FAQ

January 25, 2011 v.1

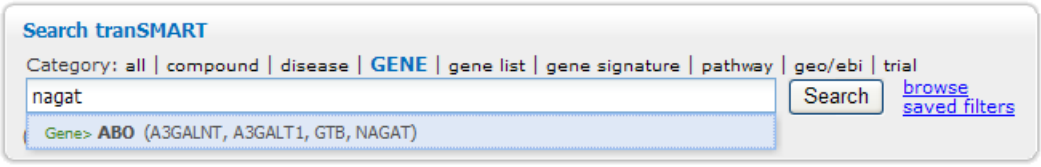
Frequently Asked Questions...

Are searches case-sensitive?

No. Searches are not case sensitive.

Can I search for a gene alias?

Yes. Aliases appear in parentheses in the dropdown list of search filters. In the figure below, tranSMART finds the search filter for the gene **ABO** after **nagat** was typed in the search field:

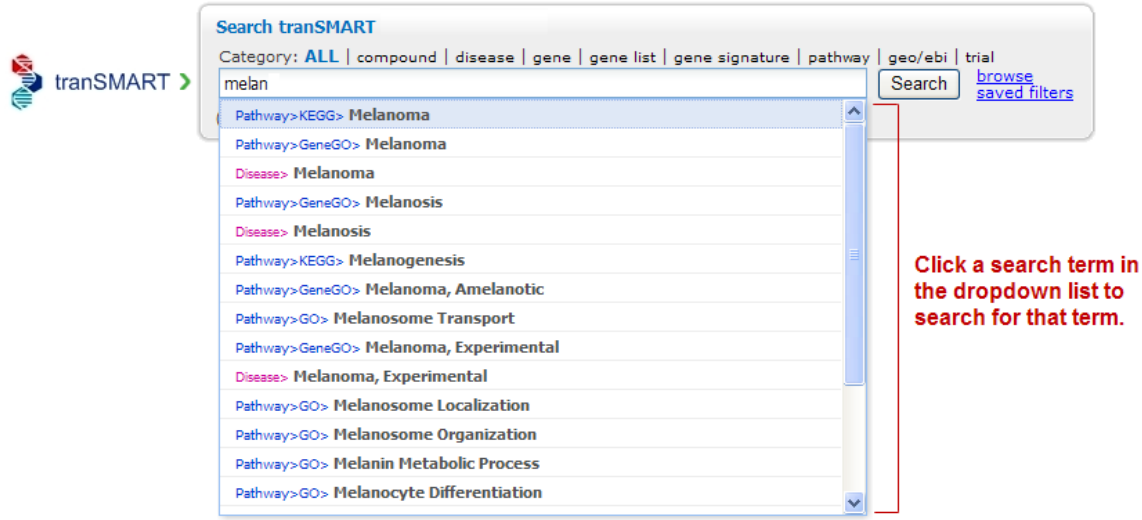


Can I use wild cards in my searches?

The search tool does not work with wild card characters such as '*' and '?'.

What is the 'autocomplete' feature?

When you type a few characters of text in the tranSMART search field, tranSMART looks for complete search terms (or aliases) that begin with the text you typed, and displays the terms in a dropdown list below the search field. For example, if you type **melan** in the search field, tranSMART displays the following possible matches:



When you click a search term in the list, tranSMART immediately searches for that term.

tranSMART displays up to 20 search terms in the dropdown list. If you don't see the text you want to search for, type more text in the search field. This narrows the possible matches for the text you typed.

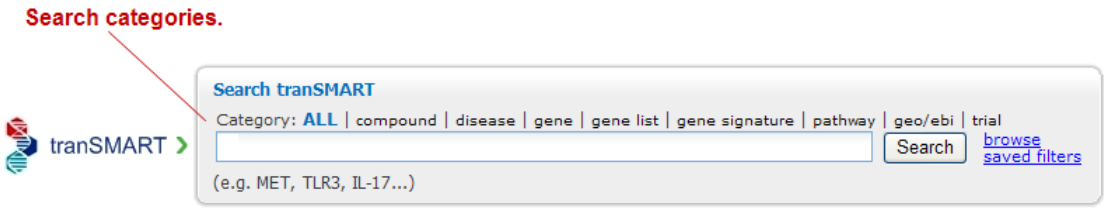
Why am I only seeing search results on the Documents tab?

