

The Innate Immune Database (IIDB) Quick Tutorial Guide

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Version 1.0

About IIDB

- The Innate Immune Database (IIDB) is a repository of genomic annotations and experimental data for over 2000 genes associated with immune response behavior in the mouse genome. A specific focus of IIDB is on Toll-like Receptor (TLR) genes, which are key components of innate immunity. As part of our research a customized Affymetrix gene chip was developed to generate and explore ChIP-chip binding data specific to TLR mouse genes. The selection of genes on the customized gene chip was based on the mouse assembly NCBI Build 33 and as such, the annotations in IIDB are by necessity mapped to this assembly.
- The annotations contained within IIDB are derived using data from over 100 microarray experiments, the NCBI and ENSEMBL annotation databases, computationally predicted transcription factor binding sites, co-expression clusters, predicted cis-regulatory modules, evolutionary conserved regulatory sequences, and sample ChIP-chip data. For each gene, we have analyzed the sequence from at least 20 kb upstream of the transcription start site to at least 10kb downstream of the transcription end site, including all exons and introns. Annotations for DNase hypersensitive sites, as well as exon/intron boundaries, CpG islands, repeats, Affymetrix GeneChip expression array probes (Mouse 320 2.0) are included in the database to facilitate analysis for users with ChIP-chip data.

Quick Facts

- The customized Affymetrix gene chip was developed upon sequence slices based around specific genes. Upon investigating these sequences it was found that the gene names and annotations defined by NCBI and ENSEMBL did not agree in all cases. Hence for each source of gene annotation, we include the genes that they respectively report within the specific gene sequences laid on the gene chip. IIDB users can choose which gene annotations they wish to use.
- The computational scans for putative transcription factor binding sites were undertaken using different levels of stringency, to reduce the reporting of false positive predictions. Each binding site matrix used in IIDB was assessed to determine the expectation that it would make a prediction with respect to a random background model. Three thresholds were used: 0.1 indicates the expectation of recording a prediction once in 1000 bases; 0.05 once in 2000 and 0.01 once in 10,000 bases (the most stringent).

IIDB Homepage

IIDB: Welcome Page - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

InnateImmunity-SystemsBiology.org | Aderem Group | Shmulevich Group ISB Home

Innate Immune Database (IIDB)

The development of IIDB is supported by a grant from the National Institute of Allergy and Infectious Disease (NIAID), a division of the National Institutes of Health (NIH).

<p>? Your Favorite Gene</p> <p>Search for a Gene</p> <p>Gene Aliases</p> <p>List of Annotated Genes</p> <p>? NCBI mm5 Version 33</p> <p>? ENSEMBL Version 29e</p>	<p>Computationally Predicted Co-regulated Genes</p> <p>? ISB Co-regulated Gene Clusters</p> <p>Annotated by: NCBI ENSEMBL</p> <p>? LPS Responsive Gene Clusters</p> <p>from Nilsson R et. al., Supplemental Data</p> <p>Annotated by: NCBI ENSEMBL</p>	<p>Advanced Analyses</p> <p>? Search for TFBS</p> <p>? Search Genes for Shared TFBS</p> <p>? Create Gene Groups by GO - Annotation</p> <p>? Get a Sequence File</p> <p>? Explore ChIP-chip Data: ATF3</p>
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[IIDB Home](#) [About IIDB](#) [How to Use IIDB](#) [IIDB Tutorial](#) [Site Map](#) [Questions/Contact](#)

Welcome to IIDB

The **Innate Immune Database (IIDB)** is a repository of genomic annotations and experimental data for over 2000 genes associated with **immune response behavior** in the **mouse genome**. A specific focus of IIDB is on **Toll-like Receptor (TLR)** genes, which are key components of innate immunity. As part of our research a customised Affymetrix gene chip was developed to generate and explore ChIP-chip binding data specific to TLR mouse genes. The selection of genes on the customised gene chip was based on the **mouse assembly NCBI Build 33** and as such, the annotations in IIDB are by necessity mapped to this assembly.

The annotations contained within IIDB are derived using data from over 100 microarray experiments, the NCBI and ENSEMBL annotation databases, computationally predicted transcription factor binding sites, co-expression clusters, predicted cis-regulatory modules, evolutionary conserved regulatory sequences, and sample ChIP-chip data. For each gene, we have analyzed the sequence from at least 20 kb upstream of the transcription start site to at least 10kb downstream of the transcription end site, including all exons and introns. Annotations for DNase hypersensitive sites, as well as exon/intron boundaries, CpG islands, repeats, Affymetrix geneChip probes are included in the database to facilitate analysis for users with ChIP-chip data.

IIDB offers users multiple, flexible ways to interrogate the database. Search results can be generated by analysing single genes for all available sources of annotations. Groups of co-expressed genes can also be analysed to determine, for example, whether these genes share common transcription factor binding sites. Search results are automatically annotated on the genomic DNA sequence and can be viewed using the [Argo genome browser](#) or saved to the user's own computer.

A Quick Guide to the Search Console

Single gene search

Searches on pre-computed clusters of genes

Interactive searches

The screenshot shows the Innate Immune Database (IIDB) search console. At the top, it displays the website name and navigation links. The main content area is divided into three columns. The left column has a 'Favorite Gene' section with a search box and a 'List of Annotated Genes' section with two entries: 'NCBI mm5 Version 33' and 'ENSEMBL Version 29e'. The middle column has a 'Computationally Predicted Co-regulated Genes' section with two sub-sections: 'ISB Co-regulated Gene Clusters' and 'LPS Responsive Gene Clusters'. The right column has an 'Advanced Analyses' section with several interactive search options. A navigation bar at the bottom contains links for 'IIDB Home', 'About IIDB', 'How to Use IIDB', 'IIDB Tutorial', 'Site Map', and 'Questions/Contact'. Red arrows point from text labels to specific features: 'Single gene search' points to the 'Search for a Gene' box; 'Searches on pre-computed clusters of genes' points to the 'ISB Co-regulated Gene Clusters' and 'LPS Responsive Gene Clusters' sections; 'Interactive searches' points to the 'Advanced Analyses' section; 'Lists of analyzed genes' points to the 'List of Annotated Genes' section; 'Homepage' points to the 'IIDB Home' link; 'On-line guide' points to the 'How to Use IIDB' link; 'This tutorial' points to the 'IIDB Tutorial' link; and 'Pop-up help pages' points to the question mark icons in the search boxes.

