

Navigating the Main Data Page



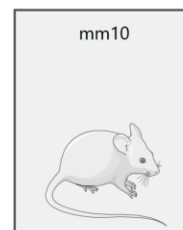
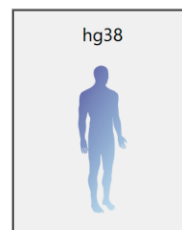
Welcome to the Loop Catalog

The Loop Catalog is a database of curated high-resolution HiChIP data from published work. Our dataset includes 763 human samples processed with hg38 and 281 mouse samples processed with mm10. In addition, it also contains 44 high-resolution HiC samples from the 4D Nucleome for auxiliary purposes. As development continues, our goal is to include various other analysis tools developed in lab and enhance various types of research such as variant prioritization.

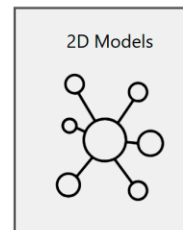
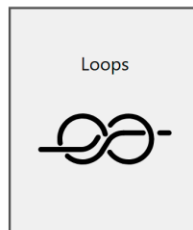
First time to the Loop Catalog? Come visit our video tutorial: [link](#)

This website is free and open to all users and login is not required.

Select Reference Genome i



Select Analysis i



GO

Welcome to the Loop Catalog

Get Help

Tutorial
FAQs
Contact Us

Dataset

Docs
Latest Build: 0.1

Publications

bioRxiv 2024

La Jolla
Institute
FOR IMMUNOLOGY

Life
Without
Disease.[®]



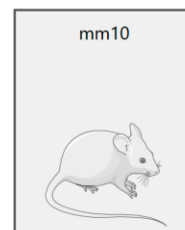
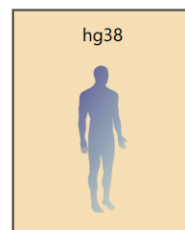
Welcome to the Loop Catalog

The Loop Catalog is a database of curated high-resolution HiChIP data from published work. Our dataset includes 763 human samples processed with hg38 and 281 mouse samples processed with mm10. In addition, it also contains 44 high-resolution HiC samples from the 4D Nucleome for auxiliary purposes. As development continues, our goal is to include various other analysis tools developed in lab and enhance various types of research such as variant prioritization.

First time to the Loop Catalog? Come visit our video tutorial: [link](#)

This website is free and open to all users and login is not required.

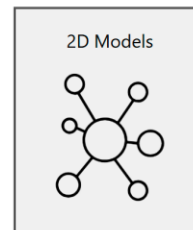
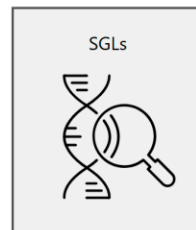
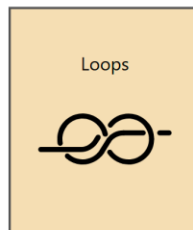
Select Reference Genome i



Select a Reference Genome



Select Analysis i



Select an Analysis



Click Go



Get Help

Tutorial
FAQs
Contact Us

Dataset

Docs
Latest Build: 0.1

Publications

bioRxiv 2024

La Jolla
Institute
FOR IMMUNOLOGY

Life
Without
Disease.[®]

Data Explorer

Tools: chr1:22000000-23000000 Viewing a 1.0 Mb region in 1291px, 1 pixel spans 774 bp



FC Loops

Unfiltered 5kb 10kb 25kb Peaks

Filtered 5kb 10kb 25kb

[All/None](#) [All/None](#)

FH Loops

Unfiltered 5kb 10kb 25kb Peaks

Filtered 5kb 10kb 25kb

[All/None](#) [All/None](#)

HiCCUPs Loops

5kb 10kb 25kb

[All/None](#)

HiC Loops

1kb 5kb

[All/None](#)

[Filter](#)
[Copy](#)
[CSV](#)
[Column visibility](#)
[Clear Browser](#)
[Clear Selection](#)
[Download Data](#)
[Download WashU JSON](#)
[Visualize](#)

Showing 1 to 10 of 1,042 entries

| Primary Name | Study | Number of Read Pairs | Bio-rep | Pulldown or HiC | 5kb FC Loops (Unfiltered) | 5kb FH Loops (Unfiltered) |
|--|----------------------|----------------------|---------|-----------------|---------------------------|---------------------------|
| <input type="checkbox"/> Wei-22RV1 (merged) | Wei et al., 2023 | 375,335,640 | 2 | CTCF | 214603 | 116360 |
| <input type="checkbox"/> H9 | Lyu et al., 2018 | 515,530,130 | 1 | Rad21 | 196151 | 230390 |
| <input type="checkbox"/> Wei-22RV1-Myc (merged) | Wei et al., 2023 | 437,453,186 | 1 | CTCF | 150379 | 131802 |
| <input type="checkbox"/> Natural Killer 1816-RH-1 (All Donors) | Chandra et al., 2021 | 1,457,921,642 | 1 | H3K27ac | 139924 | 14614 |
| <input type="checkbox"/> H9-HS | Lyu et al., 2018 | 418,316,089 | 1 | Rad21 | 134065 | 139883 |
| <input type="checkbox"/> Wei-22RV1-Control (merged) | Wei et al., 2023 | 344,429,396 | 2 | CTCF | 130218 | 115765 |
| <input type="checkbox"/> MB157-plnd20EBF1-10dox | Zhou et al., 2022 | 774,486,022 | 1 | SMC1A | 120549 | 106894 |
| <input type="checkbox"/> CD4 Naive 1815-RH-1 (All Donors) | Chandra et al., 2021 | 2,125,336,641 | 1 | H3K27ac | 119199 | 23013 |
| <input type="checkbox"/> MB157-plnd20ICF1-10dox | Zhou et al., 2022 | 732,911,273 | 1 | SMC1A | 106533 | 97695 |
| <input type="checkbox"/> Wei-22RV1 | Wei et al., 2023 | 178,763,153 | 1 | CTCF | 99754 | 44291 |

Show 10 entries Previous **1** 2 3 4 5 ... 105 Next

Can't find the sample you're looking for? Send us a message through the emails listed in the "Contact Us" section.

