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Gene Expression Omnibus

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

brg1 c2c12

Getting Started	Tools	Browse Content
Overview	Search for Studies at GEO DataSets	Repository Browser
FAQ	Search for Gene Expression at GEO Profiles	DataSets: 4348
About GEO DataSets	Search GEO Documentation	Series: 131090
About GEO Profiles	Analyze a Study with GEO2R	Platforms: 21026
About GEO2R Analysis	Studies with Genome Data Viewer Tracks	Samples: 3636188
How to Construct a Query	Programmatic Access	
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		Guidelines for Reviewers
		GEO Publications

<https://www.ncbi.nlm.nih.gov/geo/>

The screenshot shows the NCBI Gene Expression Omnibus (GEO) website at <https://www.ncbi.nlm.nih.gov/geo/>. The page features a blue header bar with the NCBI logo, a search bar, and links for "GEO Home", "Documentation", "Query & Browse", and "Email GEO". On the right side of the header, there are links for "sabrsyed", "My NCBI", and "Sign Out". Below the header, a red banner displays COVID-19 information from CDC and NIH, along with a link to NCBI SARS-CoV-2 literature.

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Getting Started

- Overview
- FAQ
- About GEO DataSets
- About GEO Profiles
- About GEO2R Analysis
- How to Construct a Query
- How to Download Data

Tools

- Search for Studies at GEO DataSets
- Search for Gene Expression at GEO Profiles
- Search GEO Documentation
- Analyze a Study with GEO2R
- Studies with Genome Data Viewer Tracks
- Programmatic Access
- FTP Site

GEO
Gene Expression Omnibus

brg1 c2c12 There are **36** results for "brg1 c2c12" in the GEO DataSets Database.
There are **29** results for "brg1 c2c12" in the GEO Profiles Database.

DataSets:	4348
Series:	131090
Platforms:	21026
Samples:	3636188

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Entry type DataSets (0) Series (9) Samples (26) Platforms (1)

Organism Customize ...

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

Author Customize ...

Attribute name tissue (28) strain (1) Customize ...

Publication dates 30 days 1 year Custom range... Clear all Show additional filters

Summary 20 per page Sort by Default order Send to: Filters: Manage Filters

Top Organisms Tree Mus musculus (36) Homo sapiens (1)

Find related data Database: Select Find items

Search details brg1[All Fields] AND c2c12[All Fields]

Search See more...

Recent activity Turn Off Clear

brg1 c2c12 (36) GEO DataSets See more...

Search results Items: 1 to 20 of 36 << First < Prev Page 1 of 2 Next > Last >>

1. [myogenic gene transcription \[ATAC-Seq\]](#)
(Submitter supplied) Functional crosstalk between histone modifications and chromatin remodeling has emerged as a key regulatory mode of transcriptional control during cell fate decisions, but the underlying mechanisms are not fully understood. Here we demonstrate that HRP2-DPF3a-BAF complex coordinates histone H3 lysine 36 methylation (H3K36me) and ATP-dependent chromatin remodeling to regulate chromatin dynamic and gene transcription during myogenic differentiation. [more...](#)
Organism: Mus musculus
Type: Genome binding/occupancy profiling by high throughput sequencing
Platform: GPL21273 6 Samples
Download data: BW
Series Accession: GSE148296 ID: 200148296
[SRA Run Selector](#)

2. [myogenic gene transcription \[ChIP-Seq\]](#)
(Submitter supplied) Functional crosstalk between histone modifications and chromatin remodeling has emerged as a key regulatory mode of transcriptional control during cell fate decisions, but the underlying mechanisms are not fully understood. Here we demonstrate that HRP2-DPF3a-BAF complex coordinates histone H3 lysine 36 methylation (H3K36me) and ATP-dependent chromatin remodeling to regulate chromatin dynamic and gene transcription during myogenic differentiation. [more...](#)
Organism: Mus musculus
Type: Genome binding/occupancy profiling by high throughput sequencing
Platform: GPL21273 21 Samples
Download data: BW



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

DataSet (0) Series (9) Samples (26) Platforms (1)

Organism Customize ...

Study type Expression profiling by RT-PCR Expression profiling by SAGE Expression profiling by SNP array Expression profiling by array Expression profiling by genome tiling array Expression profiling by high throughput sequencing Genome binding/occupancy profiling by SNP array Genome binding/occupancy profiling by array Genome binding/occupancy profiling by genome tiling array Genome binding/occupancy profiling by high throughput sequencing Genome variation profiling by SNP array Genome variation profiling by array Genome variation profiling by genome tiling array Genome variation profiling by high throughput sequencing Methylation profiling by SNP array

Author Customize ...

Attribute name tissue (28) strain (1) Custom range...

Publication date 30 days 1 year Custom range...