Lists of analyzed genes

Homepage

On-line guide

This tutorial

Pop-up help pages

Walked-through Examples

1. How are genes named?
2. How can I see which genes are in the database?
3. How do I retrieve annotations for my favorite gene?
4. How do I search the co-regulated gene clusters?
5. Can I search using my own gene clusters?
6. Can I search a gene for specific transcription factor binding sites?
7. Can I download the gene sequences?
8. What are the quick tips to using the Argo genome browser?

1. How are genes named?

- Gene names have been assigned based on immunological-relevance
- A list of aliases and synonyms has also been curated

Innate Immune Database (IIDB)

The development of IIDB is supported by a grant from the National Institute of Allergy and Infectious Disease (NIAID), a division of the National Institutes of Health (NIH).

Your Favorite Gene
Search for a Gene
Gene Aliases

List of Annotated Genes
NCBI mm5 Version 33
ENSEMBL Version 29e

Computationally Predicted Co-regulated Genes
ISB Co-regulated Gene Clusters
Annotated by: NCBI | ENSEMBL
LPS Responsive Gene Clusters
from Nilsson R et al., Supplemental Data
Annotated by: NCBI | ENSEMBL

Advanced Analyses
Search for TFBS
Search Genes for Shared TFBS
Create Gene Groups by GO - Annotation
Get a Sequence File
Explore ChIP-chip Data: ATF3

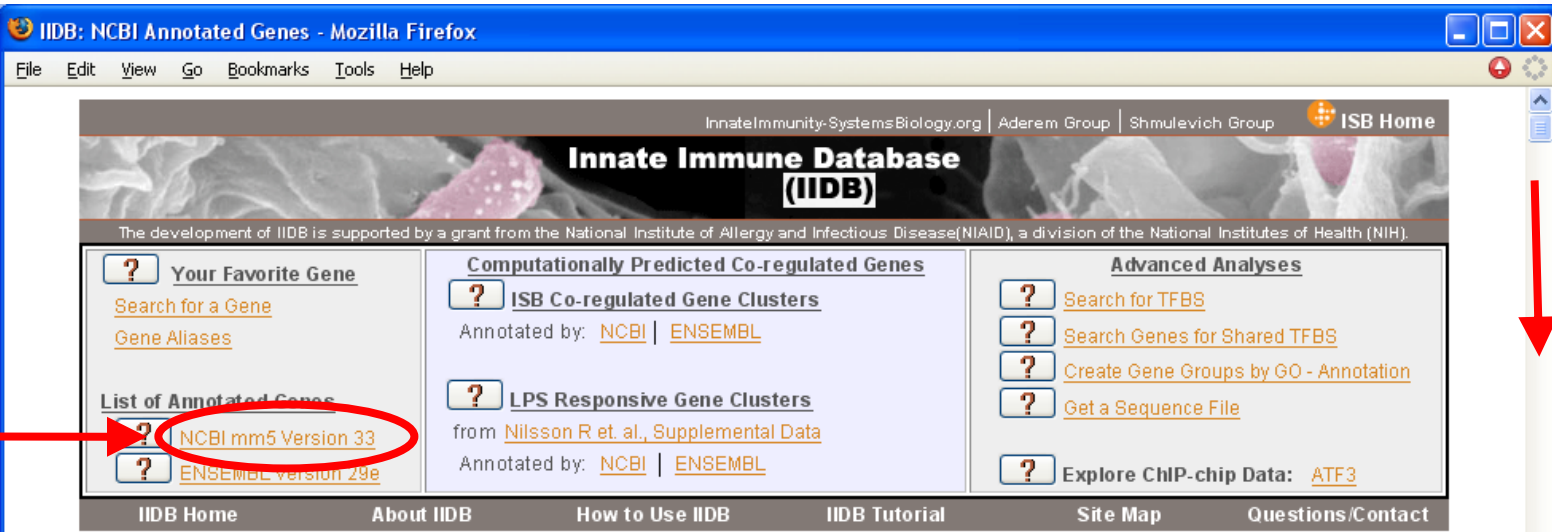
Gene Aliases

The common name of a gene is displayed as **[CommonName]**.
Use the Ctrl+F function of your browser to search for a gene name and aliases.

[0610009M14RIK] 0610009M14RIK NP_112197.1 THG-1 THG-1PIT TILZ2 Thg-1 pit Tilz2	[0610039A15RIK] EST AI225901 0610039A15RIK LOC55831 AW260416	[1110007A13RIK] 1110007A13RIK C10ORF119 FLJ13081 MGC36596 cDNA sequence BC025841	[1110007C24RIK] 9230118A01RIK 1110007C24RIK FLJ10747 9230118A01RIK
[1110007F12RIK] 1110007F12RIK FLJ11000 NP_060765.1	[1110033F14RIK] 1110033F14RIK	[1110054O05RIK] 1110054O05RIK C9ORF80 HSPC043 HSPC043 protein	[1110061O04RIK] 1110061O04RIK FLJ22405 FLJ90311
[1190002C06RIK] 1190002C06RIK	[1200009I06RIK] 1200009I06RIK	[1200014J11RIK] 1200014J11RIK	[1200015M12RIK] 1200015M12RIK

Links out to NCBI Entrez Gene data pages

2. How can I see which genes are in the database?



Use scroll bars to search

ENSEMBL annotations are also available

NCBI Annotated Genes

nce slices have been scanned with [TRANSFAC Matrices](#) and mapped with [collapsed matrix families](#).
 cl: indicates that the sequence has been analyzed for [TFBS clusters](#).
 ch: indicates that [ChIP-Chip](#) data is available for this sequence.
 con: indicates that [evolutionary conserved promoter](#) sequence is available for this sequence.
 dn: indicates that [DNase hypersensitive sites](#) data is available for this sequence.
 tes that microarray expression data from stimulated mouse macrophages is available for this sequence.

