

The manual for

ChIP-Atlas: Enrichment Analysis

1. Overview
2. Enrichment for the genomic loci (BED)
3. Enrichment around the genes (Gene symbol)
4. Tips

Overview of the Enrichment Analysis tool

ChIP-Atlas: Enrichment Analysis

Identify common epigenetic features of a given set of genomic loci and genes

 Tutorial movie ▾

H. sapiens (hg38)

H. sapiens (hg19)

M. musculus (mm10)

M. musculus (mm9)

R. norvegicus (rn6)

D. melanogaster (dm6)

D. melanogaster (dm3)

C. elegans (ce11)

C. elegans (ce10)

S. cerevisiae (sacCer3)

1. Experiment type

ChIP: Histone (33095)
ChIP: RNA polymerase (3823)
ChIP: TFs and others (30300)
ChIP: Input control (16408)
ATAC-Seq (42241)
DNase-seq (4526)
Bisulfite-Seq (20796)

2. Cell type Class

All cell types (30300)
Adipocyte (202)
Blood (6868)
Bone (803)
Breast (4675)
Cardiovascular (436)
Digestive tract (1831)
Embryo (2)

3. Threshold for Significance ⓘ

50
100
200
500

4. Enter dataset A

- ☒ Genomic regions (BED) or sequence motif ⓘ
☐ Gene list (Gene symbols) ⓘ

chr1 629298 630014
chr1 630279 630461
chr1 630767 630963
chr1 631035 631363
chr1 631888 632304
chr1 632511 632792
chr1 633411 633532
chr1 633912 634354

Data A

Choose local file

[Try with example](#)

5. Enter dataset B

- ☐ Random permutation of dataset A ⓘ
☒ BED or sequence motif ⓘ

chr1 11231 11359
chr1 29221 29377
chr1 96507 96693
chr1 104181 104302
chr1 181728 181849
chr1 273048 273271
chr1 629293 630019
chr1 630279 630465
chr1 630767 631365

Data B

Choose local file

[Try with example](#)

6. Analysis description

Analysis title ⓘ

Test

Dataset A title ⓘ

pDC

Dataset B title ⓘ

Mono

Estimated run time: 16 mins
[node status \(short.q\)](#)

The ChIP-Atlas “Enrichment Analysis” tool is useful to identify the transcription factors (TFs) whose bindings are enriched for given genomic coordinates or gene loci.

Overview of the Enrichment Analysis tool

ChIP-Atlas / Enrichment Analysis

Search for proteins significantly bound to your data.

Show entries

Search:

					Test						
ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / pDC	Overlaps / Mono	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX1023792	TFs and others	SPI1	Blood	Macrophages	112968	5339/11207	13014/18171	-324.0	-324.0	0.67	FALSE
SRX2770855	TFs and others	SPI1	Blood	Macrophages	88807	5420/11207	13855/18171	-324.0	-324.0	0.63	FALSE
SRX1287846	TFs and others	CDK8	Blood	MOLM-14	50649	5066/11207	13051/18171	-324.0	-324.0	0.63	FALSE
SRX1287844	TFs and others	CDK8	Blood	MOLM-14	50871	5084/11207	13250/18171	-324.0	-324.0	0.62	FALSE
SRX3031982	TFs and others	BRD4	Blood	MV-4-11	47241	5298/11207	14117/18171	-324.0	-324.0	0.61	FALSE
SRX9867025	TFs and others	BCL11B	Blood	TALL-1	31691	4185/11207	11317/18171	-324.0	-324.0	0.60	FALSE
SRX4484988	TFs and others	ERG	Blood	SEM	50919	4052/11207	10966/18171	-324.0	-324.0	0.60	FALSE
SRX9867024	TFs and others	BCL11B	Blood	TALL-1	29842	4111/11207	11167/18171	-324.0	-324.0	0.60	FALSE

The ChIP-Atlas “Enrichment Analysis” tool is useful for identifying the transcription factors (TFs) whose binding is enriched for given genomic coordinates or gene loci.

The manual for

ChIP-Atlas: Enrichment Analysis

1. Overview
2. Enrichment for the genomic loci (BED)
3. Enrichment around the genes (Gene symbol)
4. Tips

In this tutorial, you will identify transcription factors (TFs) whose bindings are enriched for the open chromatin regions obtained from public ATAC-seq data.

Access to the Enrichment Analysis tool

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

ChIP-Atlas

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



Peak Browser

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

Enrichment Analysis

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

Diff Analysis

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

Target Genes

[ChIP](#)

Colocalization

[ChIP](#)

Dataset Search

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

Enrichment Analysis

What's new

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

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

Settings

ChIP-Atlas: Enrichment Analysis

[Tutorial movie](#)

hg38

Identify common epigenetic features of a given set of genomic loci and genes

H. sapiens (hg38)

H. sapiens (hg19)

M. musculus (mm10)

M. musculus (mm9)

R. norvegicus (rn6)

D. melanogaster (dm6)

D. melanogaster (dm3)

C. elegans (ce11)

C. elegans (ce10)

S. cerevisiae (sacCer3)

1. Experiment type

ChIP: Histone (33095)
ChIP: RNA polymerase (3823)
ChIP: TFs and others (30300)
ChIP: Input control (16408)
ATAC-Seq (42241)
DNase-seq (4526)
Bisulfite-Seq (20796)

