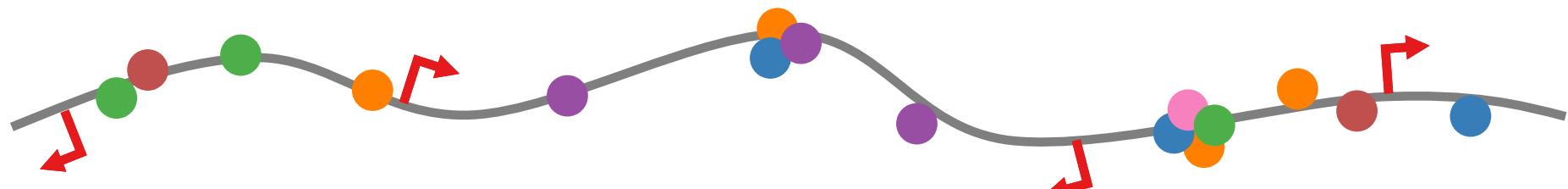


エンリッチメント解析

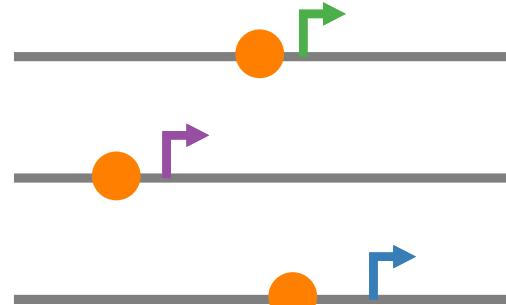
Enrichment Analysis でできること

Peak Browser

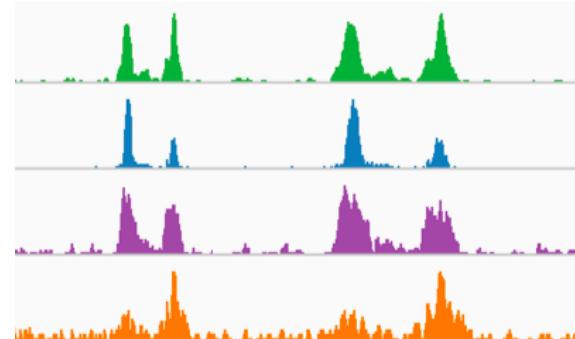


Target Genes

Enrichment Analysis



Colocalization



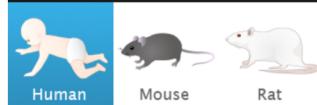
課題：肝臓特異的遺伝子群の上流因子の探索

RefEx より肝臓特異的遺伝子群を取得

Reference
Expression
Dataset
[English](#) | [日本語](#)



RefExの論文が出版されました。あなたの研究に役立ったらぜひ引用を!!
▼もっと詳しく



キーワードで検索

検索

ex) troponin, ALB

肝臓

組織特異的に発現する
遺伝子を見る

遺伝子オントロジー
Gene Ontology

遺伝子ファミリー

[refex.dbcls.jp/genelist.php?lang=ja&db=human&roku_valid=1&r\[31\]=31&order_key=score](http://refex.dbcls.jp/genelist.php?lang=ja&db=human&roku_valid=1&r[31]=31&order_key=score)



- [cellular process](#)
- [biological regulation](#)
- [metabolic process](#)

- [multicellular organismal process](#)
- [response to stimulus](#)
- [developmental process](#)

他のオントロジーを選ぶ

- [RNA recognition motif, RNP-1](#)
- [Pleckstrin homology](#)
- [Kruppel-associated box](#)

- [Protein kinase-like domain](#)
- [Zinc finger,C2H2-like](#)
- [GPCR,rhodopsin-like superfamily](#)

他のファミリーを選ぶ

Google

RefEx



RefEx より肝臓特異的遺伝子群を取得

Reference
Expression
Dataset
[English](#) | [日本語](#)

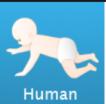

RefEx

[検索](#)

[RefExの論文が出版され](#)

[ました](#)

[ダウンロード](#)

 Human Mouse Rat

結果一覧 470 件中 1 - 10 件を表示

10

[最初](#) < > [最後](#)

ソート: Tissue Specificity, high

[リストをクリア](#)

[リストを見る 0](#)

[ダウンロード](#)

[エクセルで開く](#)

検索条件

遺伝子名

条件なし

組織

• 肝臓

オントロジー

条件なし

ファミリー

条件なし

遺伝子名

3Dマップ

相対発現量

[mannose-binding lectin \(protein C\) 2, soluble \(opsonic defect\)](#)