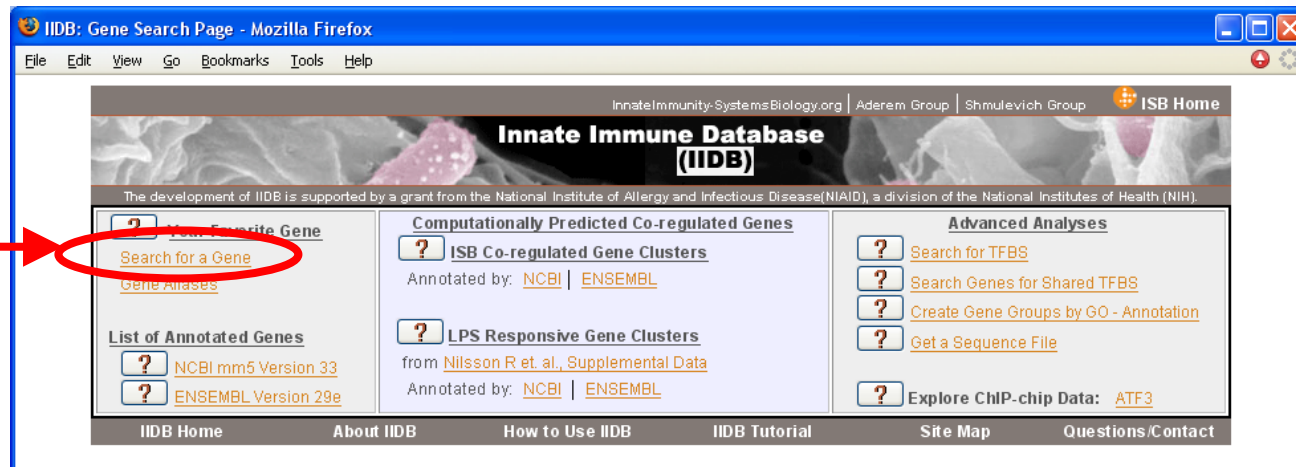
Available annotation data

Analyze Genes for Shared Transcription Factor Binding Sites

Analyze Genes for Transcription Factor Binding Site

Check for TFBS Analysis	GeneID	Chromosome Locus	Available Data	Analyze	Check for TFBS Analysis	GeneID	Chromosome Locus	Available Data	Analyze
<input type="checkbox"/>	0610007C21Rik NM_212470 381629	chr: 5 29442992 - 29496658	con,	Select Features Select TFs	<input type="checkbox"/>	0610010D20Rik NM_026152 67432	chr: 19 41315683 - 41458429	ch,	Select Features Select TFs
<input type="checkbox"/>	0610012D17Rik NM_025329 66061	chr: 16 32277480 - 32348500	ch, con,	Select Features Select TFs	<input type="checkbox"/>	0610038D11Rik NM_026306 67674	chr: 19 6614408 - 6655248	con,	Select Features Select TFs
<input type="checkbox"/>	0910001A06Rik NM_144846	chr: 15 64179208 -	ma	Select Features	<input type="checkbox"/>	1110001A07Rik NM_025377	chr: 11 86690923 -	con, ma	Select Features

3. How do I retrieve annotations for my favorite gene?



Enter your gene's
known identifier
e.g. IL12b or
a NM_ identifier



Select Gene Annotations from: NCBI ENSEMBL

Search by Gene Identifier:

Ex: gene name (IL12b), refseq (NM_008352), entrez geneID (16160), Eus Exon, NucleotideNameID, etc

Search by Chromosome location:

Ex: chr:11 44019798-44073744

Or define a gene
by chromosomal
location



You will be advised if your gene is NOT in the database

3. How do I retrieve annotations for my favorite gene?

Gene Annotation Selector Page

Gene	Chromosome	Locus	Strand	Exon Coord	Sequence Length
Name: II12B RefSeq: NM_008352 GeneID: 16160	chr:11	44019798 - 44073744	+	19999 - 33954	53946

Expression Profiles for: [R848](#) [PAM3](#) [CpG](#) [LPS](#) [All Stimuli](#)

Select Annotated and/or Computationally Generated Features to Display

Sequence Region	Annotated Features	Computational Features
5' Upstream 2000	<input type="radio"/> Check All <input type="radio"/> Reset <input checked="" type="checkbox"/> Exons/Introns <input type="checkbox"/> ChIP-chip Probes	<input type="radio"/> Check All <input type="radio"/> Reset <input type="checkbox"/> All Mouse TRANSFAC Matrices Percentile Threshold: <input type="radio"/> 0.1 <input type="radio"/> 0.05 <input checked="" type="radio"/> 0.01 Macrophage Specific Only: <input type="radio"/> Yes <input checked="" type="radio"/> No
3' Downstream 1000	<input type="checkbox"/> Verified TRANSFAC TF Sites <input type="checkbox"/> CpG Islands <input type="checkbox"/> Repeats <input type="checkbox"/> Affymetrix Mouse430_2 Probes	<input type="checkbox"/> Matrix Families Percentile Threshold: <input type="radio"/> 0.1 <input type="radio"/> 0.05 <input checked="" type="radio"/> 0.01 Macrophage Specific Only: <input type="radio"/> Yes <input checked="" type="radio"/> No <input type="checkbox"/> Matrix Cluster Percentile Threshold: <input type="radio"/> 0.1 <input type="radio"/> 0.05 <input checked="" type="radio"/> 0.01 Macrophage Specific Only: <input type="radio"/> Yes <input checked="" type="radio"/> No <input type="checkbox"/> Conserved Human/Dog/Mouse/Rat Promoter Regions <input type="checkbox"/> DNase Hypersensitive Sites ChIP-chip Segments

Check	TranscriptionFactor	Stimulus	Stimulation Time
<input type="checkbox"/>	ATF3	TGF-beta	100 240 60

Links to additional sources of biological data

Summary
Genomic regions, transcripts, and proteins
Genomic context
Bibliography
Interactions
Alleles
General gene information
General protein information
Reference Sequences
Related Sequences
Additional Links

Links
Order cDNA clone
Conserved Domains
Genome
GEO Profiles
Homologene
Map Viewer
Core/Nucleotide
Full text in PMC
Probe
Protein
SNP
PubMed
PubMed (GeneRIF)
SNP: Genotype
SNP: GeneView
Taxonomy
UniSTS
CCDS
Ensembl
Evidence Viewer
Gene Expression Database (GXD) at MGI
KEGG
MGC
MGI

All Stimuli Expression Profile for II12B == NM_008352

Normalized Expression Level

Time (min)

R848
PAM3
CpG
LPS

3. How do I retrieve annotations for my favorite gene?

Choose a sequence range in which to retrieve computational features. In this example, 2kb upstream and 1kb downstream of the gene

Select annotated features

Generate the results

Select computational features

I2DB: Advanced Search Page - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

Your Favorite Gene
Search for a Gene
Gene Aliases

List of Annotated Genes
NCBI mm5 Version 33
ENSEMBL Version 29e

Computationally Predicted Co-regulated Genes
ISB Co-regulated Gene Clusters
Annotated by: NCB1 | ENSEMBL
LPS Responsive Gene Clusters
from Nilsson R et al., Supplemental Data
Annotated by: NCB1 | ENSEMBL

Advanced Analyses
Search for TFBS
Search Genes for Shared TFBS
Create Gene Groups by GO - Annotation
Get a Sequence File
Explore ChIP-chip Data: ATF3

I2DB Home About I2DB How to Use I2DB I2DB Tutorial Site Map Questions/Contact

Gene Annotation Selector Page

Gene	Chromosome Locus	Strand	Exon Coord	Sequence Length
Name: II12E RefSeq: NM_008352 GeneID: 16160	chr:11 44019798 - 44073744	+	19999 -33954	53946

