CURATION GUIDE

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Further help and tips are available on the PI2 wiki
https://www.pathogenomics.ca/wiki/index.php/Curators_Group

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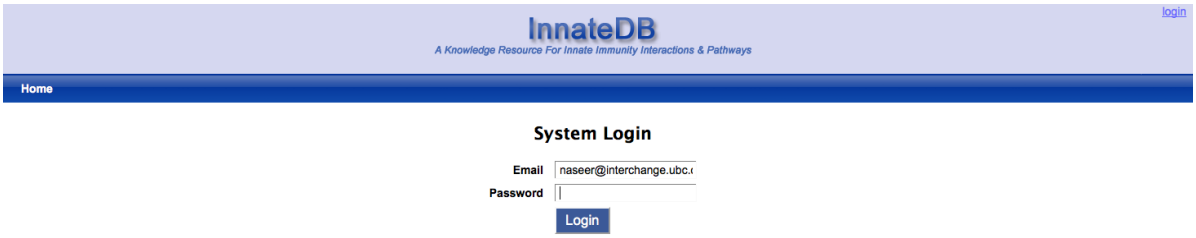
Chapter 1: A Guide To The InnateDB Submission System

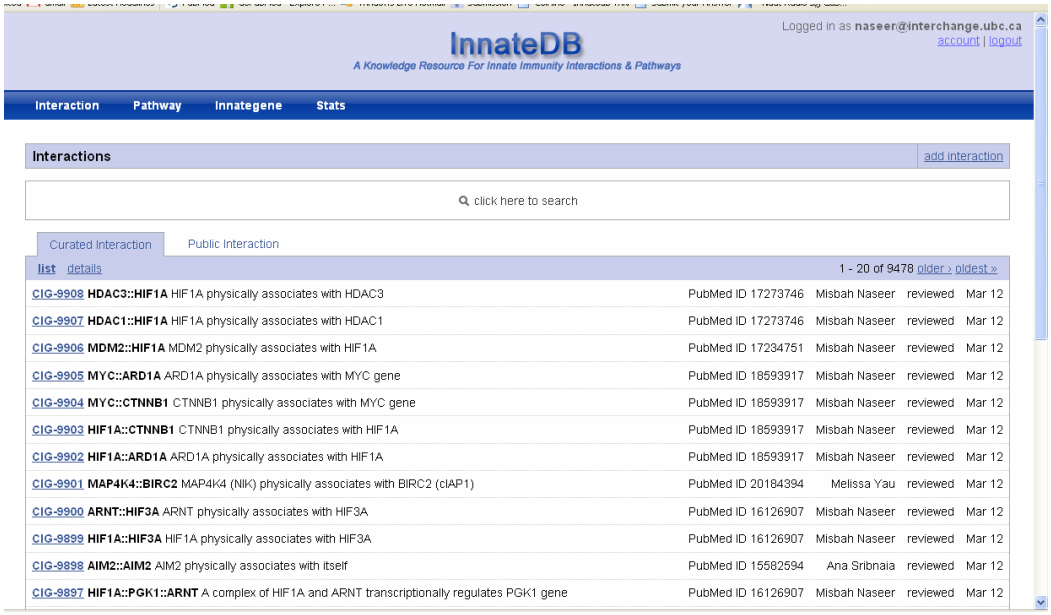
http://www.innatedb.ca/dashboard/

1.1 Logging In

A user email address and password are required to access the submission system.



First Page allows users to view & review submitted interactions:

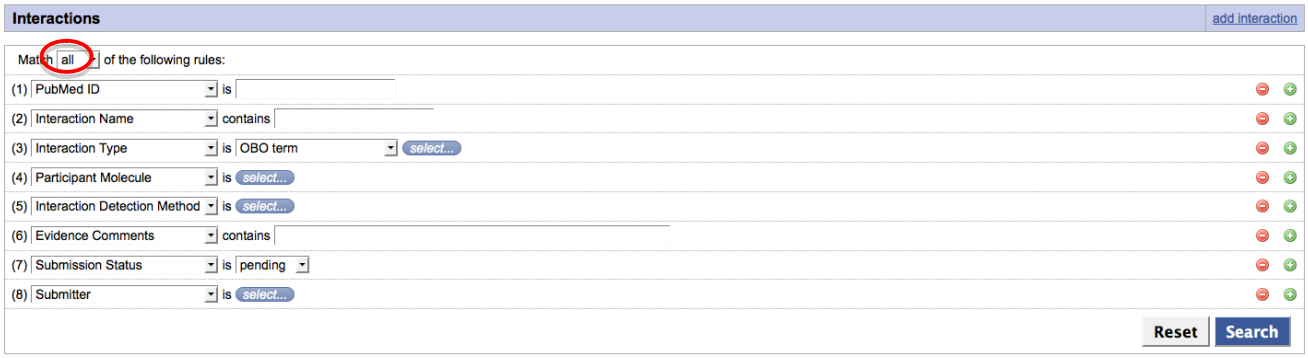


1.2 *Searching Interactions*

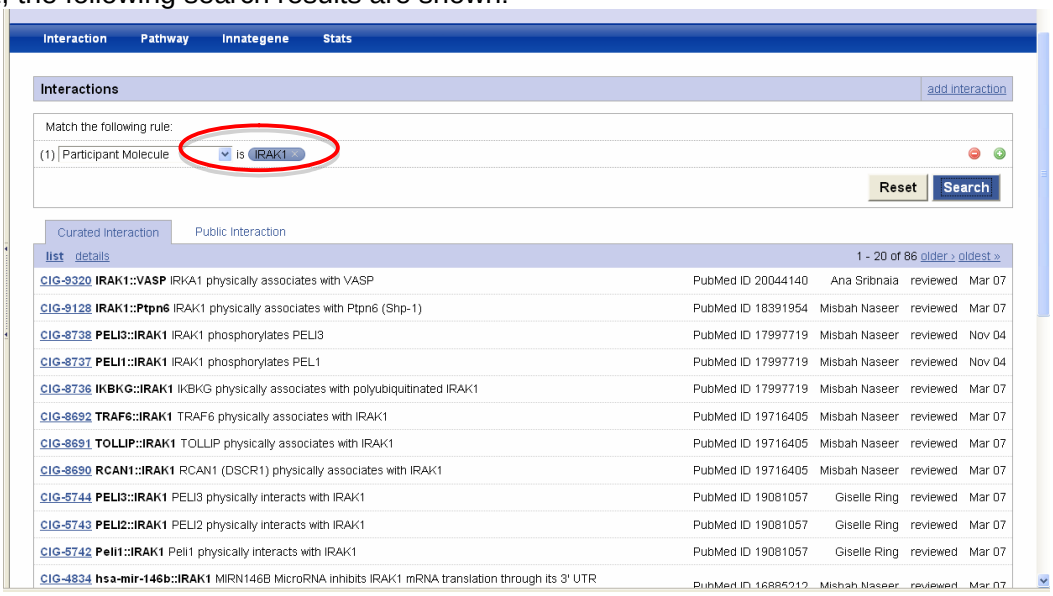
The submission system allows users to search single or multiple criteria at a time. Searchable fields include:

- PubMed ID
- Interaction Name
- Interaction Type
- Participant Molecule
- Interaction Detection Method
- Evidence Comments
- Submission Status
- Submitter

To add multiple search criteria, click the "+" icon. The user can search for interactions matching **all** criteria or **any** of the criteria selected. To take out a search criteria, click on the "-" icon.



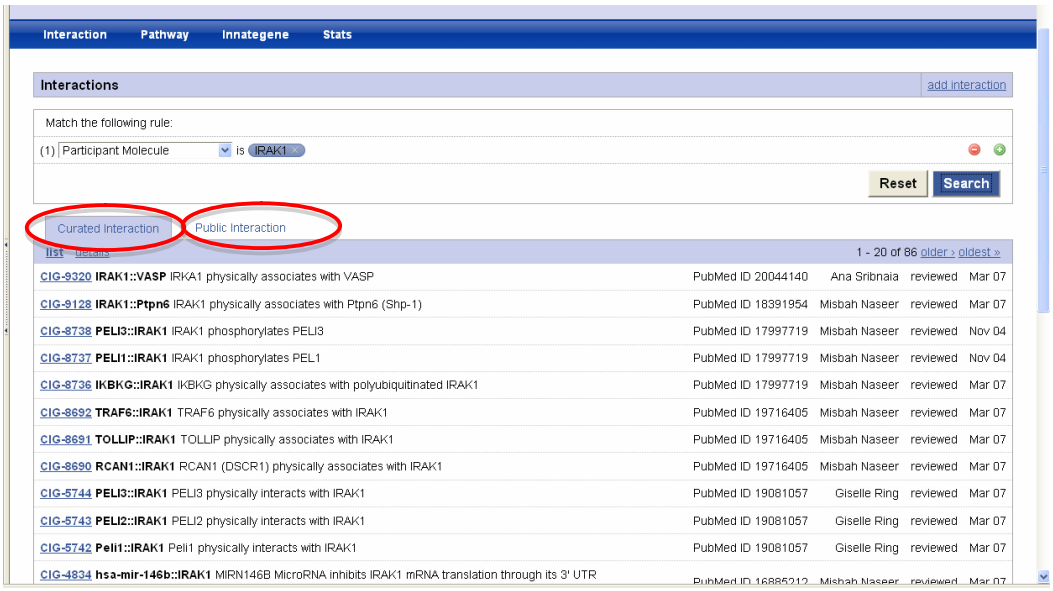
Click the "Search" button after entering the search criteria. For example, if participant molecule= IRAK1, the following search results are shown:



Results are categorized into:

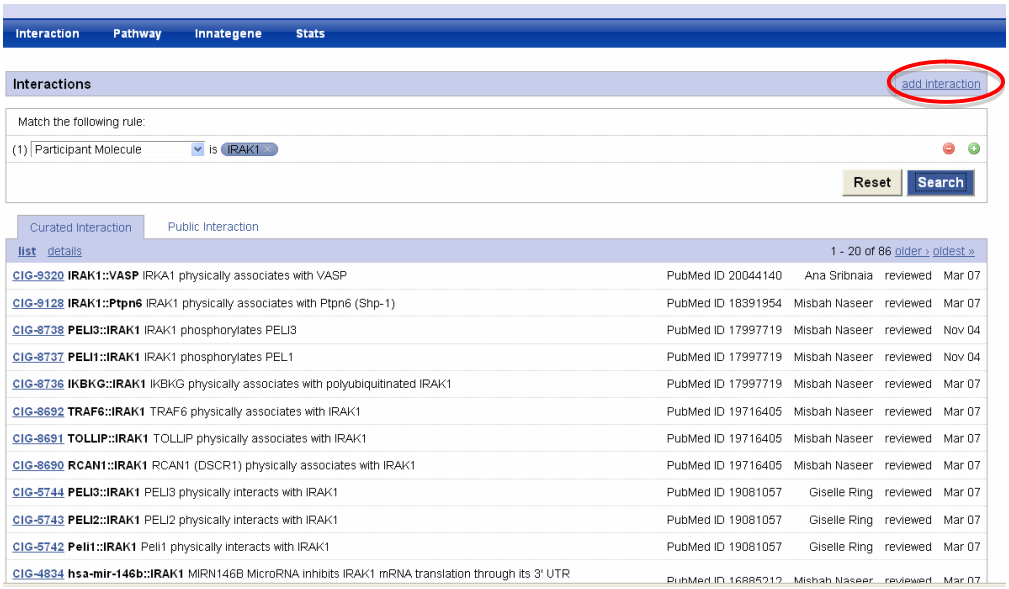
- **“Curated interactions”** which refer to interactions for IRAK1 manually curated by the InnateDB team

- **“Public Interactions”** which refer to all interactions for IRAK1 displayed on the main site (www.innatedb.ca)



1.3 Adding a New Interaction

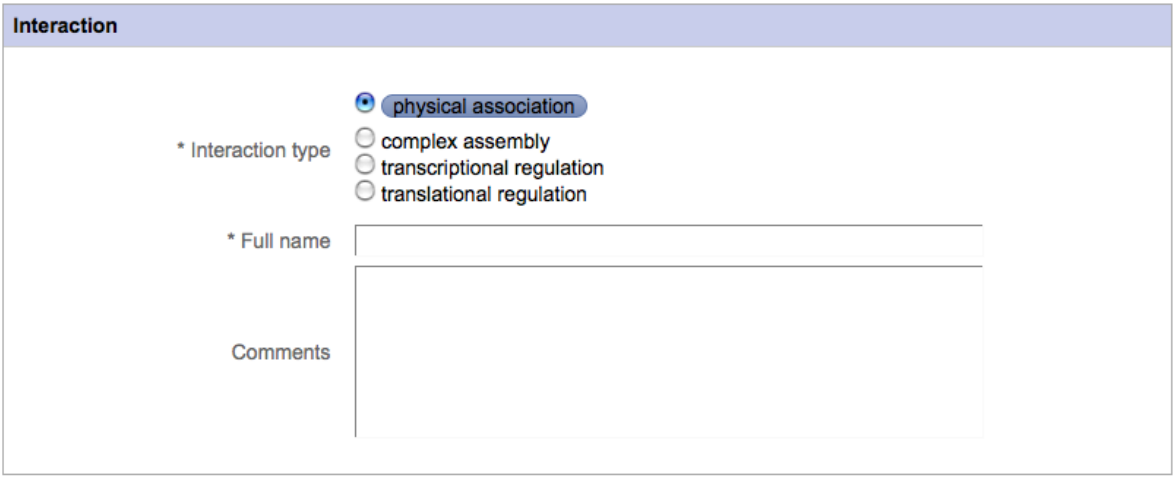
Click “Add Interaction” in the top right-hand corner of page to begin submitting a new interaction.