Probably because you clicked the **Search** button instead of clicking a search term in the dropdown list. Clicking **Search** initiates a special kind of search, limited to Johnson & Johnson document repositories for the exact text you typed.

What are search categories?

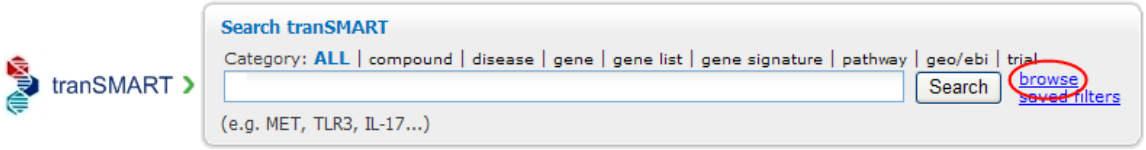
Search categories are a way to focus your search and limit your search results to a specific area, such as compounds, diseases, or genes.

Search categories are displayed above the search field. In the figure below, the search will be conducted across all search categories. To limit the search to a particular area, click the category you want to search within.



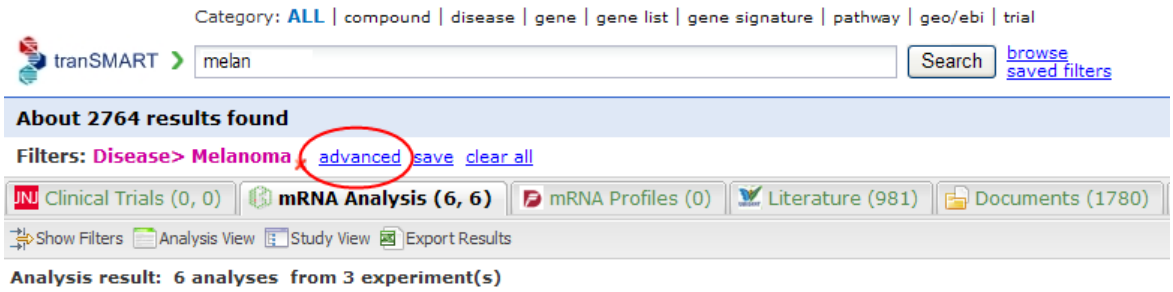
Can I browse through a list of search terms?

Yes. If you click the browse button, you can browse through all the search terms in each of the following categories: Clinical Trial, Compound, Disease, Pathway, and Gene Signature/List.



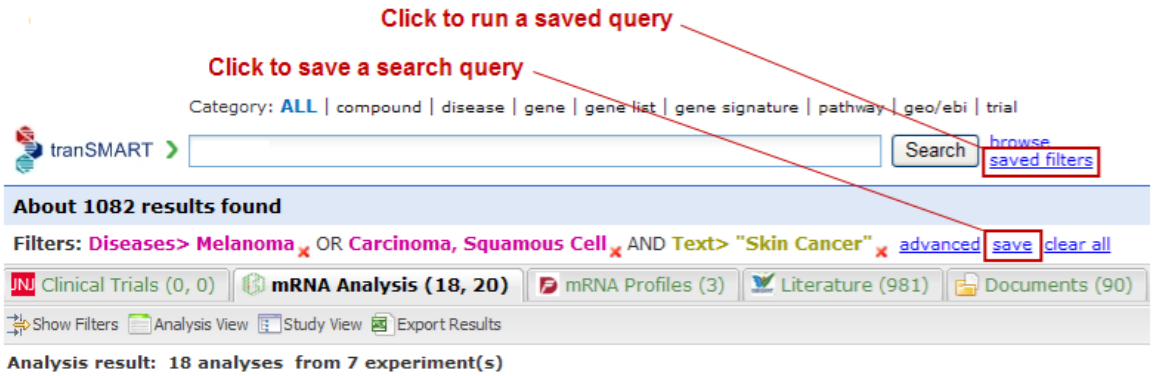
Can I create a search query with multiple criteria?

Yes. Search criteria are called filters. You can only specify one filter in the tranSMART search field. To build a search query with multiple filters, you first run the search against a single filter. When the search results are returned, click the **advanced** button to add more filters to the query:



Can I save a search query?