[リストに追加する](#)

[リストから削除する](#)

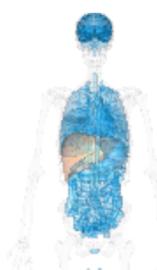
同義遺伝子名 Mannan-binding protein, MBL, MGC116833, MBL2, MBP-C, Mannose-binding protein C precursor, MGC116832, Mannose-binding lectin, COLEC1, HSMBPC, MBP1

Refseq ID NM_000242

GenelID 4153

Unigene ID Hs.499674

Probe set ID 207256_at



EST



GeneChip



CAGE



RNA-seq



[fibrinogen alpha chain](#)

refex.dbcls.jp/genelist_dl.php?lang=ja&db=human&roku_valid=1&rk[]=%20&order_key=score



RefEx



RefEx より肝臓特異的遺伝子群を取得

db=human&roku_valid=1&rk()=31&order_key=score								
#	RefseqID	GeneID	UnigeneID	ProbesetID	Description	Interpro_top	Chromosome	est10_max
1	NM_000242	4153	Hs.499674	207256_at	mannose-bin	C-type lectin	10q21.1(-)	52.799999
2	NM_000508	2243	Hs.351593	205649_s_at	fibrinogen alp	NULL	4q31.3(-)	724
3	NM_005989	6718	Hs.201667	207102_at	aldo-keto red	Aldo/keto red	7q33(+)	105.59999
4	NM_001737	725		206707_at	complement	Thrombopos	Fn12_1(+)	-
5	NM_001638							84.400001
6	NM_019844							232.19999
7	NM_005141							7473.200
8	NM_000780							15.
9	NM_000133							9
10	NM_000488							812.79998
11	NM_001872							390.60000
12	NM_016413							390.60000
13	NM_001643							1372.1999
14	NM_005577							10.600000
15	NM_001643							1372.1999
16	NM_006446	10599	Hs.449750	210500_at	solute carrier	major facilitat	12p12.2(+)	316.70001
17	NM_031479	83729	Hs.632713	210587_at	inhibin, beta	I Transforming	12q13.3(+)	42.200000
18	NM_006684	10877	-	207874_s_at	complement	Sushi/SCR/C	1q31.3(+)	-

エル エル
<http://bit.ly/2KhMLTu>

liver_genes.txt をダウンロード

Refseq ID を全てコピー

エンリッチメント解析

The screenshot shows the ChIP-Atlas website interface. At the top, there's a dark header with the title "エンリッチメント解析". Below it is a standard browser-style header with back/forward buttons, a search bar containing "chip-atlas.org", and a refresh button. The main menu includes "ChIP-Atlas", "Peak Browser", "Target Genes", "Colocalization", "Enrichment Analysis", "Documentation", "Publications", and a "Find an experiment" dropdown.

ChIP-Atlas

ChIP-Atlas is an integrative and comprehensive database for visualizing and making use of public ChIP-seq data. ChIP-Atlas covers almost all public ChIP-seq data submitted to the SRA (Sequence Read Archives) in NCBI, DDBJ, or ENA, and is based on over 78,000 experiments.

[Watch movie introduction](#)

クリック

The four main features of ChIP-Atlas are:

Peak Browser

graphically visualizes protein binding on given genomic loci with genome browser (IGV).

[Watch Movie](#)

Target Genes

predicts target genes bound by given transcription factors.

[Watch Movie](#)

Colocalization

predicts partner proteins colocalizing with given transcription factors.

[Watch Movie](#)

Enrichment Analysis

predicts proteins bound to given genomic loci and genes (formerly known as *in silico* ChIP).

[Watch Movie](#)



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エンリッチメント解析

[ChIP-Atlas](#)[Peak Browser](#)[Target Genes](#)[Colocalization](#)[Enrichment Analysis](#)[Documentation](#)[Publications](#)[Find an experiment ▾](#)

ChIP-Atlas - Enrichment Analysis

Analyze your data with public ChIP-seq data.