Welcome to the main data/loop page

Loop Catalog

Loop Catalog Loops Tools Docs Team News Tutorial hg38

Data Explorer

Tools: chr1:22000000-23000000 Viewing a 1.0 Mb region in 1291px, 1 pixel spans 774 bp

Metadata

FC Loops

Unfiltered 5k Filtered 5k

10k 10k

25k 25k

Peaks

[All/None](#) [All/None](#)

FH Loops

Unfiltered 5k Filtered 5k

10k 10k

25k 25k

Peaks

[All/None](#) [All/None](#)

HiCCUPs Loops

5k [All/None](#)

10k

25k

HiC Loops

1kb [All/None](#)

5k

Filtering Menu

[Filter](#)

[Reset All](#)

[Collapse All](#)

No. Samples: 1042

Pulldown or HiC

Organ

Biomaterial

No. of Reads

No. of 5k FC Loops

No. of 5k FH Loops

No. of 5k HiCCUPs Loops

No. of 1k HiC Loops

Copy CSV Column visibility Clear Browser Clear Selection [Download Data](#) [Download WashU JSON](#) [Visualize](#)

Showing 1 to 10 of 1,042 entries

| Primary Name | Study | Number of Read Pairs | Bio-rep | Pulldown or HiC | 5k FC Loops (Unfiltered) | 5k FH Loops (Unfiltered) |
|--|----------------------|----------------------|---------|-----------------|--------------------------|--------------------------|
| <input type="checkbox"/> Wei-22RV1 (merged) | Wei et al., 2023 | 375,335,640 | 2 | CTCF | 214603 | 116360 |
| <input type="checkbox"/> H9 | Lyu et al., 2018 | 515,530,130 | 1 | Rad21 | 196151 | 230390 |
| <input type="checkbox"/> Wei-22RV1-Myc (merged) | Wei et al., 2023 | 437,453,186 | 1 | CTCF | 150379 | 131802 |
| <input type="checkbox"/> Natural Killer 1816-RH-1 (All Donors) | Chandra et al., 2021 | 1,457,921,642 | 1 | H3K27ac | 139924 | 14614 |
| <input type="checkbox"/> H9-HS | Lyu et al., 2018 | 418,316,089 | 1 | Rad21 | 134065 | 139883 |
| <input type="checkbox"/> Wei-22RV1-Control (merged) | Wei et al., 2023 | 344,429,396 | 2 | CTCF | 130218 | 115765 |
| <input type="checkbox"/> MB157-plnd20EBF1-10dox | Zhou et al., 2022 | 774,486,022 | 1 | SMC1A | 120549 | 106894 |
| <input type="checkbox"/> CD4 Naive 1815-RH-1 (All Donors) | Chandra et al., 2021 | 2,125,336,641 | 1 | H3K27ac | 119199 | 23013 |
| <input type="checkbox"/> MB157-plnd20TCF1-10dox | Zhou et al., 2022 | 732,911,273 | 1 | SMC1A | 106533 | 97695 |
| <input type="checkbox"/> Wei-22RV1 | Wei et al., 2023 | 178,763,153 | 1 | CTCF | 99754 | 44291 |

Show 10 entries Previous 1 2 3 4 5 ... 105 Next

Can't find the sample you're looking for? Send us a message through the emails listed in the "Contact Us" section.

Get Help

Tutorial
FAQs
Contact Us

Dataset

Docs
Latest Build: 0.1

Publications

bioRxiv 2024

La Jolla Institute
FOR IMMUNOLOGY

Life Without Disease.

WashU Epigenome Embedding



Loop Submenu



Filtering Menu



Interactive buttons



Main Data Page



Submenu for FC Loops
with both Unfiltered and
Filtered Loops



Similar submenus for
FH, HiCCUPs and HiC loops

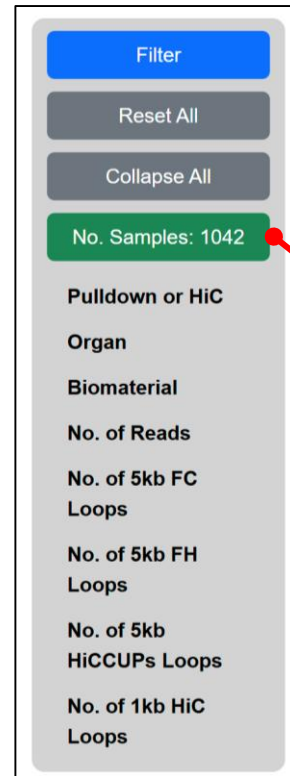


The image shows four submenus arranged horizontally. The first, 'FC Loops', is highlighted with a red border. It has a title bar with an 'i' icon, a list of radio button options under 'Unfiltered' and 'Filtered' columns, and two 'All/None' toggle buttons. The other submenus are 'FH Loops', 'HiCCUPs Loops', and 'HiC Loops', each with a similar structure but fewer options. Red lines connect the 'All/None' buttons in the FC Loops submenu to the text below.