Expression Profiles for: [R848] [PAM3] [CpG] [LPS] [All Shmuk]

Select Annotated and/or Computationally Generated Features to Display

Sequence Region
5' Upstream: 2000
Include Coding Region: Yes No
3' Downstream: 1000

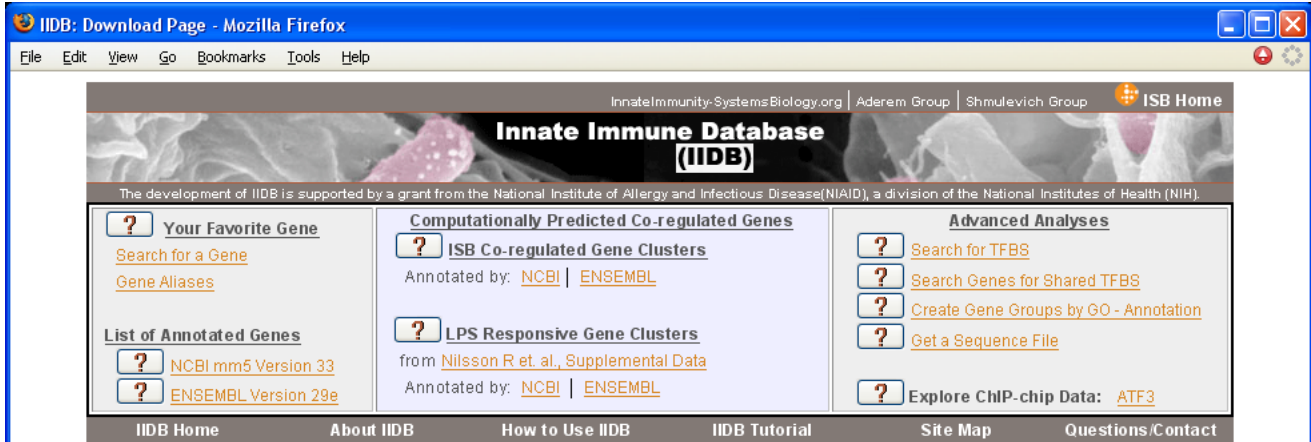
Annotated Features
 Check All
 Reset
 Exons/Introns
 ChIP-chip Probes
 Verified TRANSFAC TF Sites
 CpG Islands
 Repeats
 Affymatrix Mouse430_2 Probes

Computational Features
 Check All
 Reset
 All Mouse TRANSFAC Matrices
Percentile Threshold: 0.1 0.05 0.01
Macrophage Specific Only: Yes No
 Matrix Families
Percentile Threshold: 0.1 0.05 0.01
Macrophage Specific Only: Yes No
 Matrix Cluster
Percentile Threshold: 0.1 0.05 0.01
Macrophage Specific Only: Yes No
 Conserved Human/Dog/Mouse/Rat Promoter Regions
 DNase Hypersensitive Sites
ChIP-chip Segments

Check	TranscriptionFactor	Stimulus	Stimulation Time
<input type="checkbox"/>	ATF3	LPS	120, 240, 60,

Generate Results

3. How do I retrieve annotations for my favorite gene?



Chosen annotated features



Gene: Il12b

Annotated Features: Exon, isbProbe, transfacMatrix, CpG, Repeats, AffyFeatures,

Computationally Generated Features: all Matrix, collapsed Matrix, (threshold: 0.01) cluster, (threshold:) aligned Promoter, DNase,

