HymenopteraMine Documentation

Release 1.0

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Sep 28, 2017

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HymenopteraMine is an integrative resource for genomic data on Hymenoptera, including honeybees, ants, wasps, etc.

Link to main site: http://hymenopteragenome.org/hymenopteramine

Link to HGD YouTube Channel with HymenopteraMine Videos: https://www.youtube.com/channel/UC1NVFd9buEtlbA2mcdq0MXQ

Link to PDF version of this documentation: https://media.readthedocs.org/pdf/hymenopteramine/stable/hymenopteramine.pdf

Link to the available datasets in HymenopteraMine: http://hymenopteragenome.org/hymenopteramine/dataCategories.do

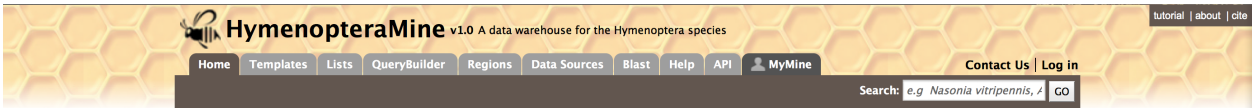
Contents:

CHAPTER 1

Welcome to HymenopteraMine

HymenopteraMine is powered by InterMine and provides a user-friendly way to access genomic, proteomic, interaction and literature data. HymenopteraMine is a part of the Hymenoptera Genome Database.

This tutorial is aimed at giving users an introduction to the different parts of HymenopteraMine and how users can make the most of HymenopteraMine.



Overview of HymenopteraMine

Before going into details, please go through this brief summary about the layout of HymenopteraMine.

Home – The home page for HymenopteraMine.

Templates – Shows the lists of templates that users can use based on the nature of their query.

Lists – Takes the user to a list page where they can upload their list of genes and perform enrichment analyses. Users, once logged in, can also save their lists for future use.

QueryBuilder – page where users can build custom queries by browsing the HymenopteraMine data model and customize their results. Users can also download the created query as XML.

Regions – a Genomic Region Search page where users can enter genomic coordinates and fetch features that fall within the interval. Users can also extend the interval to increase the range of search.

Data sources – a page where all the data sources, their links and the date of download is specified in a tabulated format.

Blast – a Blast page where users can BLAST their sequence(s) of interest with the Hymenoptera species reference genome, CDS sequences and protein sequences. *Help*- a page for guidance, when working through Hymenoptermine. *API* – a page where users can discover more about the InterMine API to programmatically access HymenopteraMine.

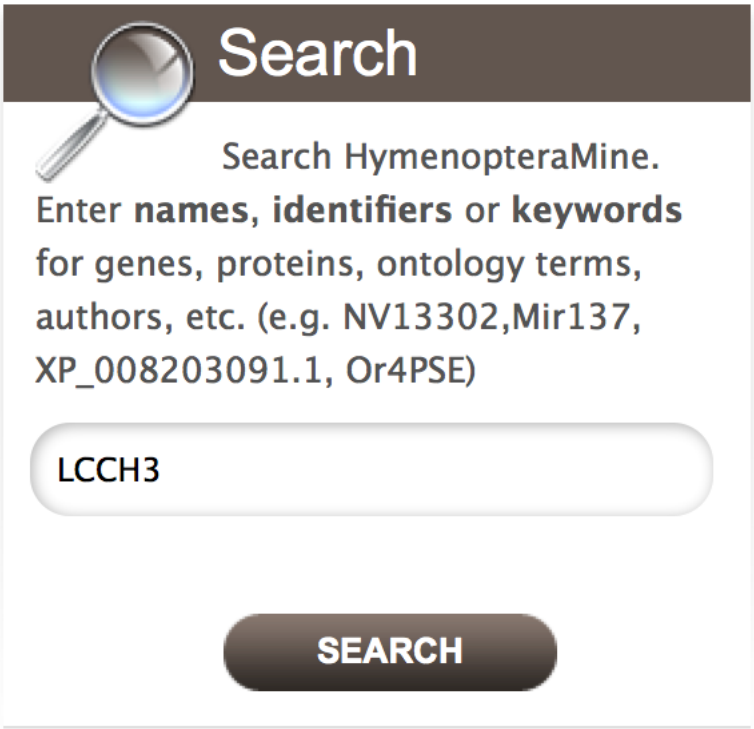
MyMine – Once users are logged in, MyMine serves as portal for accessing saved lists and saved templates. Users can also check their account details and manage their account using MyMine.

Searching in HymenopteraMine

There are several different ways for users to query HymenopteraMine.

'Quick-search'

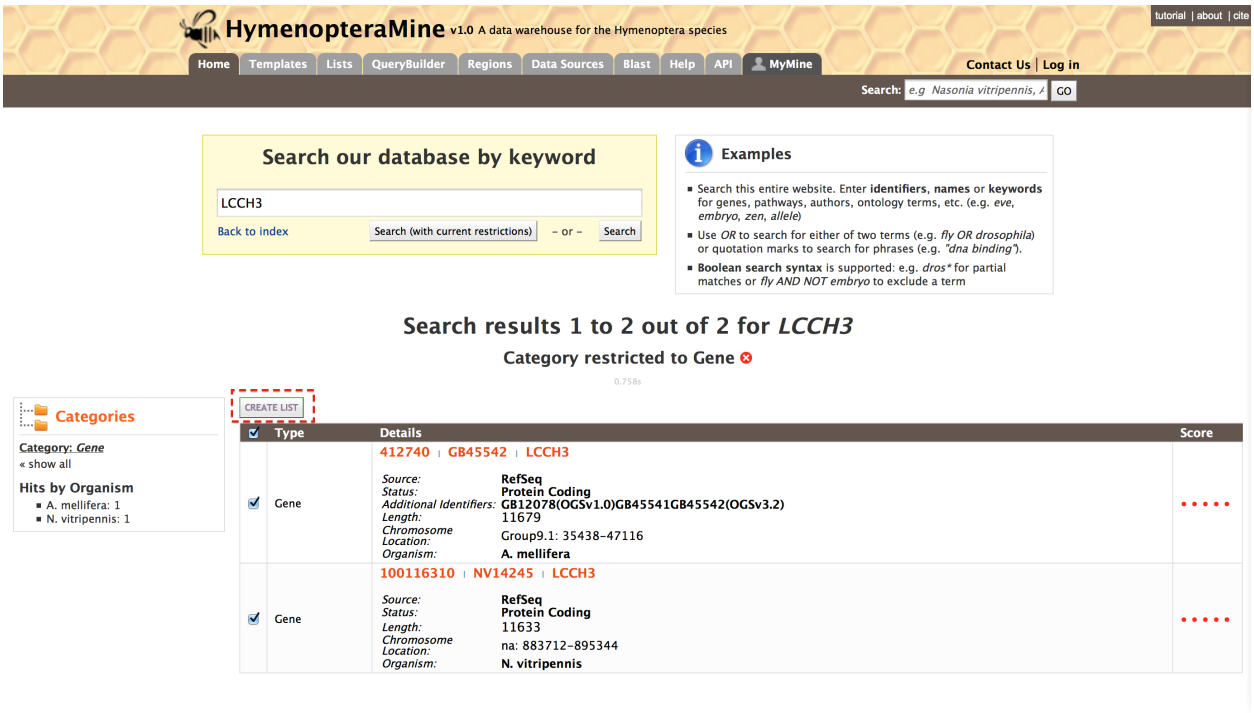
The 'Quick-search' enables users to search keywords from any of the datasets on HymenopteraMine. The quick-search box is on the main page and on the upper-right hand corner of each page