The submission page is broken into 3 main sections – Interaction, Participant & Evidence.

1.3.1 Interaction

1.3.1.1 Interaction type

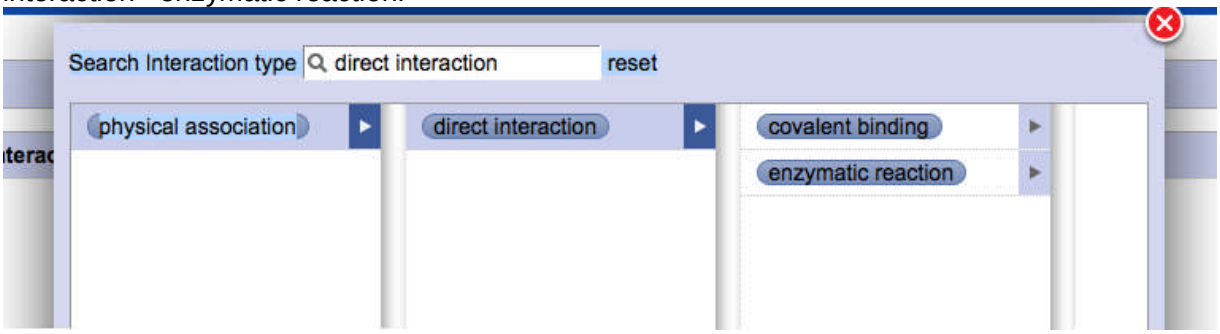


Select the appropriate interaction type from the list.

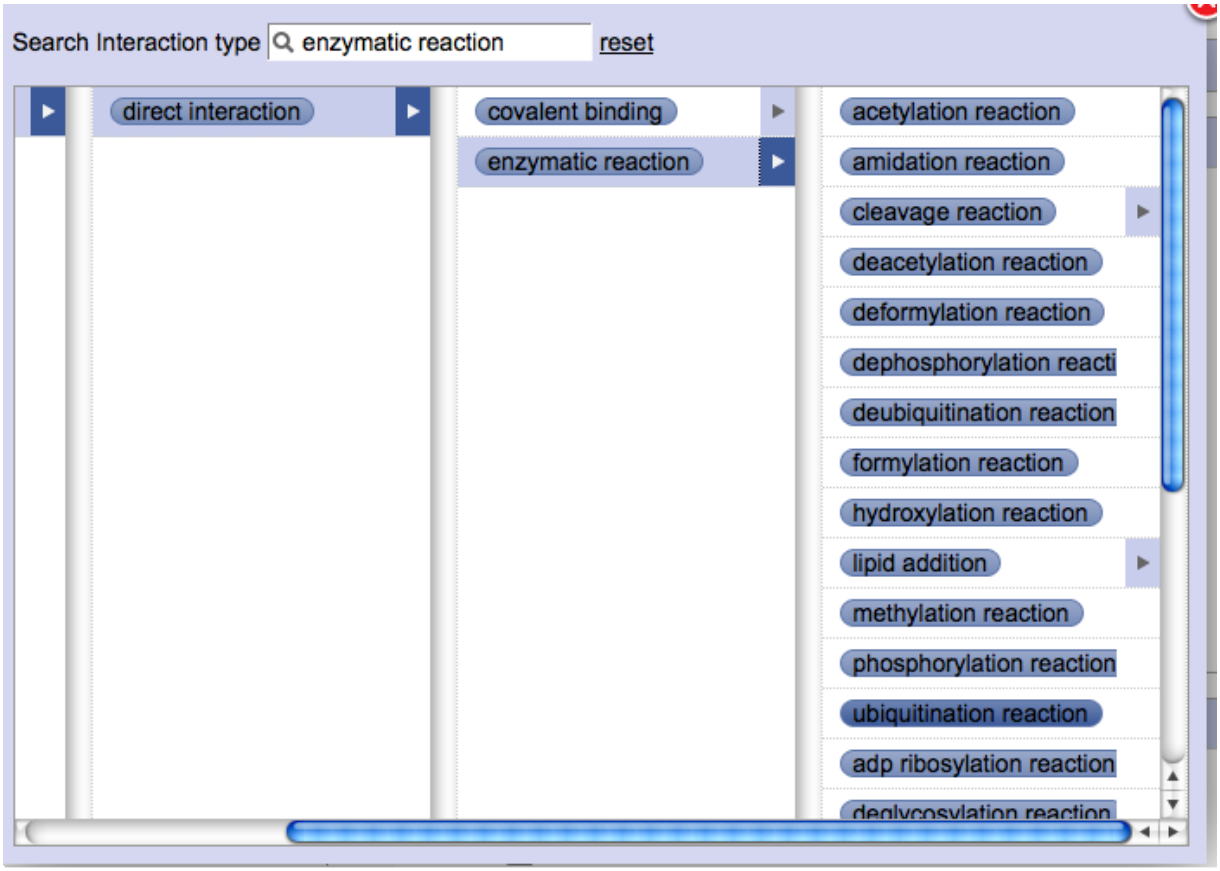
"**Physical Association**" is the most general term used to describe an interaction and should only be used when no other information is available (This is frequently the case).

"Direct Interaction" is the term used to describe an experiment in which the number of interactors equals 2 **highly purified** molecules and the interaction occurs in vitro, such that no host proteins may interfere.

For **biochemical reactions**, such as *phosphorylation*, *ubiquitination, cleavage* etc, click: "Physical Association". A search window will pop-up. The user may either manually enter the term in the search box or click on the arrow beside physical association and expand to direct interaction >enzymatic reaction.



From the list of enzymatic reactions, select the appropriate term for the interaction.



Commonly used enzymatic reactions are:

- cleavage reaction
- phosphorylation reaction
- dephosphorylation reaction
- ubiquitination reaction

"**Complex Assembly**" should be used to describe cases of complex formation i.e. A, B and C form complex ABC.

"**Transcriptional Regulation**" – remember we only describe direct, experimentally validated interactions in InnateDB. Experiments where a gene up/down regulates another gene should not be entered unless a direct interaction has been confirmed i.e. a Transcription Factor is shown to bind the promoter region of gene (via CHIP or EMSA) and up/down regulation is observed in an assay e.g. luciferase assay. When both physical interaction and gene regulation are experimentally proven, select "transcriptional regulation" as interaction type. The physical interaction evidence is described in the evidence section for the interaction with the transcriptional regulation assay is described in the comments. If no up/down regulation observed then the interaction type is just "Physical Interaction".

"**Translational Regulation**" – rarely used. See "Transcriptional Regulation". Example interaction of RNA x with gene y leads to increased/decreased translation of protein. Examples of this are very rare.

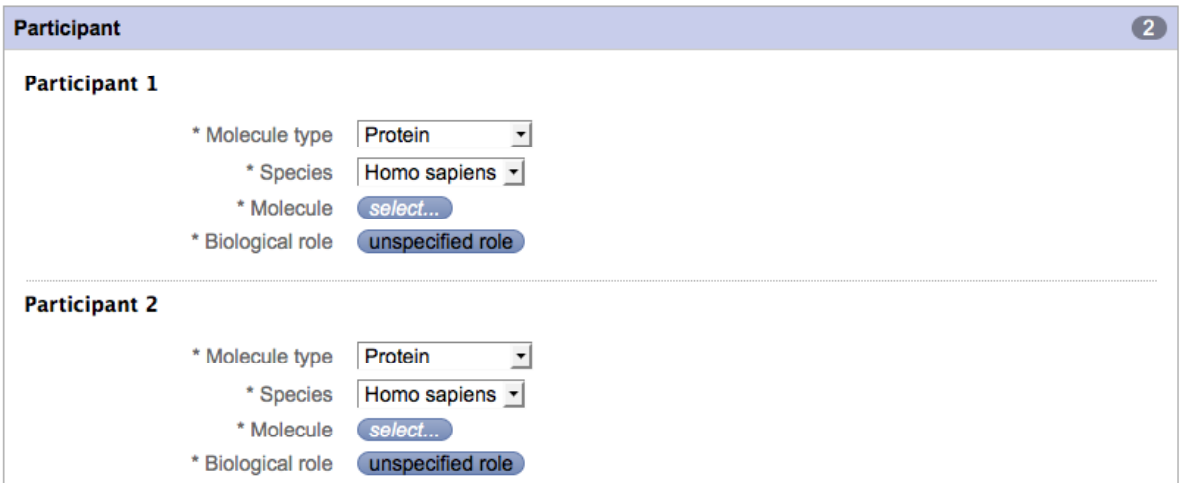
1.3.1.2 Full name

Provide one sentence describing the interaction between the interactors and any specific conditions applying to the interaction. The format of the sentence should agree with the interaction type selected e.g. IRAK4 phosphorylates IRAK1; TLR4 physically associates with LY96; ITCH autoubiquitinates itself in the presence of UBE2L3; IL1 stimulation leads to the complex formation of IRAK1, TRAF6 and MAP3K3. Use HGNC (HUGO Gene Nomenclature Committee) symbols for human participants (UPPER CASE) and Mouse Genome Informatics (MGI) symbols (Title case) for mouse participants.

1.3.1.3 Comments

If information applicable to **all** possible evidences is available, record it in the comments field e.g. a common name for a complex etc. Usually this can be left blank.

1.3.2 Participant



If there are > 2 participants in an interaction à click “add new participant”. This can be done as many times as required.

1.3.2.1 Molecule Type

Select the correct molecule type of the participant from the list (Protein, DNA, RNA). The default selection is Protein. Different participants may have different molecule types e.g. a protein (e.g. transcription factor) may interact with a gene.
Note: the ability to describe interactions between a complex and another molecule type will be added later in InnateDB development.

1.3.2.2 Species (Human & Mouse Only!)

Select the species of the participant from the list provided. InnateDB only includes interactions involving human/mouse molecules. The different participants may be of different species e.g. an experiment that shows a human protein interacts with a mouse protein. If no information about species can be gathered from the paper and references, contact the author of the paper to ensure the species.

1.3.2.3 Molecule

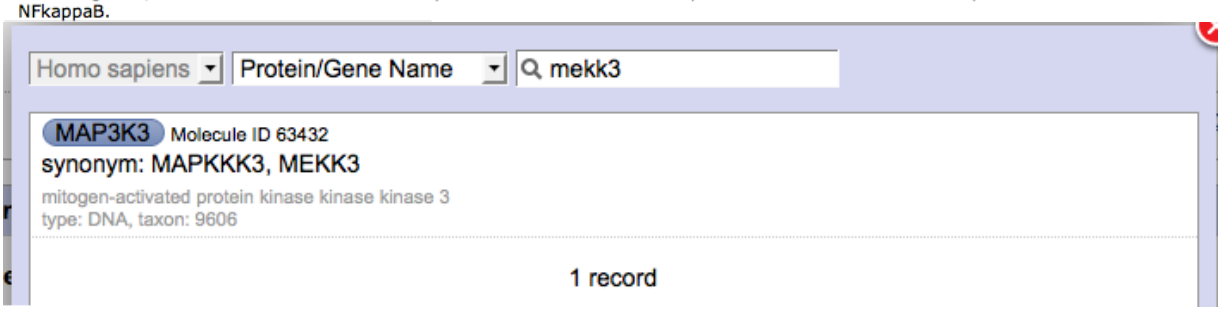
Click “select” button. Enter the symbol for the participant in the text field and hit the ENTER key. Note: Often genes are more commonly known by another name (synonym) so you will need to watch out for this and ensure you are entering the correct name. If a synonym is entered (e.g. MEKK3), the search will provide HGNC symbol for gene(s) with the entered synonym (e.g. MAP3K3).

Protein kinase C-associated kinase can activate NFkappaB in both a kinase-dependent and a kinase-independent manner.

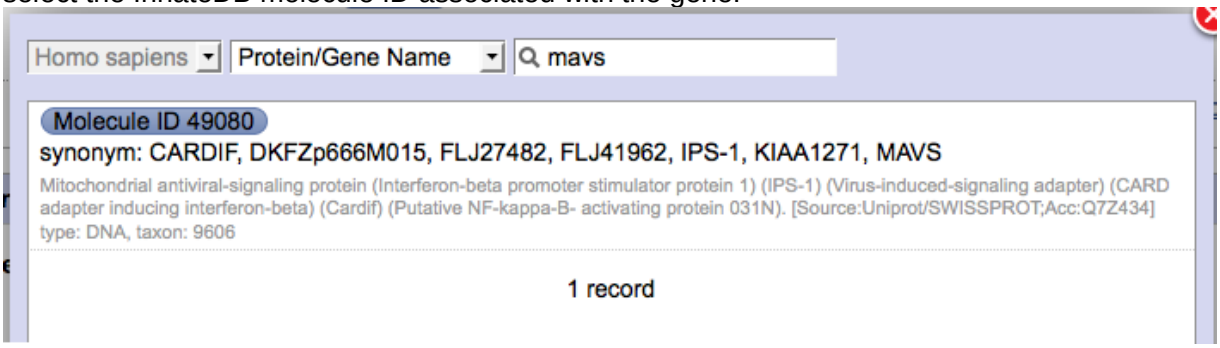
Moran ST, **Haider K**, **Ow Y**, **Milton P**, **Chen L**, **Pillai S**.