[Tutorial movie ▾](#)[H. sapiens](#)[M. musculus](#)[R. norvegicus](#)[D. melanogaster](#)[C. elegans](#)[S. cerevisiae](#)

1. Antigen Class

All antigens (43086)
DNase-seq (1632)
Histone (10578)
RNA polymerase (1532)
TFs and others (9868)
Input control (5080)
Unclassified (10053)
No description (4343)

2. Cell type Class

All cell types (43086)
Adipocyte (324)
Blood (10674)
Bone (819)
Breast (5050)
Cardiovascular (1136)
Digestive tract (2970)
Epidermis (1244)

3. Threshold for Significance ⓘ

50
100
200
500

4. Select your data

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

NM_000242
NM_000508
NM_005989
NM_001737
NM_001638
NM_019844
NM_005141
NM_000780

ファイルを選択 ファイル未選択

Choose local file

Try with example

5. Select dataset to be compared

- Refseq coding genes (excluding user data) ⓘ
 Gene list (Gene symbols) ⓘ

6. Describe datasets

User data title ⓘ

Liver genes

Compared data title ⓘ

Other genes

Project title ⓘ

Test

Distance range from TSS ⓘ

- 5000 bp ≤ TSS ≤ + 5000 bp

submit

Estimated run time: 5 mins

エンリッチメント解析

H. sapiens

Target Genes

Colocalization

Enrichment Analysis

Documentation

Publications

Find an experiment ▾

ChIP-seq - Enrichment Analysis

Analyze your data with public ChIP-seq data.

Tutorial movie ▾

H. sapiens

M. musculus

R. norvegicus

C. elegans

S. cerevisiae

1. Antigen Class

- All antigens (43086)
- DNase-seq (1632)
- Histone (10578)
- RNA polymerase (1532)
- TFs and others (9868)**
- Input control (5080)
- Unclassified (10053)
- No description (4343)

TFs and
others

Gene list

4. Select your data

- Genome regions (BED) or sequence motif ⓘ
- Refseq coding genes (excluding user data) ⓘ
- Gene list (Gene symbols) ⓘ

NM_000242
NM_000508
NM_005989
NM_001737
NM_001638
NM_019844
NM_005141
NM_000780

ペースト
Refseq ID
Official gene symbol
UniProt ID

ファイルを選択 ファイル未選択
Choose local file Try web search

Background は
その他の RefSeq
遺伝子

User data title ⓘ

Liver genes

Compared data title ⓘ

Other genes

Project title ⓘ

Test

Distance range from TSS ⓘ

- 5000 bp ≤ TSS ≤ + 5000 bp

submit

Estimated run time: 5 mins

エンリッチメント解析

[ChIP-Atlas](#)[Peak Browser](#)[Target Genes](#)[Colocalization](#)[Enrichment Analysis](#)[Documentation](#)[Publications](#)[Find an experiment ▾](#)[Tutorial movie ▾](#)

ChIP-Atlas - Enrichment Analysis

Analyze your data with public ChIP-seq data.

[H. sapiens](#)[M. musculus](#)[R. norvegicus](#)[D. melanogaster](#)[C. elegans](#)[S. cerevisiae](#)

1. Antigen Class

- All antigens (43086)
- DNase-seq (1632)
- Histone (10578)
- RNA polymerase (1532)
- TFs and others (9868)**
- Input control (5080)
- Unclassified (10053)
- No description (4343)

2. Cell type Class

- All cell types
- Adipocyte
- Blood
- Bone
- Breast
- Cardio
- Digestive
- Epidermis

3. Threshold for Significance ⓘ

- 50
- 100**
- 200
- 500

4. Select your data

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

- NM_000242
- NM_000508
- NM_005989
- NM_001737
- NM_001638
- NM_019844
- NM_005141
- NM_000780

[ファイルを選択](#)[ファイル未選択](#)[Try with example](#)

Choose local file

4. の名前
(任意)

5. Select dataset to be compared

- Refseq coding genes (excluding user data) ⓘ
- Gene list (Gene symbols) ⓘ

6. Describe datasets

[User data title ⓘ](#)[Compared data title ⓘ](#)[Project title ⓘ](#)[Distance range from TSS ⓘ](#)

- bp ≤ TSS ≤ + bp

[submit](#)

プロジェクト名
(任意)

Estimated run time: 5 mins

エンリッチメント解析

[ChIP-Atlas](#)[Peak Browser](#)[Target Genes](#)[Colocalization](#)[Enrichment Analysis](#)[Documentation](#)[Publications](#)[Find an experiment ▾](#)

ChIP-Atlas - Enrichment Analysis

Analyze your data with public ChIP-seq data.