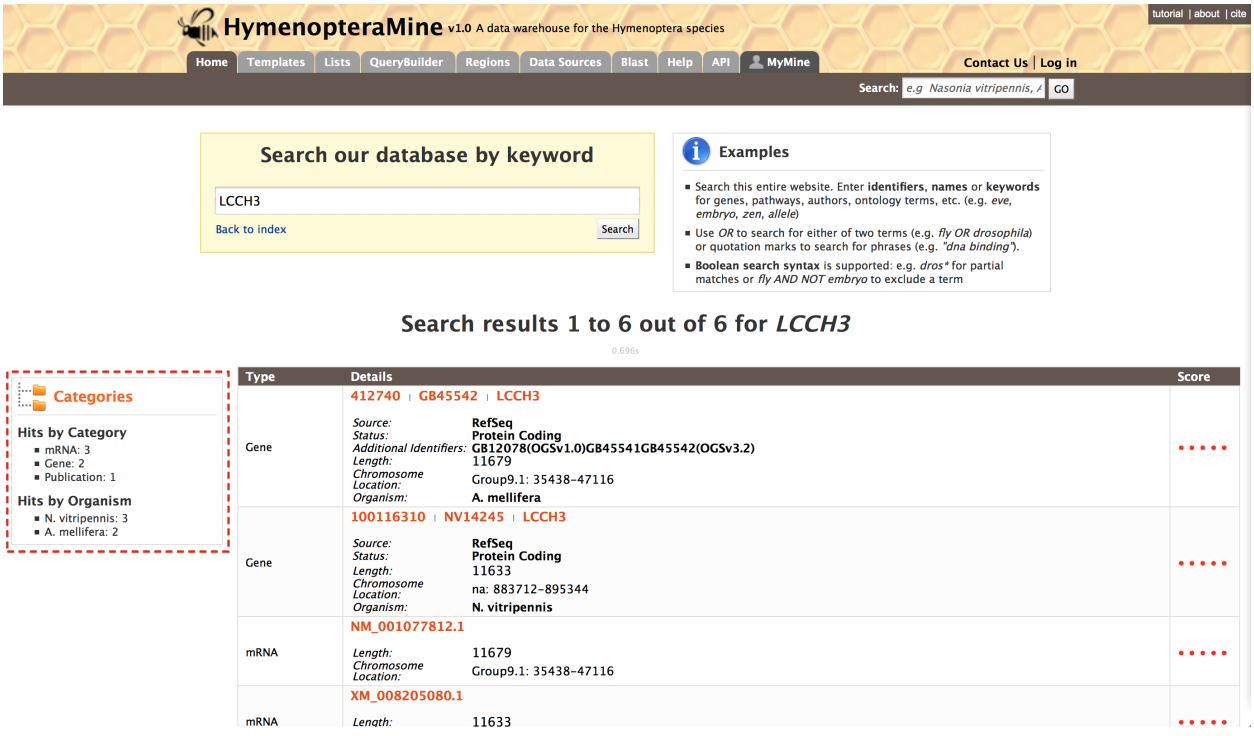
Users can input their gene name, gene identifiers or keywords and search HymenopteraMine. Users can make use of wildcard character '*' to get all results that matches their query.

Lets consider gene 'LCCH3' as an example. Enter 'LCCH3' in the search box and click 'Search'. The results page is tabulated and shows a summary about your query.



Users can filter the results based on 'Category' or 'Organism'. The score column in the result table indicates the similarity of your query to the result fetched by HymenopteraMine.

The results page can also be converted to a list. To enable this feature click on 'Gene' in 'Hits by Category', marked with a red box.

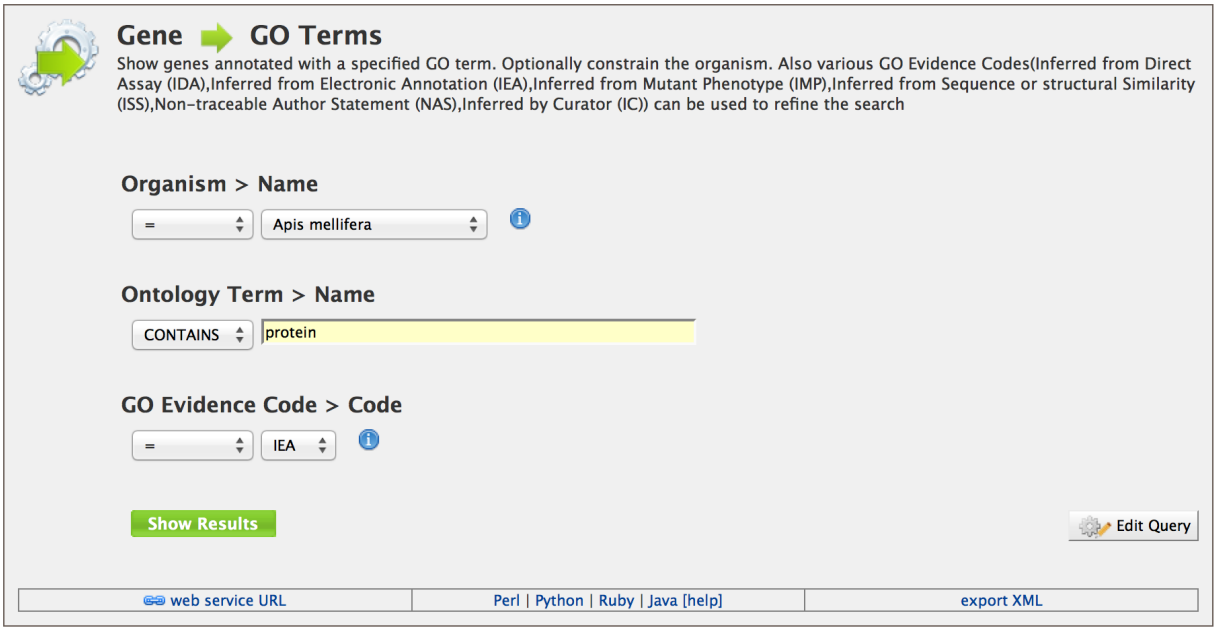


This will filter the results for the feature type 'Gene' and checkboxes will be available for users to select genes they would like to add to their list. Once the genes are selected, click on 'CREATE LIST'. List features described later.

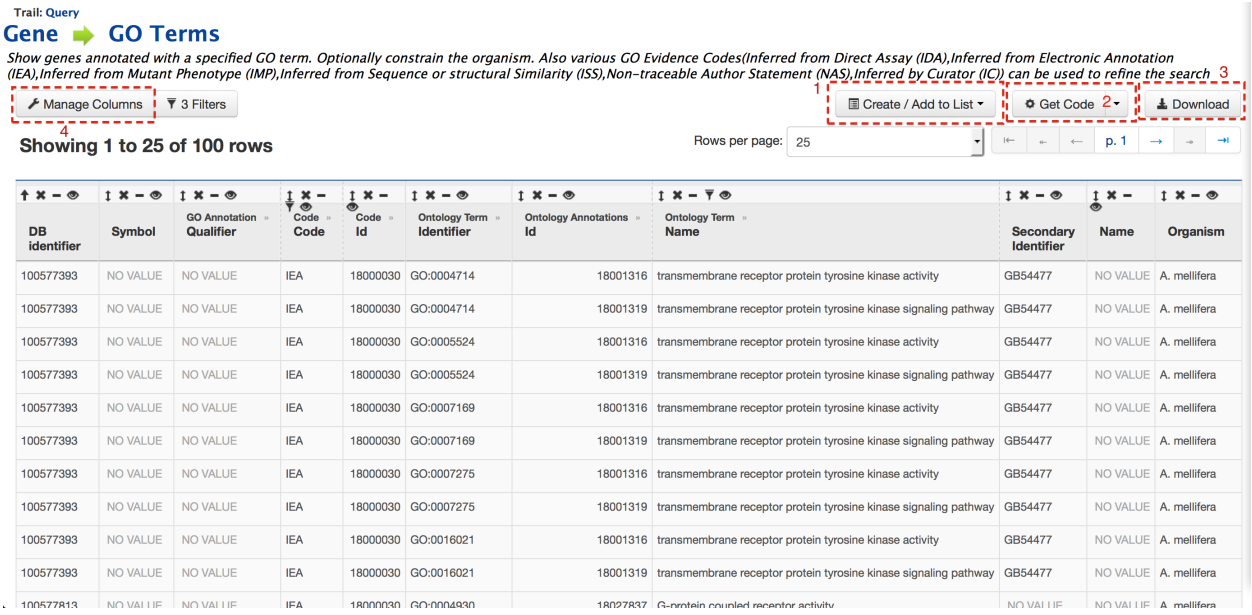
Templates

Apart from the search box, users can make use of predefined templates by clicking on the 'Templates' tab.

The Templates page provides users with a list of templates users can choose based on the nature of their query.



Users can also specify a filter for GO evidence code. Lets search for the GO term 'protein' with GO evidence code 'IEA'. Click on 'Show Results'.



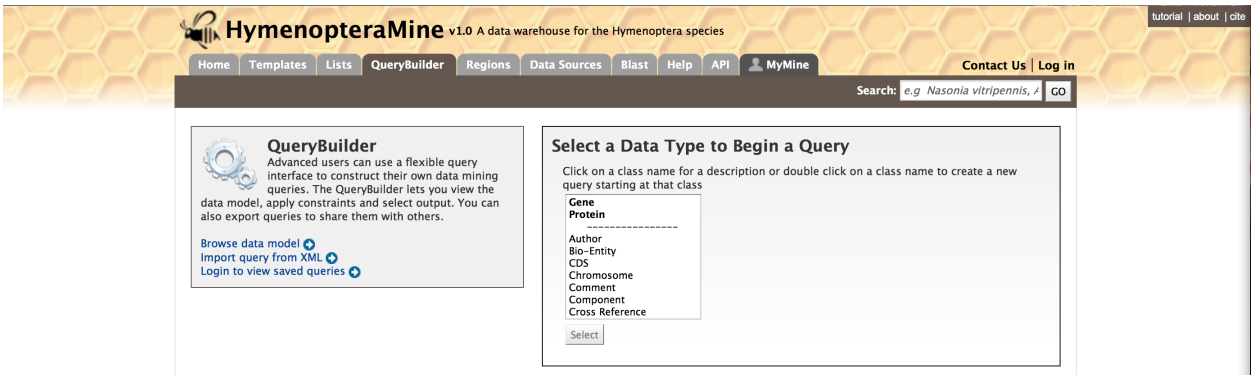
The result page shows all the genes having the Gene Ontology term 'protein' in their annotation. Users can create or add these genes to a list, by clicking on 'Create/Add to List' (Box 1) to perform further analyses. List function described later Users can get the code for the query in Perl, Python, Java, Ruby, JavaScript or XML by clicking on 'Get Code' (Box 2). Users can also download the search results, by clicking on 'Download' (Box 3), as tab-delimited, comma-separated values, XML or JSON. If the results are genomic features, which is true for the current example,

then users can download the results in GFF3 and BED format.