Search results

Study type

- Expression profiling by RT-PCR
- Expression profiling by SAGE
- Expression profiling by SNP array
- Expression profiling by array
- Expression profiling by genome tiling array
- Expression profiling by high throughput sequencing
- Genome binding/occupancy profiling by SNP array
- Genome binding/occupancy profiling by array
- Genome binding/occupancy profiling by genome tiling array
- Genome binding/occupancy profiling by high throughput sequencing
- Genome variation profiling by SNP array
- Genome variation profiling by array
- Genome variation profiling by genome tiling array
- Genome variation profiling by high throughput sequencing
- Methylation profiling by SNP array

coordinates histone modification and chromatin remodeling to regulate [ATAC-Seq]

crosstalk between histone modifications and chromatin remodeling has made of transcriptional control during cell fate decisions, but the underlying stood. Here we demonstrate that HRP2-DPF3a-BAF complex coordinates n (H3K36me) and ATP-dependent chromatin remodeling to regulate chromatin during myogenic differentiation. [more...](#)

us

binding/occupancy profiling by high throughput sequencing

ID: 200148296

coordinates histone modification and chromatin remodeling to regulate [ChIP-Seq]

crosstalk between histone modifications and chromatin remodeling has made of transcriptional control during cell fate decisions, but the underlying stood. Here we demonstrate that HRP2-DPF3a-BAF complex coordinates n (H3K36me) and ATP-dependent chromatin remodeling to regulate chromatin during myogenic differentiation. [more...](#)

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binding/occupancy profiling by high throughput sequencing

Send to: Filters: Manage Filters

Top Organisms Tree

Mus musculus (36)
Homo sapiens (1)

Find related data Database: Select

Find items

Search details

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Entry type

Summary ▾ 20 per page ▾ Sort by Default order ▾

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Filters: [Manage Filters](#)

DataSets (0)

Series (9)

Samples (26)

Platforms (1)

Organism

[Customize ...](#)

Study type

Expression profiling by high throughput sequencing

Genome binding/occupancy profiling by high throughput sequencing

Methylation profiling by array

[Customize ...](#)

Author

[Customize ...](#)

Attribute name

tissue (28)

strain (1)

[Customize ...](#)

Publication dates

30 days

1 year

Custom range...

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Search results

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 [HRP2-DPF3a-BAF complex coordinates histone modification and chromatin remodeling to regulate](#)

1. [myogenic gene transcription \[ATAC-Seq\]](#)

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Organism: Mus musculus

Type: Genome binding/occupancy profiling by high throughput sequencing

Platform: GPL21273 6 Samples

Download data: BW

Series Accession: GSE148296 ID: 200148296

[SRA Run Selector](#) [HRP2-DPF3a-BAF complex coordinates histone modification and chromatin remodeling to regulate](#)

2. [myogenic gene transcription \[ChIP-Seq\]](#)

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Organism: Mus musculus

Type: Genome binding/occupancy profiling by high throughput sequencing

Platform: GPL21273 21 Samples

Download data: BW

Top Organisms [Tree]

Mus musculus (36)

Homo sapiens (1)

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Database: Select

[Find items](#)

Search details

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Entry type Summary Sort by Default order Send to: Filters: Manage Filters

DataSet (0) Series (4) Samples (0) Platforms (0)

Organism Customize ...

Study type clear Expression profiling by high throughput sequencing
Genome binding/occupancy profiling by high throughput sequencing
Methylation profiling by array Customize ...

Author Customize ...

Attribute name tissue (2) strain (0) Customize ...

Publication dates 30 days 1 year Custom range... Clear all Show additional filters

Search results Items: 4

Filters activated: Expression profiling by high throughput sequencing. [Clear all](#) to show 36 items.

HRP2-DPF3a-BAF complex coordinates histone modification and chromatin remodeling to regulate myogenic gene transcription [RNA-Seq]

(Submitter supplied) Functional crosstalk between histone modifications and chromatin remodeling has emerged as a key regulatory mode of transcriptional control during cell fate decisions, but the underlying mechanisms are not fully understood. Here we demonstrate that HRP2-DPF3a-BAF complex coordinates histone H3 lysine 36 methylation (H3K36me) and ATP-dependent chromatin remodeling to regulate chromatin dynamic and gene transcription during myogenic differentiation. [more...](#)

Organism: Mus musculus
Type: Expression profiling by high throughput sequencing
Platform: GPL23479 10 Samples

Download data: TXT
Series Accession: GSE148294 ID: 200148294
[SRA Run Selector](#)

HRP2-DPF3a-BAF complex coordinates histone modification and chromatin remodeling to regulate myogenic gene transcription

(Submitter supplied) This SuperSeries is composed of the SubSeries listed below.