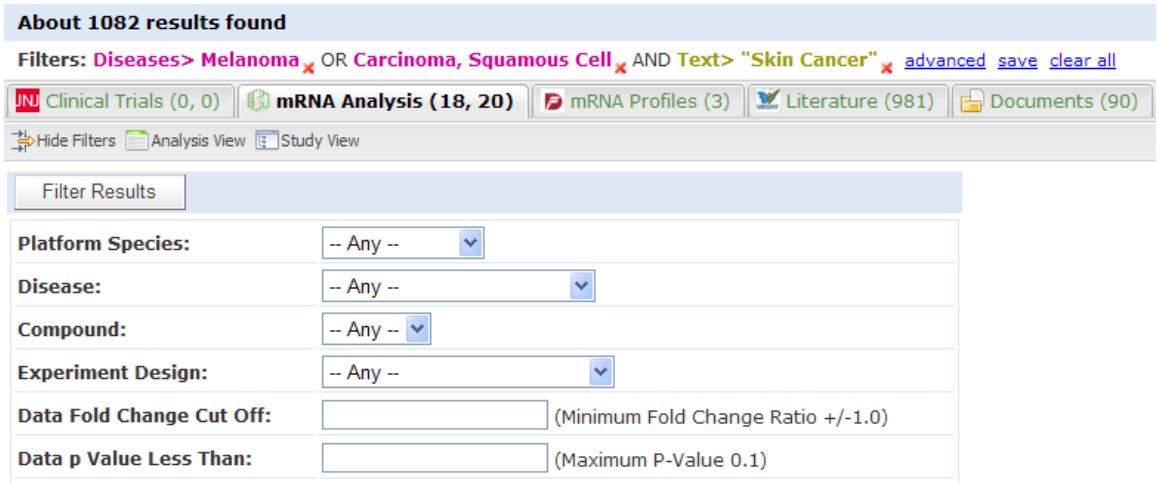
Yes. Click the **save** button to save a search query. When you want to run a saved search query, click **saved filters**.



After I run a search, can I further refine the search results?

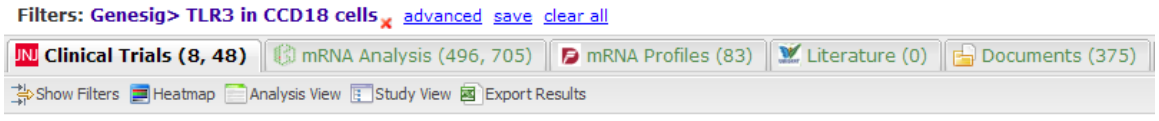
Yes. To do so, click the **Show Filters** button.

The following figure shows the kinds of filters you can select for an mRNA Analysis search result:



What do the numbers on the tabs in the results window represent?

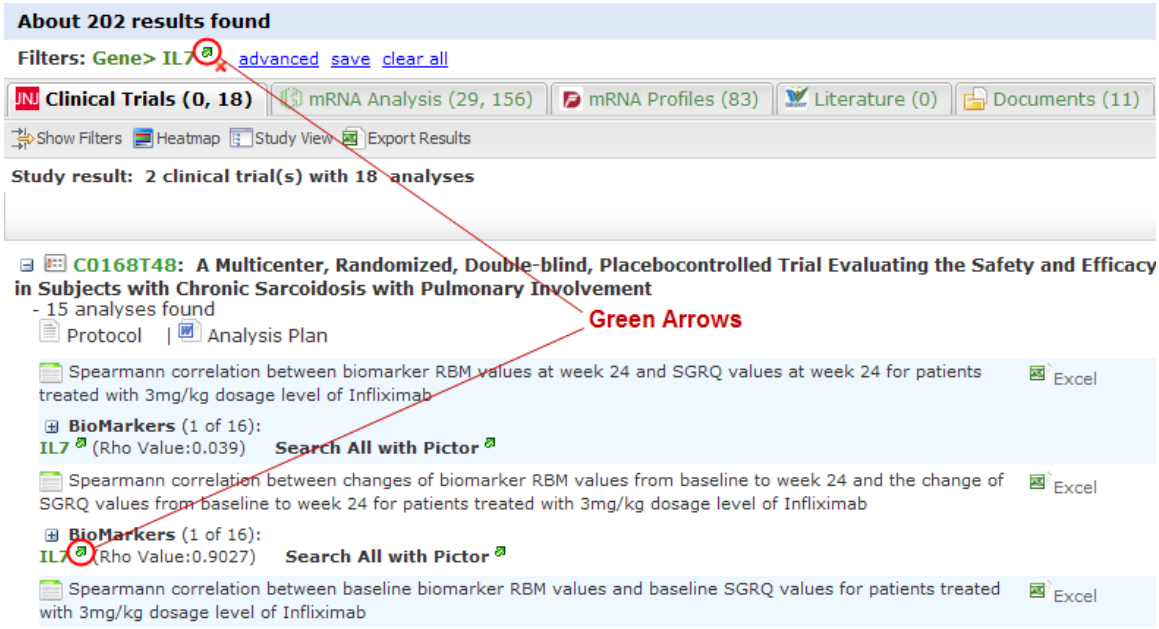
- The numbers on the mRNA Profiles, Literature, and Documents tabs represent the number of items returned within each result category.
- The pairs of numbers on the Clinical Trials and mRNA Analysis tabs represent the number of analyses found that satisfied the TEA threshold for meaningful analyses (first number) and the total number of analyses found (second number).