Massachusetts General Hospital Cancer Center, Harvard Medical School, Building 149, 13th Street, Charlestown, MA 02129, USA.

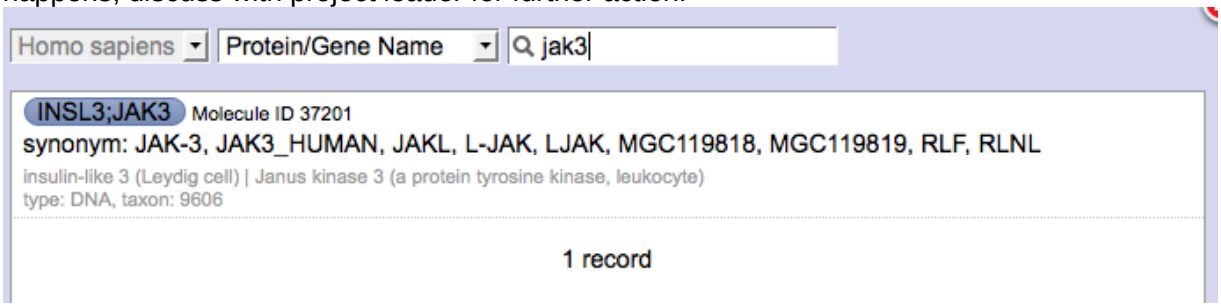
Protein kinase C-associated kinase (PKK, also known as RIP4/DIK) activates NFkappaB when overexpressed in cell lines and is required for keratinocyte differentiation in vivo. However, very little is understood about the factors upstream of PKK or how PKK activates NFkappaB. Here we show that certain catalytically inactive mutants of PKK can activate NFkappaB, although to a lesser degree than wild type PKK. The deletion of specific domains of wild type PKK diminishes the ability of this enzyme to activate NFkappaB; the same deletions made on a catalytically inactive PKK background completely ablate NFkappaB activation. PKK may be phosphorylated by two specific mitogen-activated protein kinase kinase kinases, MEKK2 and MEKK3, and this interaction may in part be mediated through a critical activation loop residue, Thr184. Catalytically inactive PKK mutants that block phorbol ester-induced NFkappaB activation do not interfere with, but unexpectedly enhance, the activation of NFkappaB by these two mitogen-activated protein kinase kinase kinases. Taken together, these data indicate that PKK may function in both a kinase-dependent as well as a kinase-independent manner to activate NFkappaB.



***Special case 1**:* If a HGNC symbol has not been assigned to a gene, search the gene and select the InnateDB molecule ID associated with the gene.

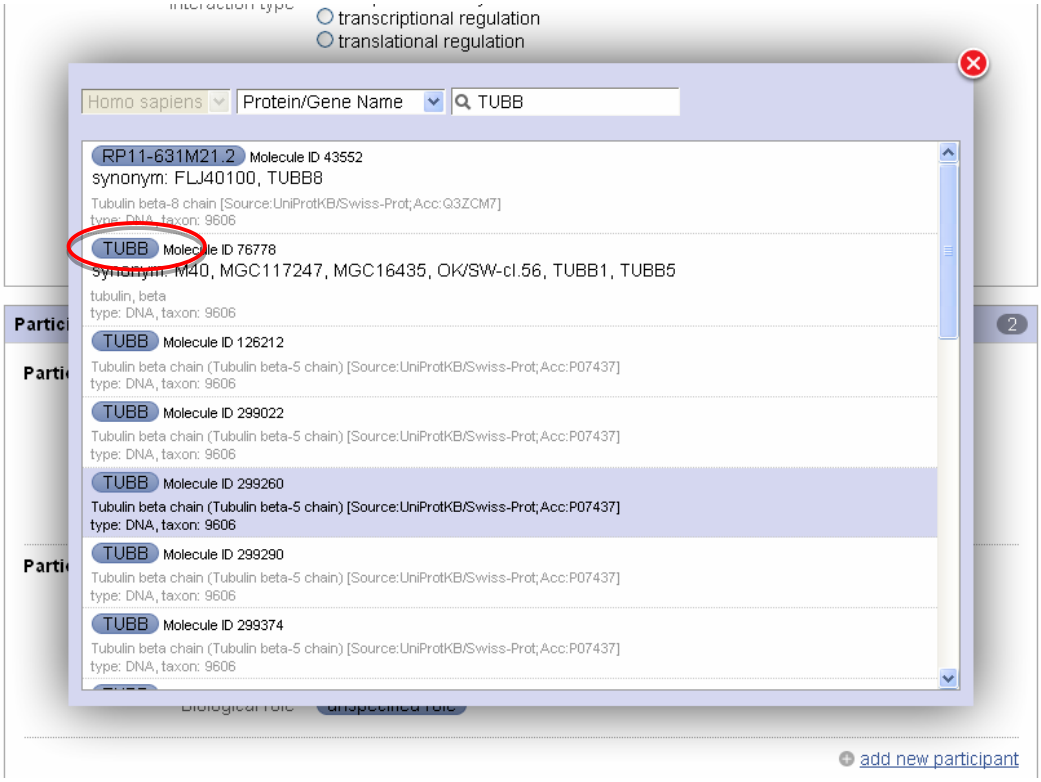


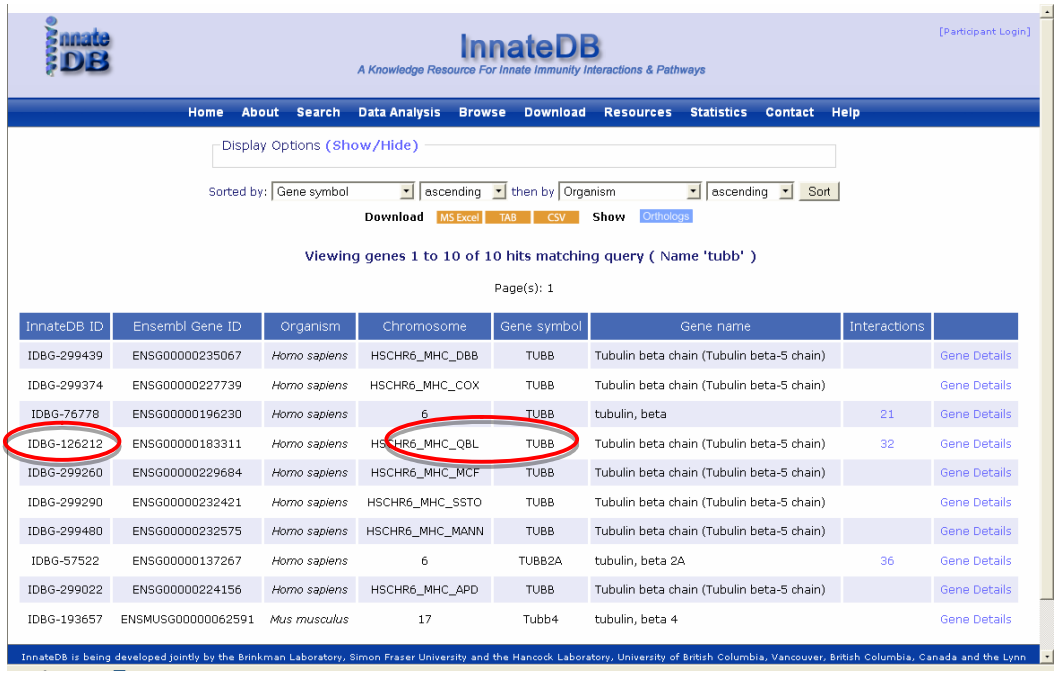
Special case 2: Sometimes 2 HGNC IDs are assigned to the same InnateDB gene. If this happens, discuss with project leader for further action.



Special case 3: Since 2009, ENSEMBL has included nine haplotypic regions, mainly in the MHC region of chromosome 6 in its gene database. Consequently, search for a gene may generate several results with identical HGNC IDs but different InnateDB molecule IDs.

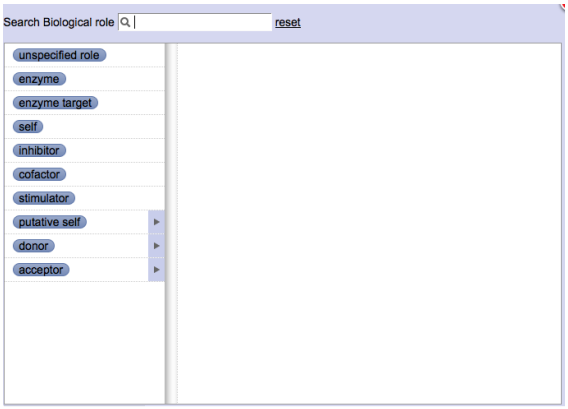
If this happens, search the gene on the main site (www.innatedb.ca). Note the InnateDB molecule ID of the gene which is located on Chromosome 6 (not the MHC regions). Use this molecule ID for submitting interactions for the gene.





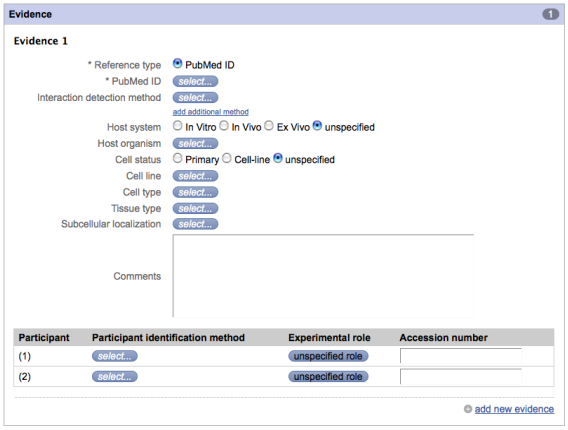
1.3.2.4 Biological Role

Select an appropriate term for the biological role for the interactor in context of the interaction e.g. *unspecified* for physical interactions, *enzyme and enzyme target* for phosphorylation, ubiquitination, dephosphorylation etc.



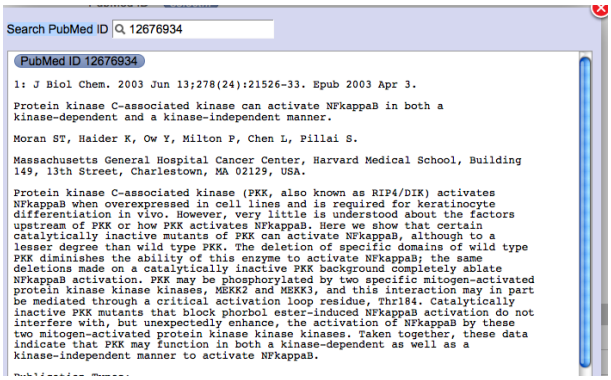
1.3.3 Evidence

Multiple evidences are possible for an interaction; either from the same PubMed ID where different experiments prove the same interaction or where two or more papers describe evidence of an interaction. Click “+ add new evidence” to add additional evidence either with the same PubMed ID or with a different one.



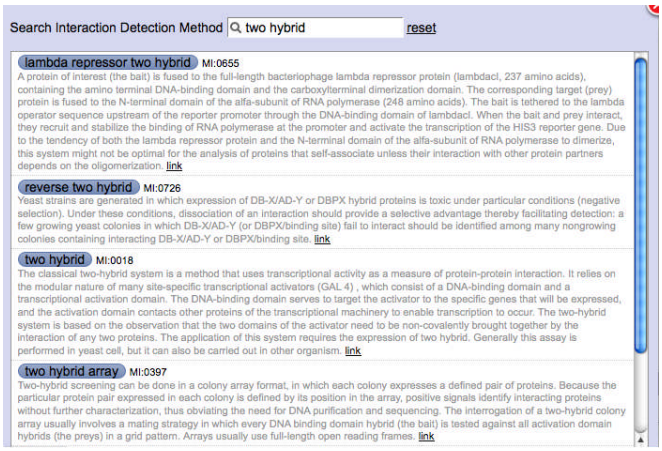
1.3.3.1 PubMed ID

Enter the PubMed ID (PMID) for the publication in which the interaction and its evidence is described. The search box will display the abstract for the entered PMID. Ensure that the correct paper is retrieved.