TFs

2. Cell type Class

All cell types (30300)
Adipocyte (202)
Blood (6868)
Bone (803)
Breast (4675)
Cardiovascular (436)
Digestive tract (1831)
Embryo (2)

All

3. Threshold for Significance ⓘ

50
100
200
500

100

4. Enter dataset A

☒ Genomic regions (BED) or sequence motif ⓘ

☐ Gene list (Gene symbols) ⓘ

chr1 629298 630014
chr1 630279 630461
chr1 630767 630963
chr1 631035 631363
chr1 631888 632304
chr1 632511 632792
chr1 633411 633532
chr1 633912 634354

Choose local file

[Try with example](#)

5. Enter dataset B

☐ Random permutation of dataset A ⓘ

☒ BED or sequence motif ⓘ

chr1 11231 11359
chr1 29221 29377
chr1 96507 96693
chr1 104181 104302
chr1 181728 181849
chr1 273048 273271
chr1 629293 630019
chr1 630279 630465
chr1 630767 631365

Choose local file

[Try with example](#)

6. Analysis description

Analysis title ⓘ

Test

Dataset A title ⓘ

pDC

Dataset B title ⓘ

Mono

Estimated run time: 16 mins
[node status \(short.q\)](#)

Set to examine the enrichment of TF peaks in all cell types with >100 MACS2 scores.

[↗ Tips: Threshold for significance](#)

Settings

ChIP-Atlas: Enrichment Analysis

Identify common epigenetic features of a given set of genomic loci and genes

[Tutorial movie](#)

[H. sapiens \(hg38\)](#)

[H. sapiens \(hg19\)](#)

[M. musculus \(mm10\)](#)

[M. musculus \(mm9\)](#)

[R. norvegicus \(rn6\)](#)

[D. melanogaster \(dm6\)](#)

[D. melanogaster \(dm3\)](#)

[C. elegans \(ce11\)](#)

[C. elegans \(ce10\)](#)

[S. cerevisiae \(sacCer3\)](#)

1. Experiment type

ChIP: Histone (33095)
ChIP: RNA polymerase (3823)
ChIP: TFs and others (30300)
ChIP: Input control (16408)
ATAC-Seq (42241)
DNase-seq (4526)
Bisulfite-Seq (20796)

2. Cell type Class

All cell types (30300)
Adipocyte (202)
Blood (6868)
Bone (803)
Breast (4675)
Cardiovascular (436)
Digestive tract (1831)
Embryo (2)

3. Threshold for Significance

50
100
200
500

4. Enter dataset A

- ☒ Genomic regions (BED) or sequence motif
☐ Gene list (Gene symbols)

chr1 629298 630014
chr1 630279 630461
chr1 630767 630963
chr1 631035 631363
chr1 631888 632304
chr1 632511 632792
chr1 633411 633532
chr1 633912 634354

[ファイルを選択](#) [ファイル未選択](#)

Choose local file

[Try with example](#)

BED

pDC

5. Enter dataset B

- ☐ Random permutation of dataset A
☒ BED or sequence motif

chr1 11231 11359
chr1 29221 29377
chr1 96507 96693
chr1 104181 104302
chr1 181728 181849
chr1 273048 273271
chr1 629293 630019
chr1 630279 630465
chr1 630767 631365

[ファイルを選択](#) [ファイル未選択](#)

Choose local file

[Try with example](#)

Mono

6. Analysis description

Analysis title

Test

Dataset A title

pDC

Dataset B title

Mono

submit

Enter the tab-delimited genomic coordinates in BED format. For example:

Dataset A: ATAC-seq peaks of plasmacytoid dendritic cells (pDC; [SRX790284](#))

Dataset B: ATAC-seq peaks of monocytes (Mono; [SRX7902871](#))

[Tips: Acceptable BED data](#)

Settings

ChIP-Atlas: Enrichment Analysis

Identify common epigenetic features of a given set of genomic loci and genes

[Tutorial movie](#)

H. sapiens (hg38)

H. sapiens (hg19)

M. musculus (mm10)

M. musculus (mm9)

R. norvegicus (rn6)

D. melanogaster (dm6)

D. melanogaster (dm3)

C. elegans (ce11)

C. elegans (ce10)

S. cerevisiae (sacCer3)

1. Experiment type

ChIP: Histone (33095)
ChIP: RNA polymerase (3823)
ChIP: TFs and others (30300)
ChIP: Input control (16408)
ATAC-Seq (42241)
DNase-seq (4526)
Bisulfite-Seq (20796)

2. Cell type Class

All cell types (30300)
Adipocyte (202)
Blood (6868)
Bone (803)
Breast (4675)
Cardiovascular (436)
Digestive tract (1831)
Embryo (2)

3. Threshold for Significance ⓘ

50
100
200
500

4. Enter dataset A

☒ Genomic regions (BED) or sequence motif ⓘ

☐ Gene list (Gene symbols) ⓘ

chr1 629298 630014
chr1 630279 630461
chr1 630767 630963
chr1 631035 631363
chr1 631888 632304
chr1 632511 632792
chr1 633411 633532
chr1 633912 634354

Choose local file

[Try with example](#)

5. Enter dataset B

☐ Random permutation of dataset A ⓘ

☒ BED or sequence motif ⓘ

chr1 11231 11359
chr1 29221 29377
chr1 96507 96693
chr1 104181 104302
chr1 181728 181849
chr1 273048 273271
chr1 629293 630019
chr1 630279 630465
chr1 630767 631365

Choose local file

pDC

Mono

[Try with example](#)

6. Analysis description

Analysis title ⓘ

Test

Test

Dataset A title ⓘ

pDC

Dataset B title ⓘ

Mono

Submit

Estimated run time: 16 mins
[node status \(short.q\)](#)

Enter the titles of this project (Test) and datasets A (pDC) and B (Mono), which will be used to label the result data. Click on the “submit” button.