Toggle buttons to select
all unfiltered or filtered
options

Filtering at the loop calling and sample levels

2) Click Filter



Filter

Reset All

Collapse All

No. Samples: 1042

Pulldown or HiC

Organ

Biomaterial

No. of Reads

No. of 5kb FC Loops

No. of 5kb FH Loops

No. of 5kb HiCCUPs Loops

No. of 1kb HiC Loops

Helper functions

Displays current
number of samples

1) Select filtering criteria

Copy table to clipboard or save to CSV

Hide/show columns from table

Clear the browser

Clear the sample selection

Download tracks from selected samples

Download WashU hub for selected samples

Visualize selected samples

Table with HiChIP/HiC samples & loop calls

Click on sample link to visit sample summary page

Select samples for interactive functions

Showing 1 to 10 of 1,042 entries

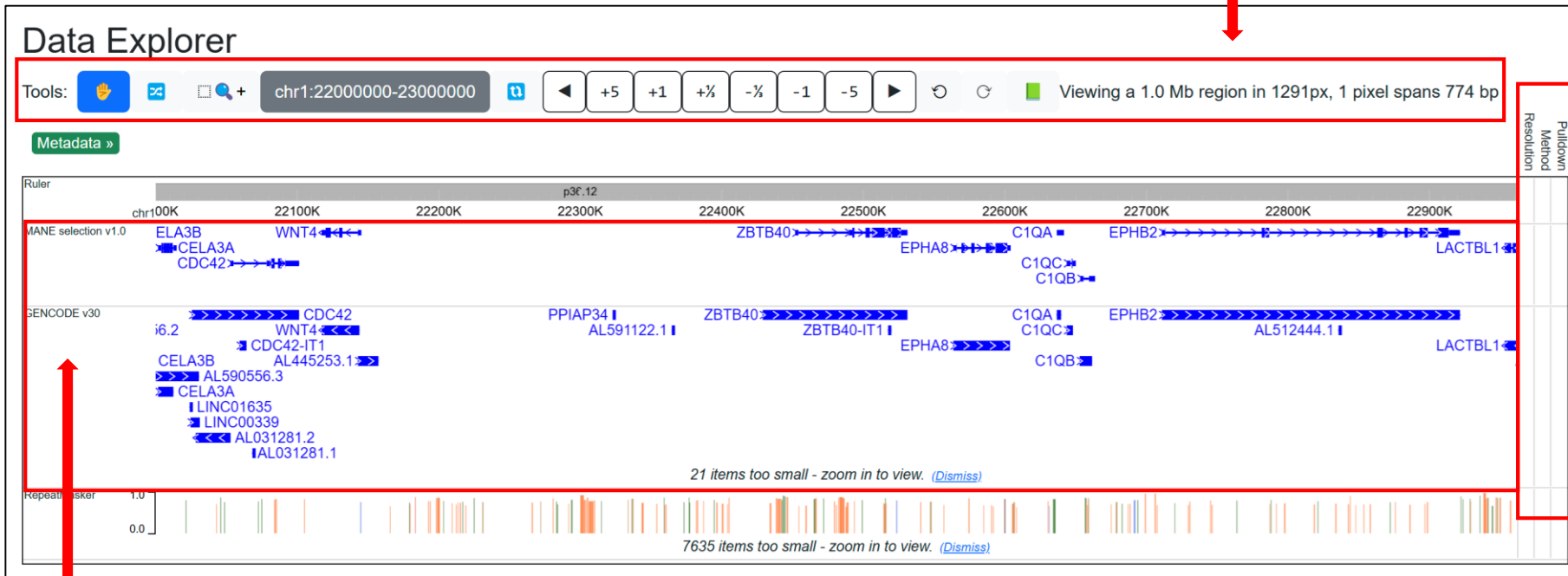
Search:

| <input type="checkbox"/> | Primary Name | Study | Number of Read Pairs | Bio-rep | Pulldown or HiC | 5kb FC Loops (Unfiltered) | 5kb FH Loops (Unfiltered) |
|--------------------------|---|----------------------|----------------------|---------|-----------------|---------------------------------|---------------------------------|
| <input type="checkbox"/> | Wei-22RV1 (merged) | Wei et al., 2023 | 375,335,640 | 2 | CTCF | 214603 <input type="checkbox"/> | 116360 <input type="checkbox"/> |
| <input type="checkbox"/> | H9 | Lyu et al., 2018 | 515,530,130 | 1 | Rad21 | 196151 <input type="checkbox"/> | 230390 <input type="checkbox"/> |
| <input type="checkbox"/> | Wei-22RV1-Myc (merged) | Wei et al., 2023 | 437,453,186 | 1 | CTCF | 150379 <input type="checkbox"/> | 131802 <input type="checkbox"/> |
| <input type="checkbox"/> | Natural Killer 1816-RH-1 (All Donors) | Chandra et al., 2021 | 1,457,921,642 | 1 | H3K27ac | 139924 <input type="checkbox"/> | 14614 <input type="checkbox"/> |
| <input type="checkbox"/> | H9-HS | Lyu et al., 2018 | 418,316,089 | 1 | Rad21 | 134065 <input type="checkbox"/> | 139883 <input type="checkbox"/> |
| <input type="checkbox"/> | Wei-22RV1-Control (merged) | Wei et al., 2023 | 344,429,396 | 2 | CTCF | 130218 <input type="checkbox"/> | 115765 <input type="checkbox"/> |
| <input type="checkbox"/> | MB157-plnd20EBF1-10dox | Zhou et al., 2022 | 774,486,022 | 1 | SMC1A | 120549 <input type="checkbox"/> | 106894 <input type="checkbox"/> |
| <input type="checkbox"/> | CD4 Naive 1815-RH-1 (All Donors) | Chandra et al., 2021 | 2,125,336,641 | 1 | H3K27ac | 119199 <input type="checkbox"/> | 23013 <input type="checkbox"/> |
| <input type="checkbox"/> | MB157-plnd20TCF1-10dox | Zhou et al., 2022 | 732,911,273 | 1 | SMC1A | 106533 <input type="checkbox"/> | 97695 <input type="checkbox"/> |
| <input type="checkbox"/> | Wei-22RV1 | Wei et al., 2023 | 178,763,153 | 1 | CTCF | 99754 <input type="checkbox"/> | 44291 <input type="checkbox"/> |