[Tutorial movie ▾](#)[H. sapiens](#)[M. musculus](#)[R. norvegicus](#)[D. melanogaster](#)[C. elegans](#)[S. cerevisiae](#)

1. Antigen Class

All antigens (43086)
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Bone (819)
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Cardiovascular (1136)
Digestive tract (2970)
Epidermis (1244)

3. Threshold for Significance ⓘ

50
100
200
500

4. Select your data

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

NM_000242
NM_000508
NM_005989
NM_001737
NM_001638
NM_019844
NM_005141
NM_000780

ファイルを選択 ファイル未選択
Choose local file Try with example

転写開始点 (TSS)
からの距離幅
例：± 5 kb

5. Select dataset to be compared

- Refseq coding genes (excluding user data) ⓘ

6. Describe datasets

User data title ⓘ

Liver genes

Compared data title ⓘ

Other genes

Project title ⓘ

Test

Distance range from TSS ⓘ

5000 bp ≤ TSS ≤ + 5000 bp

submit

submit

Estimated run time: 5 mins

エンリッチメント解析

chip-atlas.org

ChIP-Atlas Peak Browser Target Genes Colocalization Enrichment Analysis Documentation Publications Find an experiment ▾

ChIP-Atlas - Enrichment Analysis

Analyze your data with public ChIP-seq data.

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

Project title	My project
Request ID	wabi_chipatlas_2018-1207-1735-03-394-748830
Submitted at:	17:35:04 (Dec-07-2018)
Estimated finishing time:	17:37:04 (Dec-07-2018)
Current time:	17:35:09 (Dec-07-2018)
Status	Requesting
Result URL:	http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2018-1207-1735-03-394-748830?info=result&format=html
Download TSV:	http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2018-1207-1735-03-394-748830?info=result&format=tsv



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計算終了まで数分間かかる

エンリッチメント解析

The screenshot shows the ChIP-Atlas website interface. At the top, there's a navigation bar with links for ChIP-Atlas, Peak Browser, Target Genes, Colocalization, Enrichment Analysis, Documentation, Publications, and a search bar labeled "Find an experiment". Below the navigation, the main title "ChIP-Atlas - Enrichment Analysis" is displayed, followed by the subtitle "Analyze your data with public ChIP-seq data.". A note says "Result page URL will be available for a week from the time when 'status' is 'finished'." To the right of this note, there's a large orange speech bubble containing the Japanese word "クリック" (Click). Below the note, there's a table of project details:

Project title	My project
Request ID	wabi_chipatlas_2018-1207-1735-03-394-748830
Submitted at:	17:35:04 (Dec-07-2018)
Estimated finishing time:	17:37:04 (Dec-07-2018)
Current time:	17:40:23 (Dec-07-2018)
Status	finished
Result URL:	http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2018-1207-1735-03-394-748830?info=result&format=html
Download TSV:	http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2018-1207-1735-03-394-748830?info=result&format=tsv

クリック

エル いちエル
http://bit.ly/2GLzA1l



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URL を控えておくと、後日また閲覧できる

エンリッチメント解析

ChIP-Atlas / Enrichment Analysis

Search for proteins significantly bound to your data.

Show 100 entries Search:

Test

ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / Liver genes	Overlaps / Other genes	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX100505	TFs and others	HNF4A	Liver	Hep G2	21265	120/219	3428/18220	-31.2	-27.2	2.91	TRUE
SRX100544	TFs and others	EP300	Liver	Hep G2	24336	123/219	4003/18220	-26.9	-23.1	2.56	TRUE
SRX100497	TFs and others	RXRA	Liver	Hep G2	13022	93/219	2350/18220	-26.2	-22.6	3.29	TRUE
SRX100449	TFs and others	HNF4G	Liver	Hep G2	15922	105/219	3100/18220	-24.9	-21.5	2.82	TRUE
SRX100448	TFs and others	FOXA2	Liver	Hep G2	45142	134/219	5318/18220	-21.6	-18.4	2.10	TRUE
SRX190234	TFs and others	CEPB	Liver	Hep G2	12489	85/219	2290/18220	-21.6	-18.4	3.09	TRUE
SRX100506	TFs and others	FOXA1	Liver	Hep G2	50949	140/219	6058/18220	-19.4	-16.2	1.92	TRUE
SRX100552	TFs and others	SP1	Liver	Hep G2	19079	131/219	5588/18220	-17.9	-14.8	1.95	TRUE
SRX100477	TFs and others	FOXA1	Liver	Hep G2	40732	126/219	5229/18220	-17.8	-14.7	2.00	TRUE
SRX150698	TFs and others	HNF4A	Liver	Hep G2	10069	79/219	2321/18220	-17.6	-14.6	2.83	TRUE
SRX150701	TFs and others	CEPB	Liver	Hep G2	18637	106/219	4145/18220	-15.6	-12.6	2.13	TRUE
SRX100625	TFs and others	HNF4A	Liver	Hep G2	2654	24/219	512/18220	-14.7	-11.7	5.52	TRUE

Showing 1 to 100 of 10,585 entries

Previous 1 2 3 4 5 ... 106 Next

エンリッチメント解析

ChIP-Atlas / Enrichment Analysis

Search for proteins significantly bound to your data.