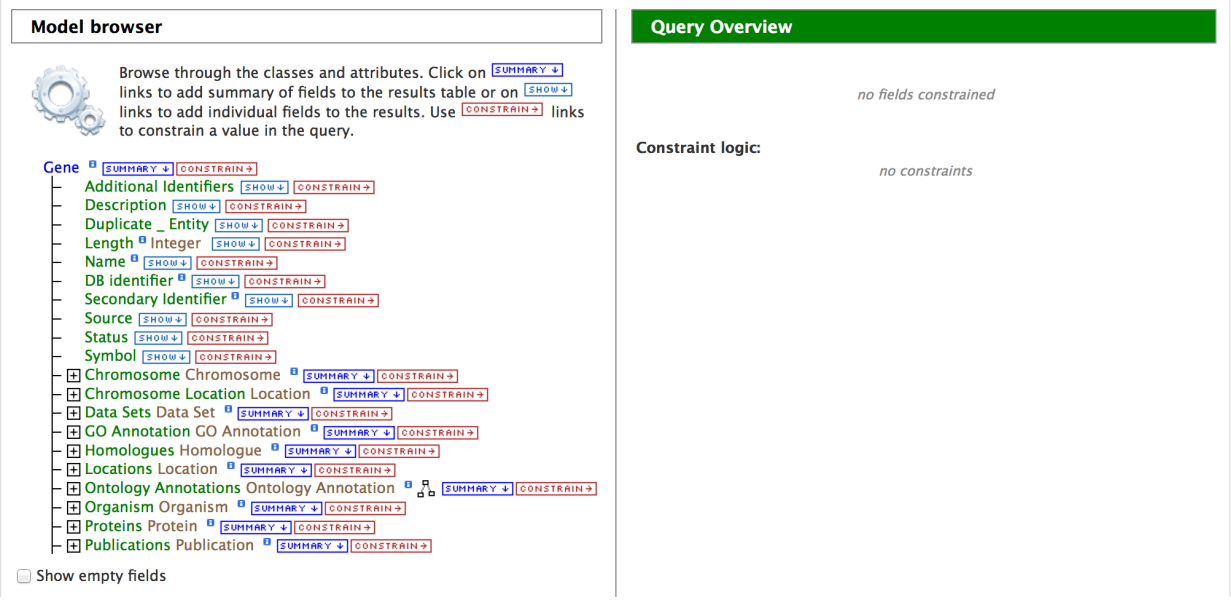
Users can also customize the layout of the result page by clicking on 'Manage Columns' (Box 4).

Query Builder

We have provided templates suitable for different types of queries but if users need more fidelity in their search they can make use of the QueryBuilder. The possibilities of queries using the QueryBuilder are endless. You can format the output the way you want and constrain your queries to perform complex search operations.



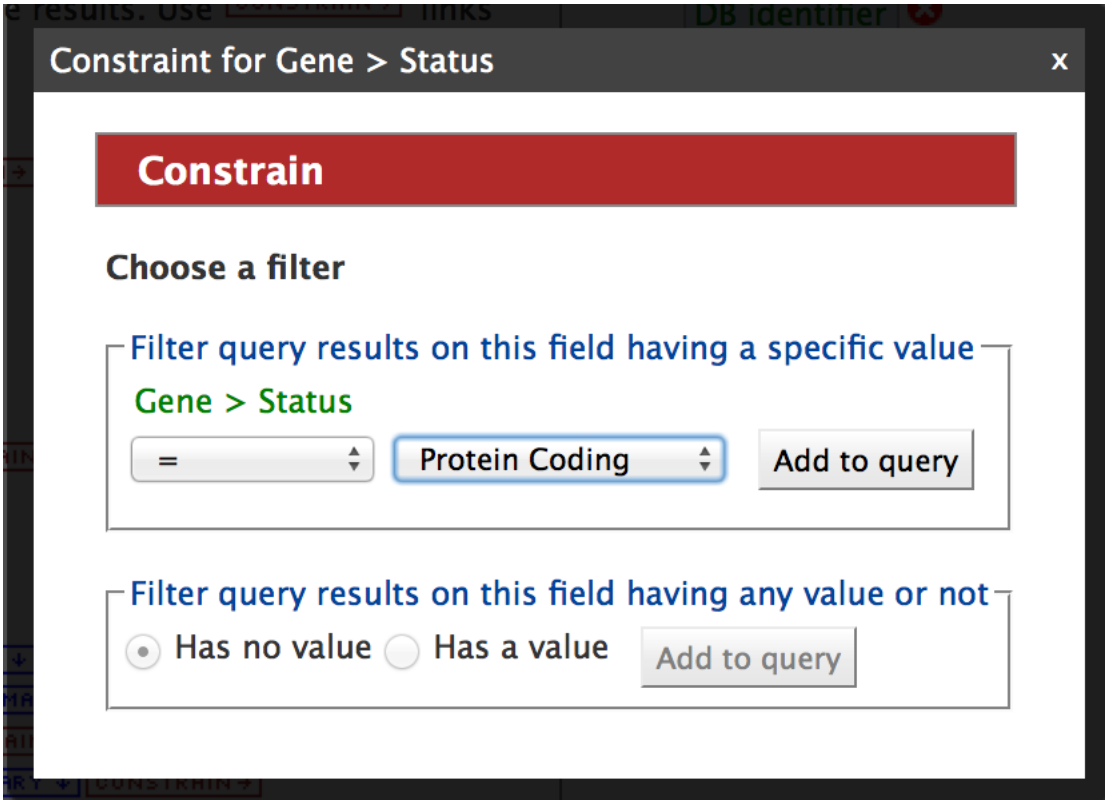
First lets select 'Gene' as a Data Type in the QueryBuilder. Then click on 'Select'. This will take you to a Model browser where you can select the attributes for the feature class 'Gene'.



Lets consider three scenarios for using the QueryBuilder,

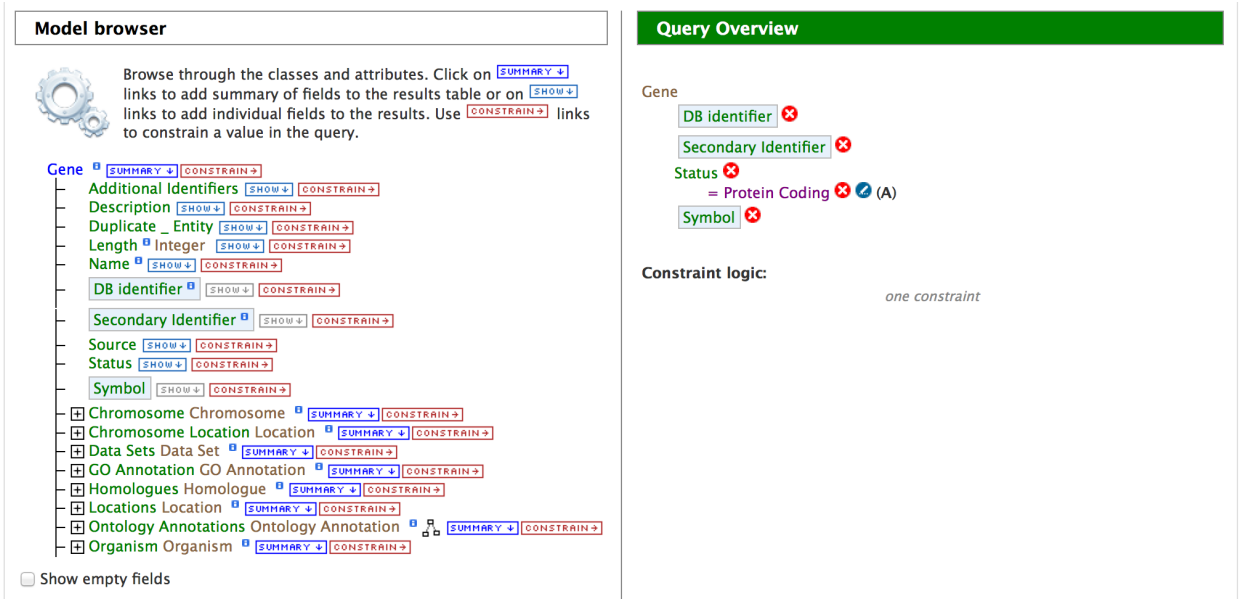
Querying for Protein Coding genes:

Click on 'Show' tab for the attributes 'DB identifier', 'Secondary Identifier', and 'Symbol'. This indicates the QueryBuilder to show the DB identifier (Primary Identifier), Secondary Identifier and the Symbol for 'Gene'. Then click on 'Constrain' tab for the attribute 'Status'.