Show entries

Previous 2 3 4 5 ... 105 Next

Navigation buttons for the WashU Browser



Meta data for each track including resolution, method and pulldown

Two gene tracks. One derived from the MANE selection and the other from GENCODE v30

Understanding the Single Sample Page

Standard Sample Name



Study & General Information



Links to download interaction level data



Table for FC Loops and links to download the raw loop files



Table for FH Loops and links to download the raw loop files



Table for HiCCUPS Loops and links to download the raw loop files



Table for CHIP-seq Peaks and links to download the raw peak files



Table for FH Peaks and links to download the raw peak files



Wei-22RV1.GSE200165.Homo_Sapiens.CTCF.biorep_merged

Study name: Wei et al., 2023
 Organism: Homo sapiens
 ChIP Pulldown: CTCF
 GEO ID: [GSE200165](#)
 GSM ID(s): [GSM6856446](#), [GSM6856447](#)
 Number of Read Pairs: 375,335,640

Interactions

| File Type | Download Link |
|------------|----------------------|
| validPairs | Link |
| hic | Link |
| cool | Link |

FC Loops

| Loop Merging | Stringency | Resolution | Number of Loops | QC Flag | Download Link |
|--------------|------------|------------|-----------------|---------|-----------------------|
| Unfiltered | Strict | 5000 | 214603 | Good | Link |
| Unfiltered | Strict | 10000 | 275621 | Good | Link |
| Unfiltered | Strict | 25000 | 299711 | Good | Link |
| Unfiltered | Loose | 5000 | 552545 | Good | Currently Unavailable |
| Unfiltered | Loose | 10000 | 621197 | Good | Currently Unavailable |
| Unfiltered | Loose | 25000 | 523471 | Good | Currently Unavailable |

FH Loops

| Loop Merging | Stringency | Resolution | Number of Loops | QC Flag | Download Link |
|--------------|------------|------------|-----------------|---------|-----------------------|
| Unfiltered | Strict | 5000 | 116360 | Good | Link |
| Unfiltered | Strict | 10000 | 171750 | Good | Link |
| Unfiltered | Strict | 25000 | 210113 | Good | Link |
| Unfiltered | Loose | 5000 | 438940 | Good | Currently Unavailable |
| Unfiltered | Loose | 10000 | 522934 | Good | Currently Unavailable |
| Unfiltered | Loose | 25000 | 463790 | Good | Currently Unavailable |

HICCUPS Loops

| Resolution | Number of Loops | QC Flag | Download Link |
|------------|-----------------|---------|-----------------------|
| 5000 | 16735 | Good | Currently Unavailable |
| 10000 | 17714 | Good | Currently Unavailable |
| 25000 | 18074 | Good | Currently Unavailable |

ChIP-seq Peaks

| Number of Peaks | QC Flag | Download Link |
|-----------------|---------|-----------------------|
| 147535 | TBD | Currently Unavailable |

FH Peaks

| Number of Peaks | QC Flag | Download Link |
|-----------------|---------|-----------------------|
| 80282 | TBD | Currently Unavailable |

Basic Single Sample Page

cytoscapeJS powered network



Enhancer-Promoter Network for FC Loops at 5kb

Recenter Network

Center on Node:
Gene Name or Anchor ID

Community Detection Results

Showing 1 to 10 of 34,009 entries

| Gene Name | Chrom | Anchor | Community | Community CRank | Community Nodes | Community Edges | Subcommunity | Subcommunity CRank |
|-----------|-------|--------------------------|-----------|-----------------|-----------------|-----------------|--------------|--------------------|
| 5S_rRNA | chr1 | chr1-182940000-182945000 | comm15 | 1 | 134 | 184 | Subcmt5 | 0.770657 |
| 5S_rRNA | chr16 | chr16-47445000-47450000 | comm4 | 0.598417 | 125 | 182 | Subcmt2 | 0.882296 |
| 5S_rRNA | chr19 | chr19-7885000-7890000 | comm30 | 1 | 47 | 81 | Subcmt3 | 1 |
| 5S_rRNA | chr7 | chr7-152590000-152595000 | comm52 | 1 | 63 | 84 | Subcmt2 | 0.823443 |
| 7SK | chr6 | chr6-52990000-52995000 | comm80 | 0.368615 | 46 | 93 | Subcmt2 | 1 |
| A2M-AS1 | chr12 | chr12-9060000-9065000 | comm26 | 0.692129 | 88 | 128 | Subcmt1 | 0.823443 |
| A2ML1 | chr12 | chr12-8820000-8825000 | comm90 | 0.211318 | 35 | 57 | Subcmt2 | 0.806095 |
| A2ML1-AS1 | chr12 | chr12-8825000-8830000 | comm90 | 0.211318 | 35 | 57 | Subcmt1 | 1 |
| A2ML1-AS2 | chr12 | chr12-8815000-8820000 | comm90 | 0.211318 | 35 | 57 | Subcmt1 | 1 |
| A2MP1 | chr12 | chr12-9270000-9275000 | comm26 | 0.692129 | 88 | 128 | Subcmt3 | 0.823443 |

Show 10 entries

Previous 1 2 3 4 5 ... 3,401 Next

Reset Table Filter

Community Detection Filters

Chromosome(s)

Community CRank Score Max: 1

Subcommunity CRank Score Max: 1

Table of community detection results



Filtering buttons for table above



Single Sample Pages with the Community Detection Module

Accessing SGL Results



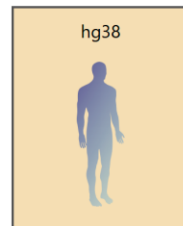
Welcome to the Loop Catalog

The Loop Catalog is a database of curated high-resolution HiChIP data from published work. Our dataset includes 763 human samples processed with hg38 and 281 mouse samples processed with mm10. In addition, it also contains 44 high-resolution HiC samples from the 4D Nucleome for auxiliary purposes. As development continues, our goal is to include various other analysis tools developed in lab and enhance various types of research such as variant prioritization.