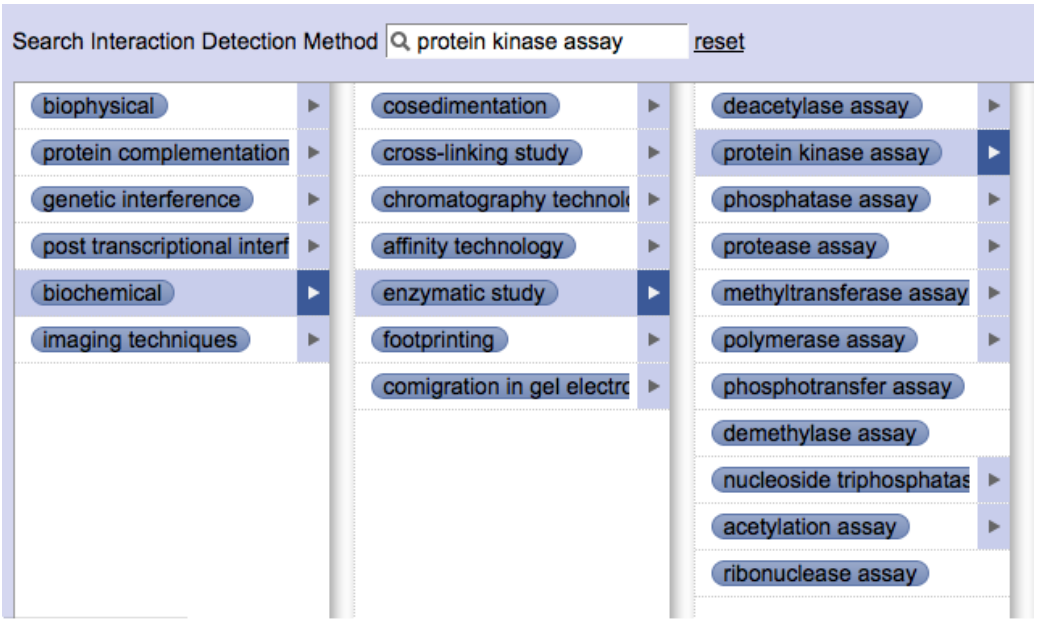


1.3.3.2 Interaction Detection Method

This is the experimental method used to detect the interaction, usually the basis for evidence of an interaction. Interaction detection method terms are controlled Open Biomedical Ontology (OBO) terms for Molecular Interactions. These terms are searchable by typing a term (or part of a term) into the box and hitting the ENTER key. Once search terms are entered, a selection of controlled vocabulary terms appear in a drop down menu, select the interaction term which best fits the experiment performed.



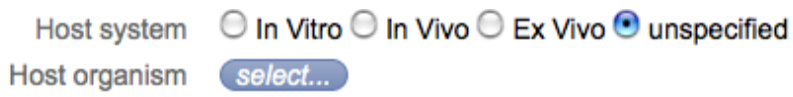
Alternatively, different OBO terms listed in the search menu can be expanded until the appropriate term is found.



Following are some OBO terms used for common detection methods:

- *coimmunopercipiation/ anti-tag coimmunoprecipitation:* coimmunoprecipitation
- *protease assay:* cleavage reactions
- *enzymatic study:* luciferase assay, ubiquitination/conjugation assay
- *protein kinase assay/ in-gel kinase assay*: phosphorylation reaction
- *phosphatase assay*: dephosphorylation reaction
- *pull down: GST pull down assay*

1.3.3.6 Host System and Host Organism



Host System:

In Vitro – experiments performed in a cell-free system; also used for experiments involving immortalized and commercially sold cell lines.

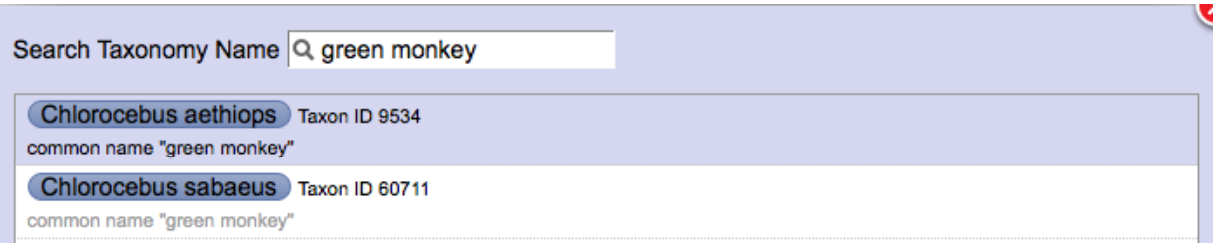
In Vivo – experiments performed in an organism or with cells extracted from an organism which have not been subject to any treatment.

Ex Vivo – experiments performed on cells extracted from a living organism that have been subjected to some form of treatment e.g. TNF, LPS stimulation , also cells derived/cultured from living cells e.g. monocytes cultured from PBMCs.

Unspecified – Experiments performed in a foreign system such as yeast two hybrid experiment.

Host Organism:

The host system is the species where the interaction was shown to take place. This is NOT to be confused with the species of the participant molecules (human and mouse only). For example yeast two hybrid would be “yeast” and HEK293 cells would be “human”. This is a searchable field with controlled vocabulary, thus the host system species must be selected from the drop menu of controlled vocabulary which appears in the search box. Any species can be added here e.g. African green monkey, yeast. Sometimes there are several possible options for a common name – make sure you choose the correct species based on the scientific name.



1.3.3.7 Cell Status

Primary - Cells were taken directly from a living organism, which is not immortalized. Cells may be cultured following isolation e.g. monocytes derived from peripheral blood mononuclear cells (PBMCs), bone-marrow derived macrophages

Cell-line - Cells which are grown under controlled conditions e.g. HeLa.

Unspecified - when primary cells or cell line were not used or not indicated in the experiment.

1.3.3.8 Cell Line

Enter the name of the cell line in which the interaction was found to occur. Where possible use the ATCC cell line names found at **http://www.atcc.org/**. Other details such as what cell type, tissue and species a cell line is derived from can also be looked up here. See **https://www.pathogenomics.ca/wiki/index.php/Curators_Group** for cell line details that have already been looked up and for information about standards used to classify a cell line not listed on the page.

Example: Caco 2: cell type: epithelial cell; Tissue type: colorectal adenocarcinoma cell line; *Homo sapiens*

1.3.3.9 Cell Type

Enter the distinct morphological or functional form of cell e.g. macrophage, epithelial etc. Cell line names should not be entered here. The cell type of a cell line should be entered. Cell type terms are OBO controlled terms and can be searched similarly to interaction detection method.

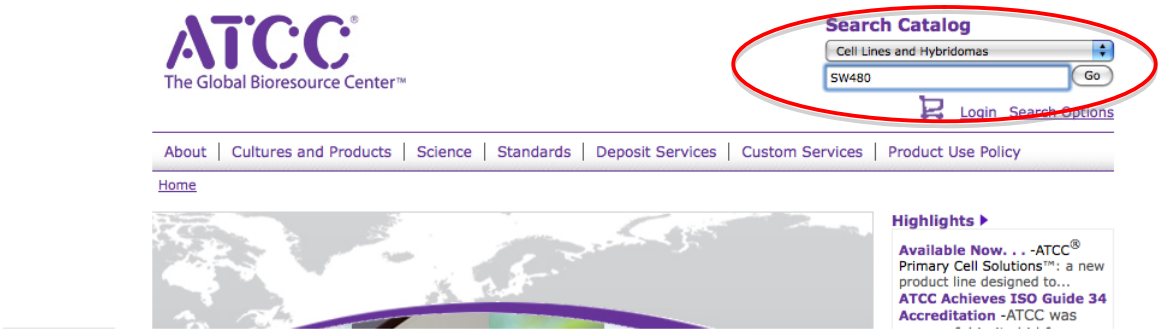
1.3.3.10 Tissue Type

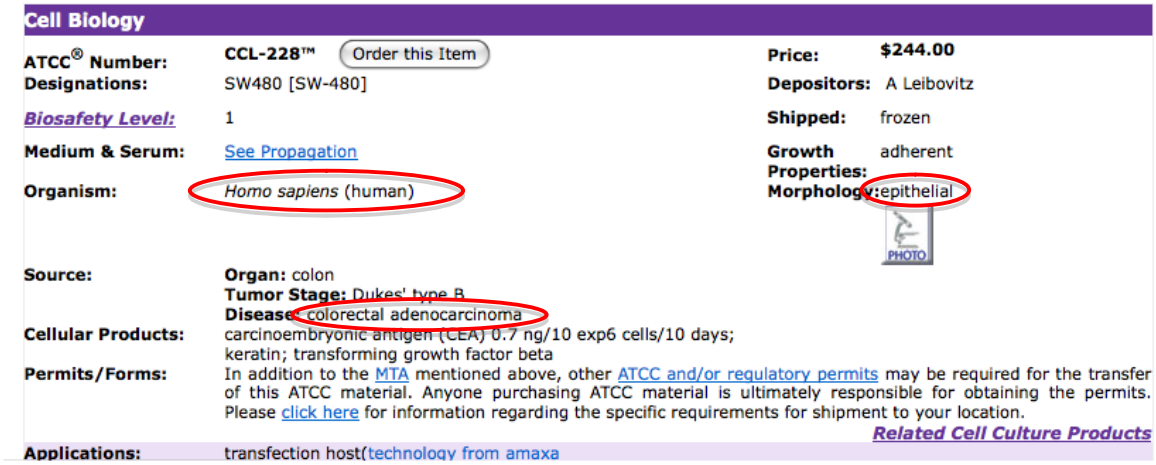
The tissue in which the cells were derived from e.g. lung, heart, brain etc. Tissue terms are OBO controlled terms and can be searched similarly to interaction detection method.

Example

To determine the cell type, tissue type and species of the cell line, search the ATCC cultures to find most of the cell line descriptions.

For example if a paper mentions SW480 cells:



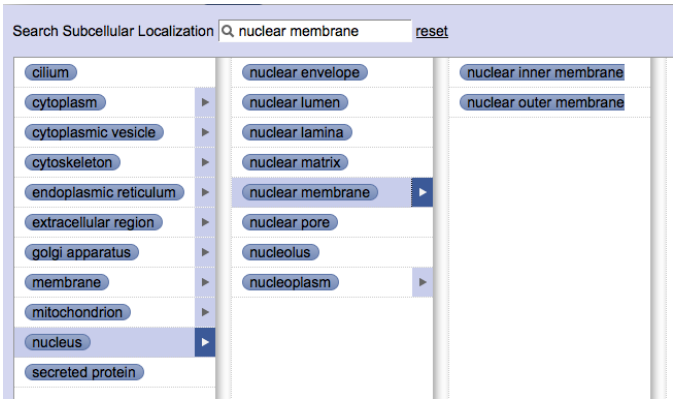


Hence, the following information will be entered:

Cell line: SW480
Cell type: epithelial cell
Tissue type: colorectal adenocarcinoma cell line

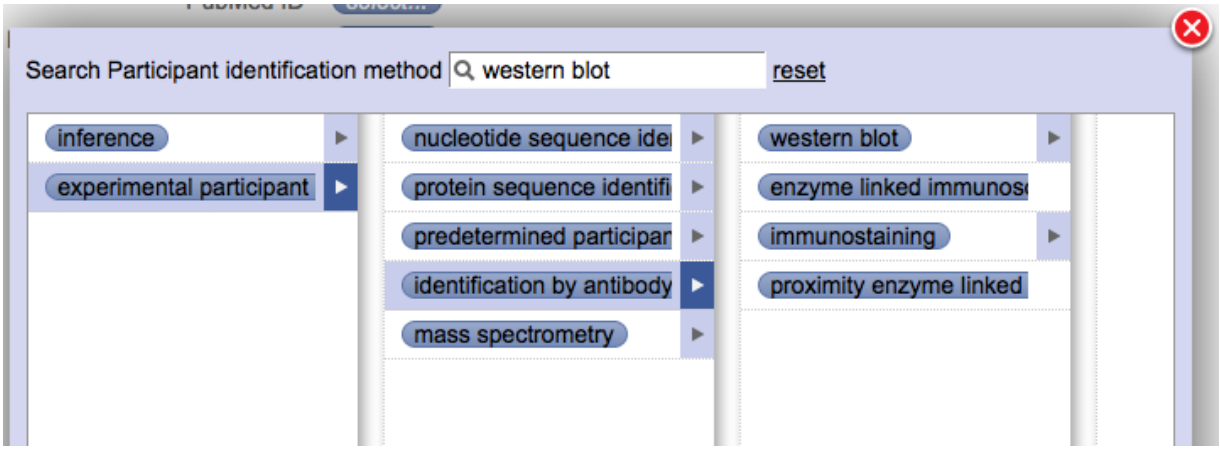
1.3.3.11 Subcellular localization

If specified, this is where the location within the cell in which the **interaction** is observed and NOT the subcellular localization of where a protein is normally located. When inputting subcellular localization, only controlled terms are allowed and thus this is a searchable field. Once search terms are entered, a selection of controlled vocabulary terms appear in the search window, select the term which best fits the subcellular localization. Alternatively, the given list in the search box can be expanded to the appropriate term.

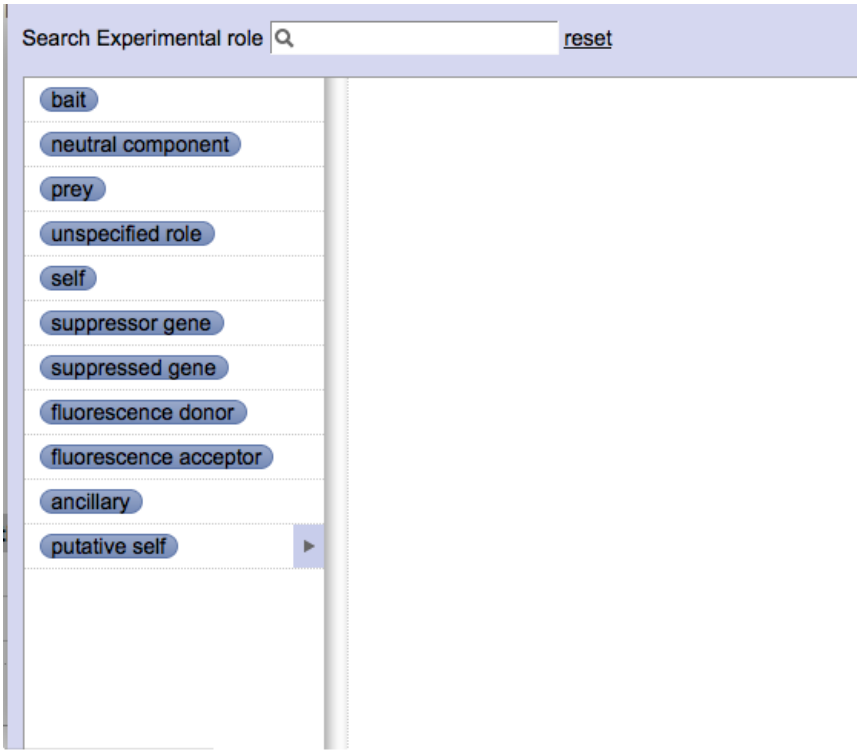

Search Subcellular Localization
nuclear membrane
reset
cilium
cytoplasm
cytoplasmic vesicle
cytoskeleton
endoplasmic reticulum
extracellular region
golgi apparatus
membrane
mitochondrion
nucleus
secreted protein
nuclear envelope
nuclear lumen
nuclear lamina
nuclear matrix
nuclear membrane
nuclear pore
nucleolus
nucleoplasm
nuclear inner membrane
nuclear outer membrane

1.3.3.12 Participant Identification Method and Experimental Role

The method used to identify or determine the participant in the interaction detection experiment is entered in this field. The participant identification method is usually found in the Materials and Methods sections of papers describing interactions and there may more than one used. If more than one method is used, add the one which is more specific in identifying the participant.