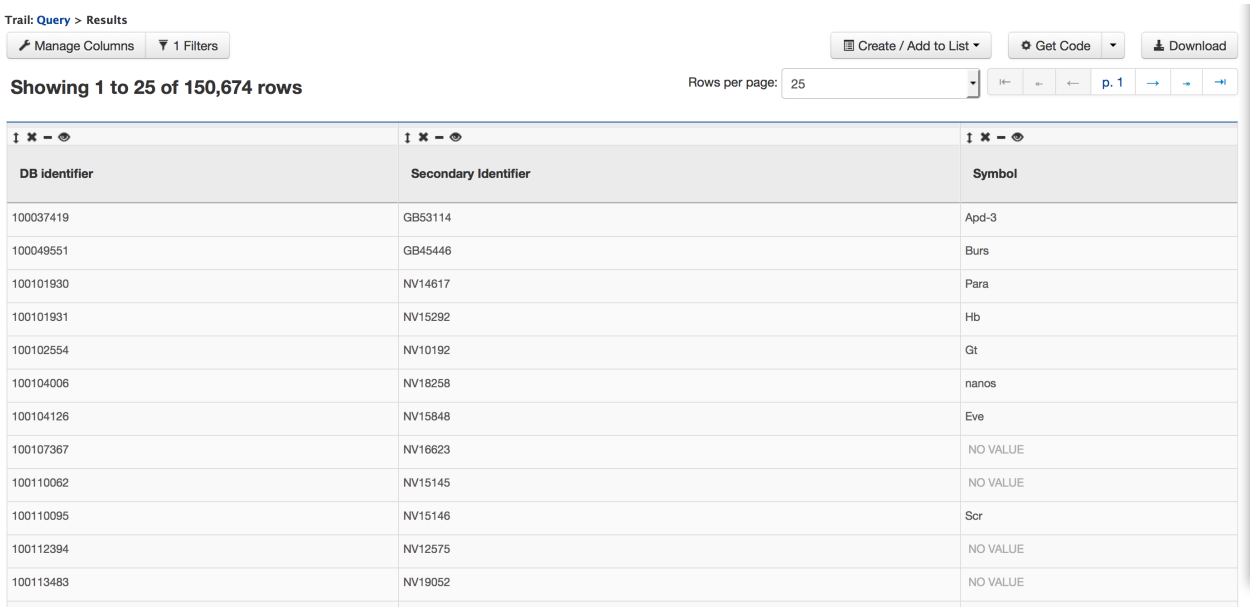


Click on the drop down list for Status and select 'Protein Coding'. Then click on 'Add to Query'.

The Model Browser should resemble the image below,

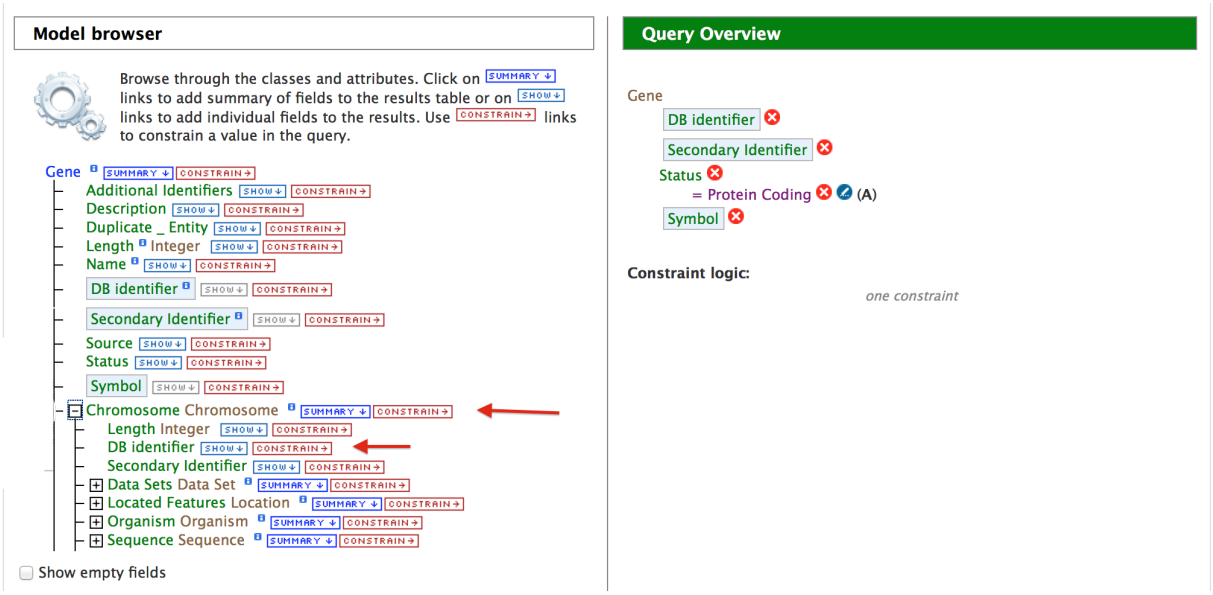


Now if you click on 'Show results' it would show all the genes that have status 'Protein Coding' as shown below:

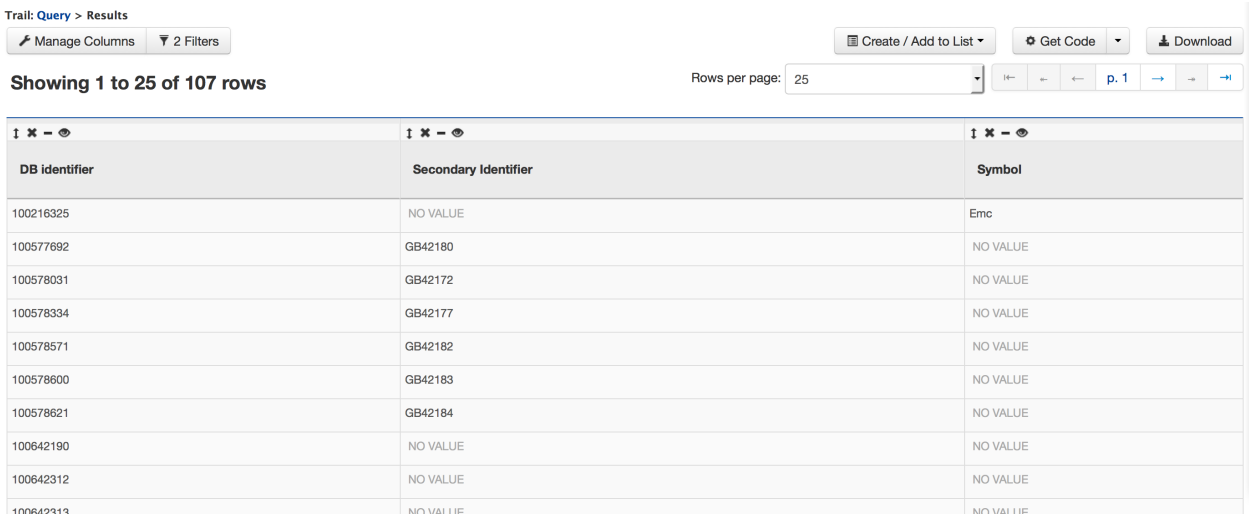


DB identifier	Secondary Identifier	Symbol
100037419	GB53114	Apd-3
100049551	GB45446	Burs
100101930	NV14617	Para
100101931	NV15292	Hb
100102554	NV10192	Gt
100104006	NV18258	nanos
100104126	NV15848	Eve
100107367	NV16623	NO VALUE
100110062	NV15145	NO VALUE
100110095	NV15146	Scr
100112394	NV12575	NO VALUE
100113483	NV19052	NO VALUE