ChIP-Atlas: Enrichment Analysis

identify common epigenetic features of a given set of genomic loci and genes

Result page URL will be available for a week from the time when 'status' is 'finished'.

Project title	Test
Request ID	wabi_chipatlas_2024-0121-1545-55-143-974837
Submitted at:	15:45:55 (Jan-21-2024)
Estimated finishing time:	16:01:55 (Jan-21-2024)
Current time:	15:47:10 (Jan-21-2024)
Status	running
Result URL:	http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2024-0121-1545-55-143-974837?info=result&format=html
Download TSV:	http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2024-0121-1545-55-143-974837?info=result&format=tsv

running

As this function uses the NIG supercomputer system, it may take time to start your job when the nodes are busy. Please check computation node status [here](#) (short.q)



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

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

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

The job has been submitted. Wait while the “Status” is indicated as “running”. This may take several minutes.



ChIP-Atlas: Enrichment Analysis

identify common epigenetic features of a given set of genomic loci and genes

Result page URL will be available for a week from the time when 'status' is 'finished'.

Project title	Test
Request ID	wabi_chipatlas_2024-0121-1545-55-143-974837
Submitted at:	15:45:55 (Jan-21-2024)
Estimated finishing time:	16:01:55 (Jan-21-2024)
Current time:	16:10:59 (Jan-21-2024)
Status	finished
Result URL:	http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2024-0121-1545-55-143-974837?info=result&format=html
Download TSV:	http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2024-0121-1545-55-143-974837?info=result&format=tsv

Result

finished

As this function uses the NIG supercomputer system, it may take time to start your job when the nodes are busy. Please check computation node status [here](#) (short.q)



THIS WORK IS SUPPORTED BY NIG SUPERCOMPUTER SYSTEM AND JST NBDC JPMJND2202.

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

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

When the “Status” changes to “finished”, click on the result URL. Take a note of the URL so that you can review the results for up to one month.

The result page

ChIP-Atlas / Enrichment Analysis

Search for proteins significantly bound to your data.

Show entries

Search:

Test											
ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / pDC	Overlaps / Mono	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX1023792	TFs and others	SPI1	Blood	Macrophages	112968	5339/11207	13014/18171	-324.0	-324.0	0.67	FALSE
SRX2770855	TFs and others	SPI1	Blood	Macrophages	88807	5420/11207	13855/18171	-324.0	-324.0	0.63	FALSE
SRX1287846	TFs and others	CDK8	Blood	MOLM-14	50649	5066/11207	13051/18171	-324.0	-324.0	0.63	FALSE
SRX1287844	TFs and others	CDK8	Blood	MOLM-14	50871	5084/11207	13250/18171	-324.0	-324.0	0.62	FALSE
SRX3031982	TFs and others	BRD4	Blood	MV-4-11	47241	5298/11207	14117/18171	-324.0	-324.0	0.61	FALSE
SRX9867025	TFs and others	BCL11B	Blood	TALL-1	31691	4185/11207	11317/18171	-324.0	-324.0	0.60	FALSE
SRX4484988	TFs and others	ERG	Blood	SEM	50919	4052/11207	10966/18171	-324.0	-324.0	0.60	FALSE
SRX9867024	TFs and others	BCL11B	Blood	TALL-1	29842	4111/11207	11167/18171	-324.0	-324.0	0.60	FALSE

The result is displayed. Each line indicates TF ChIP-seq data whose bindings are enriched for open chromatin regions of pDC or Mono.

[Link to the download](#)

The result page

ChIP-Atlas / Enrichment Analysis

Search for proteins significantly bound to your data.

Show entries

Search:

Test											
1	2	3	4	5	6	7	8	9	10	11	12
ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / pDC	Overlaps / Mono	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX1023792	TFs and others	SPI1	Blood	Macrophages	112968	5339/11207	13014/18171	-324.0	-324.0	0.67	FALSE

For example, the first line (SRX1023792 ①) indicates that this is the SPI1 ChIP-seq data in macrophages (②③④⑤). This data has 112,968 peaks (⑥), of which 5,339 peaks overlap with the ATAC-seq peaks of pDC ($n = 11,207$ ⑦), whereas 13,014 peaks overlap with the ATAC-seq peaks of Mono ($n = 18,171$ ⑧). By creating the 2×2 cross table, the following calculations were performed:

- ⑨ $\log_{10}[P \text{ values}]$ calculated **using** two-tailed Fisher's exact test (Min = -324).
- ⑩ $\log_{10}[Q \text{ values}]$ calculated **using** Benjamini-Hochberg method (Min = -324).
- ⑪ Fold-enrichment = $\text{pDC} / \text{Mono} = (5,339 / 11,207) / (13,014 / 18,171)$
- ⑫ TRUE: The fold-enrichment (FE) > 1 .
FALSE: The fold-enrichment (FE) ≤ 1 .