Organism: Mus musculus
Type: Expression profiling by high throughput sequencing; Genome binding/occupancy profiling by high throughput sequencing
Platforms: GPL21273 GPL23479 37 Samples
Download data: BW, TXT
Series Accession: GSE141407 ID: 200141407

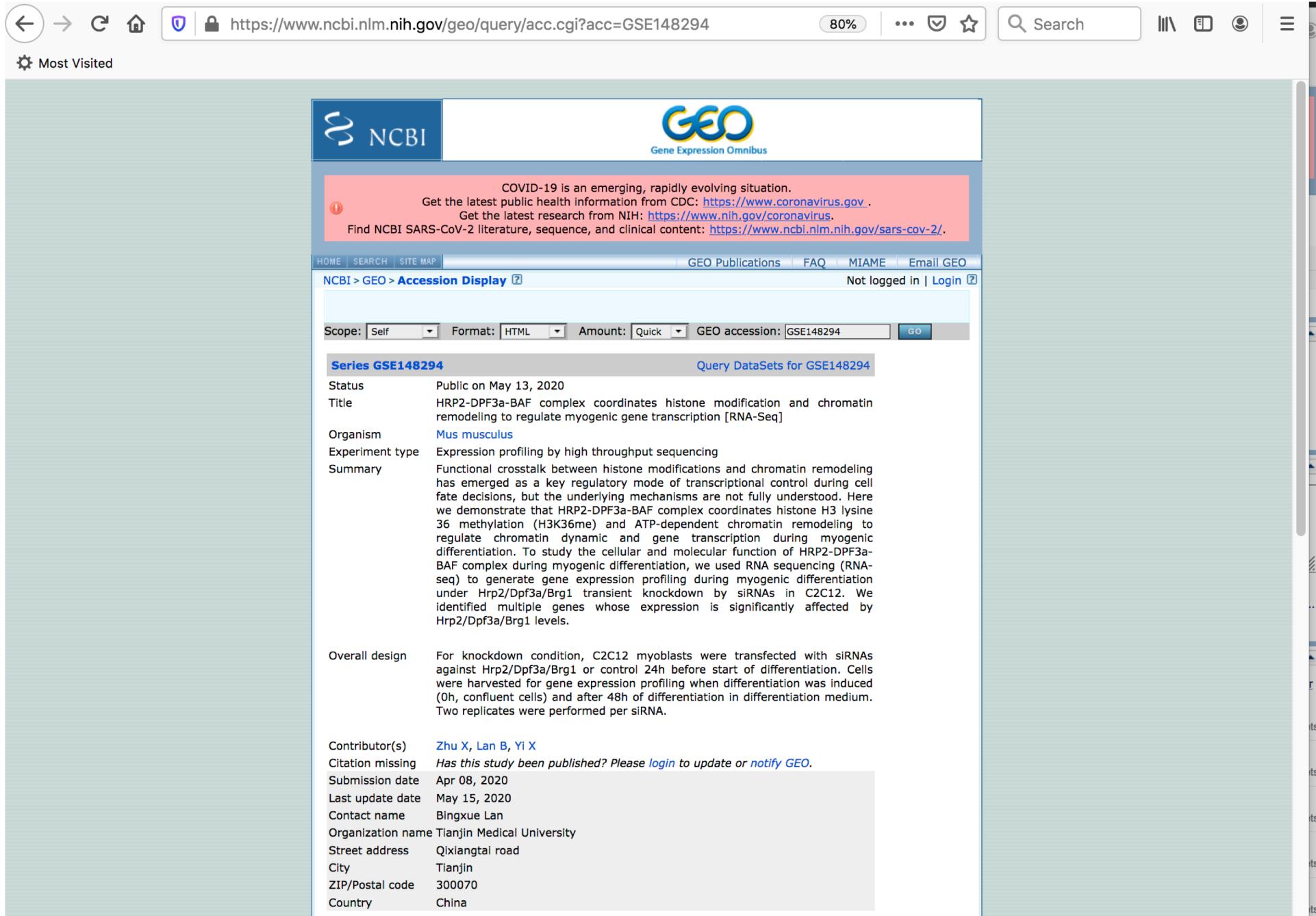
Top Organisms Tree Mus musculus (4)