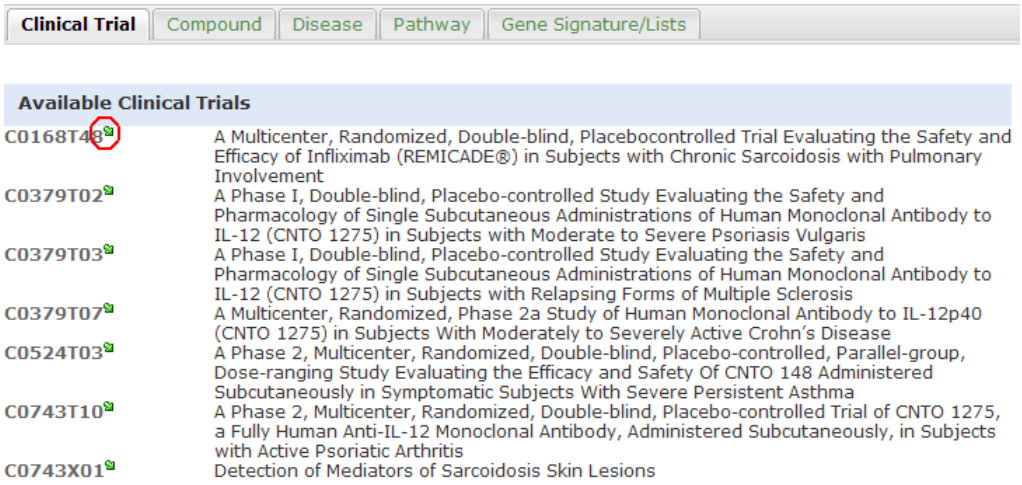
What do all of the green arrows represent?

Clicking a green arrow pointing upward and to the right after a gene name opens a window containing links to the following external sites:

- Entrez Gene (NCBI)
- Entrez Global (NCBI)
- Pictor (Johnson & Johnson)
- Hydra (Johnson & Johnson)
- Gene Cards (Xennex)
- TargetCV (Johnson & Johnson)
- Google Scholar



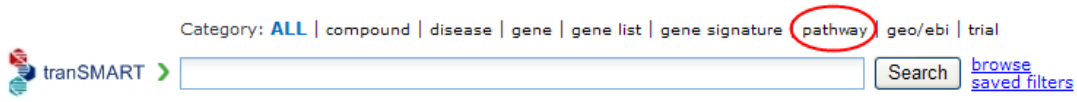
Clicking a green arrow pointing downward and to the right opens an internal tranSMART window – for example, search results are displayed when the green arrow after the clinical trial C0168T48 below is clicked (or when the trial name is clicked):



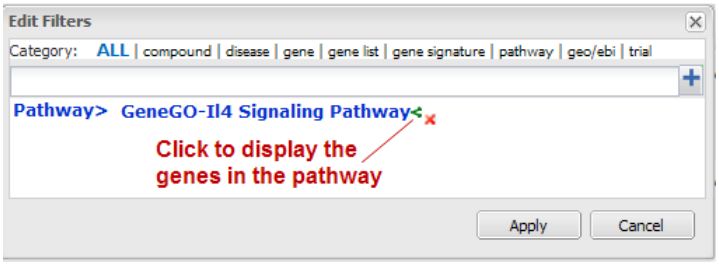
Can I remove some of a pathway's genes from the search filter?