Show 100 entries Search:

Test											
ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / Liver genes	Overlaps / Other genes	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX100505	TFs and others	HNF4A	Liver	Hep G2	21265	120/219	3428/18220	-31.2	-27.2	2.91	TRUE

Liver 由来の Hep G2 細胞における HNF4A ChIP-seq データ

- ヒトゲノムの 21,265 箇所に結合。
 - ・ 肝臓特異的遺伝子 (219 個) のうち、120 個に結合
 - ・ その他の遺伝子 (18,220 個) のうち、3428 個に結合
- 両者の比 = $(120/219) / (3428/18220) = 2.91$
- Fisher の正確確率検定: $P = 1E-31.2$

エンリッチメント解析

ChIP-Atlas / Enrichment Analysis

Search for proteins significantly bound to your data.

Show 100 entries Search:

Test

ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / Liver genes	Overlaps / Other genes	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX100505	TFs and others	HNF4A	Liver	Hep G2	21265	120/219	3428/18220	-31.2	-27.2	2.91	TRUE
SRX100544	TFs and others	EP300	Liver	Hep G2	24336	123/219	4003/18220	-26.9	-23.1	2.56	TRUE
SRX100497	TFs and others	RXRA	Liver	Hep G2	13022	93/219	2350/18220	-26.2	-22.6	3.29	TRUE
SRX100449	TFs and others	HNF4G	Liver	Hep G2	15922	105/219	3100/18220	-24.9	-21.5	2.82	TRUE
SRX100448	TFs and others	FOXA2	Liver	Hep G2	45142	134/219	5318/18220	-21.6	-18.4	2.10	TRUE
SRX190234	TFs and others	CEPB	Liver	Hep G2	12489	85/219	2290/18220	-21.6	-18.4	3.09	TRUE
SRX100506	TFs and others	FOXA1	Liver	Hep G2	50949	140/219	6058/18220	-19.4	-16.2	1.92	TRUE
SRX100552	TFs and others	SP1	Liver	Hep G2	19079	131/219	5588/18220	-17.9	-14.8	1.95	TRUE
SRX100477	TFs and others	FOXA1	Liver	Hep G2	40732	126/219	5229/18220	-17.8	-14.7	2.00	TRUE
SRX150698	TFs and others	HNF4A	Liver	Hep G2	10069	79/219	2321/18220	-17.6	-14.6	2.83	TRUE
SRX150701	TFs and others	CEPB	Liver	Hep G2	18637	106/219	4145/18220	-15.6	-12.6	2.13	TRUE
SRX100625	TFs and others	HNF4A	Liver	Hep G2	2654	24/219	512/18220	-14.7	-11.7	5.52	TRUE

Showing 1 to 100 of 10,585 entries

Previous 1 2 3 4 5 ... 106 Next

エンリッチメント解析

chip-atlas.org

ChIP-Atlas Peak Browser Target Genes Colocalization Enrichment Analysis Documentation Publications Find an experiment ▾

ChIP-Atlas - Enrichment Analysis

Analyze your data with public ChIP-seq data.

H. sapiens M. musculus R. norvegicus D. melanogaster C. elegans S. cerevisiae

1. Antigen Class
All antigens (34390)
DNA (1000)

2. Cell type Class
All cell types (34390)
Adipocyte (292)
Blood (9096)
Bone (655)
Breast (3699)
Cardiovascular (1080)
Digestive tract (2447)
Epidermis (1089)

3. Threshold for Significance ⓘ
50
100
200
500

4. Select your data
 Genomic regions (BED) or sequence motif ⓘ
 Gene list (Gene symbols) ⓘ

chr8 134339107 134339325
chr15 41548749 41548861
chr15 25207262 25207383
chr1 190561786 190561937
chr3 142208484 142208615
chr9 115544616 115544762
chr15 59846350 59846560
chr15 81109164 81109289

Choose File no file selected
Choose local file Try with example

5. Select dataset to be compared
 Random permutation of user data ⓘ
 BED or sequence motif ⓘ

chr15 32568482 32568742
chr16 17650550 17650705
chr6 134138703 134138846
chr17 43176564 43176809
chr14 100850102 100850298
chr20 48158343 48158558
chr18 43728802 43728955
chr15 88993498 88993718

Choose File no file selected
Choose local file Try with example

6. Describe datasets

User data title ⓘ
My data

Compared data title ⓘ
Control

Project title ⓘ
My project

submit

Estimated run time: 5 mins

Tutorial movie ▾



ゲノム座標を入れることもできる。