Find related data Database: Select Find items

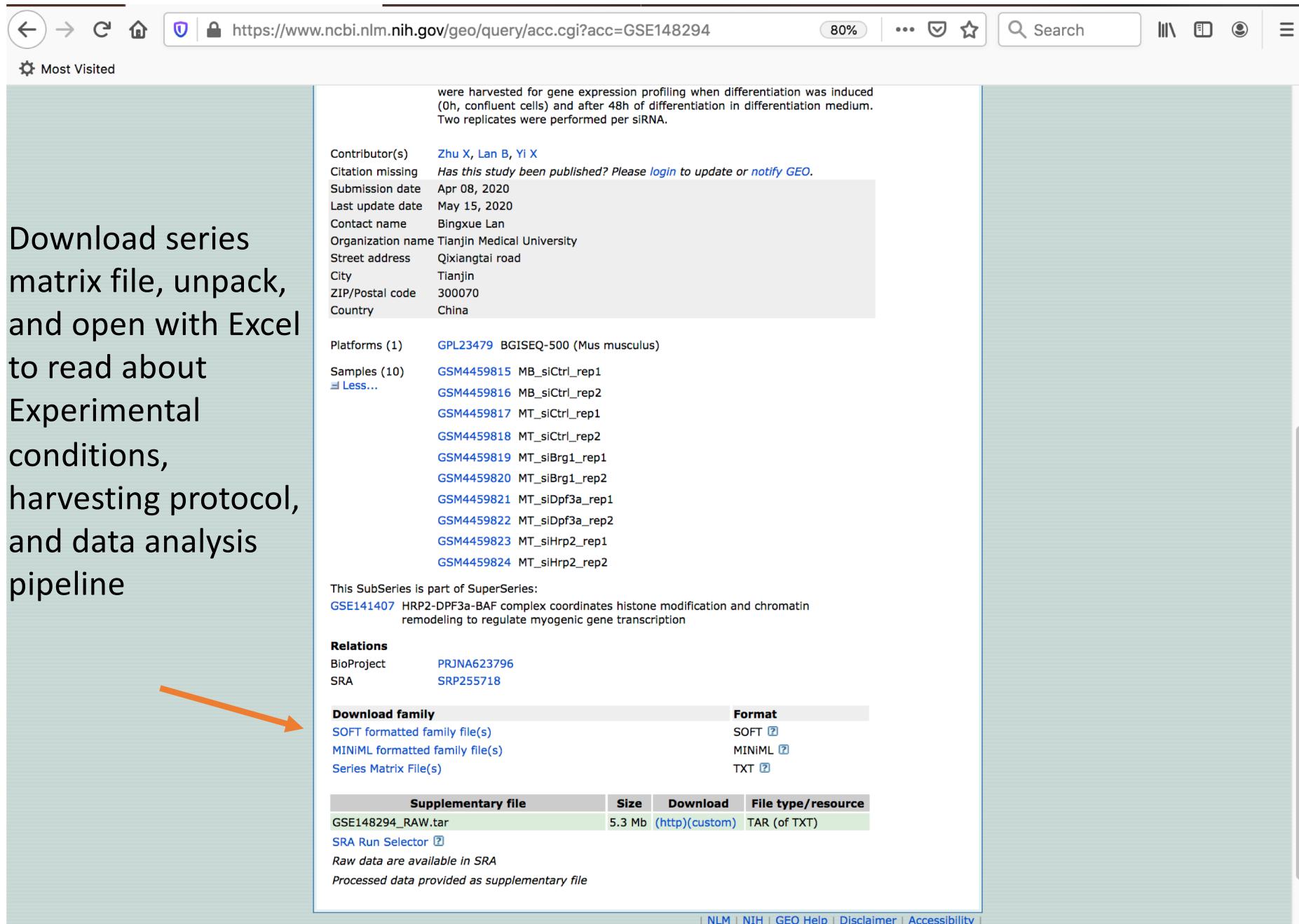
Search details (brg1[All Fields] AND c2c12[All Fields] AND "Expression profiling by high throughput sequencing" [Filter])

Search See more...

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brg1 c2c12 AND ("Expression profiling by high throughput sequencing" (4) GEO DataSets
brg1 c2c12 (36) GEO DataSets See more...



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were harvested for gene expression profiling when differentiation was induced (0h, confluent cells) and after 48h of differentiation in differentiation medium. Two replicates were performed per siRNA.

Contributor(s) Zhu X, Lan B, Yi X
Citation missing Has this study been published? Please [login](#) to update or [notify GEO](#).
Submission date Apr 08, 2020
Last update date May 15, 2020
Contact name Bingxue Lan
Organization name Tianjin Medical University
Street address Qixiangtai road
City Tianjin
ZIP/Postal code 300070
Country China

Platforms (1) [GPL23479](#) BGISEQ-500 (Mus musculus)

Samples (10) [GSM4459815](#) MB_siCtrl_rep1
[GSM4459816](#) MB_siCtrl_rep2
[GSM4459817](#) MT_siCtrl_rep1
[GSM4459818](#) MT_siCtrl_rep2
[GSM4459819](#) MT_siBrg1_rep1
[GSM4459820](#) MT_siBrg1_rep2
[GSM4459821](#) MT_siDpf3a_rep1
[GSM4459822](#) MT_siDpf3a_rep2
[GSM4459823](#) MT_siHrp2_rep1
[GSM4459824](#) MT_siHrp2_rep2

This SubSeries is part of SuperSeries:
[GSE141407](#) HRP2-DPF3a-BAF complex coordinates histone modification and chromatin remodeling to regulate myogenic gene transcription

Relations

BioProject [PRJNA623796](#)
SRA [SRP255718](#)

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SOFT formatted family file(s)
MINIML formatted family file(s)
Series Matrix File(s)

Supplementary file	Size	Download	File type/resource
GSE148294_RAW.tar	5.3 Mb	(http)(custom)	TAR (of TXT)

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Raw data are available in SRA
Processed data provided as supplementary file

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Platforms (1) [GPL23479 BGISEQ-500 \(Mus musculus\)](#)

Samples (10)
[Less...](#)

[GSM4459815](#) MB_siCtrl_rep1
[GSM4459816](#) MB_siCtrl_rep2
[GSM4459817](#) MT_siCtrl_rep1
[GSM4459818](#) MT_siCtrl_rep2
[GSM4459819](#) MT_siBrg1_rep1
[GSM4459820](#) MT_siBrg1_rep2
[GSM4459821](#) MT_siDpf3a_rep1
[GSM4459822](#) MT_siDpf3a_rep2
[GSM4459823](#) MT_siHrp2_rep1
[GSM4459824](#) MT_siHrp2_rep2