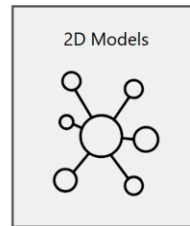
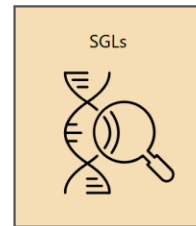
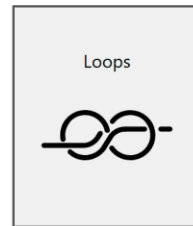
First time to the Loop Catalog? Come visit our video tutorial: [link](#)

This website is free and open to all users and login is not required.

Select Reference Genome i



Select Analysis i



GO

Get Help

Tutorial
FAQs
Contact Us

Dataset

Docs
Latest Build: 0.1

Publications

bioRxiv 2024

La Jolla
Institute
FOR IMMUNOLOGY

Life
Without
Disease.[®]

**Access via the main
page**

Alternatively, access from the Navigation Bar after a previous query

Tools → GWAS SGLs

The screenshot displays the Loop Catalog interface. At the top is a blue header with the 'Loop Catalog' logo. Below it is a dark navigation bar with links for 'Loop Catalog', 'Loops', 'Tools', 'Docs', 'Team', 'News', and 'Tutorial'. The 'Tools' link is highlighted with a red box, and a red arrow points to it from the text 'Tools → GWAS SGLs' above. A dropdown menu is open under 'Tools', listing 'GWAS SGLs', 'eQTL SGLs', 'Motifs', '2D Embeddings', and 'Statistics'. The 'GWAS SGLs' option is highlighted in blue. Below the navigation bar is the 'Data Explorer' section, which includes a 'Tools' toolbar with icons for a hand, a list, a search, and a plus sign, and a 'Metadata' button. A ruler at the bottom shows genomic coordinates from 22100K to 22900K on chromosome 10, with gene models for ELA3B, CELA3A, CDC42, WNT4, ZBTB40, EPHA8, C1QA, C1QC, C1QB, EPHB2, and LACTBL1. A status bar at the bottom right indicates 'Viewing a 1.0 Mb region in 1275px, 1 pixel spans 785 bp'.

Disease [i](#)

- Arthritis, Rheumatoid
- Dermatitis, Atopic
- Diabetes Mellitus, Type 1
- Psoriasis

Locus [i](#)

Locus:

Slop:

Samples [i](#)

- Toggle select none/all
- CD4_Naive_1800-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
- CD4_Naive_1814-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
- CD4_Naive_1815-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
- CD4_Naive_1815-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b2
- CD4_Naive_1816-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
- CD4_Naive_1829-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
- CD4_Naive_1829-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b2
- CD4_Naive_1831-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
- CD4_Naive_1831-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b2
- CD4_Naive_1831-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b2

Query

Example

Get Help

[Tutorial](#)
[FAQs](#)
[Contact Us](#)

Dataset

[Docs](#)
Latest Build: 0.1

Publications

[bioRxiv 2024](#)

La Jolla Institute
FOR IMMUNOLOGY

Life Without Disease.[®]



Select disease



Select locus



Select samples

SGL Analysis for Arthritis, Rheumatoid

Tools: Viewing a 303.8 Kb region in 1385px, 1 pixel spans 219 bp

Locus

Step: +/- slop for chr:pos (default=100)

SGLs Derived from FitHiChIP with ChIP-seq Peaks (FC Loops)

Showing 1 to 10 of 42 entries

| rsID | Chrom | SNP BP | SNP FINEMAP PPA | Gene Name | Anchor1 | Anchor2 | Distance | Loop log(Q) | Sample | GWAS Study (Causal DB) |
|---------------------------|-------|--|-----------------|----------------------------|--------------------------|--------------------------|----------|-------------|-----------------------------------|------------------------|
| rs2230926 | chr6 | <input type="text" value="137874929"/> | 0.0687607 | AL356234.1 | chr6:137705000-137710000 | chr6:137870000-137875000 | 165000 | 3.24 | CD4_Naive_1814-RH-1.phs001703v... | Okada Y - PH378 |
| rs2230926 | chr6 | <input type="text" value="137874929"/> | 0.0687607 | AL356234.1 | chr6:137705000-137710000 | chr6:137870000-137875000 | 165000 | 9.43 | CD4_Naive_1800-RH-1.phs001703v... | Okada Y - PH378 |
| rs5029928 | chr6 | <input type="text" value="137868805"/> | 0.00604524 | HECA | chr6:137865000-137870000 | chr6:139135000-139140000 | 1270000 | 7.09 | CD4_Naive_1800-RH-1.phs001703v... | Okada Y - PH378 |
| rs5029928 | chr6 | <input type="text" value="137868805"/> | 0.00604524 | AL356234.1 | chr6:137705000-137710000 | chr6:137870000-137875000 | 160000 | 158.78 | CD4_Naive_1800-RH-1.phs001703v... | Okada Y - PH378 |
| rs5029928 | chr6 | <input type="text" value="137868805"/> | 0.00604524 | LINC02539 | chr6:137790000-137795000 | chr6:137865000-137870000 | 75000 | 10.68 | CD4_Naive_1815-RH-1.phs001703v... | Okada Y - PH378 |
| rs5029928 | chr6 | <input type="text" value="137868805"/> | 0.00604524 | RF00019 | chr6:137780000-137785000 | chr6:137865000-137870000 | 85000 | 4.42 | CD4_Naive_1814-RH-1.phs001703v... | Okada Y - PH378 |
| rs5029928 | chr6 | <input type="text" value="137868805"/> | 0.00604524 | HECA | chr6:137865000-137870000 | chr6:139135000-139140000 | 1270000 | 8.54 | CD4_Naive_1815-RH-1.phs001703v... | Okada Y - PH378 |
| rs5029928 | chr6 | <input type="text" value="137868805"/> | 0.00604524 | RF00019 | chr6:137780000-137785000 | chr6:137865000-137870000 | 85000 | 5.26 | CD4_Naive_1815-RH-1.phs001703v... | Okada Y - PH378 |
| rs5029928 | chr6 | <input type="text" value="137868805"/> | 0.00604524 | IFNGR1 | chr6:137215000-137220000 | chr6:137865000-137870000 | 650000 | 7.40 | CD4_Naive_1800-RH-1.phs001703v... | Okada Y - PH378 |
| rs5029928 | chr6 | <input type="text" value="137868805"/> | 0.00604524 | HECA | chr6:137865000-137870000 | chr6:139135000-139140000 | 1270000 | 2.38 | CD4_Naive_1814-RH-1.phs001703v... | Okada Y - PH378 |