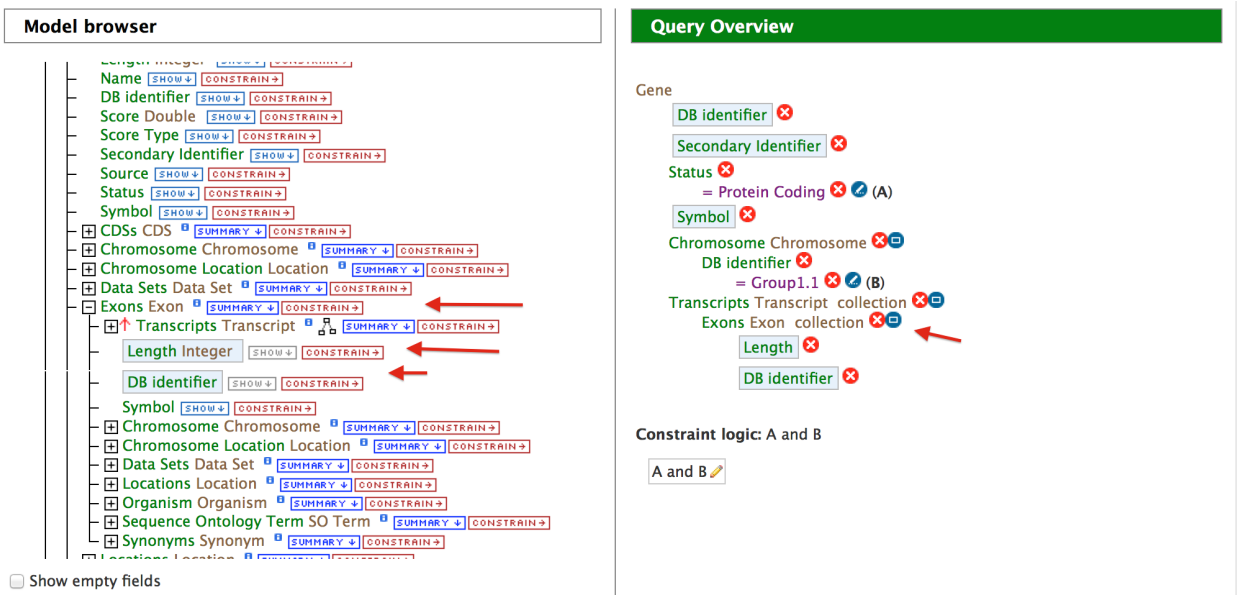
ii. Querying for Protein Coding genes on a particular chromosome Users can customize this query by adding another constraint for Chromosome.



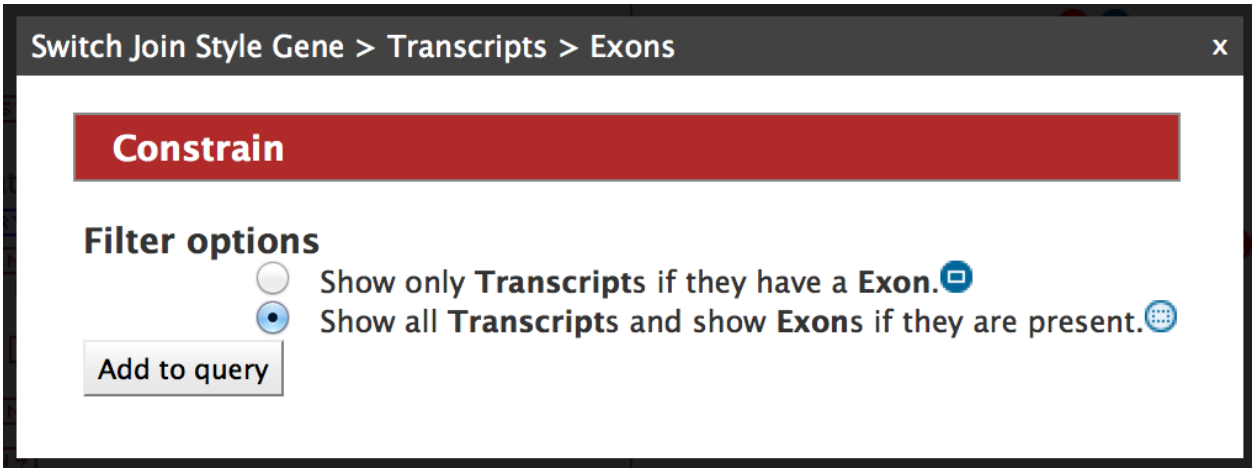
While building the query in the QueryBuilder, expand the 'Chromosome' feature class and select the 'Constrain' tab for attribute 'DB Identifier'. Enter 'Group1.1' in the text box of the pop-up window and then click on 'Add to Query'. Now if you click on 'Show results' the query will result in all the genes that are of type 'Protein Coding' on Chromosome with DB Identifier 'Group1.1'.



iii. Querying for Protein Coding genes on a particular chromosome and theirs exons Users can customize this further by configuring the query to show all the exons for each Gene.

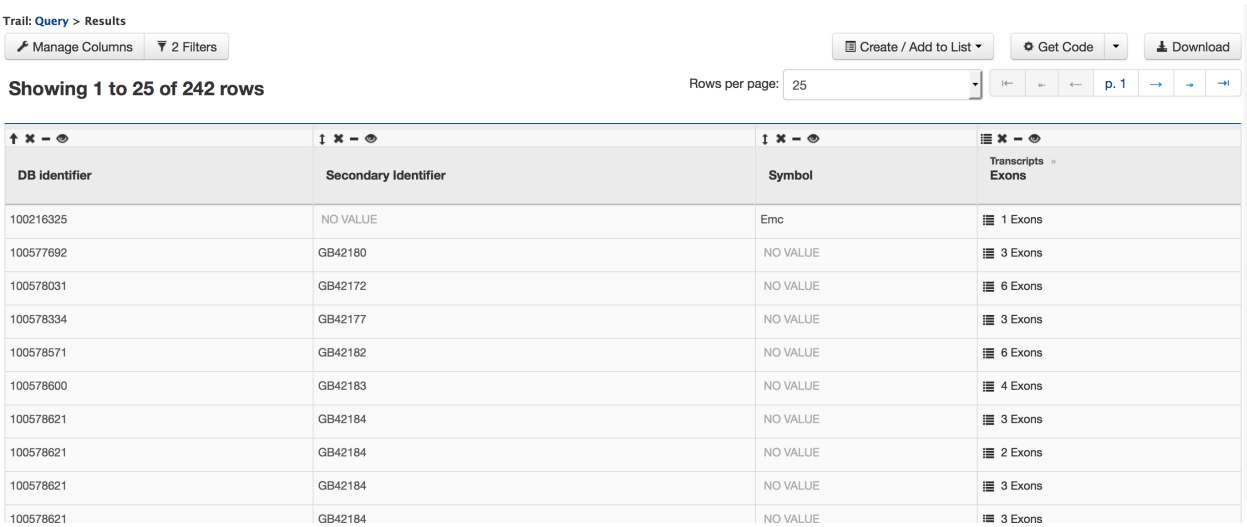


Expand the 'Exon' feature class and select on 'DB identifier' and 'Length'. To make the output more visually pleasing, click on the blue square near Exon collection in the query overview and you will see a popup like below,

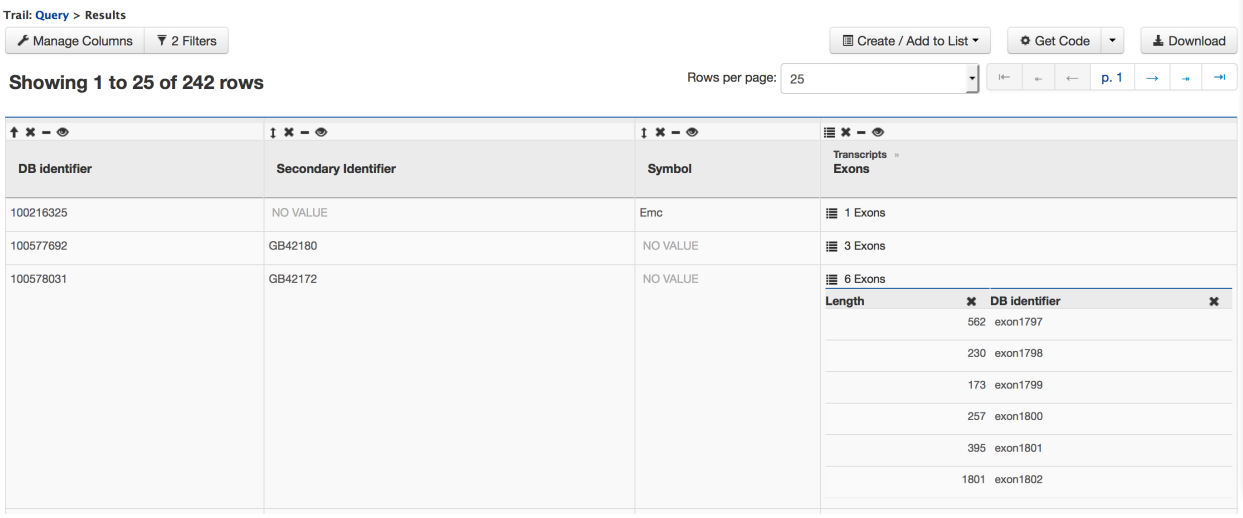


Select 'Show all Genes and show Exons if they are present' and click on 'Add to query'.

Now run the query and you should see the following results page,

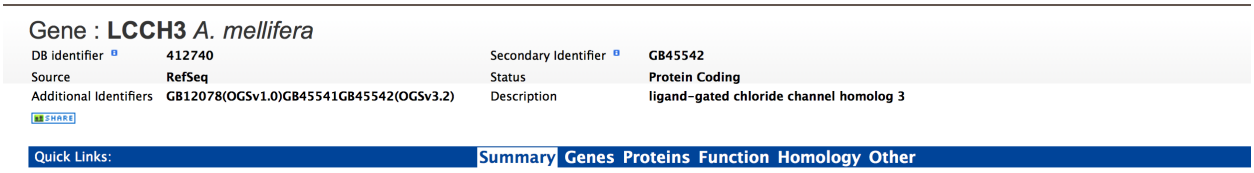


There are 107 genes on Chromosome Group1.1 and the gene with NCBI GeneID 100578031 has 6 exons. Users can click on the '6 exons' to expand the table with additional rows describing the length and DB identifier for each of the 6 exons.