This SubSeries is part of SuperSeries:
[GSE141407](#) HRP2-DPF3a-BAF complex coordinates histone modification and chromatin remodeling to regulate myogenic gene transcription

Relations

BioProject [PRJNA623796](#)
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	Format
SOFT formatted family file(s)	SOFT
MINIML formatted family file(s)	MINIML
Series Matrix File(s)	TXT

Supplementary file **Size** **Download** **File type/resource**

Supplementary file	Size	Download	File type/resource
GSE148294_RAW.tar	5.3 Mb	(http)(custom)	TAR (of TXT)

[SRA Run Selector](#)

Raw data are available in SRA
Processed data provided as supplementary file

Custom GSE148294_RAW.tar archive:

Supplementary file	File size
GSM4459815_MB_siCtrl_rep1.txt.gz	544.6 K
GSM4459816_MB_siCtrl_rep2.txt.gz	542.5 K
GSM4459817_MT_siCtrl_rep1.txt.gz	546.9 K
GSM4459818_MT_siCtrl_rep2.txt.gz	547.5 K
GSM4459819_MT_siBrg1_rep1.txt.gz	544.3 K
GSM4459820_MT_siBrg1_rep2.txt.gz	545.5 K
GSM4459821_MT_siDpf3a_rep1.txt.gz	546.1 K
GSM4459822_MT_siDpf3a_rep2.txt.gz	543.2 K
GSM4459823_MT_siHrp2_rep1.txt.gz	542.9 K

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Series Matrix File

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B27 MB_siCtrl_rep1

	A	B	C	D	E	F	G	H
1	ISeries_title	HRP2-DPF3a-BAF complex coordinates histone modification and chromatin remodeling to regulate myogenic gene transcri						
2	ISeries_geo_accession	GSE148294						
3	ISeries_status	Public on May 13 2020						
4	ISeries_submission_date	Apr 08 2020						
5	ISeries_last_update_date	May 15 2020						
6	ISeries_summary	Functional crosstalk between histone modifications and chromatin remodeling has emerged as a key regulatory mode of t						
7	ISeries_overall_design	For knockdown condition, C2C12 myoblasts were transfected with siRNAs against Hrp2/Dpf3a/Brg1 or control 24h before s						
8	ISeries_type	Expression profiling by high throughput sequencing						
9	ISeries_contributor	Xu,Zhu						
10	ISeries_contributor	Bingxue,Lan						
11	ISeries_contributor	Xianfu,Yi						
12	ISeries_sample_id	GSM4459815 GSM4459816 GSM4459817 GSM4459818 GSM4459819 GSM4459820 GSM4459821 GSM4459822 GSM4459823						
13	ISeries_contact_name	Bingxue,Lan						
14	ISeries_contact_institute	Tianjin Medical University						
15	ISeries_contact_address	Qixiangtai road						
16	ISeries_contact_city	Tianjin						
17	ISeries_contact_zip/postal_code	300070						
18	ISeries_contact_country	China						
19	ISeries_supplementary_file	ftp://ftp.ncbi.nlm.nih.gov/geo/series/GSE148nnn/GSE148294/suppl/GSE148294_RAW.tar						
20	ISeries_platform_id	GPL23479						
21	ISeries_platform_taxid	10090						
22	ISeries_sample_taxid	10090						
23	ISeries_relation	SubSeries of: GSE141407						
24	ISeries_relation	BioProject: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA623796						
25	ISeries_relation	SRA: https://www.ncbi.nlm.nih.gov/sra?term=SRP255718						
26	ISample_title	MB_siCtrl_rep1	MB_siCtrl_rep2	MT_siCtrl_rep1	MT_siCtrl_rep2	MT_siBrg1_rep1	MT_siBrg1_r	MT_siDpf
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29	ISample_submission_date	Apr 08 2020	Apr 08 2020	Apr 08 2020	Apr 08 2020	Apr 08 2020	Apr 08 2020	Apr 08 2020
30	ISample_last_update_date	May 14 2020	May 14 2020	May 14 2020	May 14 2020	May 14 2020	May 14 2020	May 14 2020
31	ISample_type	SRA	SRA	SRA	SRA	SRA	SRA	SRA
32	ISample_channel_count	1	1	1	1	1	1	1
33	ISample_source_name_ch1	muscle	muscle	muscle	muscle	muscle	muscle	muscle
34	ISample_organism_ch1	Mus musculus	Mus musculus	Mus musculus	Mus musculus	Mus musculus	Mus musculus	Mus musculus