Show 10 entries

Previous Next



WashU Browser



Re-select locus



Table of SGL results



SNP nav button

Anchor 1 Navigation

Anchor 2 Navigation

Loop Navigation

Showing 1 to 10 of 42 entries

Search:

| rsID | Chrom | SNP BP | SNP FINEMAP PPA | Gene Name | Anchor1 | Anchor2 | Distance | Loop -log(Q) | Sample | GWAS Study (CAUSAL DB) |
|---------------------------|-------|---------------------------|-----------------|----------------------------|--|--|-------------------------|--------------|-----------------------------------|------------------------|
| rs2230926 | chr6 | 137874929 | 0.0687607 | AL356234.1 | chr6:137705000-137710000 | chr6:137870000-137875000 | 165000 | 3.24 | CD4_Naive_1814-RH-1.phs001703v... | Okada Y - PH378 |
| rs2230926 | chr6 | 137874929 | 0.0687607 | AL356234.1 | chr6:137705000-137710000 | chr6:137870000-137875000 | 165000 | 9.43 | CD4_Naive_1800-RH-1.phs001703v... | Okada Y - PH378 |
| rs5029928 | chr6 | 137868805 | 0.00604524 | HECA | chr6:137865000-137870000 | chr6:139135000-139140000 | 1270000 | 7.09 | CD4_Naive_1800-RH-1.phs001703v... | Okada Y - PH378 |
| rs5029928 | chr6 | 137868805 | 0.00604524 | AL356234.1 | chr6:137705000-137710000 | chr6:137865000-137870000 | 160000 | 158.78 | CD4_Naive_1800-RH-1.phs001703v... | Okada Y - PH378 |
| rs5029928 | chr6 | 137868805 | 0.00604524 | LINC02539 | chr6:137790000-137795000 | chr6:137865000-137870000 | 75000 | 10.68 | CD4_Naive_1815-RH-1.phs001703v... | Okada Y - PH378 |
| rs5029928 | chr6 | 137868805 | 0.00604524 | RF00019 | chr6:137780000-137785000 | chr6:137865000-137870000 | 85000 | 4.42 | CD4_Naive_1814-RH-1.phs001703v... | Okada Y - PH378 |
| rs5029928 | chr6 | 137868805 | 0.00604524 | HECA | chr6:137865000-137870000 | chr6:139135000-139140000 | 1270000 | 8.54 | CD4_Naive_1815-RH-1.phs001703v... | Okada Y - PH378 |
| rs5029928 | chr6 | 137868805 | 0.00604524 | RF00019 | chr6:137780000-137785000 | chr6:137865000-137870000 | 85000 | 5.26 | CD4_Naive_1815-RH-1.phs001703v... | Okada Y - PH378 |
| rs5029928 | chr6 | 137868805 | 0.00604524 | IFNGR1 | chr6:137215000-137220000 | chr6:137865000-137870000 | 650000 | 7.40 | CD4_Naive_1800-RH-1.phs001703v... | Okada Y - PH378 |
| rs5029928 | chr6 | 137868805 | 0.00604524 | HECA | chr6:137865000-137870000 | chr6:139135000-139140000 | 1270000 | 2.38 | CD4_Naive_1814-RH-1.phs001703v... | Okada Y - PH378 |

Show entries

Previous Next

Each row represents an SGL

Anchor1 and **Anchor2** contain the bins corresponding to the left and right sides of a loop

Distance is measured as the start of Anchor2 minus the start of Anchor1

Loop -log₁₀(Q) stores the significance value derived from FitHiChIP)

GWAS Study (CAUSALdb) contains the publication authors followed by the CAUSALdb ID

Link to dbSNP

Link to OpenTargets

Accessing 2D Embeddings

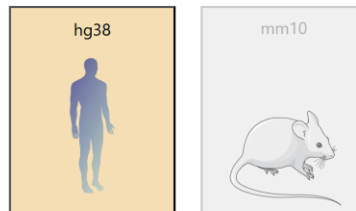
Welcome to the Loop Catalog

The Loop Catalog is a database of curated high-resolution HiChIP data from published work. Our dataset includes 763 human samples processed with hg38 and 281 mouse samples processed with mm10. In addition, it also contains 44 high-resolution HiC samples from the 4D Nucleome for auxiliary purposes. As development continues, our goal is to include various other analysis tools developed in lab and enhance various types of research such as variant prioritization.

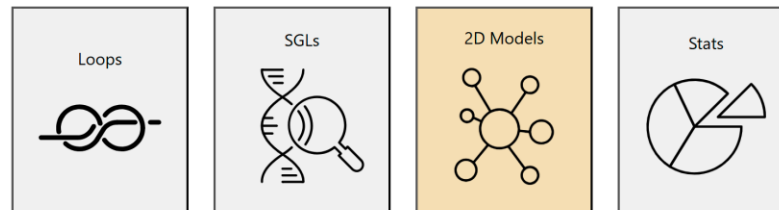
First time to the Loop Catalog? Come visit our video tutorial: [link](#)

This website is free and open to all users and login is not required.