Yes. To split a pathway into its component genes, click the green Split icon (<) after the pathway name on the Edit Filters dialog. You can then delete one or more of the pathway's genes from the search filter. For example:

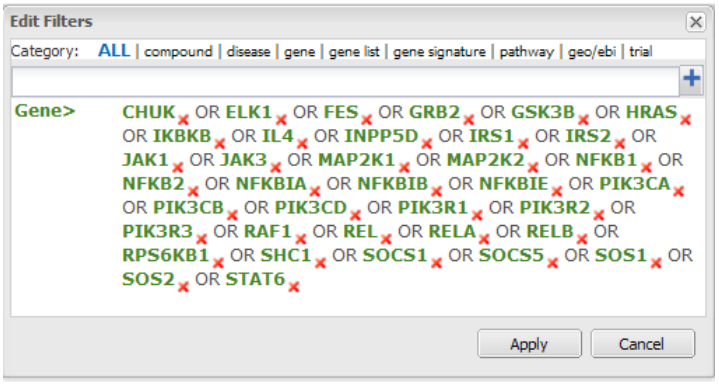
1. Click the filter category **pathway** in the tranSMART search window:



2. Type **il4** in the Search field, then select **Pathway>GeneGO> Il4 Signaling Pathway**.
3. Click the **advanced** button to display the Edit Filters dialog.
4. Click the Split icon (<) after the pathway name:



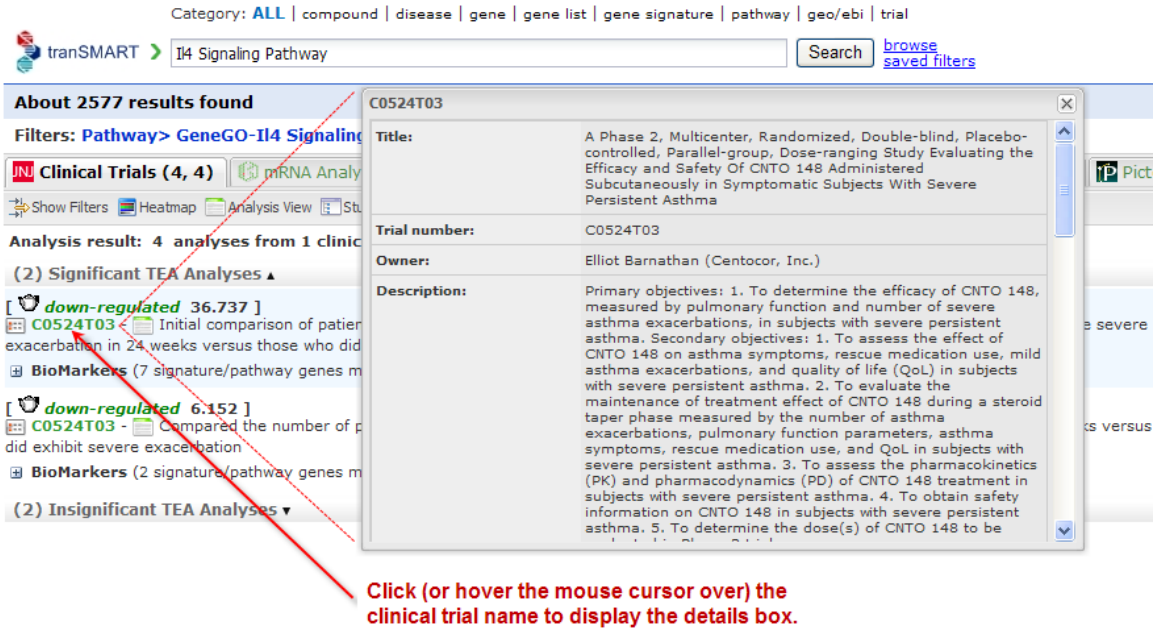
The Edit Filters dialog now looks as follows:



5. To remove one or more genes from the search filter, click the red x (x) after the name of each gene to remove.

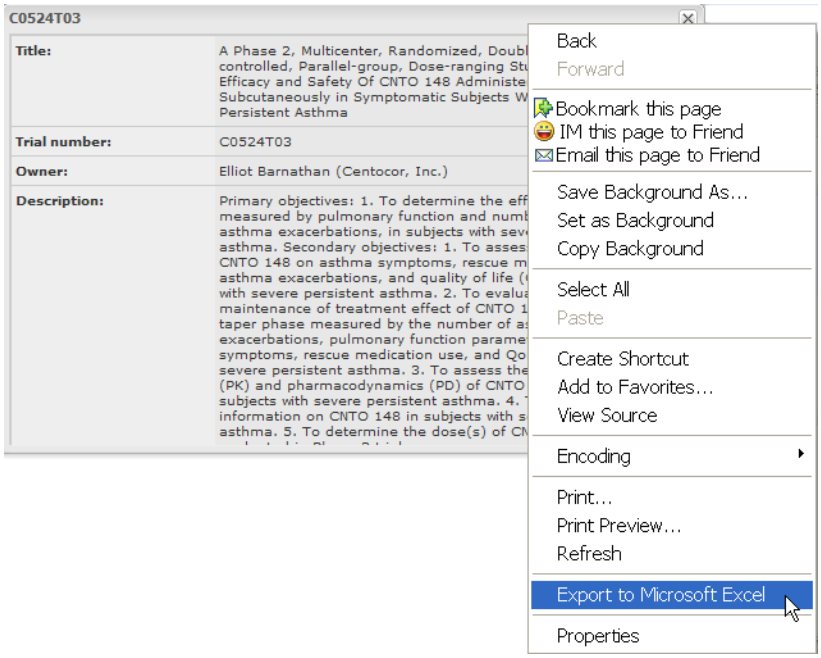
How can I open a details box for an item such as a clinical trial?

A details box contains information about subjects such as clinical trials, experiments, analyses, and gene signatures. You can open a details box by clicking the name of the item (such as a clinical trial) – for example:



How can I print the contents of a details box, or export the contents to Excel?

When the details box is open, right-click the details box and select the action you want:



Can I export statistics and measurements from a clinical trial or experiment?

Yes. tranSMART lets you export search results to Microsoft Excel. You can also export search results to other applications – for example, Johnson & Johnson's Pictor site, and Ariadne Genomics ResNet and Pathway Studio – where you can perform additional search operations on the tranSMART results.

What does the heat map show me?

A heat map is a matrix of colored squares. The color of each square represents the level of up- or down-regulation of an analyte in a given experiment, as follows:

- Red: Up-regulated.
- Green or Blue: Down-regulated.
- Black: Neither up-regulated or down-regulated.
- Gray: No relevant data exists for the analyte.

The brighter the color, the more strongly up-regulated (bright red) or down-regulated (bright green or blue) the analyte was in the experiment.

Are there different kinds of heat maps?

Yes. A heat map generated from Dataset Explorer represents a different kind of data than a heat map generated from a tranSMART search result:

- In Dataset Explorer, a heat map is a matrix of data points for a particular set of biomarkers, such as genes or RBM antigens, at a particular point in time in the study, as measured for a particular subject in the study.

  Up-regulation is expressed in shades of red. Down-regulation is expressed in shades of blue.

- In a tranSMART search result, a heat map is a matrix of data points for a particular set of genes, as measured in one or more study analyses.

  Up-regulation is expressed in shades of red. Down-regulation is expressed in shades of green.

Can I display heat maps if I have pop-up blocker enabled on my browser?

Yes. To allow heat maps to be displayed in Microsoft Internet Explorer 8 if you have pop-up blocker enabled, do the following:

1. Internet Explorer, click the **Tools** menu, then click **Internet Options**.
2. Click the **Privacy** tab.
3. In the Pop-up Blocker group box, click **Settings**.
4. In **Address of website to allow**, type the following:

   `jnj.com`

5. Click **Add**.
6. Click **Close**, then click **OK** to close the Internet Options dialog.

> **Note:** If your security software blocks pop-ups, refer to the documentation to learn how to allow pop-ups from the tranSMART site.

What is the TEA algorithm?

Target Enrichment Analysis (TEA) measures the enrichment of the genes in a gene signature, gene list, or pathway in a microarray expression experiment.