Report Page

Every query result has a report page and the layout of the report page depends on the data available for a given query. Continuing with the example of 'Hb', the report page for this gene is shown below



The report page provides a complete description for gene Hb. The header of the report page shows the DB identifier. The 'status' indicates the type of gene, in this case a protein coding gene. Other possible values are,

· Non Coding – for non coding RNAs

· Pseudogene – for pseudogenes

· Immunogenes – for protein coding genes that are annotated to be a part of the immune system

· Frameshift – for protein coding genes that have a frameshift in their coding frame

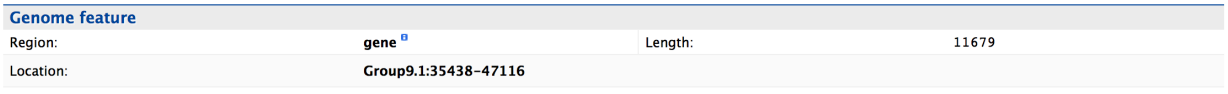
· miRNA – for micro RNAs

· rRNA – for ribosomal RNAs

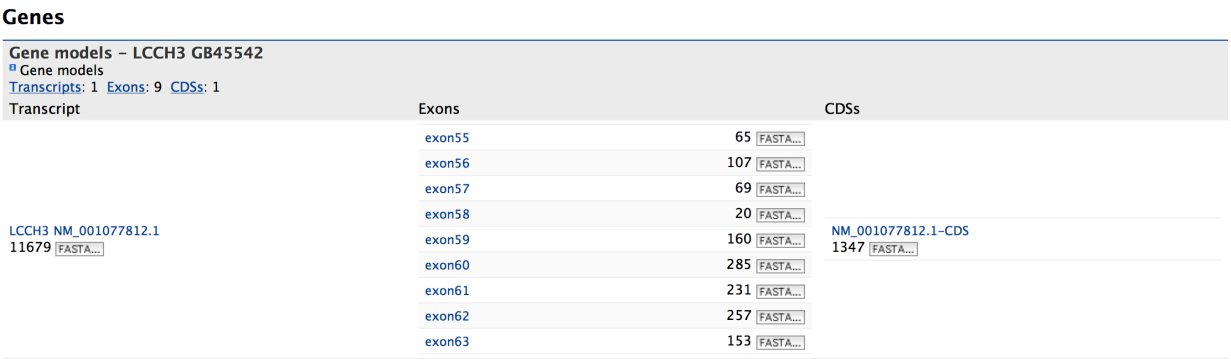
· tRNA – for transfer RNAs

The contents of the report page are divided into categories based on the type of information provided,

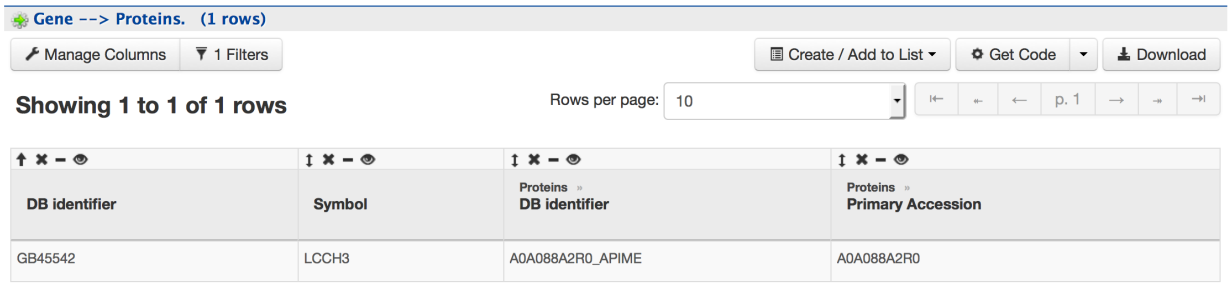
Summary:



Provides a summary about a gene such as length, chromosome location and strand information. Users can also get the complete FASTA sequence of the gene by clicking on the FASTA tab.

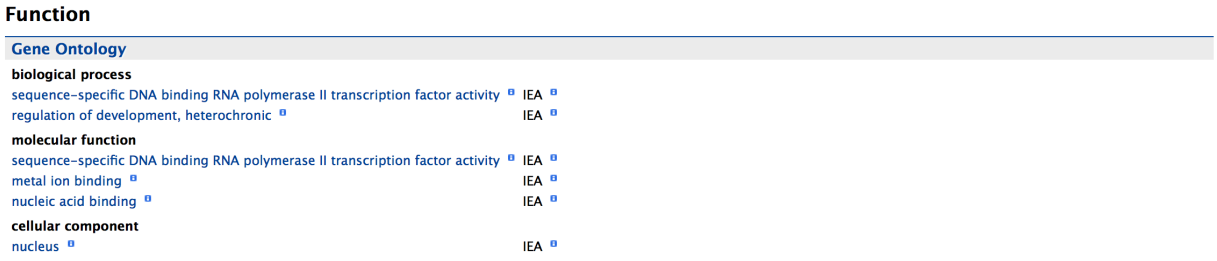


This section provides information about the gene model. It displays all the transcripts and exons for a gene. The FASTA sequence of each transcript or exon can be downloaded by clicking on the FASTA tab. Users can also download the coding sequence for a transcript, when available, by clicking on the FASTA tab in the CDS column.



This section provides information about the protein product of gene LLCH3. The comments section gives a brief description about the protein along with the UniProt accession.

Function:



This section provides Gene Ontology annotations for a gene. Annotations are divided into three categories,

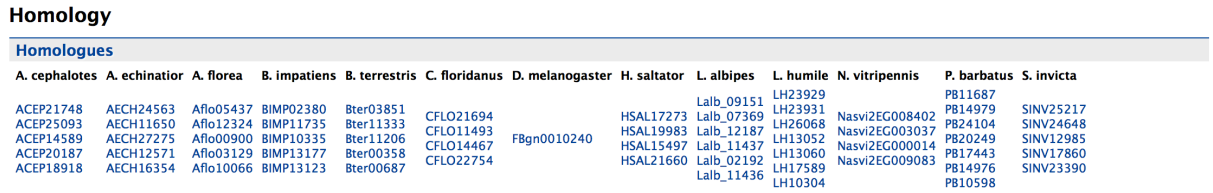
· Biological process

· Molecular function

· Cellular Component

The GO terms are displayed along with the evidence code indicating how the annotations were derived.

Homology:



Homology

Homologues

A. cephalotes	A. echinatior	A. florea	B. impatiens	B. terrestris	C. floridanus	D. melanogaster	H. saltator	L. albipes	L. humile	N. vitripennis	P. barbatus	S. invicta
ACEP21748	AECH24563	Aflo05437	BIMP02380	Bter03851	CFLO21694	FBgn0010240	HSAL17273	Lalb_09151	LH23929	Nasvi2EG008402	PB11687	SINV25217
ACEP25093	AECH11650	Aflo12324	BIMP11735	Bter11333	CFLO11493		HSAL19983	Lalb_07369	LH23931	Nasvi2EG003037	PB14979	SINV24648
ACEP14589	AECH27275	Aflo00900	BIMP10335	Bter11206	CFLO14467		HSAL15497	Lalb_12187	LH26068	Nasvi2EG000014	PB24104	SINV12985
ACEP20187	AECH12571	Aflo03129	BIMP13177	Bter00358	CFLO22754		HSAL21660	Lalb_11437	LH13052	Nasvi2EG009083	PB20249	SINV17860
ACEP18918	AECH16354	Aflo10066	BIMP13123	Bter00687				Lalb_02192	LH13060		PB17443	SINV23390
								Lalb_11436	LH17589		PB14976	
									LH10304		PB10598	

The table below gives a detailed information about the homologue, the type of homologue and from which dataset the information was obtained.

Others:

This section provides information such as,

Child features – lists all the features that are sub features of the current gene

Flanking regions – lists all the features flanking the current gene

Overlapping features – lists all the features that overlap with current gene

Publications – Publications related to the current gene

Genomic Regions Search

The Genomic Region Search is a tool to fetch features that are within a given set of genomic coordinates or to fetch features that are within a given number of bases flanking a given set of genomic coordinates.