GSE148294_series_matrix +

Average: 1 Count: 9 Sum: 1 INDEX 200 2000 20000

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A1 geneID

	A	B	C	D	E	F
1	geneID	symbol	MB_siCtrl_rep1			
2	ENSMUSG00000000001.4	Gna13	34.0254			
3	ENSMUSG00000000003.15	Pbsn	0			
4	ENSMUSG00000000028.14	Cdc45	11.554539			
5	ENSMUSG00000000031.16	H19	371.97713			
6	ENSMUSG00000000037.16	Scml2	0.270659514			
7	ENSMUSG00000000049.11	Apoh	0.0513898			
8	ENSMUSG00000000056.7	Narf	4.28981			
9	ENSMUSG00000000058.6	Cav2	23.690881			
10	ENSMUSG00000000078.7	Klf6	24.347099			
11	ENSMUSG00000000085.16	Scmh1	55.585639			
12	ENSMUSG00000000088.7	Cox5a	162.508525			
13	ENSMUSG00000000093.6	Tbx2	0.0787586			
14	ENSMUSG00000000094.12	Tbx4	0.0089221			
15	ENSMUSG00000000103.12	Zfy2	0			
16	ENSMUSG00000000120.6	Ngfr	0.192973			
17	ENSMUSG00000000125.5	Wnt3	0			
18	ENSMUSG00000000126.11	Wnt9a	1.85143			
19	ENSMUSG00000000127.14	Fer	9.330532			
20	ENSMUSG00000000131.15	Xpo6	72.2776574			
21	ENSMUSG00000000134.17	Tfe3	33.2450223			
22	ENSMUSG00000000142.15	Axin2	0.903051			
23	ENSMUSG00000000148.17	Brat1	2.59088779			
24	ENSMUSG00000000149.10	Gna12	7.983382			
25	ENSMUSG00000000154.16	Slc22a18	0.2761048			
26	ENSMUSG00000000157.15	Itgb2l	0			
27	ENSMUSG00000000159.15	Igfs5	0.185279			
28	ENSMUSG00000000167.14	Pih1d2	1.589434738			
29	ENSMUSG00000000168.9	Dlat	44.494524			
30	ENSMUSG00000000171.5	Sdhb	49.2688			
31	ENSMUSG00000000182.9	Fgf23	0			
32	ENSMUSG00000000183.6	Fgf6	0.00551568			
33	ENSMUSG00000000184.12	Ccnd2	14.83693513			
34	ENSMUSG00000000194.13	Gpr107	24.1048899			
35	ENSMUSG00000000197.8	Nalcn	0.1254481			
36	ENSMUSG00000000202.9	Btbd17	0.017648807			
37	ENSMUSG00000000204.16	Sifn4	0.00814198			
38	ENSMUSG00000000214.11	Th	0			
39	ENSMUSG00000000215.11	Ins2	0			
40	ENSMUSG00000000216.8	Serpin1a	0			

Series Matrix File

A	B
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28	!Sample_geo_accession GSM4459815
29	!Sample_status Public on May 13 2020
30	!Sample_submission_date Apr 08 2020
31	!Sample_last_update_date May 14 2020
32	!Sample_type SRA
33	!Sample_channel_count
34	!Sample_source_name_ch1 muscle
35	!Sample_organism_ch1 Mus musculus
36	!Sample_characteristics_ch1 cell line: C2C12
37	!Sample_characteristics_ch1 tissue: muscle
38	!Sample_characteristics_ch1 cell type: myoblast
39	!Sample_characteristics_ch1 treatment: siCtrl
40	!Sample_treatment_protocol_ch1 C2C12 cells were transfected with siRNAs against Hrp2/Dpf3a/Brg1 or control.
41	!Sample_growth_protocol_ch1 C2C12 cells were cultured in DMEM medium supplemented with 20% fetal bovine serum (FBS).
42	!Sample_molecule_ch1 total RNA
43	!Sample_extract_protocol_ch1 Total RNA isolation was performed using TRIzol (Invitrogen). Total RNAs from cultured cells were subjected to Oligo dT se.
44	!Sample_extract_protocol_ch1 Construction of RNA-seq library was completed by BGI company (Shenzhen,China).
45	!Sample_taxid_ch1
46	!Sample_data_processing FastQC (version 0.11.8) was used to do quality control checks on clean reads.
47	!Sample_data_processing The expression of genes was quantified by Salmon (version 0.8.0) with default parameters.
48	!Sample_data_processing DEGs (differential expressed genes) between samples were generated by DESeq2.
49	!Sample_data_processing Genome_build: mm10
50	!Sample_data_processing Supplementary_files_format_and_content: TPM for each sample.
51	!Sample_platform_id GPL23479
52	!Sample_contact_name Bingxue,,Lan
53	!Sample_contact_institute Tianjin Medical University
54	!Sample_contact_address Qixiangtai road
55	!Sample_contact_city Tianjin
56	!Sample_contact_zip/postal_co
57	!Sample_contact_country China
58	!Sample_data_row_count
59	!Sample_instrument_model BGISEQ-500
60	!Sample_library_selection cDNA
61	!Sample_library_source transcriptomic