The TEA algorithm assigns scores to each expression experiment. A TEA score is based on the level of co-regulation or anti-regulation of the genes within a gene signature or list when compared with the corresponding genes in the experiment. With pathways, the TEA score is based on the level of up-regulation or down-regulation of the genes in the pathway and in the experiment.

TEA identifies experiments where the signature genes are differentially modulated, indicating that the associated target or pathway is affected by the treatment, disease, or other topic examined in the experiment.

What is Jubilant data?

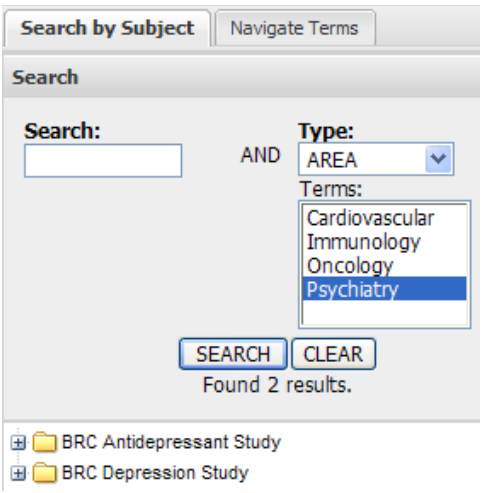
The **Literature** tab presents the user with information about the search terms that have been found in published literature. Jubilant is the name of a company that was sourced to curate thousands of peer-reviewed journal articles in the fields of oncology and immunology. Each article was reviewed and categorized into a 2009 MeSH (Medical Subject Headings via the National Library of Medicine) ontology. Jubilant also extracted mechanisms of action from most of the research articles so that each article can be explored in Ariadne's Pathway Studio software – exposing the underlying biochemistry.

What do I do if I get a Java security warning?

You may encounter a Java security warning when you try to generate visualizations such as heat maps and principal component analyses in Dataset Explorer. For information about these security warnings, see the document Configuration Tips.

In Dataset Explorer, can I search for a study according to my area of interest?

Yes. You can search for studies involving a particular research area, compound, or disease. In the following figure, two studies were found in a search for studies within the area of psychiatric research:



In Dataset Explorer, why do some of the elements in the ontology navigation pane have letter icons while others have numeric icons?

Nodes in the ontology that have numeric icon can be represented by numeric values. For example, IL-13 expression levels would be preceded by the icon **123**.

These numeric nodes are important for two reasons:

- When a user defines the criteria that subjects in the study groups must satisfy, he can specify numeric values in the Set Value dialog box, which lets the user specify logical operators (such as "equals" or "greater than") for the numeric criteria. For example, the user may want to specify that a study group be populated with subjects 50 years old or older.
- When the concept is dragged into the Results/Analysis view of Dataset Explorer, the values of each subset population will be analyzed.

Nodes in the ontology that have the icon of letters (**abc**) cannot be represented by numeric values. For example, the user may want to specify that a study group be populated with males only. These nodes cannot be filtered further with the Set Values dialog box.

Why is this trial-folder grayed out?

You don't have authorization to access the folder. See the next FAQ.

How do I gain access to additional clinical studies?

