

metabolicMine

Data & Tools To Support Metabolic Disease Research

Michael Lyne, Adrian Carr, Richard Smith, Radek Stepan & Gos Micklem
University of Cambridge, UK.

<http://metabolicMine.org>
metabolicmine@intermine.org

metabolicMine...

- is a data warehouse that integrates diverse biological data sets and the tools to explore them.
- supports research into the genomics, genetics and proteomics of common metabolic disease
- brings together information covering genes, proteins, interactions, orthologues (including key data sets from mouse and rat), pathways, ontologies, diseases, GWAS & SNPs.
- has an intuitive web interface, a library of 'Template' searches, List Analysis and advanced QueryBuilder which provide many different ways to interrogate the data.
- provides programming interfaces for bioinformaticians.

A Need For metabolicMine

Common metabolic diseases (including diabetes, obesity and related metabolic and endocrine illnesses) are a leading cause of mortality world wide. Great efforts have been made to elucidate the underlying genetic bases of these complex human diseases, so generating near-overwhelming quantities of data. Exploiting these data poses a significant challenge for biomedical researchers.

Developed in collaboration with leading UK metabolic disease groups, metabolicMine enables the metabolic disease research community to search across domains of biological knowledge by integrating diverse data, and the tools for their exploration, into one resource.

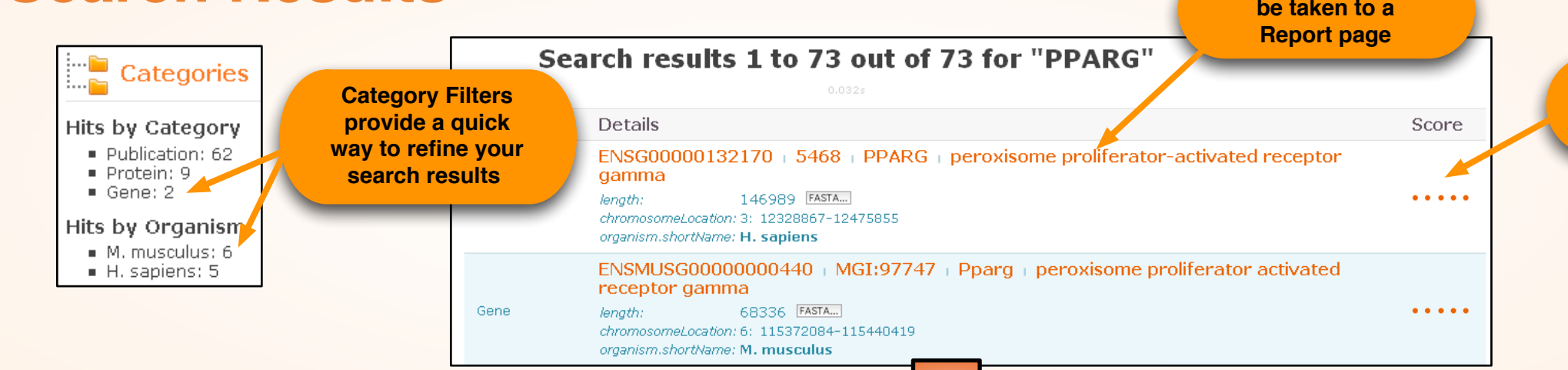
metabolicMine is freely available at metabolicmine.org.