Supplementary files are displaying TPM data for RNA-Seq

What is TPM RNA seq? ^

TPM unit of transcript expression

Transcripts Per Million (**TPM**) is a normalization method for **RNA-seq**, should be read as "for every 1,000,000 **RNA** molecules in the **RNA-seq** sample, x came from this gene/transcript." Aug 4, 2016

[www.arrayserver.com › wiki › title=TPM](http://www.arrayserver.com/wiki/title=TPM)

[TPM - Array Suite Wiki](#)

To get raw FASTQ files for a sequencing run, copy SRA number

Contributor(s) Zhu X, Lan B, Yi X
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Submission date Apr 08, 2020
Last update date May 15, 2020
Contact name Bingxue Lan
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Platforms (1) GPL23479 BGISEQ-500 (Mus musculus)

Samples (10)
[GSM4459815](#) MB_siCtrl_rep1
[GSM4459816](#) MB_siCtrl_rep2
[GSM4459817](#) MT_siCtrl_rep1
[GSM4459818](#) MT_siCtrl_rep2
[GSM4459819](#) MT_siBrg1_rep1
[GSM4459820](#) MT_siBrg1_rep2
[GSM4459821](#) MT_siDpf3a_rep1
[GSM4459822](#) MT_siDpf3a_rep2
[GSM4459823](#) MT_siHrp2_rep1
[GSM4459824](#) MT_siHrp2_rep2

This SubSeries is part of SuperSeries:
[GSE141407](#) HRP2-DPF3a-BAF complex coordinates histone modification and chromatin remodeling to regulate myogenic gene transcription

Relations

BioProject PRJNA623796
SRA SRP255718

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Supplementary file	Size	Format
GSE148294_RAW.tar	5.3 Mb (http (custom))	TAR (of TXT)

[SRA Run Selector](#)

Raw data are available in SRA
Processed data provided as supplementary file

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SRP255718

Examples: BN000065, histone

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Advanced Sequence

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The European Nucleotide Archive (ENA) provides a comprehensive record of the world's nucleotide sequencing information, covering raw sequencing data, sequence assembly information and functional annotation. [More about ENA](#)

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Text Search

Examples: BN000065, histone

search

Advanced search

Sequence Search

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- Submitting environmental sequences
- Citing ENA data
- Rest URLs for data retrieval
- Rest URLs to search ENA

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16 Apr 2020: Release 143 of ENA's assembled/annotated sequences is now available

...

06 Apr 2020: Submissions to ENA through all tools and interfaces are in operation and open for all data types

Submissions to ENA through...

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SRP255718 Examples: BN000065, histone Search Advanced Sequence

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Message posted 21.4.20.

We recommend that you subscribe to the [ENA-announce mailing list](#) for updates on services.

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Experiment (10)
Run (10)

Study

Study (1)



Experiment (10 results found)

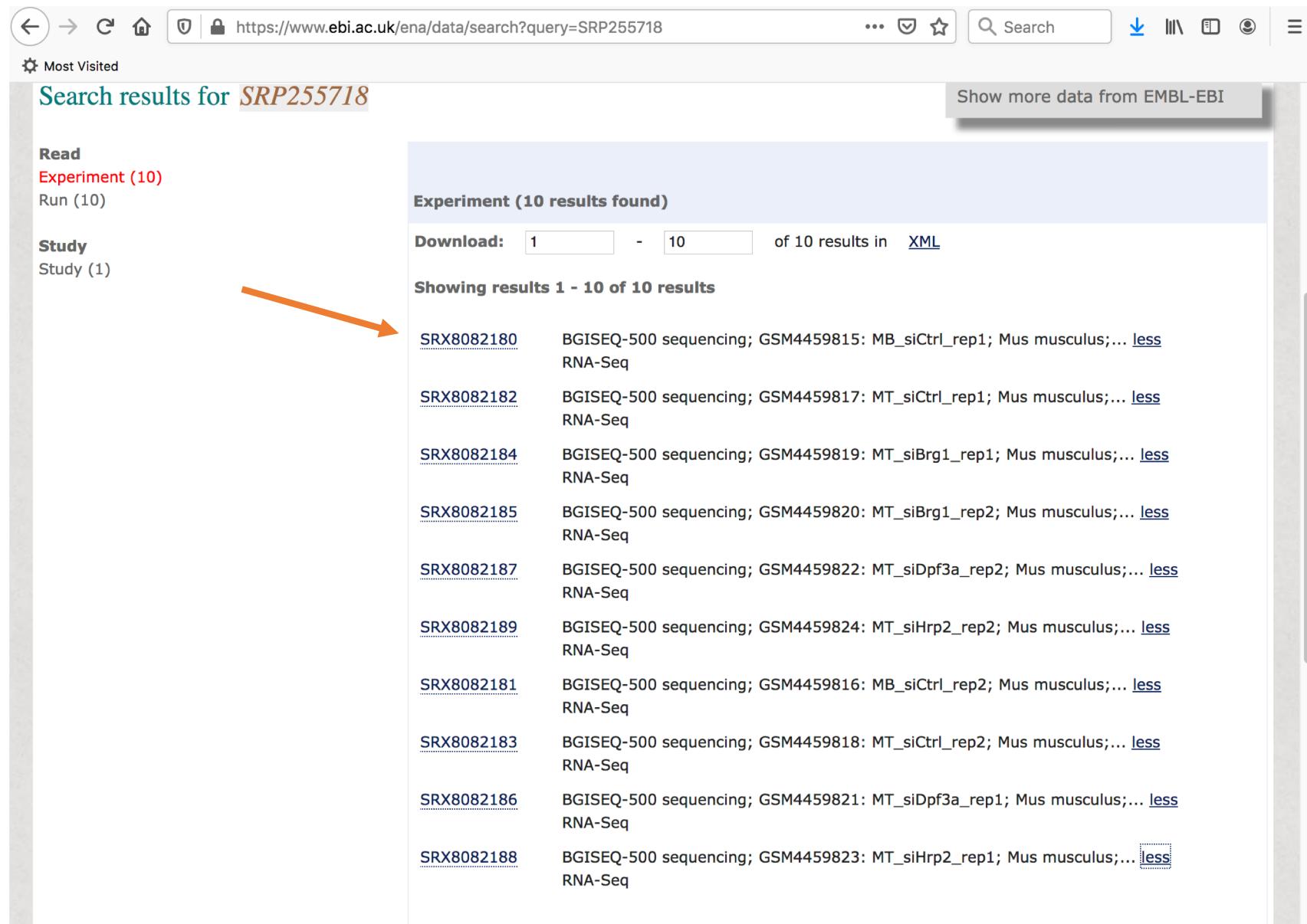
SRX8082180 BGISEQ-500 sequencing; GSM4459815: MB_siCtrl_rep1; Mus musculus; RNA-Seq
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Run (10 results found)