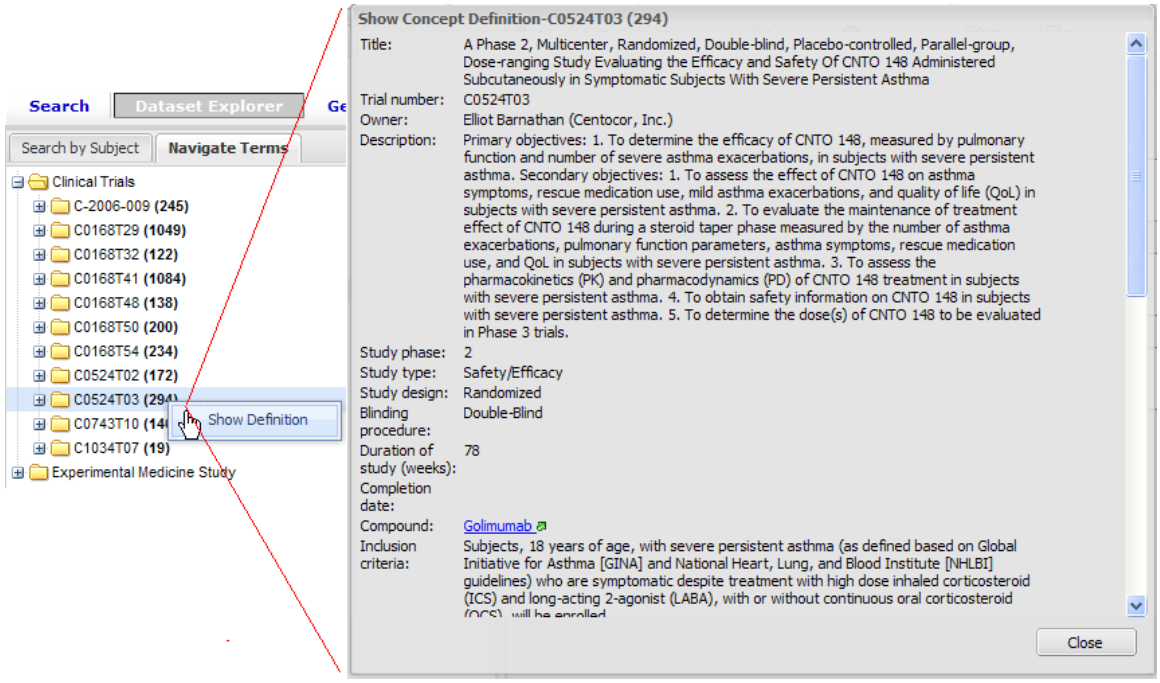
There is a formal process by which an individual will gain access to additional sources of data in tranSMART. An individual requesting read, read and export, or read, export and administrative access must write for permission from the individual denoted as the study owner. The study owner changes from study to study. If the study owner approves the request he will send an e-mail to Dr. Sandor Szalma (sszalma@its.jnj.com), who will enact the access request.

How do I determine the study owner of a given clinical study?

It depends where you are:

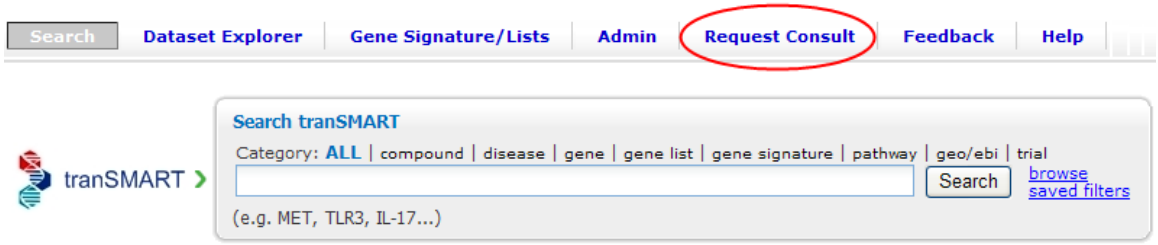
- If viewing a search result, click (or hover the cursor over) the study name. A dialog appears containing the name of the study owner and other details about the study:

- If in Dataset Explorer, right click the name of the study, then click Show Definition:



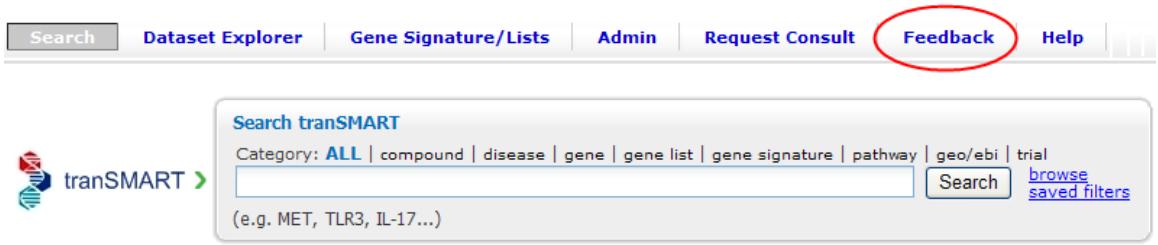
What do I do if I can't find the data I'm looking for?

Click the **Request Consult** button. An email window will open pre-addressed to the tranSMART consultation desk.



What do I do if I have a suggestion to improve tranSMART or find a bug?

Click the **Feedback** button. An email window will open pre-addressed to the tranSMART feedback desk.



What do I do if I have a suggestion to improve tranSMART or find a bug?