Experimental Role explains the role of each interaction participant in the experiment demonstrating the interaction.



bait – The participant was used as a “bait” to find the other participant(s). For example, in a GST pulldown experiment, the GST fusion protein is the bait since it is used to detect other interacting proteins. This is usually the stationary/immobilized participant.

prey – The participant that interacts with the bait; the interactor that is detected because of its interaction with the bait.

ancillary – This is the participant(s) in a complex which links other components of a complex together.

neutral component – An interaction participant that has a neutral role in the interaction; for example in a non-screening yeast two hybrid, neither component is the bait or prey, but instead come together to demonstrate an interaction.

suppressor gene – The gene which suppresses another gene.

suppressed gene – The gene which is suppressed by a suppressor gene.

fluorescence donor – In experiments where fluorescence energy transfer is used (such as in FRET), this is the participant which is the source of fluorescence energy.

fluorescence acceptor – In experiments where fluorescence energy transfer is used (such as in FRET), this is the participant which receives fluorescence energy from the fluorescence donor.

fluorescence acceptor donor pair – Comprised of a fluorescence acceptor and donor.

self – When there is only one participant i.e. an interaction with itself (dimer formation, auto-phosphorylation).

unspecified role – Used when the role of the participant is unknown. This option is rarely used.

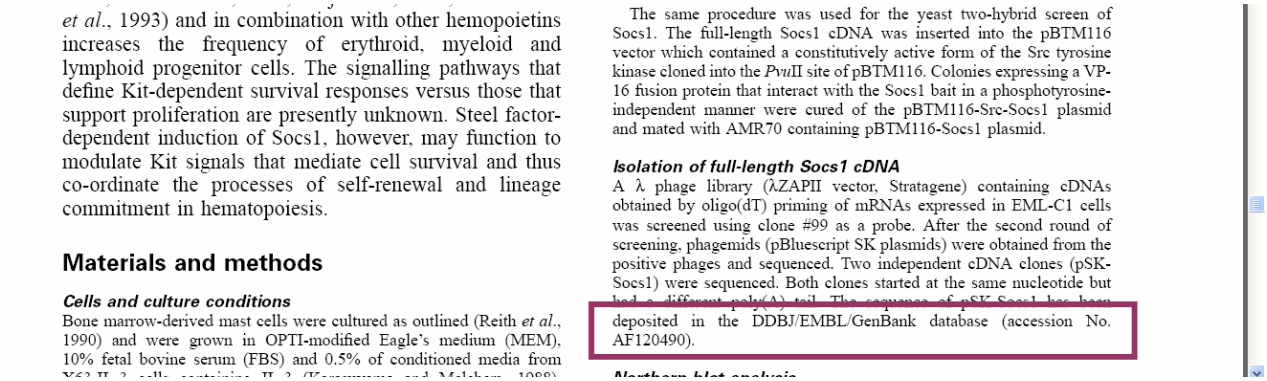
In general, there are <u>many</u> methods which may be used in an article to detect the participant in the interaction, however here are some common ones:

Interaction Detection Method	Expt. Role	Participant Identification Method
Yeast two hybrid	• **Bait** • **Prey**	Plasmid verified by nucleotide sequencing Positive clones verified by nucleotide sequencing
Coimmunoprecipitation	• **Bait** • **Prey**	- Western blot (mono/polyclonal if specified) or - Plasmid was verified by nucleotide sequencing Western blot (mono/polyclonal if specified)
Anti Tag Coimmunoprecipitation	• **Bait** • **Prey**	Western blot (mono/polyclonal if specified) or tag western blot - Anti tag western blot or - Western blot (mono/polyclonal if specified)
Pull down	• **Bait** • **Prey**	Predetermined participant - Western blot (mono/polyclonal if specified) or - Autoradiography if used in vitro translated 35S-labelled protein
Chromatin Immunopercipitation Assays	• **Neutral Component** • **Neutral Component**	- Primer specific PCR (gene) - Identification by antibody (protein)
Electrophoretic Mobility Shift Assay	• **Neutral Component** • **Neutral Component**	- Autoradiography (gene) - Identification by antibody (protein)

1.3.3.13 Accession Number

A unique identifier given to a biological polymer sequence (DNA, protein) when it is submitted to a sequence database. If an accession number for a participant(s) is given in the paper please record it as it can be used to identify the exact variant of a gene or protein used in the experiment. Many different identifiers could be named in articles; the more common identifiers are GenBank, Swiss-Prot, RefSeq and are usually found in material and methods section.

****TIP: It is best to verify the accession number by going to NCBI to make sure that it is the protein you are interested in and it also verifies the species of the protein.**



et al., 1993) and in combination with other hemopoietins increases the frequency of erythroid, myeloid and lymphoid progenitor cells. The signalling pathways that define Kit-dependent survival responses versus those that support proliferation are presently unknown. Steel factor-dependent induction of Socs1, however, may function to modulate Kit signals that mediate cell survival and thus co-ordinate the processes of self-renewal and lineage commitment in hematopoiesis.

Materials and methods

Cells and culture conditions

Bone marrow-derived mast cells were cultured as outlined (Reith *et al*., 1990) and were grown in OPTI-modified Eagle's medium (MEM), 10% fetal bovine serum (FBS) and 0.5% of conditioned media from

The same procedure was used for the yeast two-hybrid screen of Socs1. The full-length Socs1 cDNA was inserted into the pBTM116 vector which contained a constitutively active form of the Src tyrosine kinase cloned into the *Pvu*II site of pBTM116. Colonies expressing a VP-16 fusion protein that interact with the Socs1 bait in a phosphotyrosine-independent manner were cured of the pBTM116-Src-Socs1 plasmid and mated with AMR70 containing pBTM116-Socs1 plasmid.

Isolation of full-length Socs1 cDNA

A λ phage library (λZAPII vector, Stratagene) containing cDNAs obtained by oligo(dT) priming of mRNAs expressed in EML-C1 cells was screened using clone #99 as a probe. After the second round of screening, phagemids (pBluescript SK plasmids) were obtained from the positive phages and sequenced. Two independent cDNA clones (pSK-Socs1) were sequenced. Both clones started at the same nucleotide but

deposited in the DDBJ/EMBL/GenBank database (accession No. AF120490).

1.3.3.14 Comments

Any additional comments or clarification about the experiment can be entered here. Special conditions or treatments in the experiment must be specified. For common additional information, the format for entry into comments is:

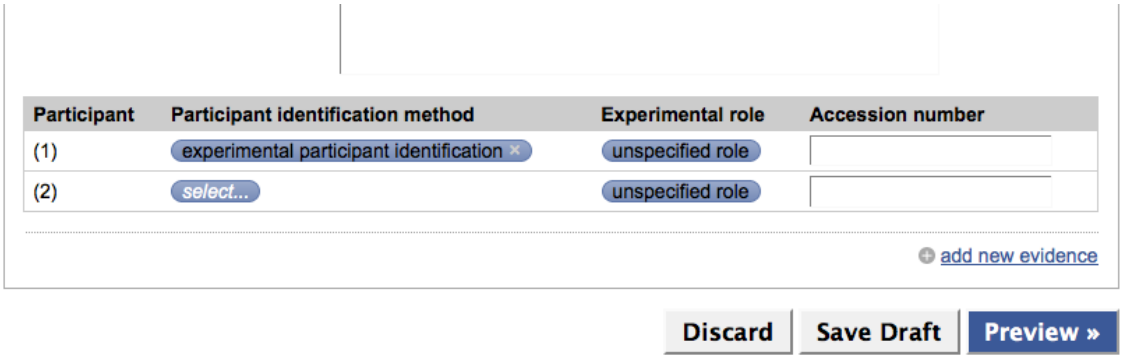
Tags: _____; Treatment:_____; interacting domain:_____; [any other information.]

Example Comments:

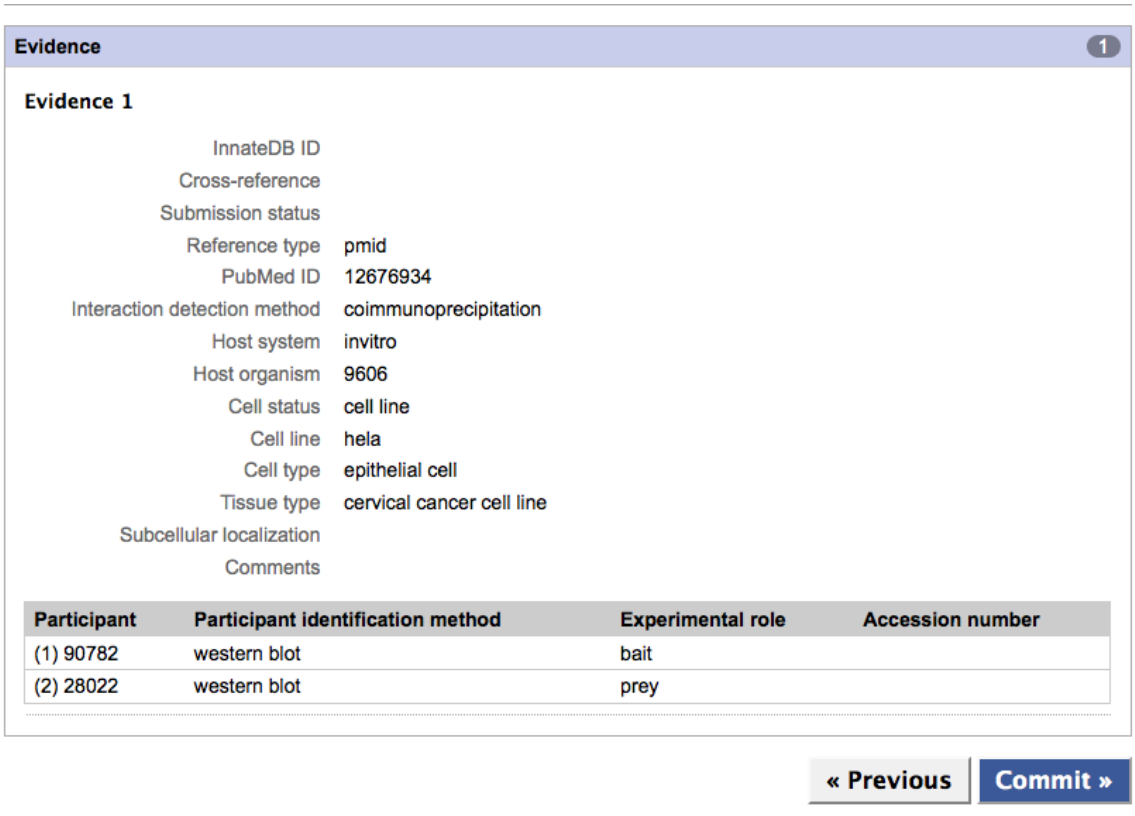
- The interaction was only present in absence of serum stimulation or very low in serum stimulated cells. Also cells treated with 200 ng/ml EGF for 10 min found to inhibit the interaction.
- Tags: CFLAR (Casper) - Flag, NFKB1 (p105) - HA;
- NFKB1 (p50) is 35S labeled
- Interaction strengthened after IL-1 beta stimulation whereas interaction between IRAK2 and AKT1 weakened after stimulation; When LY294002, inhibitor of Akt1 phosphorylation was added simultaneously with IL-1 beta treatment, interaction with IRAK2 was restored while interaction with IL1R1 weakened.

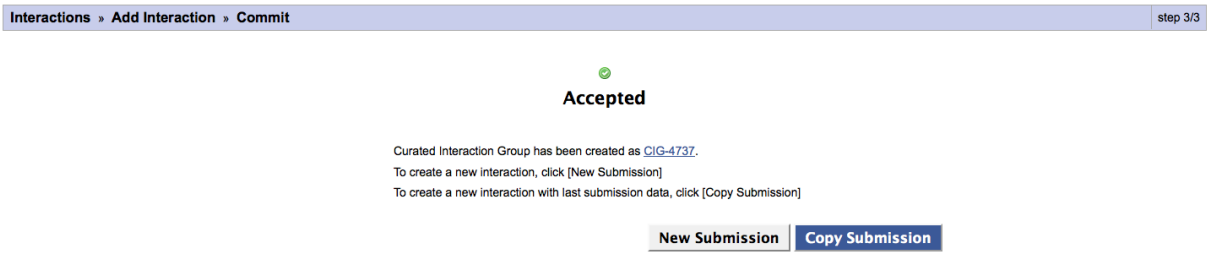
Preview and Submit

After all information has been entered, select preview to view the record and confirm the accuracy prior to submission. If interaction is not ready to be submitted, select 'Save Draft'. All information of the submission page will be saved for later access.