By default, this table is sorted by $\log_{10}[P \text{ values}]$ in the 9th column.

The result page

ChIP-Atlas / Enrichment Analysis

Search for proteins significantly bound to your data.

Show entries

Search:

Test											
ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / pDC	Overlaps / Mono	FE < 1		Fold Enrichment	FE > 1?
SRX1023792	TFs and others	SPI1	Blood	Macrophages	112968	5339/11207	13014/18171	-324.0	-324.0	0.67	FALSE
SRX2770855	TFs and others	SPI1	Blood	Macrophages	88807	5420/11207	13855/18171	-324.0	-324.0	0.63	FALSE
SRX1287846	TFs and others	CDK8	Blood	MOLM-14	50649	5066/11207	13051/18171	-324.0	-324.0	0.63	FALSE
SRX1287844	TFs and others	CDK8	Blood	MOLM-14	50871	5084/11207	13250/18171	-324.0	-324.0	0.62	FALSE
SRX3031982	TFs and others	BRD4	Blood	MV-4-11	47241	5298/11207	14117/18171	-324.0	-324.0	0.61	FALSE
SRX9867025	TFs and others	BCL11B	Blood	TALL-1	31691	4185/11207	11317/18171	-324.0	-324.0	0.60	FALSE
SRX4484988	TFs and others	ERG	Blood	SEM	50919	4052/11207	10966/18171	-324.0	-324.0	0.60	FALSE
SRX9867024	TFs and others	BCL11B	Blood	TALL-1	29842	4111/11207	11167/18171	-324.0	-324.0	0.60	FALSE

This result indicates that SPI1 is one of the most enriched TFs for the open chromatin regions of Mono because the fold-enrichment (FE) is less than 1.

The result page

ChIP-Atlas / Enrichment Analysis

Search for proteins significantly bound to your data.

Show entries

Search:

TRUE

Test

ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / pDC	Overlaps / Mono	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX1491252	TFs and others	TCF4	Blood	GEN2.2	48362	6418/11207	6792/18171			1.53	TRUE
SRX1491250	TFs and others	TCF4	Blood	CAL-1	29027	4342/11207	4025/18171	-201.6	-200.2	1.75	TRUE
SRX220960	TFs and others	TCF4	Blood	CAL-1	4012	825/11207	315/18171	-125.5	-124.3	4.25	TRUE
SRX158106	TFs and others	TCF3	Blood	RPMI 8402	6547	620/11207	302/18171	-72.9	-71.9	3.33	TRUE
SRX725589	TFs and others	TAL1	Blood	T-ALL	22746	1572/11207	1378/18171	-68.4	-67.5	1.85	TRUE
SRX158111	TFs and others	TAL1	Blood	RPMI 8402	11091	774/11207	503/18171	-61.0	-60.1	2.49	TRUE
SRX475794	TFs and others	SPI1	Blood	GM12878	23939	2675/11207	2989/18171	-53.5	-52.6	1.45	TRUE
SRX1041802	TFs and others	GATA3	Blood	Jurkat	13079	958/11207	757/18171	-52.1	-51.2	2.05	TRUE

FE > 1

TFs enriched for pDC are filtered by searching with the keyword “TRUE” in the text box. The most enriched factor is TCF4, which is an essential factor for the differentiation of pDCs.

Download the data



Peak Browser



Enrichment Analysis



Diff Analysis



Target Genes



Colocalization



Publications



Docs

Find By ID

GSM469863

Go

Search



ChIP-Atlas: Enrichment Analysis

identify common epigenetic features of a given set of genomic loci and genes

Result page URL will be available for a week from the time when 'status' is 'finished'.

Project title	Test
Request ID	wabi_chipatlas_2024-0121-1545-55-143-974837
Submitted at:	15:45:55 (Jan-21-2024)
Estimated finishing time:	16:01:55 (Jan-21-2024)
Current time:	16:10:59 (Jan-21-2024)
Status	finished
Result URL:	http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2024-0121-1545-55-143-974837?info=result&format=html
Download TSV:	http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2024-0121-1545-55-143-974837?info=result&format=tsv

As this function uses the NIG supercomputer system, it may take time to start your job when the nodes are busy. Please check computation node status [here](#) (short.q)



THIS WORK IS SUPPORTED BY NIG SUPERCOMPUTER SYSTEM AND JST NBDC JPMJND2202.