Search

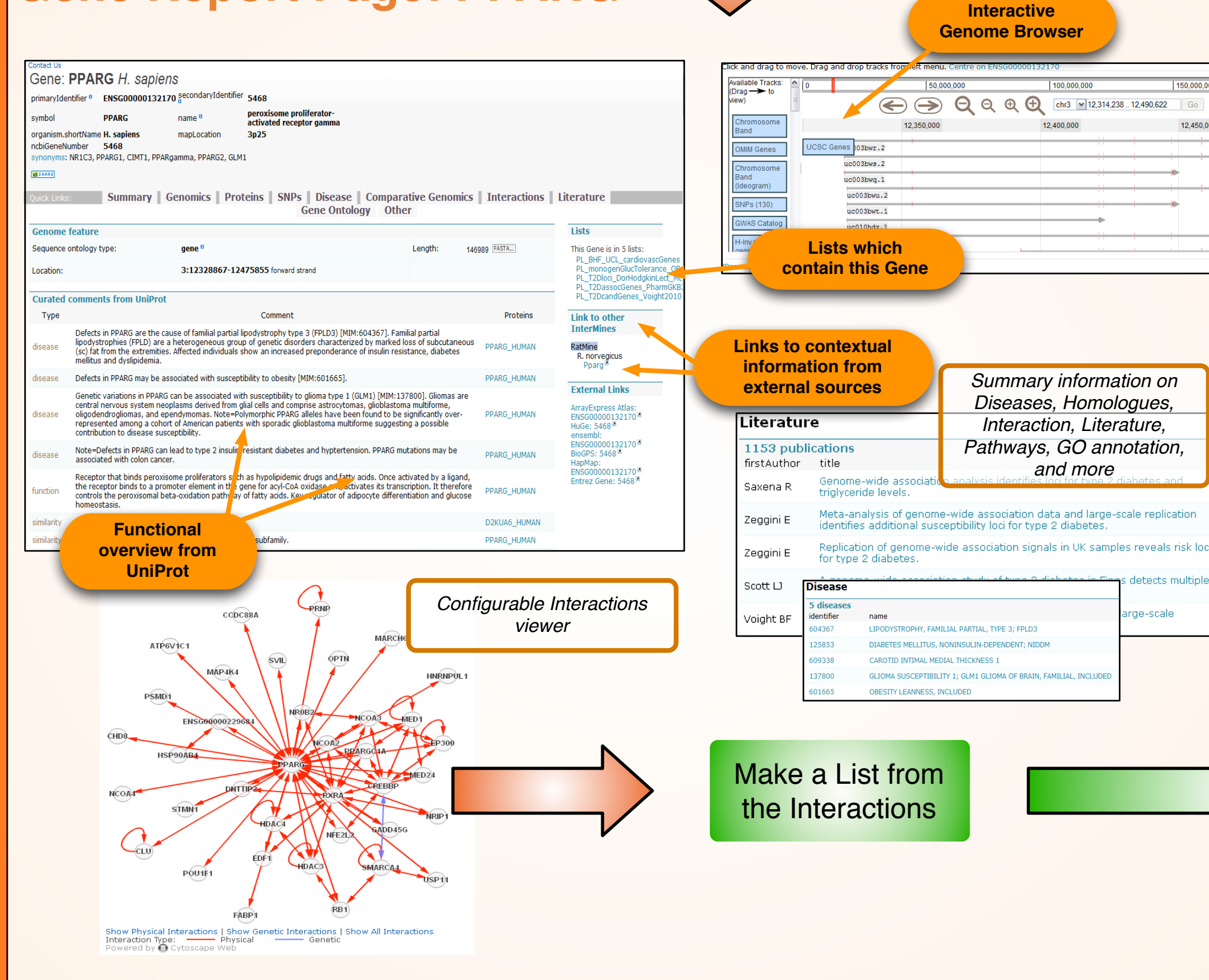
Task: Search for all relevant information on your favourite Gene without having to visit several sites and formats.

Solution: Use metabolicMine's Search to retrieve Gene information covering many different data sources and types. Search accepts a range of Identifiers including Gene symbol, Ensembl ID, Entrez Gene ID and also synonyms.