If changes are needed, select "previous" and make the desired changes. If no changes need to be made to the submission, click "commit".





You have now successfully submitted a new interaction. In order to submit another interaction, you can select:

New submission: a blank submission page will open OR
Copy submission: a submission page with data from your previous submission will open. This option is usually used for similar interactions in the same paper.

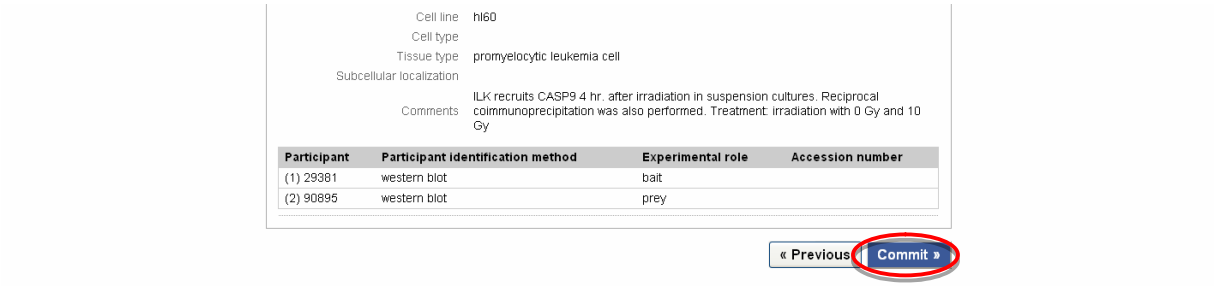
1.4 Editing an Interaction

An interaction in InnateDB may need to be edited due to misspelled words or further details may be needed to be added in the comment section after discussion among the curators. More importantly, an interaction may need to be edited due to incorrect species or missing information in uploaded interactions from other databases (MINT, BIND, etc) which were not manually curated by our own team.

1.4.1 Editing a Curated Interaction

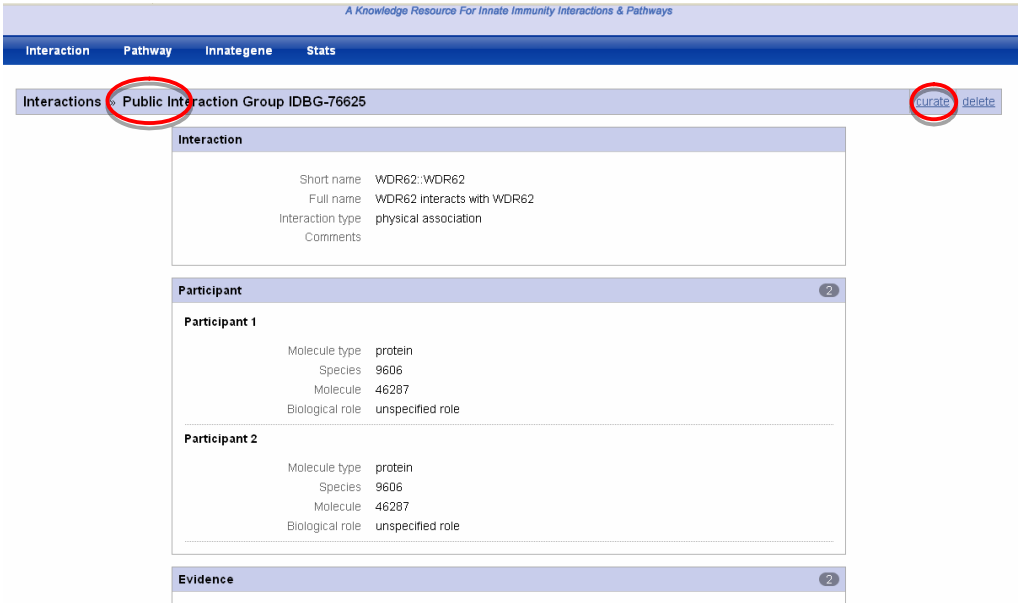
Search the desired interaction using the search criteria (see section 1.2). Click on the interaction from "**Curated Interaction"** Tab (make sure it is not the "Public Interaction" Tab). Click on "Edit" button and the make the appropriate changes. Click on "Preview" to review the interaction.

Click on “Commit” to when changes have been verified.

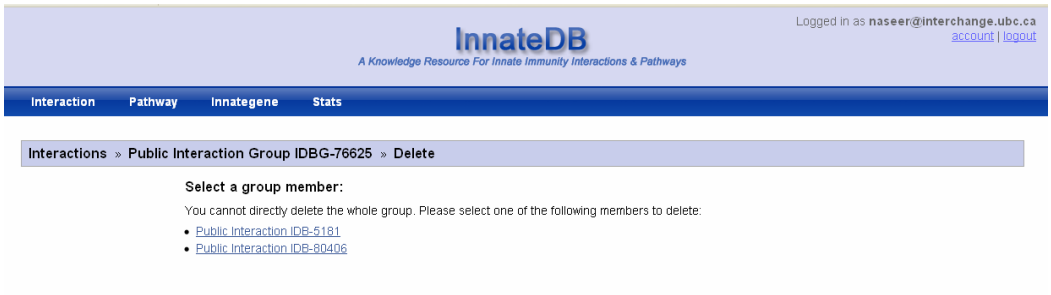


1.4.2 Editing a Public Interaction

Search the desired interaction using the search criteria (see section). Click on the interaction from Public Interaction Tab. Click on “Curate” button and the make the appropriate changes. Click on “Preview” to review the interaction.



If more than one public interaction belongs to the interaction group, you will need to click on the specific interaction you are referring to.



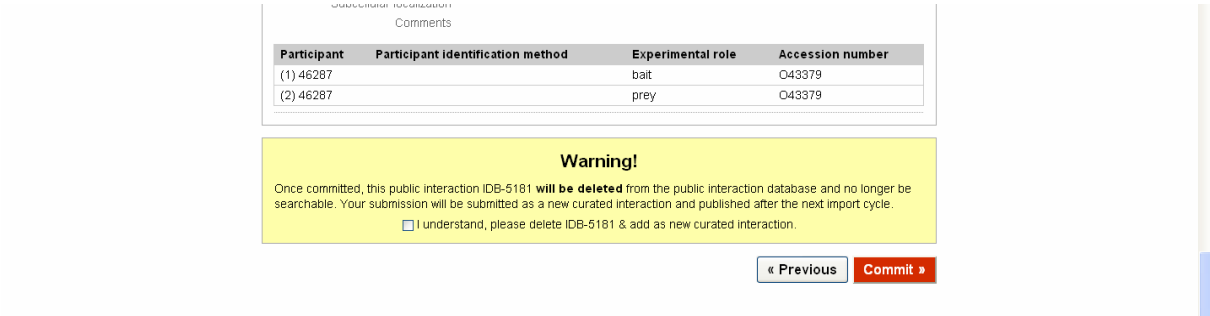
Make the appropriate changes to the interaction and click on “Preview”.

The preview page will display the following warning:

“Once committed, this public interaction IDB-XXXXX **will be deleted** from the public interaction database and no longer be searchable. Your submission will be submitted as a new curated interaction and published after the next import cycle.”

Click on the check box to confirm the deletion of the published interaction.

☐ I understand, please delete IDB-XXXXX & add as new curated interaction.



Click on “Commit” to successfully delete the published interaction and submitted a new curated interaction.

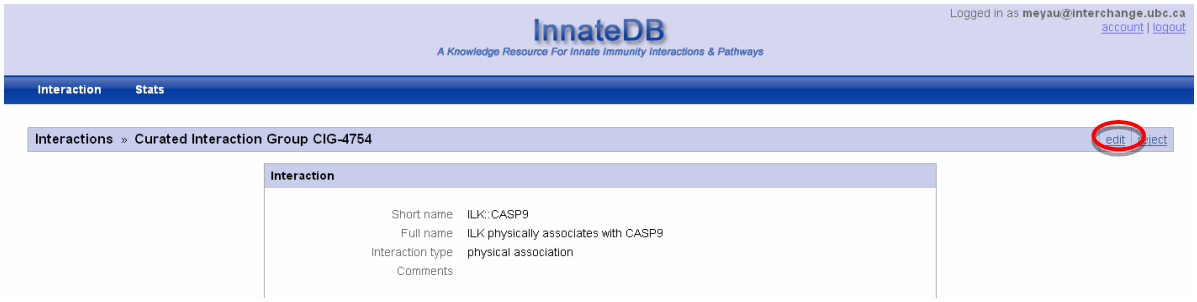
1.5 Deleting an interaction

Deleting an interaction results when published interactions uploaded into InnateDB:

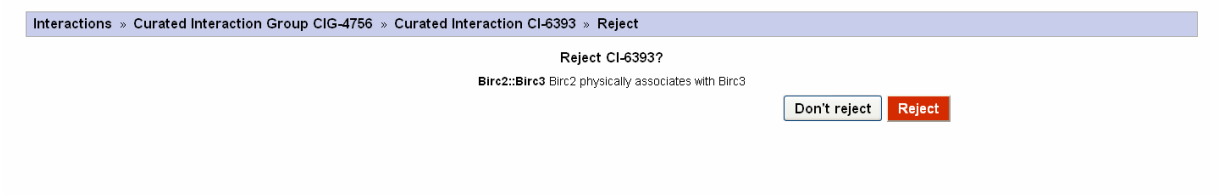
- used an interaction detection method which our curation team has decided is insufficient direct evidence to support an interaction (e.g. interaction detection method using confocal microscopy),
- when the public interaction is not found in the paper when manually curated,
- when the interaction involves other species other than human or mouse.

1.5.1 Deleting a Curated interaction

Search the desired interaction using the search criteria (see 1.2 in this chapter). Click on the interaction from the Curated Interaction Tab. Click on “Reject”. If more than one interaction belongs to the interaction group, you will need to click on the specific interaction you are referring to.

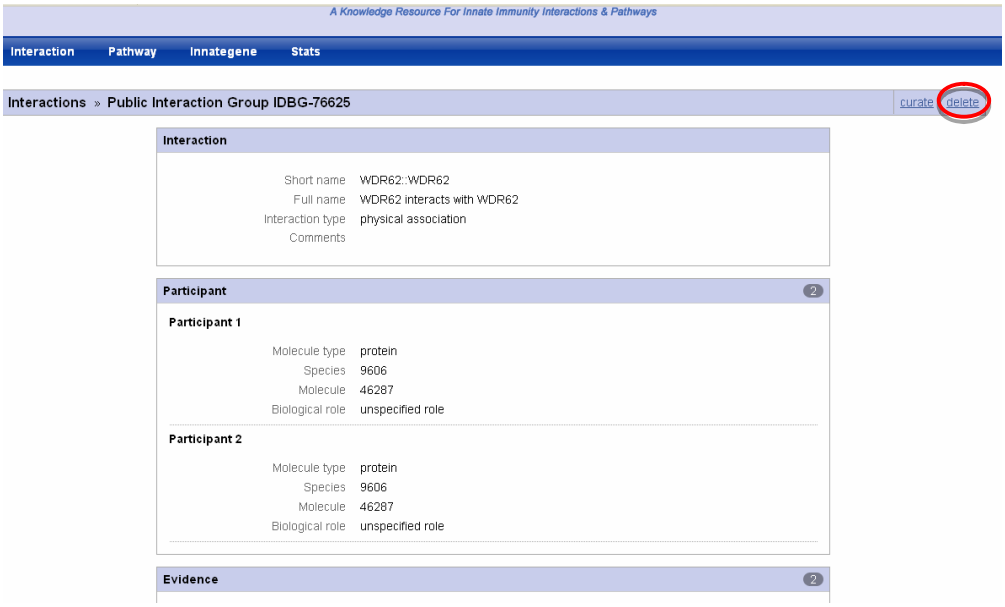


Confirm the rejection by clicking on the “Reject” button.