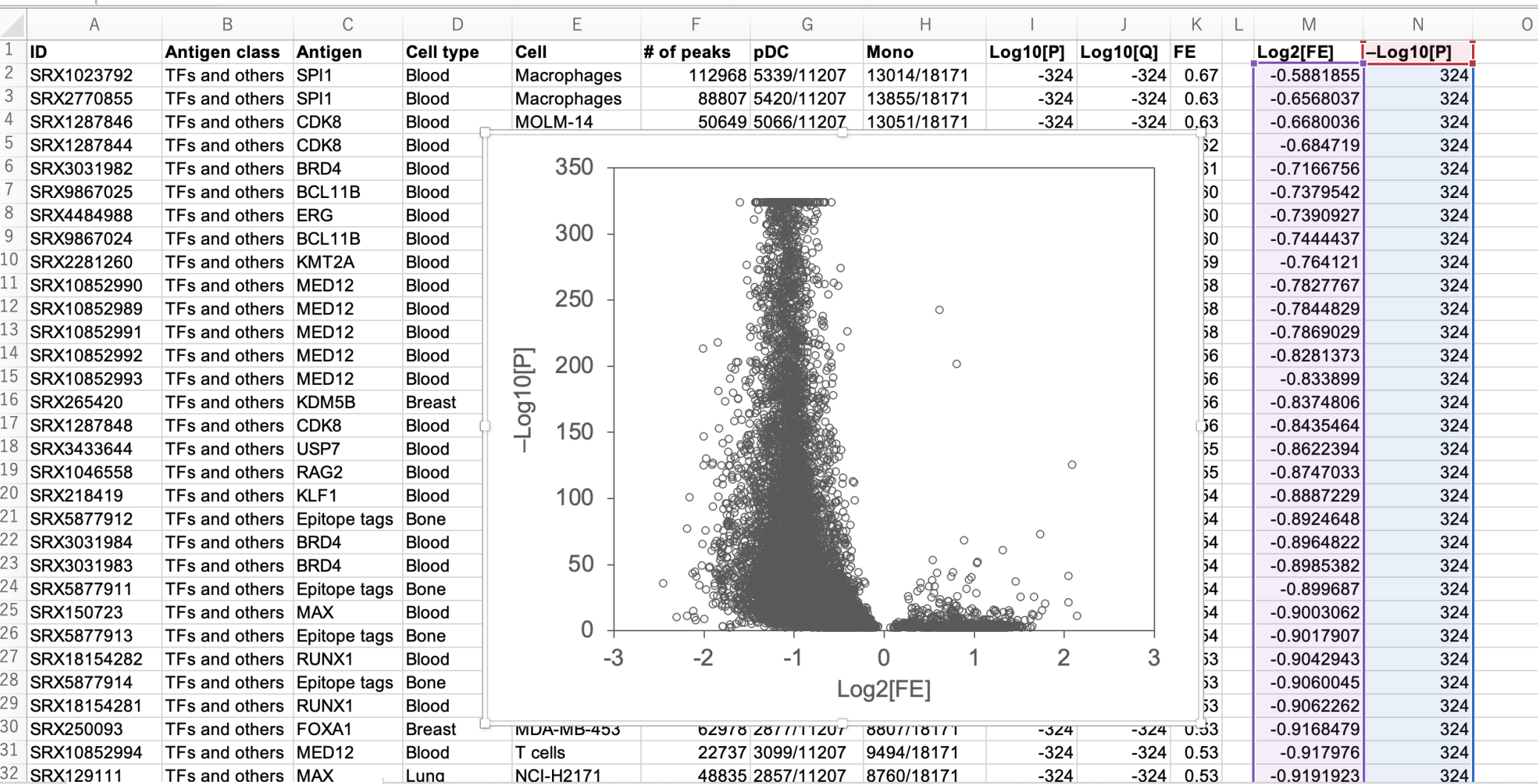
ALL DATA AND ANALYSIS TOOLS PROVIDED BY CHIP-ATLAS ARE LICENSED UNDER CC-BY 4.0 . ATTRIBUTION SHOULD BE MADE TO OUR PUBLICATION WHEN USING THESE RESOURCES.

NEED HELP? CREATE AN ISSUE ON GITHUB OR CONTACT US

The table can be downloaded in the Tab-Separated Values (TSV) format and used for further analysis, such as drawing the volcano plot shown on the next slide.

Volcano plot

グラフ 1



wabi_chipatlas_2024-0121-1545-5

準備完了 アクサシビリティ: 利用不可

Volcano plots are useful to visualize the distribution of P and FE values simultaneously. This can be done on Microsoft Excel® using a downloaded TSV file.

The manual for

ChIP-Atlas: Enrichment Analysis

1. Overview
2. Enrichment for the genomic loci (BED)
3. Enrichment around the genes (Gene symbol)
4. Tips

Next, let us try to identify the TFs whose bindings are enriched around the genes that are specifically expressed in liver cells.

Settings

ChIP-Atlas: Enrichment Analysis

[Tutorial movie](#)

Identify common peaks of a given set of genomic loci and genes

mm10
H. sapiens (hg19) M. musculus (mm10) M. musculus (mm9) R. norvegicus (rn6) D. melanogaster (dm6) D. melanogaster (dm3)
C. elegans (ce11) C. elegans (ce10) S. cerevisiae (sacCer3)

1. Experiment type

ChIP: Histone (38742)
ChIP: RNA polymerase (3273)
ChIP: TFs and others (20865)
ChIP: Input control (12128)
ATAC-Seq (40007)
DNase-seq (1632)
Bisulfite-Seq (35459)

TFs

2. Cell type Class

All cell types (20865)
Adipocyte (353)
Blood (5233)
Bone (137)
Breast (486)
Cardiovascular (322)
Digestive tract (215)
Embryo (628)

All

3. Threshold for Significance ⓘ

50
100
200
500

100

4. Enter dataset A

☐ Genomic regions (BED) or sequence motif ⓘ
☒ Gene list (Gene symbols) ⓘ

NM_144836
NM_001003893
NM_007824
NM_007618
NM_008555
NM_010775
NM_011316
NM_010767

[ファイルを選択](#) [ファイル未選択](#)

Choose local file

[Try with example](#)

5. Enter dataset B

☒ Refseq coding genes (excluding dataset A) ⓘ
☐ Gene list (Gene symbols) ⓘ

6. Analysis description

Analysis title ⓘ

Test

Dataset A title ⓘ

Liver

Dataset B title ⓘ

Others

Distance range from TSS ⓘ

- 5000 bp ≤ TSS ≤ + 5000 bp

submit

Set to examine the enrichment of TF peaks in all cell types with >100 MACS2 scores.