Search Results



Gene Report Page: PPARG



metabolicMine

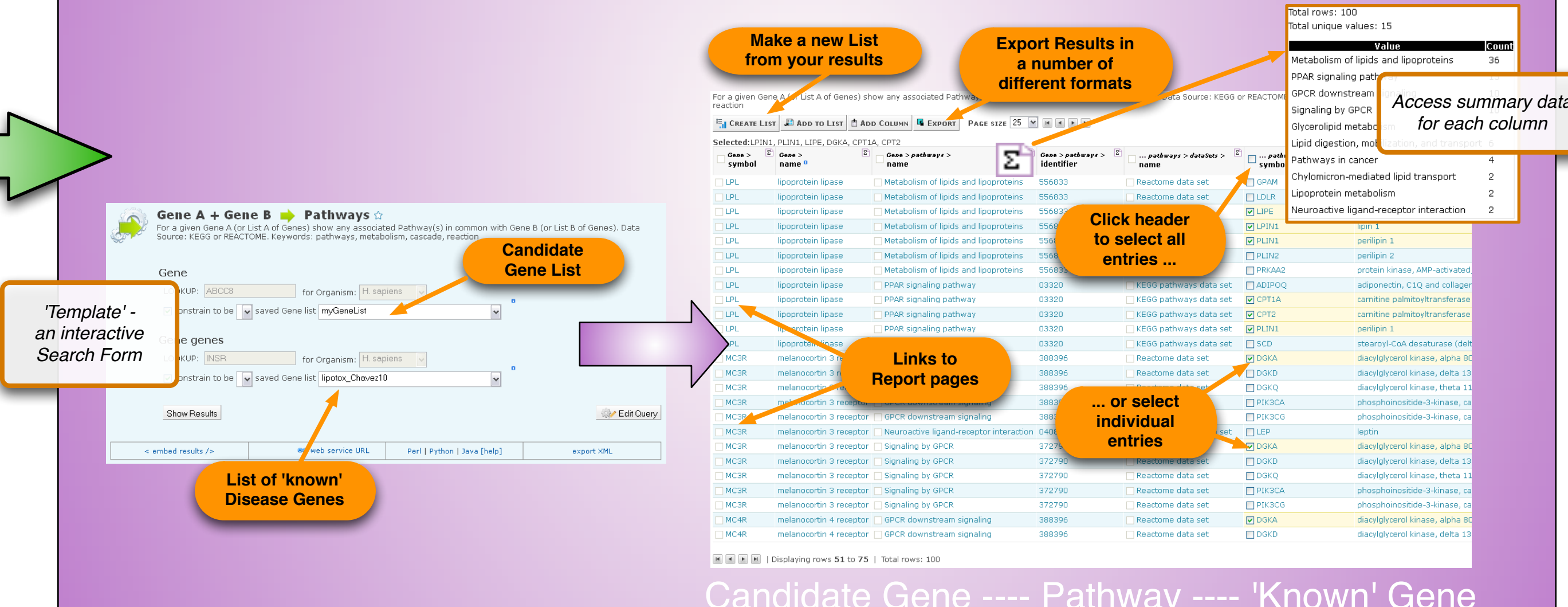


A Community-driven Search Library

Task: You have a set of Disease candidate Genes and want to know if there is a relationship with 'known' Disease Genes.

Solution: Use metabolicMine's List comparison Template to search for common Pathways with the 'known' Disease Genes.

metabolicMine has a Library of 'Template' searches covering questions frequently asked by the research community. Each member of the library has an interactive search form representing a common task. For example, we can explore relationships between two Lists of Genes through the elements that they have in common, like shared Pathways or their Interactions.



Candidate Gene ---- Pathway ---- 'Known' Gene

More Template Solutions

Genes --> Proteins
Genes --> all SNPs
Genes --> Diseases
Gene --> Pathways
Proteins --> Protein Domains
Proteins --> Interactions
Proteins --> GO terms
Protein Domain --> all Proteins

Go term --> Proteins
SNPs --> GWA study
SNPs --> Type + Consequences
GWAS term --> SNPs
GWA study --> Genes
Region --> Genes
Region --> SNPs
Gene A --> Interactions <-- Gene B

Data Sources

metabolicMine integrates information from many different sources and types including, Genes, Proteins, Diseases, SNPs, GWAS, Homologues, Pathways, Interactions and more!