1.5.2 Deleting a Public interaction

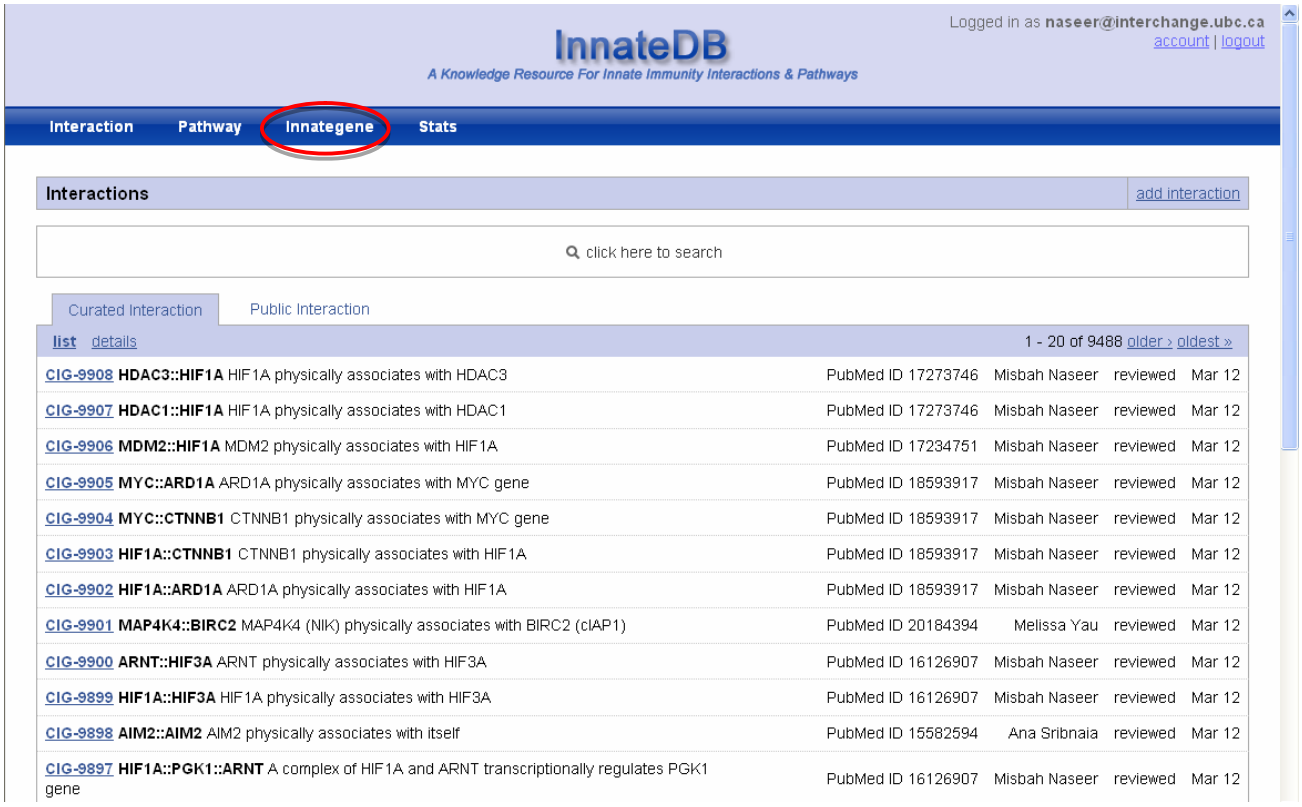
Search the desired interaction using the search criteria (see 1.2 in this chapter). Click on the interaction from the Public Interaction Tab. Click on “Delete”. If more than one interaction belongs to the interaction group, you will need to click on the specific interaction you are referring to.



Confirm the rejection by clicking on the “Delete” button.

1.6 Annotating Innate Immune Genes

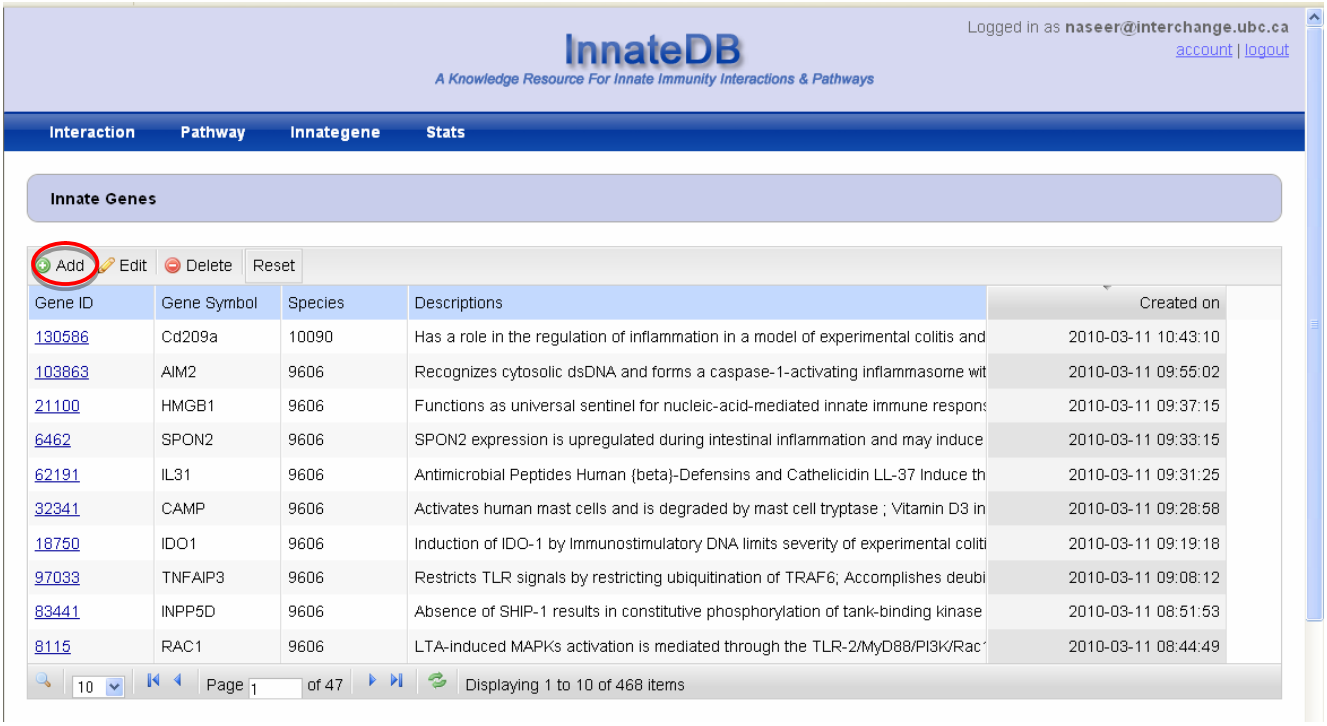
The **Innategene** function on the main page is used to record immune genes and their function in innate immunity as described in specific scientific publications. This information can also be extracted from review articles, however experimentally defined role of the gene/protein is preferred. This information is displayed on the gene card on the main site, under the section “InnateDB annotation.”



1.6.1 Adding annotation for a gene

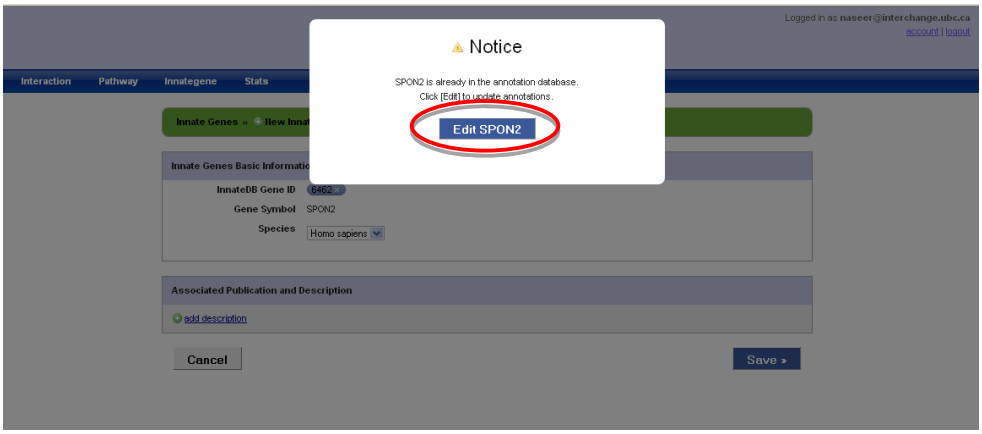
Click **Innategene** in the top right-hand corner of page to begin submitting a new annotation.

The main Innate Genes page displays the most recently annotated genes. Click **Add** icon on the main page.



On the **New Innate Genes** page, enter the gene symbol in InnateDB Gene ID field. Select the desired gene as per section 1.3.2.3.

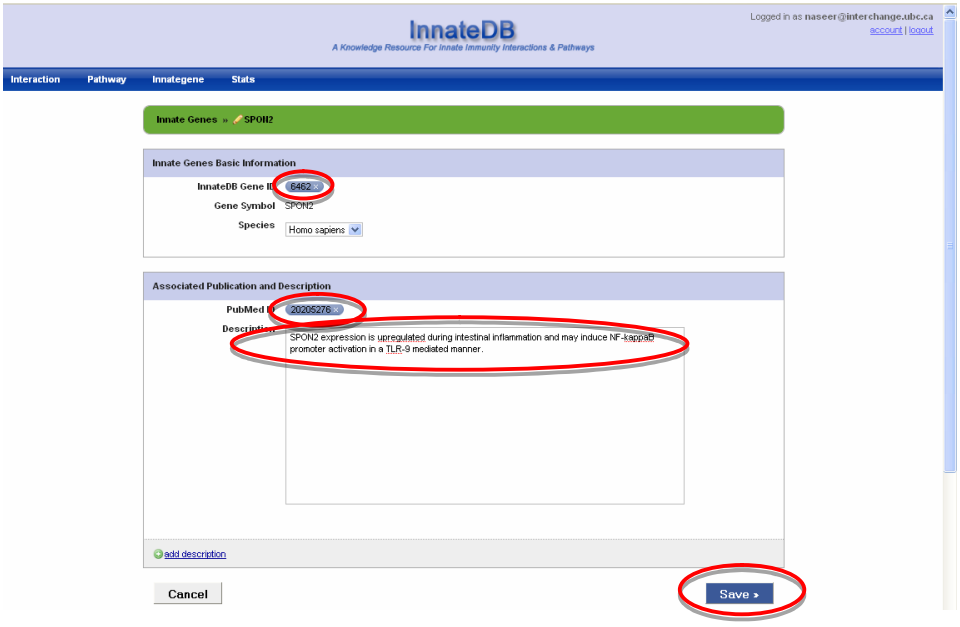
Note: When looking up a gene ID, a pop-up screen may appear notifying the user of an existing annotation for the gene. Click **EDIT [GENE SYMBOL]** button to continue.



Click **add description** to enter a new annotation.

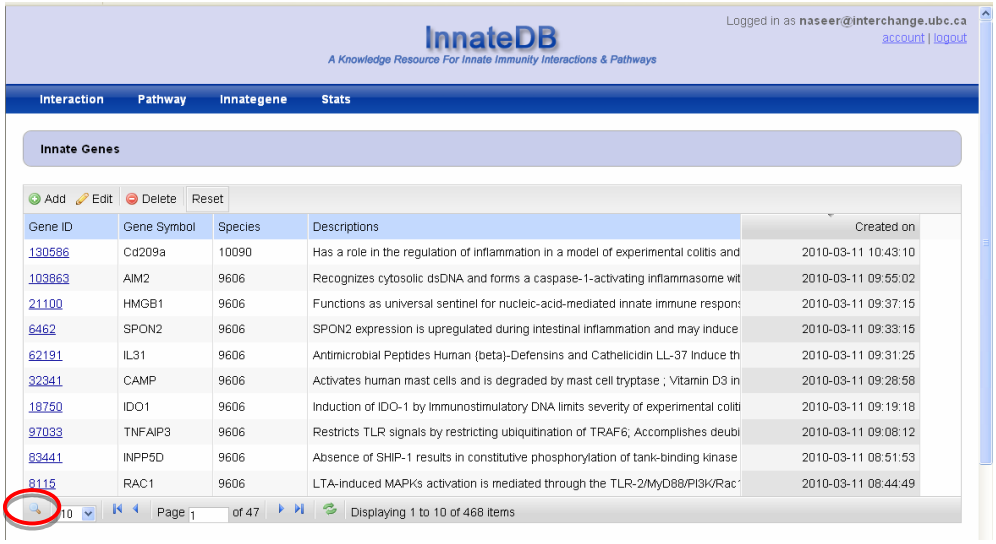
Enter the PMID of the source journal article in the **Pubmed ID** field. In the **Description** field, enter a one-sentence description of the gene in relation to its function in innate immunity. This information can usually be derived from the conclusion statement of the abstract of the source journal article.

After entering the required information, click **Save** button. The information will be updated instantly on the gene card on www.innatedb.ca.

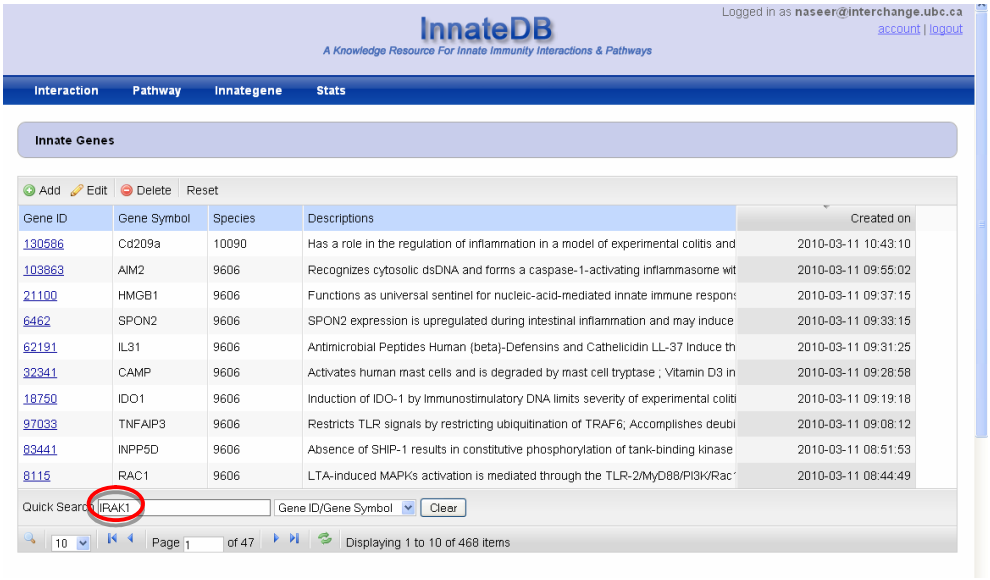


1.6.2 Editing/Deleting an annotation

Click on the magnifying glass icon in the bottom right-hand corner to search for all annotations of the gene entered in InnateDB.