Select Reference Genome



Select Analysis



GO

Get Help

Tutorial
FAQs
Contact Us

Dataset

Docs
Latest Build: 0.1

Publications

bioRxiv 2024

La Jolla
Institute
FOR IMMUNOLOGY

Life
Without
Disease.[®]

Alternative access:
Nav bar → Tools → 2D
Embeddings

Gene *i*

Gene:

Samples *i*

- Toggle select none/all
- Aortic-VIC.GSE154513.Homo_Sapiens.H3K27ac.b1
- CD4_Naive_1800-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
- CD4_Naive_1814-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
- CD4_Naive_1816-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
- CD8_Naive_1800-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
- CD8_Naive_1815-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
- CD8_Naive_1816-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
- CD8_Naive_1831-RH-1.phs001703v3p1.Homo_Sapiens.H3K27ac.b1
- COLO320-DM.GSE159985.Homo_Sapiens.H3K27ac.b1
- DMS1_MT.GSE180104.Homo_Sapiens.H3K27ac.b1

Query

Example

Select Gene

Select Samples

Get Help

Tutorial
FAQs
Contact Us

Dataset

Docs
Latest Build: 0.1

Publications

bioRxiv 2024

La Jolla
Institute
FOR IMMUNOLOGY

Life
Without
Disease.

2D embedding model

with overlap of *raw counts*
(sum of contacts for a given bin
within this subregion)

Quickly query a new
gene with the same
sample set

Select the
overlapping 1D signal

2D Models

Gene [i](#)

Gene:

1D Signal [i](#)

Raw Counts CHIP-seq

Std Sample Name: H9-HS.GSE105028.Homo_Sapiens.Rad21.b1

Gene ID | Gene Name | Signal Value | Significant Level

| | | | |
|-----------------|---------|------|----|
| ENSG00000171408 | PDE7B | 0.0 | ns |
| ENSG00000146410 | MTFR2 | 0.0 | LL |
| ENSG00000029363 | BCLAF1 | 0.0 | LL |
| ENSG00000135525 | MAP7 | 0.0 | LL |
| ENSG00000197442 | MAP3K5 | 0.38 | ns |
| ENSG00000112357 | PEX7 | 0.0 | LL |
| ENSG00000182747 | SLC35D3 | 0.0 | LL |
| ENSG0000016402 | IL20RA | 0.0 | LL |
| ENSG00000164485 | IL22RA2 | 0.0 | ns |
| ENSG00000027697 | IFNGR1 | 0.0 | LL |
| ENSG00000177468 | OLIG3 | 0.0 | LL |
| ENSG00000118503 | TNFAIP3 | 0.0 | LL |
| ENSG00000112378 | PERP | 0.0 | ns |
| ENSG00000254440 | PBOV1 | 0.0 | HL |
| ENSG00000112379 | ARFGEF3 | 0.0 | ns |
| ENSG00000262543 | SMIM28 | 0.0 | LL |
| ENSG00000051620 | HEBP2 | 0.0 | LL |

↑
Visualization of the 2D
embedding model

↙
Results table where each
row is a gene with its signal
value and (local Moran's)
significance level

2D embedding model with overlap of *ChIP-seq* signal

2D Models

Gene i

Gene: TNFAIP3 Query

1D Signal i

Raw Counts ChIP-seq

Std Sample Name: H9-HS.GSE105028.Homo_Sapiens.Rad21.b1

Colored based on ChIP-seq

Normalized ChIP-seq Levels

- 1.59, -1.28
- 1.28, -0.96
- 0.96, -0.64
- 0.64, -0.32
- 0.32, 0.00

TNFAIP3
start: 135.88 mb
end: 139.88 mb

| Gene ID | Gene Name | Signal Value | Significant Level |
|-----------------|-----------|--------------|-------------------|
| ENSG00000171408 | PDE7B | -1.09 | LH |
| ENSG00000146410 | MTFR2 | -1.28 | ns |
| ENSG00000029363 | BCLAF1 | -1.08 | ns |
| ENSG00000135525 | MAP7 | -1.12 | ns |
| ENSG00000197442 | MAP3K5 | -1.22 | ns |
| ENSG00000112357 | PEX7 | -1.15 | ns |
| ENSG00000182747 | SLC35D3 | -0.72 | ns |
| ENSG00000016402 | IL20RA | -1.13 | ns |
| ENSG00000164485 | IL22RA2 | -1.07 | ns |
| ENSG00000027697 | IFNGR1 | -1.25 | ns |
| ENSG00000177468 | OLIG3 | -0.62 | ns |
| ENSG00000118503 | TNFAIP3 | -0.85 | LL |
| ENSG00000112378 | PERP | -1.12 | ns |
| ENSG00000254440 | PBOV1 | -1.1 | ns |
| ENSG00000112379 | ARFGEF3 | -1.27 | LL |
| ENSG00000262543 | SMIM28 | -0.85 | ns |
| ENSG00000051620 | HEBP2 | -1.14 | ns |
| ENSG00000135510 | MAP3K4 | -0.92 | ns |



Same 2D structure



Results are now based on local
Moran's I using ChIP-seq signal
values

Other: Accessing Basic Statistics

Access Basic Statistics

Loop Catalog

Welcome to the Loop Catalog

The Loop Catalog is a database of curated high-resolution HiChIP data from published work. Our dataset includes 763 human samples processed with hg38 and 281 mouse samples processed with mm10. In addition, it also contains 44 high-resolution HiC samples from the 4D Nucleome for auxiliary purposes. As development continues, our goal is to include various other analysis tools developed in lab and enhance various types of research such as variant prioritization.

First time to the Loop Catalog? Come visit our video tutorial: [link](#)

This website is free and open to all users and login is not required.