YOUR DB SUGGESTIONS

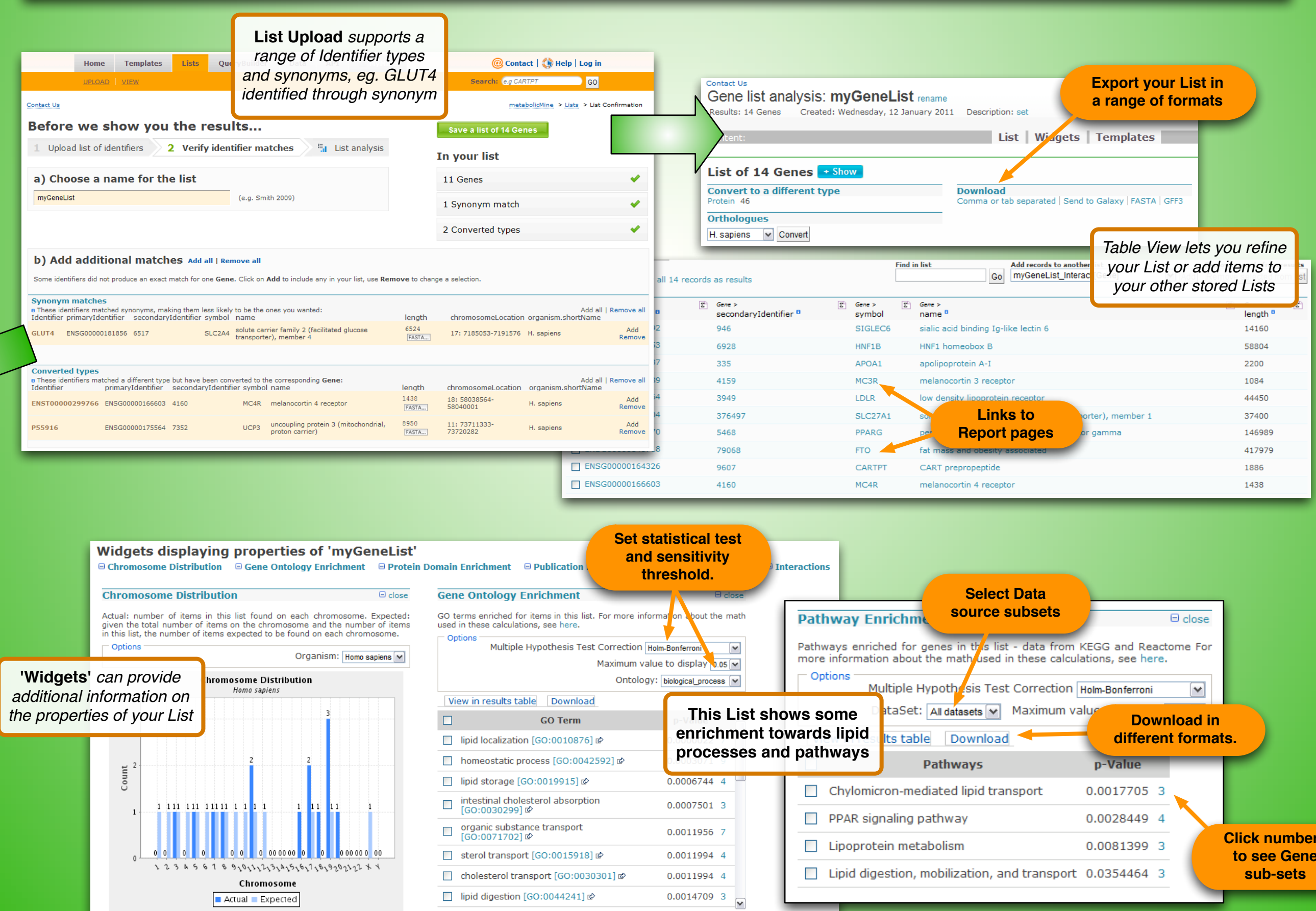
Please send us your suggestions for 'public' datasources that you'd like included in metabolicMine

Upload and Analyse Lists of Data

Task: You have a set of Disease Candidate Genes and wish to understand how the members may be related

Solution: Use metabolicMine's List Upload and Analysis.

List Upload recognises all common types of identifiers and synonyms and lets you store your List for further analysis. List Analysis provides an overview of your List across a range of properties including GO terms, Pathways, Interactions, Publications and Expression and display 'widgets' highlight statistically enriched results.



We plan to add more widgets and functionality to the List Analysis page so if you have suggestions on what you'd like to see, please let us know.

Help to Improve metabolicMine!

We welcome all suggestions and feedback.

To contact us you can click the @Contact button, top right of every metabolicMine page or e-mail us: metabolicmine@intermine.org

metabolicMine is a community resource!

In addition to using metabolicMine, you can also help by suggesting:

- Datasets that you think we should include (that are 'Open Access'). An example would be 'HMDB' (www.hmdb.ca).
- Publications with interesting Gene or SNP lists that could contribute to our 'known' Gene sets. For example, Chavez & Summers (2010): Genes linked to lipotoxicity and metabolic disease. Even better, if you make a List from a publication please share it with us.
- Tasks that we can turn into Template Searches to add to metabolicMine's Library.
- Workflows and Functionality improvements.

Are you a Bioinformatician?

metabolicMine includes a RESTful web service API allowing you to access data directly from programs you write. There are three main ways to use the web services:

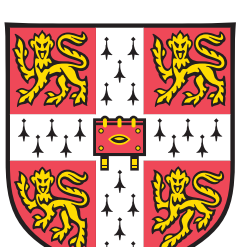
1. Run a Template search with the values you choose using the REST URL. Each Template in the web interface has an 'Embed' link which will give you the URL to do this.
2. Export an XML representation of a Template or custom search created in QueryBuilder and run it from the command line or a script.
3. Use the Java or Perl client code to build and execute custom searches from within your program.

For more information, see the API tab on any metabolicMine page

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Systems Biology Centre, University of Cambridge, Tennis Court Road, Cambridge CB2 1QR, UK
Tel: +44 1223 760262 Email: metabolicmine@intermine.org

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