[Tips: Threshold for significance](#)

Settings

ChIP-Atlas: Enrichment Analysis

Identify common epigenetic features of a given set of genomic loci and genes

[Tutorial movie](#)

[H. sapiens \(hg38\)](#)

[H. sapiens \(hg19\)](#)

[M. musculus \(mm10\)](#)

[M. musculus \(mm9\)](#)

[R. norvegicus \(rn6\)](#)

[D. melanogaster \(dm6\)](#)

[D. melanogaster \(dm3\)](#)

[C. elegans \(ce11\)](#)

[C. elegans \(ce10\)](#)

[S. cerevisiae \(sacCer3\)](#)

1. Experiment type

ChIP: Histone (38742)
ChIP: RNA polymerase (3273)
ChIP: TFs and others (20865)
ChIP: Input control (12128)
ATAC-Seq (40007)
DNase-seq (1632)
Bisulfite-Seq (35459)

2. Cell type Class

All cell types (20865)
Adipocyte (353)
Blood (5233)
Bone (137)
Breast (486)
Cardiovascular (322)
Digestive tract (215)
Embryo (628)

3. Threshold for Significance ⓘ

50
100
200
500

4. Enter dataset A

- ☐ Genomic regions (BED) or sequence motif ⓘ
☒ **Gene list (Gene symbols) ⓘ**

NM_144836
NM_001003893
NM_007824
NM_007618
NM_008555
NM_010775
NM_011316
NM_010767

[ファイルを選択](#) [ファイル未選択](#)

Choose local file

[Try with example](#)

Refseq

5. Enter dataset B

- ☒ **Refseq coding genes (excluding dataset A) ⓘ**
☐ Gene list (Gene symbols) ⓘ

Liver-specific
genes

6. Analysis description

Analysis title ⓘ

Test

Dataset A title ⓘ

Liver

Dataset B title ⓘ

Others

Distance range from TSS ⓘ

- 5000 bp ≤ TSS ≤ + 5000 bp

Gene

You can enter the gene symbols or IDs in the text box of “dataset A”, e.g., the genes specifically expressed in the liver ([Download](#)) obtained from the tissue-specific gene database, RefEx. The other Refseq coding genes are set as the background.

[Tips: Acceptable gene list](#)

Settings

ChIP-Atlas: Enrichment Analysis

[? Tutorial movie](#)

Identify common epigenetic features of a given set of genomic loci and genes

[H. sapiens \(hg38\)](#)[H. sapiens \(hg19\)](#)[M. musculus \(mm10\)](#)[M. musculus \(mm9\)](#)[R. norvegicus \(rn6\)](#)[D. melanogaster \(dm6\)](#)[D. melanogaster \(dm3\)](#)[C. elegans \(ce11\)](#)[C. elegans \(ce10\)](#)[S. cerevisiae \(sacCer3\)](#)

1. Experiment type

ChIP: Histone (38742)
ChIP: RNA polymerase (3273)
ChIP: TFs and others (20865)
ChIP: Input control (12128)
ATAC-Seq (40007)
DNase-seq (1632)
Bisulfite-Seq (35459)

2. Cell type Class

All cell types (20865)
Adipocyte (353)
Blood (5233)
Bone (137)
Breast (486)
Cardiovascular (322)
Digestive tract (215)
Embryo (628)

3. Threshold for Significance ⓘ

50
100
200
500

4. Enter dataset A

- ☐ Genomic regions (BED) or sequence motif ⓘ
☒ Gene list (Gene symbols) ⓘ

NM_144836
NM_001003893
NM_007824
NM_007618
NM_008555
NM_010775
NM_011316
NM_010767
NM_010767

ファイルを選択 ファイル未選択

Choose local file

[Try with example](#)

5. Enter dataset B

- ☒ Refseq coding genes (excluding dataset A) ⓘ
☐ Gene list (Gene symbols) ⓘ

6. Analysis description

Analysis title ⓘ

Test

Test

Dataset A title ⓘ

Liver

Liver

Dataset B title ⓘ

Others

Others

TSS ± 5kb

Distance range from TSS ⓘ

- 5000 bp ≤ TSS ≤ + 5000 bp

Submit

submit

Enter the titles of this project (Test) and datasets A (Liver) and B (Others), which will be used to label the result data. Regions of ±5,000 bp are specified to examine the TF binding. Click on the “submit” button.



ChIP-Atlas: Enrichment Analysis

identify common epigenetic features of a given set of genomic loci and genes

Result page URL will be available for a week from the time when 'status' is 'finished'.