No data for feature: transfacMatrix

No data for feature: CpG

No data for feature: DNase

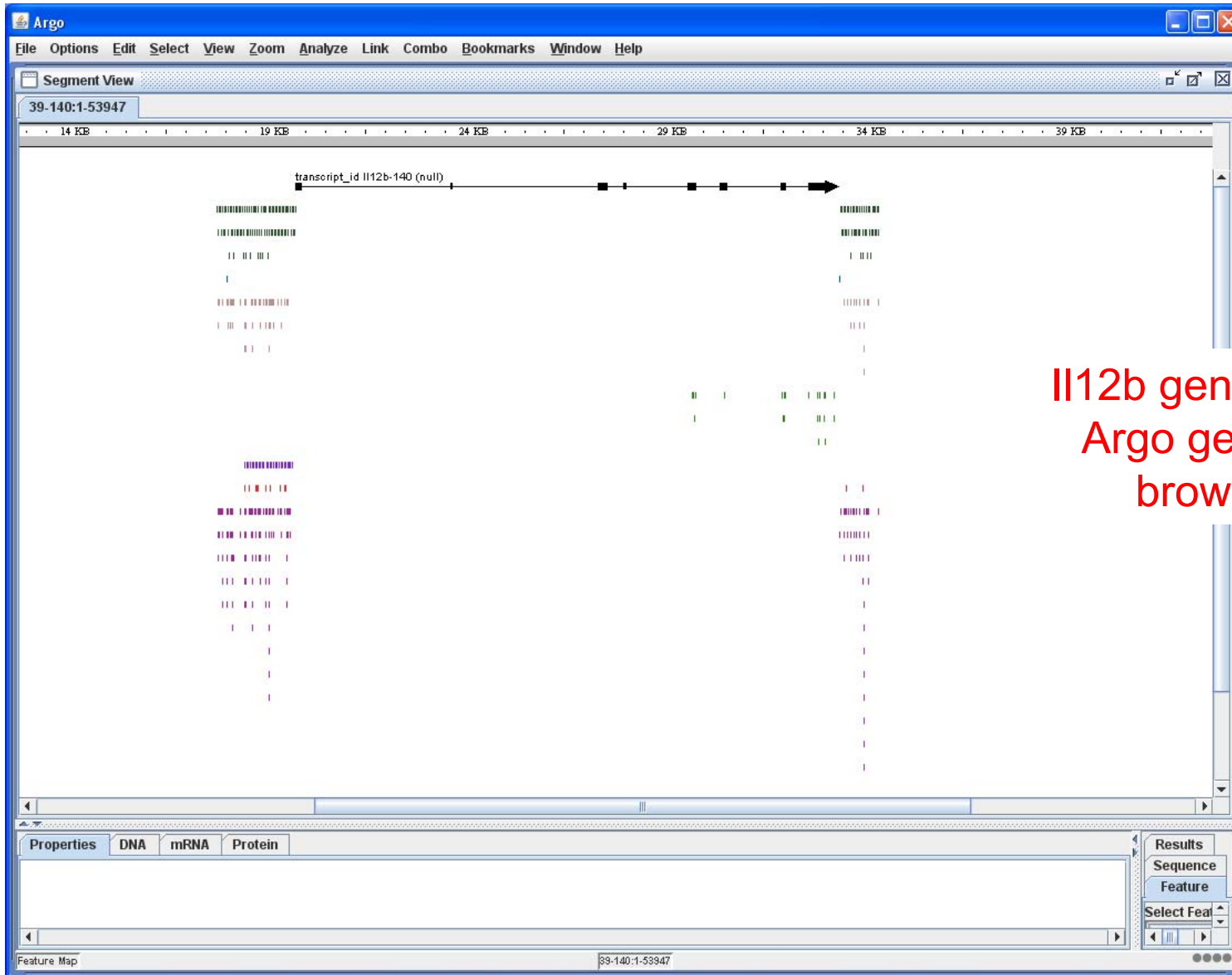
Available computational features



Download a zip file of gff files

Run the Argo genome browser

3. How do I retrieve annotations for my favorite gene?



II12b gene in the Argo genome browser

4. How do I search the co-regulated gene clusters?

The screenshot shows the IIBD website interface. A red arrow points from the 'ISB Co-regulated Gene Clusters' link in the 'Computationally Predicted Co-regulated Genes' section to the 'ISB Co-regulated Gene Clusters' link in the 'Advanced Analyses' section. Another red arrow points from the 'ISB Co-regulated Gene Clusters' link in the 'Advanced Analyses' section to the 'Analyze Individual Genes of this Group' link in the 'Genes up regulated by all Stimuli at mid and late time point' category.

This option goes to a similar search page as described in the previous example when searching for a single gene

ISB Co-regulated Gene Clusters Annotated Using NCBI

The screenshot displays four categories of gene clusters. The first category, 'Genes up regulated by Pam2, Pam3 at late time point', is highlighted with a yellow box. The second category, 'Genes up regulated by Poly-IC at late time point', is highlighted with a red box. The third category, 'Genes up regulated by all Stimuli at mid and late time point', is highlighted with a red box. The fourth category, 'Genes up regulated by all Stim at mid and down regulated at late time point', is highlighted with a red box. A red arrow points from the 'Analyze this Gene Group Further' button in the second category to the 'Analyze this Gene Group Further' button in the third category.

One group

Let's choose this group for simplicity and "Analyze this Gene Group Further"

NB: The LPS responsive gene cluster can be analyzed in the same way

4. How do I search the co-regulated gene clusters?

Not all genes
need be
selected

Uncheck Gene(s) to Eliminate Them From Subsequent TFBS Analysis

- Uncheck All
- Check All
- [2610018G03RIK chr.X\(43167325-43241106\)](#)
- [ABCA1 chr.4\(52267105-52424936\)](#)
- [BIRC4 chr.X\(34399610-34473791\)](#)

Analyze Genes for Transcription Factor Binding Sites

Analyze Genes for Shared Transcription Factor Binding Sites

Selected genes can now be analyzed for:

- ANY binding sites – (we'll do this next...)
- Binding sites that are SHARED by the genes

4. How do I search the co-regulated gene clusters?

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Your Favorite Gene
Search for a Gene
Gene Aliases

Computationally Predicted Co-regulated Genes
ISB Co-regulated Gene Clusters
Annotated by: [NCBI](#) | [ENSEMBL](#)
LPS Responsive Gene Clusters
from [Nilsson R et al., Supplemental Data](#)
Annotated by: [NCBI](#) | [ENSEMBL](#)

Advanced Analyses
[Search for TFBS](#)
[Search Genes for Shared TFBS](#)
[Create Gene Groups by GO-Annotation](#)
[Get a Sequence File](#)
[Explore ChIP-chip Data](#)

List of Annotated Genes
[NCBI mm5 Version 33](#)
[ENSEMBL Version 29e](#)

IIDB Home About IIDB How to Use IIDB IIDB Tutorial Site Map Questions/Contact

Search for binding sites within the gene cluster

Search a Gene for Transcription Factor Binding Sites

Transcription Factor	Matrix Threshold	Upstream Region	Selected Genes to be Analyzed
<ul style="list-style-type: none">ALLAhrAlx4ArArntArf3Bach1Bach2Bhlhb2Bhlhb3Cart1Cdx2	<ul style="list-style-type: none"><input checked="" type="radio"/> 0.01<input type="radio"/> 0.05<input type="radio"/> 0.1	<input type="text" value="2000"/>	<p>ABCA1 chr:4 (52267105-52424936) 2610018G03RIK chr:X (43167325-43241106) BIRC4 chr:X (34399610-34473791)</p>

- Show Repeats
- Show Matrix Clusters
- Show Conserved Sequences
- Show DNase Sites
- Show ChIP-chip Data
- ATF3

Genes selected on the previous page

Choose:

- Binding sites to search for
- A threshold value
- A common region upstream of the genes

SUBMIT

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List of Annotated Genes
[NCBI mm5 Version 33](#)
[ENSEMBL Version 29e](#)

IIDB Home About IIDB How to Use IIDB IIDB Tutorial Site Map Questions/Contact

Your Username: IIDBUser-PXMwHxGE
[Download Data Files](#)

[Run App](#)

4. How do I search the co-regulated gene clusters?

Innate Immune Database (IIDB)

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Your Favorite Gene
Search for a Gene
Gene Aliases

Computationally Predicted Co-regulated Genes
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Annotated by: [NCBI](#) | [ENSEMBL](#)

Advanced Analyses
Search for TFBS
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List of Annotated Genes
NCBI mm5 Version 33
ENSEMBL Version 29e

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Search for SHARED binding sites within the cluster

Search Genes for **Shared** Transcription Factor Binding Sites

Transcription Factor	Matrix Threshold	Upstream Region	Specify TF Window	Selected Genes to be Analyzed
ALL Ahr Alx4 Ar Amt Atf3 Bach1 Bach2 Bhlhb2 Bhlhb3 Cart1 Cdx2	<input checked="" type="radio"/> 0.01 <input type="radio"/> 0.05 <input type="radio"/> 0.1	<input type="text" value="2000"/>	<input type="text" value="500"/>	ABCA1 chr:4 (52267105-52424936) 2610018G03RIK chr:X (43167325-43241106) BIRC4 chr:X (34399610-34473791)

Choose other annotation data

- Show Repeats
- Show Matrix Clusters
- Show Conserved Sequences
- Show DNase Sites
- Show ChIP-chip Data
- ATF3

SUBMIT

Almost the same search as before except a value is specified within which binding sites must occur to be considered SHARED by the genes in the cluster

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Your Favorite Gene
Search for a Gene
Gene Aliases