SRR11510070 BGISEQ-500 sequencing; GSM4459815: MB_siCtrl_rep1; Mus musculus; RNA-Seq
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SRP255718 HRP2-DPF3a-BAF complex coordinates histone modification and chromatin remodeling to regulate myogenic gene transcription [RNA-Seq]
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Experiment (10)

Run (10)

Study

Study (1)

Experiment (10 results found)

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Showing results 1 - 10 of 10 results

Sample ID	Description
SRX8082180	BGISEQ-500 sequencing; GSM4459815: MB_siCtrl_rep1; Mus musculus;... less RNA-Seq
SRX8082182	BGISEQ-500 sequencing; GSM4459817: MT_siCtrl_rep1; Mus musculus;... less RNA-Seq
SRX8082184	BGISEQ-500 sequencing; GSM4459819: MT_siBrg1_rep1; Mus musculus;... less RNA-Seq

GSE148294_series_matrix

Office Update To keep up-to-date with security updates, fixes, and improvements, ch

B27	x ✓ fx	MB_siCtrl_rep1
27	A	
27	!Sample_title	MB_siCtrl_rep1
28	!Sample_geo_accession	GSM4459815
29	!Sample_status	Public on May 13 2020
30	!Sample_submission_date	Apr 08 2020
31	!Sample_last_update_date	May 14 2020
32	!Sample_type	SRA
33	!Sample_channel_count	
34	!Sample_source_name_ch1	muscle
35	!Sample_organism_ch1	Mus musculus
36	!Sample_characteristics_ch1	cell line: C2C12
37	!Sample_characteristics_ch1	tissue: muscle
38	!Sample_characteristics_ch1	cell type: myoblast
39	!Sample_characteristics_ch1	treatment: siCtrl
40	!Sample_treatment_protocol_ch1	C2C12 cells were transfected with siRNAs against Hrp2/Dpf3a/
41	!Sample_growth_protocol_ch1	C2C12 cells were cultured in DMEM medium supplemented wit

Experiment: SRX8082180

BGISEQ-500 sequencing; GSM4459815: MB_siCtrl_rep1; Mus musculus; RNA-Seq

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Submitting Centre GEO	Platform	Model		
Library Layout SINGLE	Library Strategy RNA-Seq	Library Source TRANSCRIPTOMIC	Library Selection cDNA	Library Name
Broker Name NCBI				
Library Construction Protocol Total RNA isolation was performed using TRIzol (Invitrogen). Total RNAs from cultured cells were subjected to Oligo dT selection and adaptor ligation. Construction of RNA-seq library was completed by BGI company (Shenzhen,China).				

This table contains the files for experiment SRX8082180

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Showing results 1 - 1 of 1 results

Study accession	Sample accession	Secondary sample accession	Experiment accession	Run accession	Tax ID	Scientific name	Instrument model	Library layout	FASTQ files (FTP)	FASTQ files (Galaxy)	Submitted files (FTP)	Submitted files (Galaxy)	NCBI SRA file (FTP)	NCBI SRA file (Galaxy)	CRAM Index files (FTP)
PRJNA623796	SAMN14558854	SRS6450280	SRX8082180	SRR11510070	10090	Mus musculus	BGISEQ-500	SINGLE	File 1	File 1			File 1	File 1	

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FASTQ file can be used for further data analysis