Select Reference Genome

hg38 mm10

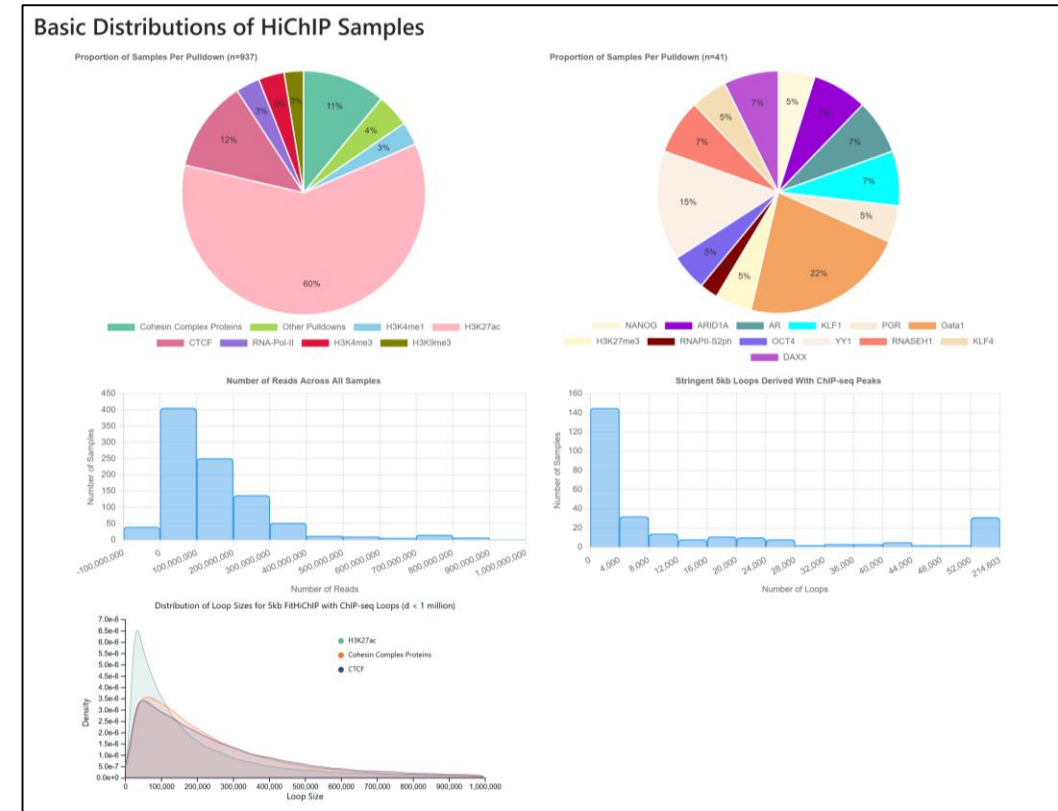
Select Analysis

Loops SGLs 2D Models Stats

GO

Get Help: Tutorial, FAQs, Contact Us
 Dataset: Docs, Latest Build: 0.1
 Publications: bioRxiv 2024
 La Jolla Institute FOR IMMUNOLOGY | Life Without Disease.

Select and GO!

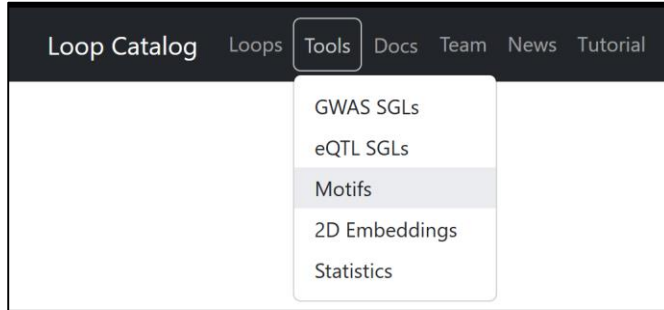


Breakdown of pulldowns, number of reads, number of loops and loop size

Alternative access:

Nav bar → Tools → Statistics

Accessing 1D Motif Results



Alternative access:
Nav bar → Tools → Motifs

Access from Tools

Results for each of the SEA analysis using different subsets of the High Confidence HiChIP Sample Set, this includes:

- 1) All samples
- 2) Immune only
- 3) Non-immune only
- 4) CTCF only

SEA Analysis with the High Confidence HiChIP Sample Set

For further information on how to interpret these results please access <https://meme-suite.org/meme/doc/sea-output-format.html>.
To get a copy of the MEME software please access <https://meme-suite.org>.

If you use SEA in your research, please cite the following paper:
Timothy L. Bailey and Charles E. Grant, "SEA: Simple Enrichment Analysis of motifs", *BioRxiv*, August 24, 2021. [\[full text\]](#)

[ENRICHED MOTIFS](#) | [INPUT FILES](#) | [PROGRAM INFORMATION](#) | [RESULTS IN TSV FORMAT](#) | [MATCHING SEQUENCES](#) | [MATCHING SITES](#)

ENRICHED MOTIFS

Found 382 motifs with E-values ≤ 10 .

| Logo | Database | ID | Alt ID | P-value | E-value | Q-value | TP | FP | Enrichment Ratio |
|------|-------------------------------|--------------------------|--------|-----------|-----------|-----------|--------------------|--------------------|------------------|
| | Jaspar CORE 2022 latest human | MA1713.1 | ZNF610 | 4.74e-127 | 3.44e-124 | 1.07e-124 | 978 / 1044 (93.7%) | 499 / 1035 (48.2%) | 1.94 |
| | Jaspar CORE 2022 latest human | MA1122.1 | TFDP1 | 1.23e-102 | 8.96e-100 | 1.40e-100 | 959 / 1044 (91.9%) | 526 / 1035 (50.8%) | 1.81 |
| | Jaspar CORE 2022 latest human | MA0506.1 | NRF1 | 5.07e-100 | 3.68e-97 | 3.83e-98 | 721 / 1044 (69.1%) | 243 / 1035 (23.5%) | 2.93 |