Computationally Predicted Co-regulated Genes
ISB Co-regulated Gene Clusters
Annotated by: [NCBI](#) | [ENSEMBL](#)

Advanced Analyses
Search for TFBS
Search Genes for Shared TFBS
Create Gene Groups by GO-Annotation
Get a Sequence File
Explore ChIP-chip Data: [ATF3](#)

List of Annotated Genes
NCBI mm5 Version 33
ENSEMBL Version 29e

IIDB Home About IIDB How to Use IIDB IIDB Tutorial Site Map Questions/Contact

Your User Name: IIDBUser-PXMwHxGE
Download Data Files

4. How do I search the co-regulated gene clusters?

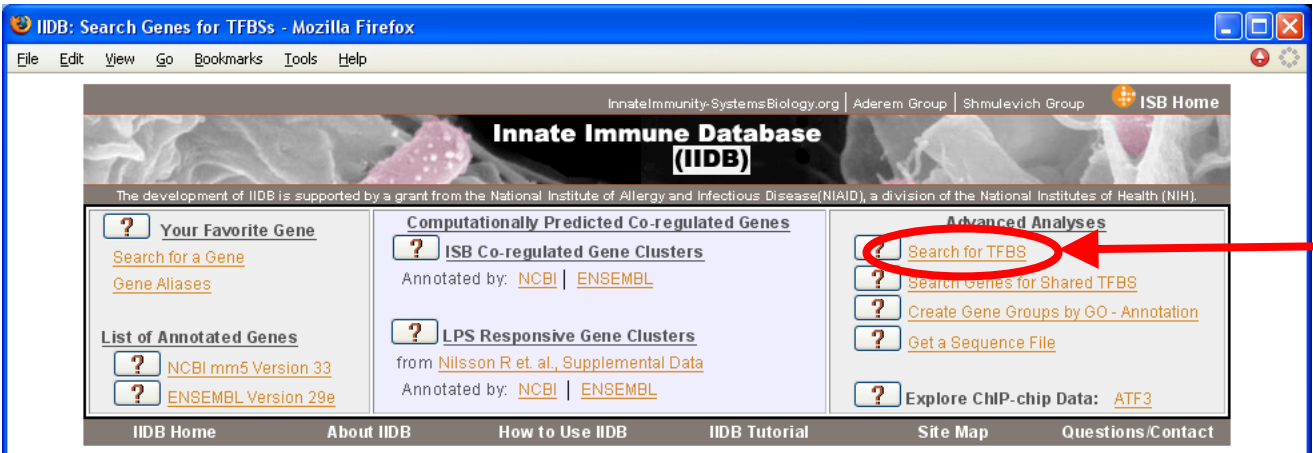
Gene cluster in the Argo genome browser

Reported
binding
sites

The screenshot displays the Argo genome browser interface. The main window shows a 'Segment View' for the region 'nn:1-60000'. The view includes a scale bar at the top with markers at 12 KB, 27 KB, 43 KB, and 58 KB. Below the scale bar, three transcripts are shown as horizontal bars with arrows indicating their orientation: 'transcript_id Abca1-Abca1 (null)', 'transcript_id 2610018G03Rik-2610018G03Rik (null)', and 'transcript_id Birc4-Birc4 (null)'. Red arrows point from the text 'Reported binding sites' to the top of the transcript bars, and from 'Coding regions of the genes are aligned' to the transcript bars themselves. The bottom of the window features a 'Properties' panel with fields for SEQUENCE, FILE, LOCATION, GENETIC_CODE, and EDITABLE?. To the right of the properties panel is a 'Feature' panel with tabs for 'Feature', 'Sequence', and 'Results', and a search interface with a 'Search' button.

Coding regions of the
genes are aligned

5. Can I search a gene for specific transcription factor binding sites?



Search a Gene for Transcription Factor Binding Sites

Transcription Factor	Matrix Threshold	Upstream Region	Gene to be Analyzed
<ul style="list-style-type: none">ALLAhrAlx4ArArntAtf3Bach1Bach2Bhlhb2Bhlhb3Cart1Cdx2	<ul style="list-style-type: none">0.010.050.1	<input type="text" value="2000"/>	Select Gene Annotations from: <input checked="" type="radio"/> NCBI <input type="radio"/> ENSEMBL Search by Gene Identifier: <input type="text" value="il12b"/> <small>Ex: gene name (IL12b), refseq (NM_008352), entrez geneID (16160), EhsExon, NucleotideNameID, etc</small> Search by Chromosome location: <input type="text"/> <small>Ex: chr:11 44019798-44073744</small>

Specify a gene

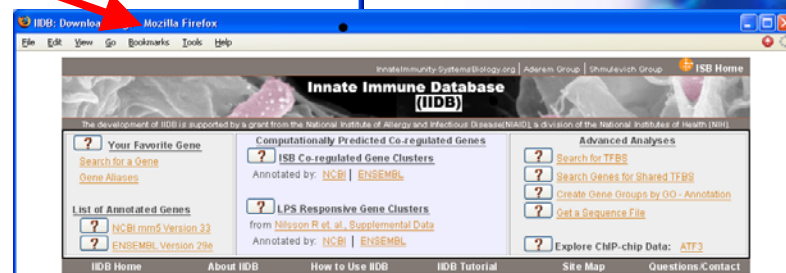
- Show Repeats
- Show Matrix Clusters
- Show Conserved Sequences
- Show DNase Sites
- Show ChIP-chip Data
- ATF3

SUBMIT

Use Ctrl-left mouse click to select a subset of specific factors to search for

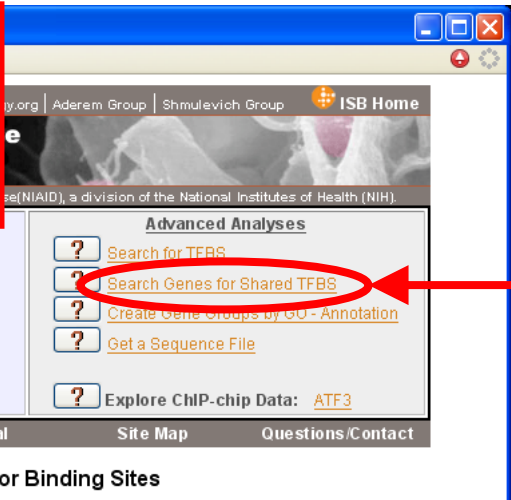
Choose parameters again

To download



6. Can I search using my own gene clusters?

In this example, we will search for shared binding sites in three genes we specify