Project title	Test
Request ID	wabi_chipatlas_2024-0121-1545-55-143-974837
Submitted at:	15:45:55 (Jan-21-2024)
Estimated finishing time:	16:01:55 (Jan-21-2024)
Current time:	16:10:59 (Jan-21-2024)
Status	finished
Result URL:	http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2024-0121-1545-55-143-974837?info=result&format=html
Download TSV:	http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2024-0121-1545-55-143-974837?info=result&format=tsv

As this function uses the NIG supercomputer system, it may take time to start your job when the nodes are busy. Please check computation node status [here](#) (short.q)



THIS WORK IS SUPPORTED BY NIG SUPERCOMPUTER SYSTEM AND JST NBDC JPMJND2202.

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

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

After waiting for several minutes, the “Status” indicates “finished”. Click on the result URL. Take a note of the URL so that you can review the results for up to one month.

The result page

ChIP-Atlas / Enrichment Analysis

Search for proteins significantly bound to your data.

Show  entries

Search:

Test											
ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / Liver	Overlaps / Others	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX2375602	TFs and others	Prox1	Liver	Liver	22246	120/176	2947/19280	-54.5	-50.2	4.46	TRUE
SRX5028147	TFs and others	Ncor1	Liver	Liver	20087	114/176	2813/19280	-50.4	-46.4	4.44	TRUE
SRX6817423	TFs and others	Hnf4a	Liver	Liver	24867	136/176	4494/19280	-50.2	-46.4	3.32	TRUE
SRX5028173	TFs and others	Ncor1	Liver	Liver	22448	125/176	3619/19280	-49.9	-46.2	3.78	TRUE
SRX377391	TFs and others	Esr1	Liver	Liver	20828	137/176	4639/19280	-49.5	-45.9	3.24	TRUE
SRX5028171	TFs and others	Ncor1	Liver	Liver	26423	132/176	4226/19280	-49.3	-45.8	3.42	TRUE
SRX20201041	TFs and others	Hnf4a	Liver	Liver	22824	131/176	4151/19280	-49.2	-45.7	3.46	TRUE
SRX6817423	TFs and others	Hnf4a	Liver	Liver	24867	136/176	4494/19280	-50.2	-46.4	3.32	TRUE

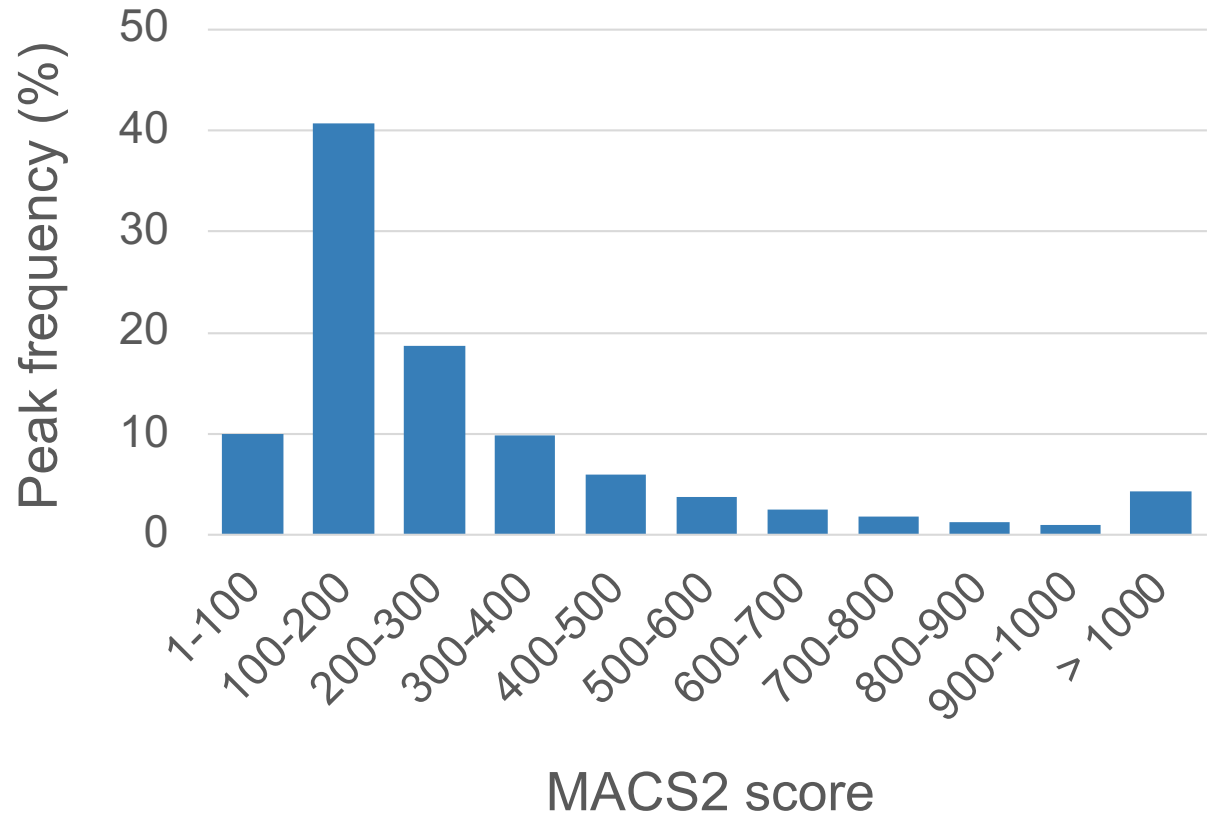
The most enriched TFs, include Prox1, Ncor1, and Hnf4a, which are known to be essential for liver development and function. This tool is therefore useful for identifying the TFs that organize cell type-specific genes.

