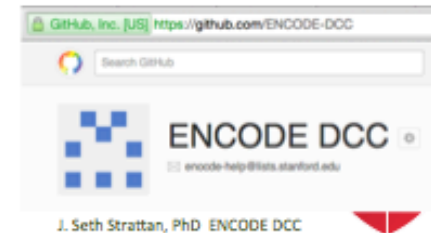
1. Deploy ENCODE-defined pipelines for ChIP-seq, RNA-seq, DNase-seq, methylation.
2. Use those pipelines to generate the standard ENCODE peaks, quantitations, CpG.
3. Capture metadata to make clear what software, versions, parameters, inputs were used.
4. Capture, accession, and distribute the output.
5. Deliver *exactly the same* pipelines in a form that *anyone can run* on their data or with ENCODE data – one experiment or 1000.

Replicability – Provenance – Ease of Use – Scalability

DNAnexus

Featured projects
ENCODE Uniform Processing Pipelines
Parliament

1



Tomorrow: ENCODE Help Desk

Need help or have a question? Contact us through:

- email: encode-help@lists.stanford.edu
- twitter: @encodedcc
 - ENCODE help desk gets an email if you direct message us

Subscribe to our mailing list for announcements about new features and data releases:

<https://mailman.stanford.edu/mailman/listinfo/encode-announce>



Acknowledgments



Mike Cherry (PI), Ben Hitz, Cricket Sloan

Data Wranglers



Esther Chan, Jean Davidson, J. Seth Strattan, Idan Gabdank, Jason Hilton

Software Engineers



Forrest Tanaka, Tim Dreszer, Bek Baymuradov, Christopher

Systems Administration, Biocuration Assistants



Stuart Miyasato, Matt Simison, Marcus Ho, Aditi Narayanan, Kathrina Onate

National Institute of General Medical Sciences of the United States AQ1215 National Institutes of Health (GM10331601); U41 grant from National Human Genome Research Institute at the U.S. National Institutes of Health (HG006992)

Cricket A Sloan ENCODE DCC