Search Genes for Shared Transcription Factor Binding Sites

Transcription Factor	Matrix Threshold	Upstream Region	Specify TF Window	Gene to be Analyzed
<ul style="list-style-type: none">ALLAhrAlx4ArArntAtf3Bach1Bach2Bhlhb2Bhlhb3Cart1Cdx2	<input type="radio"/> 0.01 <input type="radio"/> 0.05 <input checked="" type="radio"/> 0.1	<input type="text" value="2000"/>	<input type="text" value="400"/>	Select Gene Annotations from: <input checked="" type="radio"/> NCBI <input type="radio"/> ENSEMBL Search by Gene Identifier: (Comma separated List of Genes) Ex: gene name (IL12b), refseq (NM_005483), chr: chr10(100), Exon, NucleotideID <input type="text" value="1112b, 1112a, 1115"/>

Specify a list of comma separated genes

Choose parameters again

Optionally choose other annotation data

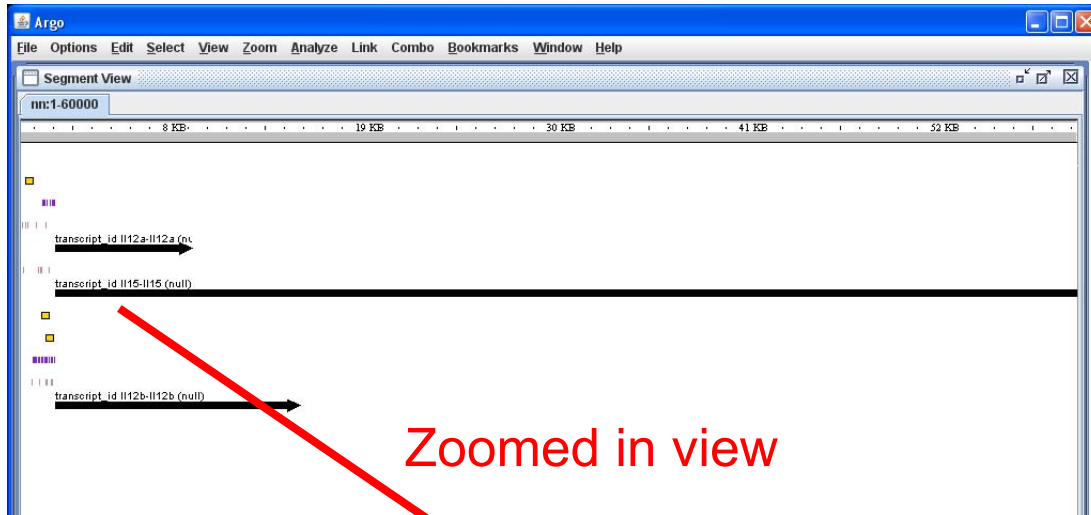
Show Repeats Show Matrix Clusters Show Conserved Sequences Show DNase Sites [Show CHIP-chip Data](#)

ATF3

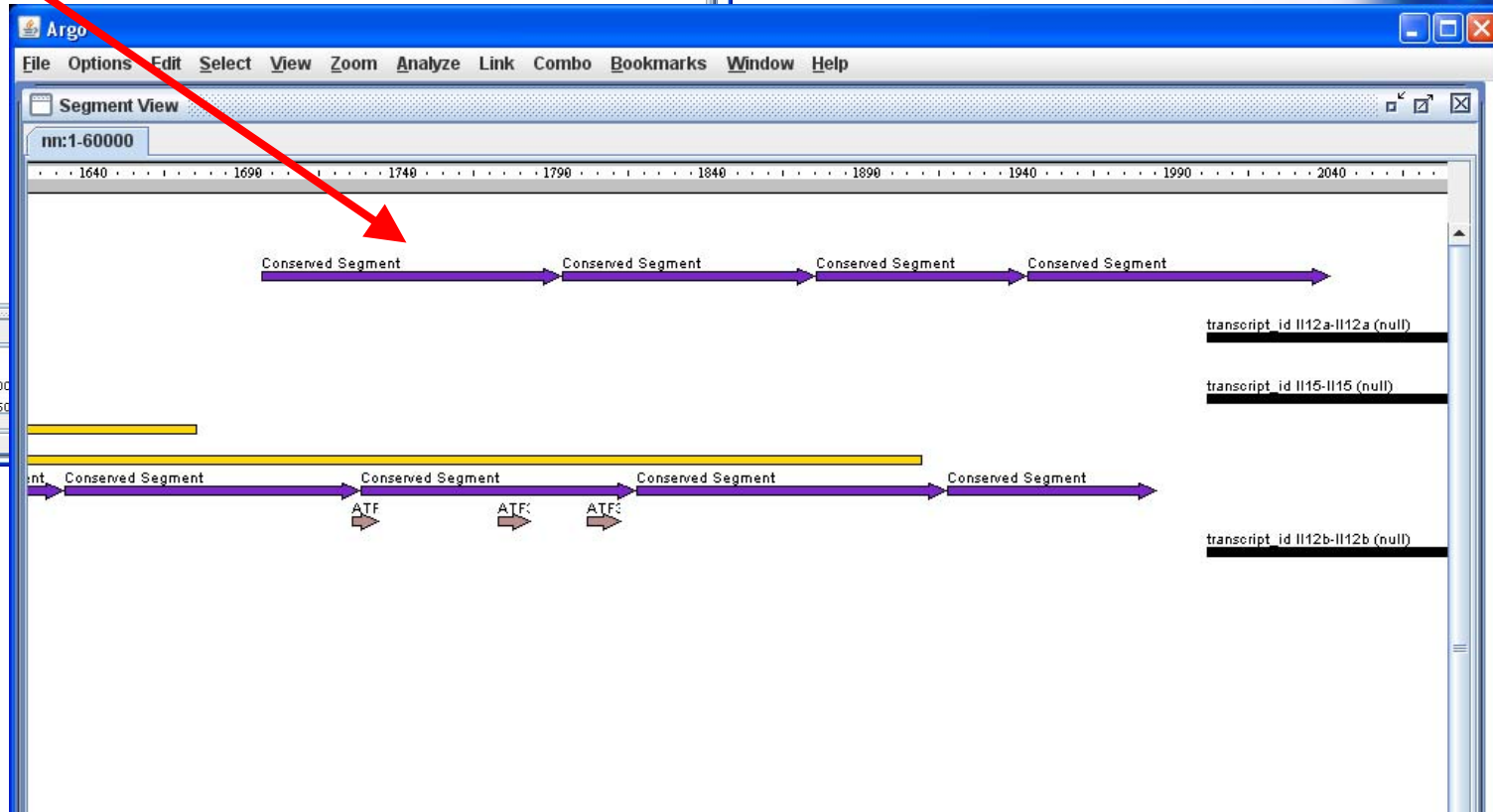
Or upload file (file format requirements)

File to Upload:

6. Can I search using my own gene clusters?



Zoomed in view



7. Can I download the gene sequences?

InnateImmunity:SystemsBiology.org | Aderem Group | Shmulevich Group | ISB Home

Innate Immune Database (IIDB)

The development of IIDB is supported by a grant from the National Institute of Allergy and Infectious Disease (NIAID), a division of the National Institutes of Health (NIH).