The coordinates have to be of the format,

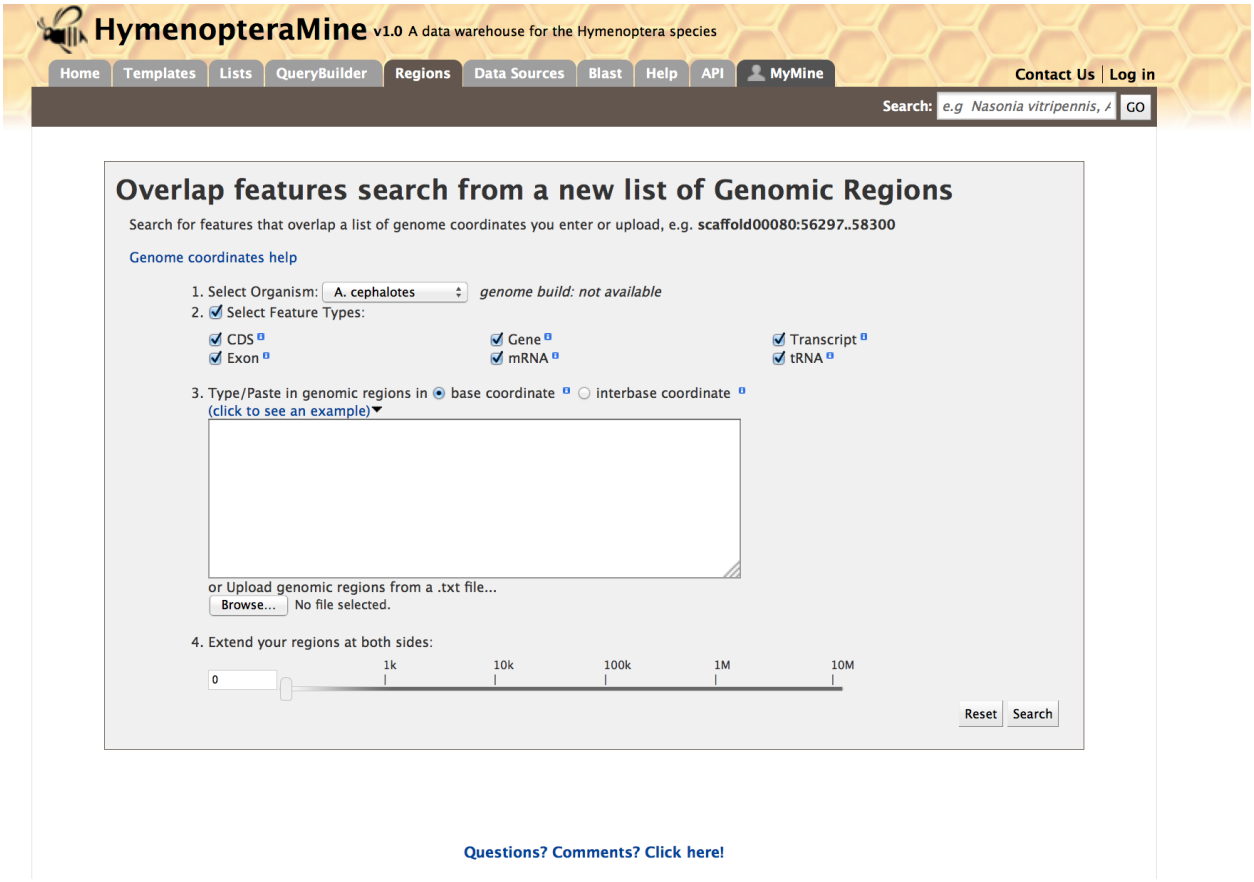
chromosome_name:start..end

OR

chromosome_name:start-end

OR

chromosome_name start end

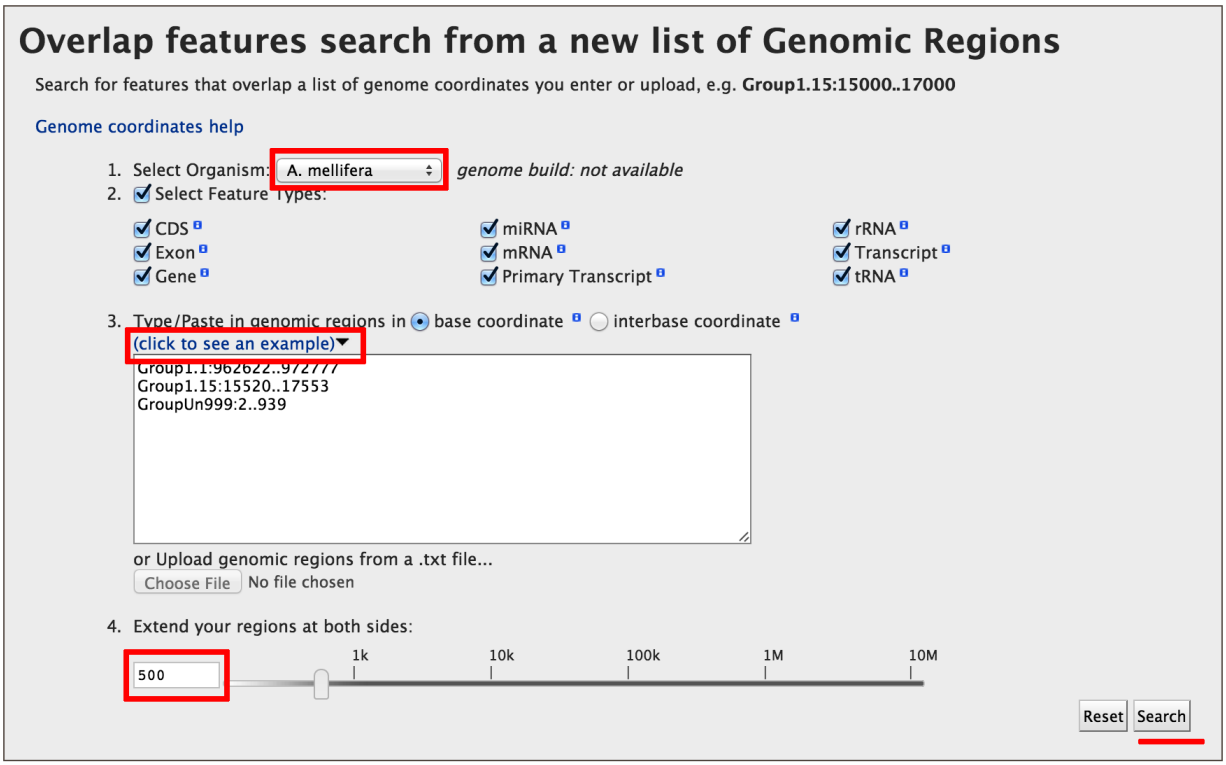


Click on 'click to see an example' for a representative set of genomic coordinates.

Users can extend the regions on either side of the genomic coordinate using the slider or using the textbox.

Users can also select the type of coordinate system they would like to use: base coordinate or interbase coordinate.

Lets consider the example,



Click on the 'click to see an example' and extend the region search by 500 bp.

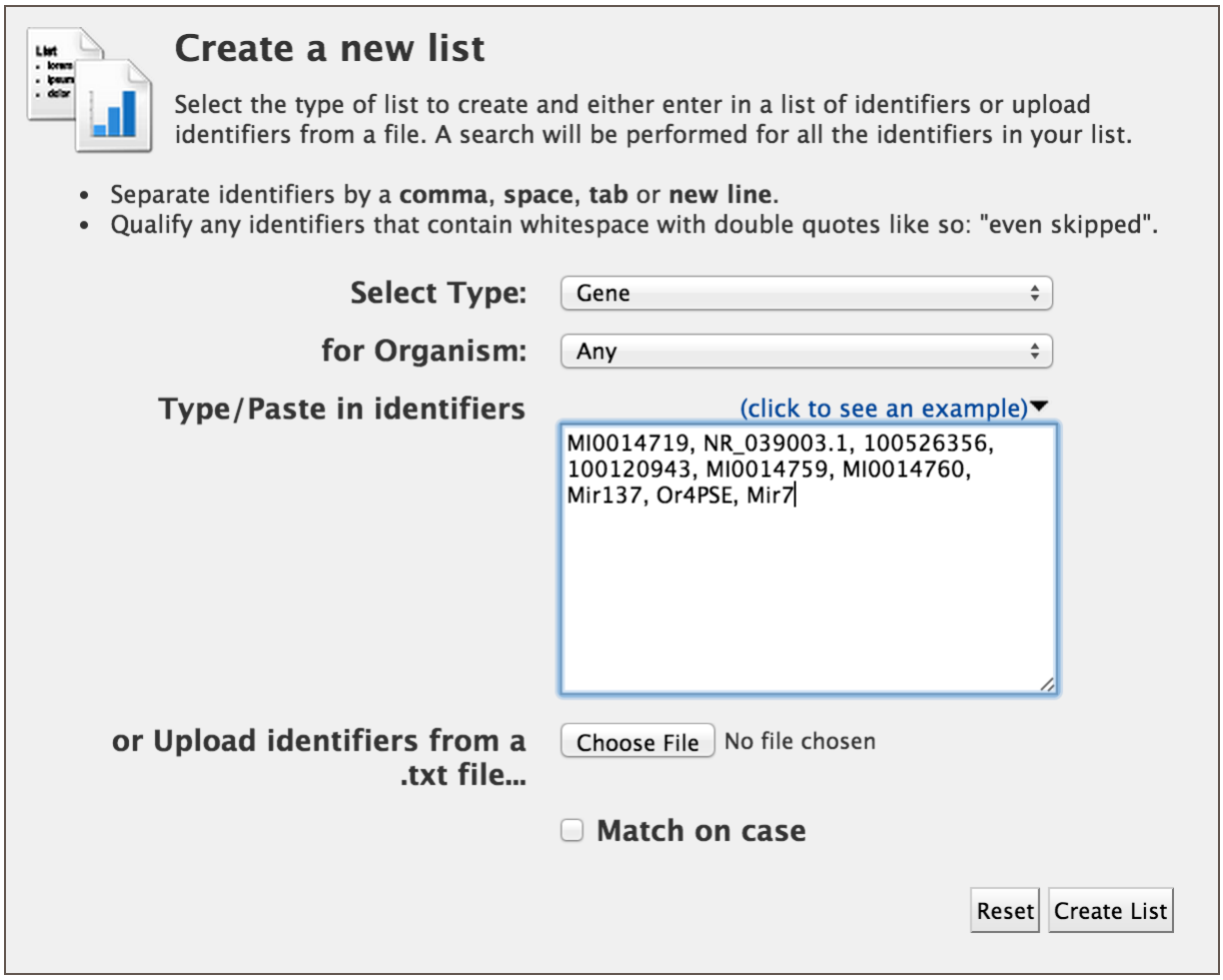
The result page will give a list of features that are present in each of the genomic interval provided in the input.