Tips: Threshold for significance

3. Threshold for Significance ⓘ

50
100
200
500

MACS2 score
 $= -10 * \log_{10} [Q \text{ value}]$



The 'Threshold for Significance' panel of the Enrichment Analysis tool specifies the cut-off value of the MACS2 scores that indicates the statistical significance of each peak call. This histogram shows the relative frequencies of the ChIP/ATAC/DNase-seq peaks according to the MACS2 score. We recommend a threshold value of >100 to display reliable data.

Tips: Acceptable BED data

Input BED file must be described as follows:

Chromosome<tab>Begin<tab>End

4. Enter dataset A

☒ Genomic regions (BED) or sequence motif ⓘ
☐ Gene list (Gene symbols) ⓘ

chr9	68493082	68493193
chr9	69503038	69503199
chr9	69564724	69564888
chr9	71766977	71767096
chr9	73832865	73832982
chr9	75820890	75821028
chr9	76272003	76272152
chr9	76793230	76793393

5. Enter dataset B

☒ Random permutation of dataset A ⓘ
Permutation times ☐ x1 ☒ x10 ☐ x100
☐ BED or sequence motif ⓘ

BED vs Random background:

Suitable if you have an input BED file, but do not have a file for comparison, such as the SNPs loci and evolutionary conserved regions. Increasing the number of 'permutation times' will generate less biased random backgrounds; however, the computation time will be longer.

4. Enter dataset A

☒ Genomic regions (BED) or sequence motif ⓘ
☐ Gene list (Gene symbols) ⓘ

chr13	102503490	102503623
chr13	103799093	103799221
chr13	104325115	104325260
chr13	105796270	105796435
chr13	106096691	106096791
chr13	110481033	110481377
chr13	111247698	111247820
chr13	19897939	19898072

5. Enter dataset B

☐ Random permutation of dataset A ⓘ
☒ BED or sequence motif ⓘ

chr13	40476711	40476829
chr13	42284129	42284238
chr13	44219021	44219176
chr13	44854670	44854964
chr13	44922588	44922776
chr13	45068166	45068289
chr13	45340399	45340540
chr13	51397482	51397609

BED vs BED:

Suitable for comparing two sets of BED files, such as the two cell types of ATAC-seq peaks or hypomethylated regions and two types of histone mark peaks from an identical cell type.

Tips: Acceptable gene list

Official gene symbols and IDs shown here are acceptable; however, the synonymous symbols are not.

Official symbol	Synonym	Refseq ID	Ensembl gene ID	Ensembl transcript ID	UniProt ID
Pou5f1	Oct4	NM_013633	ENSMUSG00000024406	ENSMUST00000025271	P20263
Trp53	p53	NM_011640	ENSMUSG00000059552	ENSMUST00000005371	P02340

4. Enter dataset A

☐ Genomic regions (BED) or sequence motif ⓘ

☒ Gene list (Gene symbols) ⓘ

ADI1
AGO1
AHCYL2
AJAP1
APOBEC3C
APOBEC3D
ARHGEF38
ATPAF2
BCL2

5. Enter dataset B

☒ Refseq coding genes (excluding dataset A) ⓘ

☐ Gene list (Gene symbols) ⓘ

Genes vs Other Refseq coding genes:

Suitable if you have a list of input genes, but do not have a list for comparison, such as the genes specifically expressed in a tissue or cell type.

4. Enter dataset A

☐ Genomic regions (BED) or sequence motif ⓘ

☒ Gene list (Gene symbols) ⓘ

ADI1
AGO1
AHCYL2
AJAP1
APOBEC3C
APOBEC3D
ARHGEF38
ATPAF2
BCL2

5. Enter dataset B

☐ Refseq coding genes (excluding dataset A) ⓘ

☒ Gene list (Gene symbols) ⓘ

AGBL5
ALOXE3
AMZ2
ANG
APBB3
ARID2
ASF1A
ATP5O
ATM

Genes vs Genes:

Suitable for comparing two sets of gene lists, such as the up- vs down-regulated genes in response to certain mutations or drug administration.

Tips: API

```
$ ls
dataA.bed
$ curl -X POST \
  -d "format=text" \
  -d "result=www" \
  -d "genome=hg19" \
  -d "antigenClass=TFs and others" \
  -d "cellClass=Pluripotent stem cell" \
  -d "threshold=50" \
  -d "typeA=bed" \
  --data-urlencode "bedAFile@dataA.bed" \
  -d "typeB=rnd" \
  -d "bedBFile=empty" \
  -d "permTime=10" \
  -d "title=10 times random permutation of my data" \
  -d "descriptionA=my data" \
  -d "descriptionB=random permutation 10 times" \
  -d "distanceUp=0" \
  -d "distanceDown=0" \
  https://ddbj.nig.ac.jp/wabi/chipatlas/
```

The API of the Enrichment Analysis tool is available for batch analysis of multiple queries. See [here](#) for details.