- Your Favorite Gene**
 - Search for a Gene
 - Gene Aliases
- Computationally Predicted Co-regulated Genes**
 - ISB Co-regulated Gene Clusters
 - Annotated by: [NCBI](#) | [ENSEMBL](#)
 - LPS Responsive Gene Clusters
 - from [Nilsson R et al., Supplemental Data](#)
 - Annotated by: [NCBI](#) | [ENSEMBL](#)
- Advanced Analyses**
 - Search for TFBS
 - Search Genes for Shared TFBS
 - Create Gene Groups by GO - Annotation
 - Get a Sequence File**
 - Explore ChIP-chip Data: [ATF3](#)

IIDB Home | About IIDB | How to Use IIDB | IIDB Tutorial | Site Map | Questions / Contact

Select Gene Annotations from: [NCBI](#) [ENSEMBL](#)

Search by Gene Identifier:

Ex: gene name (IL12b), refseq (NM_008352), entrez geneID (16160), BioExam, Nucleotide NameID, etc

Search by Chromosome location:

Ex: chr:11 44019798-44073744

InnateImmunity:SystemsBiology.org | Aderem Group | Shmulevich Group | ISB Home

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IIDB Home | About IIDB | How to Use IIDB | IIDB Tutorial | Site Map | Questions / Contact

Gene Name	RefSeq	GeneID	Chromosome Locus	Length	TxStart	TxEnd	Strand
IL12b	NM_008352	16160	chr.11 44019798-44073744	53947	19999	33954	+

```
>NM_008352
GTGTAAGTAAATGGGAGGTTAACTGAACTAAGAGATATGGAAAGCCATACAGAACTCCTGCCACATAAGCTAA
CTGCACGTATAATTACAAAGAAAGAAATGTTCAATGGAGGTGTCCTGAACATGTGGCTAATGGCTCCAGAAATCAA
TCTTTAAGTTAAAACGCCAAAGTCAGACATGAGATATTCCTTGTGAGTGTATGGCCATTGAAAGTCCCCATGTCCCAA
AATAATACAGTTTATGTTAATGGGGGTTTGTGTTGTAGTAGTGTAGTGTGTTGTTGTTGTTGTTGTTATGCCACCAA
ACCCAGACATAAAAACCATATTACTGAAGACATCAACCTGTTGTTGTTATGGGACATTAGGAAATCAAATCGAGCCAGCC
TGGAAACTCTTCCCTACTAGCTAGCTTTTATAGTCTGGGAGATGCTAGGAAGCTGGGGGTTGGGGAGACATAACA
TGACTGCAAGCCCTGCTAGTGAAGTGTGTGTGTGTCAGCTGGCCACTAGCATAGCTGTAACTGTTGTAGGCAACTGATC
ACTGTCTGATGGGCTTGAGGCCCAATCCACTGGAGGGGATTCATGCCTGGTGTGCAAACTGGTTGAAAAAATCAACAG
TGTAGAGGTCATAGGCCCTGATGTGGAAGCTAGTGTCTTGTATGTTAAATTTGATATGCTATGCTATGCTATGCTATCTT
AATGTTCTGGTATGCCAGAGATTAAGTGTGCCCTGGGGCTGGCTCAGAGAGGCTCTCTTCCAGTGAAGAACTGATT
ACTACATAAGCTCAGAGCTGGTCAGAGACTGAGAATAAGCCGCTGTTAGTCTCGGCTCAAAACAGACATCTGGCT
CACCCCTTCCAAGAAATTTTTATGGGGGATCCCTGCAAGCTCCACAGCCAGCAGAGGAGTGAGCCAAATGAGGCCAAA
GGAAAGTTGGGTTACACCACTTCCGTTAGCTAGTGTGTTGTTCAAACCTCTTTTTTTTCCAAGAGTTTATTTAGACATGT
TTAAGTACATTAACAGTCTTGGGAAAAGTTTCCTCATAAGAAATGATTTCAACCCCTTGTGCACAATAAAGCCCAAGAAAT
GACTGCATTAAAAACCTTTTTCGAAAGTGCACATGGCCCTTACCACGAAAGGTGGGCTGTGATGTTAAGGGCTTAGACTT
GGGGTAGCCTTCTTGTCTATGAAAGATAGCATAGAGGTTCCCAAGCTATAGAGTACCACCTTGTGACATCTCTGTAAAGTT
GGGTTCTATTGACTGAGAAAACAAAGCTAAGGATAAAAGTCTAGAGAGAGTCTGGAGTCAATGTCATGGTCTCCAGGATGA
GGGTGAGGCTTGGTCTAAGGATAACACAGATCACCAGGCTAATAAAGCCATCCACCCCAAGCTTGTGGTGGGAAACGG
GTATATACATCCCTCCATGAAAGAGACAAAGCCACGCTGCTTAACATTCATGTTTCCCTAGGGGTGCTCTGTGACCCACA
AAGACCTCATCCCTCTACATGTATCTACATATATGTACAGAAATAGATGTATTATAAGCACTCATGTGATTAAGCCAAAT
```

8. What are the quick tips to using the Argo genome browser?

Zoom in: +

Zoom out: -

The screenshot displays the Argo genome browser interface. At the top, a menu bar includes File, Options, Edit, Select, View, Zoom, Analyze, Link, Combo, Bookmarks, Window, and Help. Below the menu is a 'Segment View' window showing a genomic track for segment 39-140:1-53947. The track includes a scale from 19360 to 20760, a 'transcript_id III12b-140 (null)', and various annotations such as 'Cluster', 'Conserved Segment', 'ATF3-240', and 'PAX'. A yellow vertical bar highlights a specific region. Below the track is a 'Feature Map' window with tabs for Properties, DNA, mRNA, and Protein. The 'Properties' tab is active, showing details for a 'Conserved Segment' feature, including its location (+19343-19440 (98)), track (aligned Promoter), score (conserved), seqid (ConPromoterSeq), and type (AR, c-Ets-1(p54), E1k-1, PEA3). To the right of the feature map is a search interface with tabs for Feature, Sequence, and Results, and a 'Search' button.

Click on a feature to get more information

Use the slider to scroll along the sequence