The results can be exported as tab-delimited and comma-separated values. If the results have genomic features then they can be exported in GFF3 or BED format. Users can also export FASTA sequences of the features.

If users are interested in creating a list of particular features from the result page then they can filter based on feature type, shown in red box, and click on 'Go'.

Lists



Users can create a list of features. The input can either be gene IDs, transcript IDs, gene symbols, etc. The list tool tries to lookup the query throughout the database and will attempt to convert the identifiers to the type selected in the list 'Select Type' option.

Lets try the examples provided. Click on 'Click to see example' link and click on 'Create List'.

Identifier you provided	Matches							Action
	primary identifier	symbol	name	length	class	secondary identifier	organism short name	
Mir7	732510	Mir7		87	Gene		A. mellifera	Add
	100526362	Mir7		87	Gene		N. vitripennis	Add
Mir137	100315659	Mir137		100	Gene		A. mellifera	Add
	100526322	Mir137		100	Gene		N. vitripennis	Add

Summary

Download summary

Direct Hits

Identifier you provided	Match						
	primary identifier	symbol	name	length	class	secondary identifier	organism short name
Or4PSE	100463191	Or4PSE		1535	Gene	NV22749	N. vitripennis
100526356	100526356	Mir281		103	Gene		N. vitripennis
100120943	100120943	100120943		3726	Gene	NV13302	N. vitripennis

The list tool does a lookup of the identifiers and shows you the results. If there are any duplicates, users can decide to add the relevant entries individually. The summary section provides information regarding those identifiers that had a direct hit without any duplicates.

Click on the ones that have proper primary identifier and secondary identifier.

Users can download summary of the converted result.

Then click on ‘save a list of 3 genes’.

This will take users to the following page,

Manage Columns | 1 Filters | Create / Add to List | Get Code | Download

Rows per page: 10 p. 1

Showing 1 to 3 of 3 rows

DB identifier	Secondary Identifier	Symbol	Name	Length	Chromosome . Primary Identifier	Chromosome Location . Start	Chromosome Location . End	Organism . Short Name
100120943	NV13302	100120943	NO VALUE	3726	NW_001814904.1	2052084	2055809	N. vitripennis
100463191	NV22749	Or4PSE	NO VALUE	1535	NW_001815348.1	1731682	1733216	N. vitripennis
100526356	NO VALUE	Mir281	NO VALUE	103	Chr5_random049	692904	693006	N. vitripennis

Orthologues

A. cephalotes (1) A. mellifera (41)

External Links

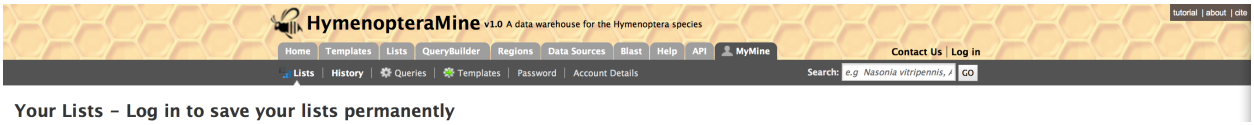
No external links.

This page provides users with widgets to perform analyses on gene lists that they have created.

List widgets

1. Chromosome Distribution
2. Gene Ontology Enrichment

3. Protein Domain Enrichment
4. Publication Enrichment
5. Pathway Enrichment
6. Orthologues

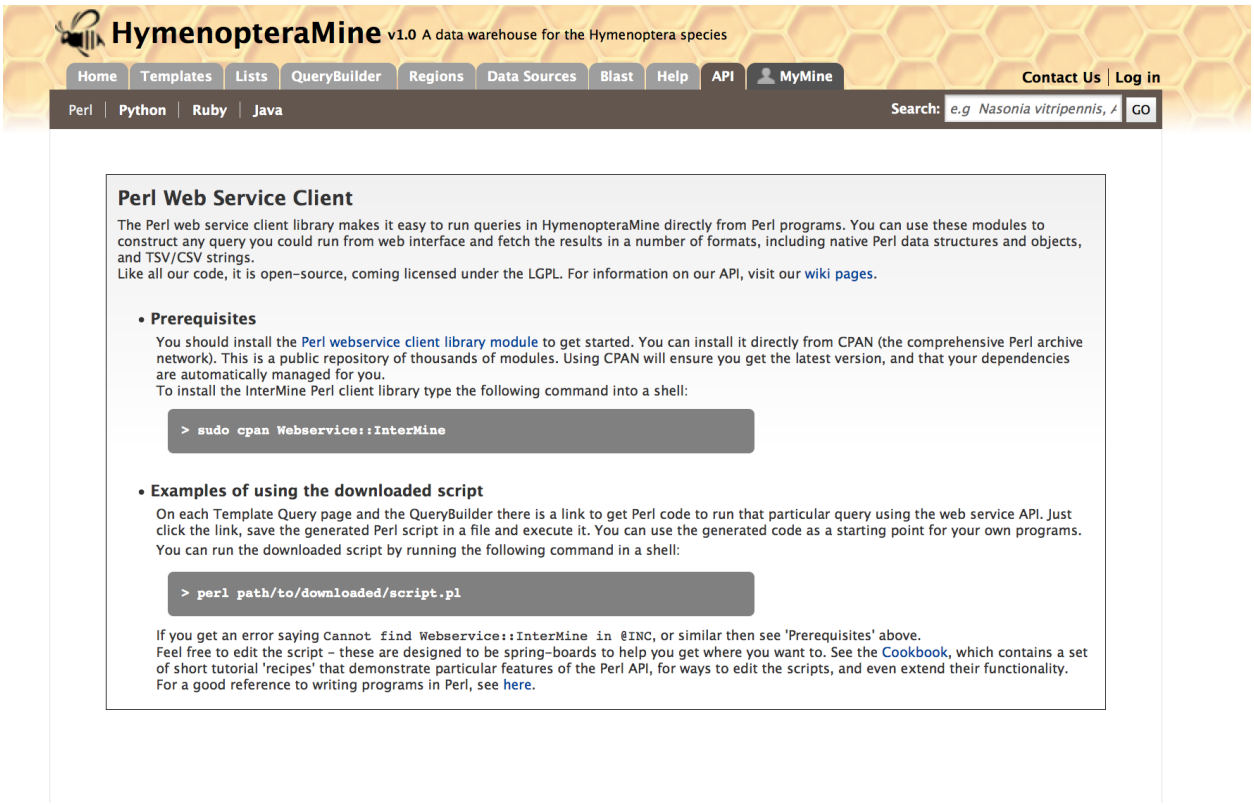


MyMine serves as a portal for users to manage their lists, queries, templates and account details.

1. Lists – lists saved by the user.
2. History of queries by user – shows a list of most recent queries performed by the user.
3. Templates – Templates created by the user or existing templates that are marked as 'favorite' by the user.
4. Password change – change the password for the user's account.
5. Account details – for updating user preferences.

API

For users who would like to programmatically access HymenopteraMine, they can make use of the API.



Perl, Python, Ruby and Java are the languages supported by the InterMine API.

For more information on the details of the API visit the InterMine Wiki

Data Sources

Provides a description of the datasets that are integrated into HymenopteraMine along with their date of download, version or release, citations wherever applicable and any additional comments.

BLAST

Users can perform BLAST against the Hymenoptera genomic, CDS or protein sequences using the BLAST page.

Click here for a video tutorial, created by FlyMine, which highlights the features of InterMine.

CHAPTER 2

Indices and tables

- genindex
- modindex
- search