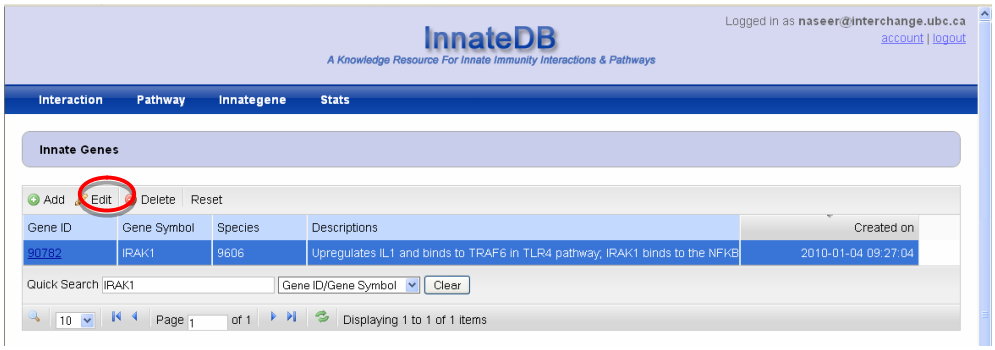


Enter the HGNC symbol for the gene and hit the **ENTER** key.



If the gene has been annotated previously, the search results page will show the entry for the desired gene.

Highlight the row displaying the gene by clicking it and click **Edit** icon.



All annotations for the selected gene will be displayed. To delete an annotation, click **remove**. To edit the text of an annotation, make the required changes on the page. Once all changes have been made, click **Save** button at the bottom of the screen.

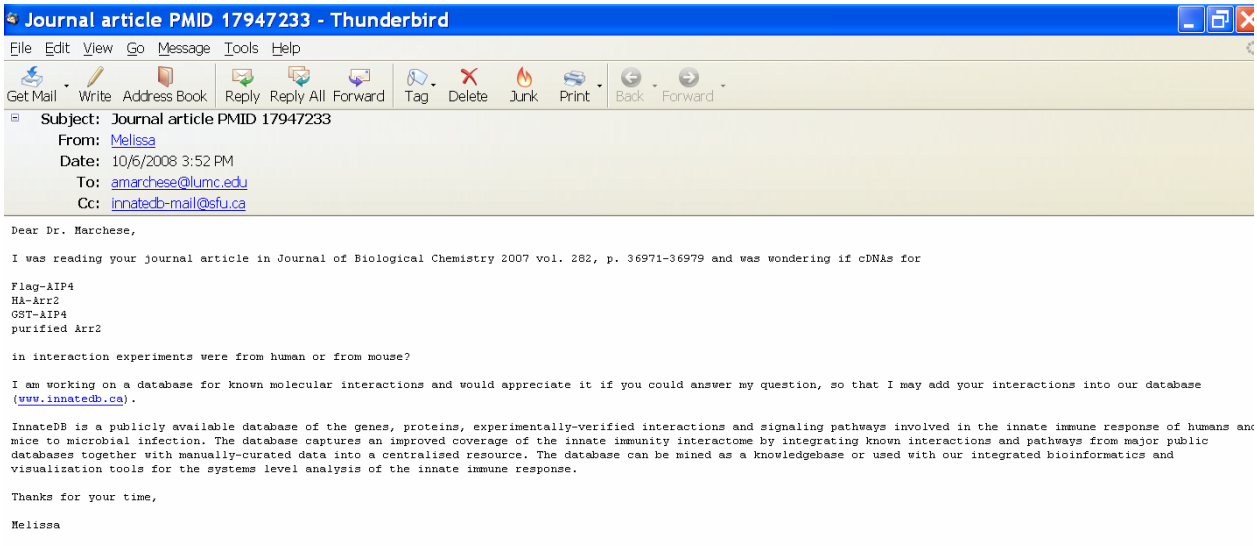
Chapter 2: Curation Related Issues

2.1 Confirming Species

If species are not specified in the scientific article, the following steps can be taken:

1) If there is an article referring to the plasmid in the Material and Methods section, looking up the species from this article.
2) Contact the corresponding author in the article for species confirmation. Note: remember to copy the email to innatedb-mail@sfu.ca

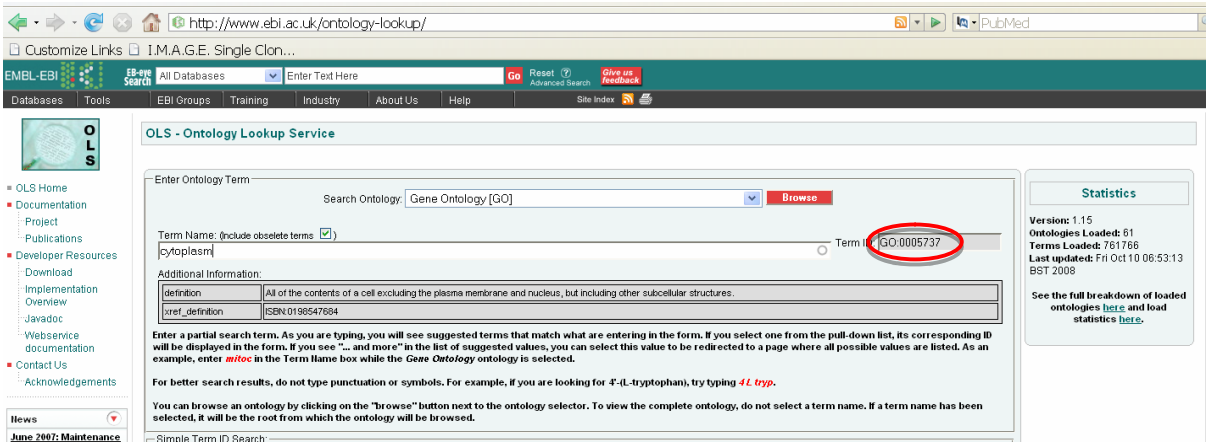
For Example:



2.2 Recording Subcellular Localization for a Gene

If the Subcellular Localization is specified for a gene in a paper, check the gene card on InnateDB to see if the subcellular localization has been recorded. If not, then record the InnateDB gene ID and the Gene ontology term referring to the subcellular localization in an excel sheet, which will be sent to the InnateDB database developer.

The gene ontology term can be looked up at the following link:
http://www.ebi.ac.uk/ontology-lookup/



2.3 Using Pathogenomics Wiki Site

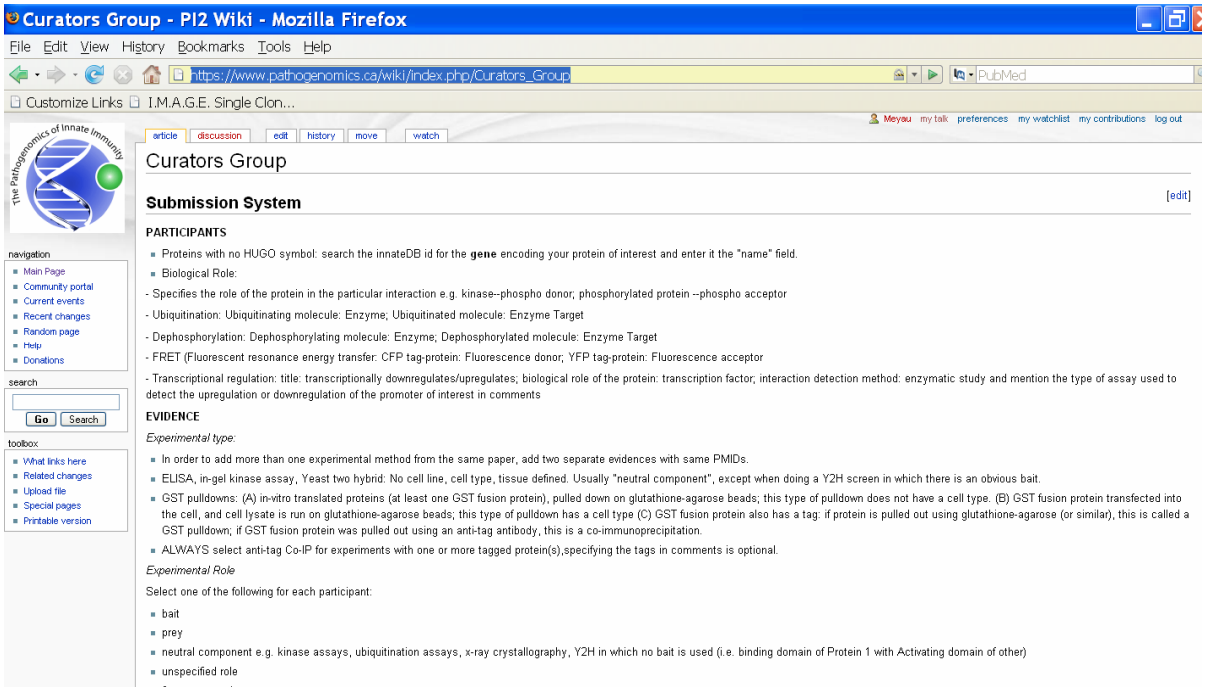
The Pathogenomics Wiki Site can be accessed at **https://www.pathogenomics.ca/wiki/index.php/Main_Page**. This site enables the curators to:

a. Guidelines for submitting interactions
b. Track curation progress (requested and curated genes)
c. Record innate immune genes and their function

2.3.1 Guidelines for submitting interactions

https://www.pathogenomics.ca/wiki/index.php/Curators_Group

To ensure consistency among curators, general rules have been outlined for submitting interactions.

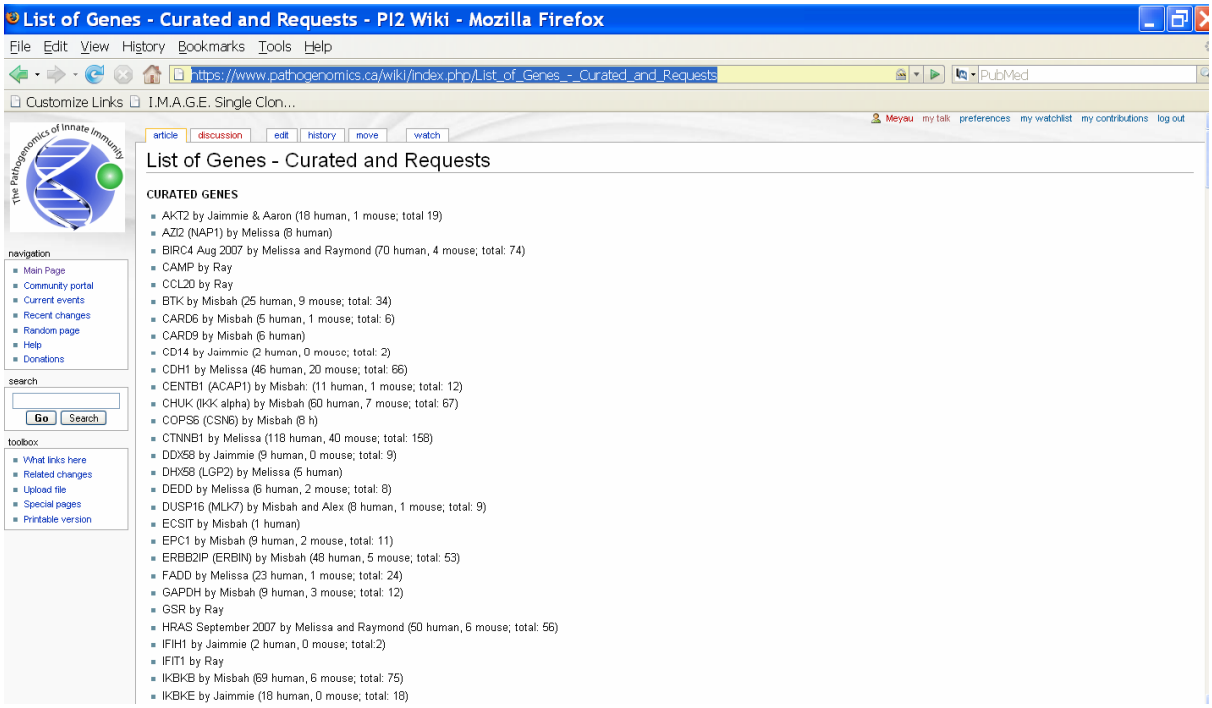


To save time and ensure consistency, tissue type, cell type and species have been recorded for curated cell lines. If a cell line is not listed, add it to the page by following the example in section 1.3.3.10 in 1.3: Adding an interaction.

2.3.2 Track Curation Progress

https://www.pathogenomics.ca/wiki/index.php/List_of_Genes_-_Curated_and_Requests

This page is used to record systematically curated genes with the number of interactions in human and mouse. And genes requested by the lab or project manager are also documented.



2.3.3 Record immune genes and their function

https://www.pathogenomics.ca/wiki/index.php/InnateDB_curators_list

This page is used to record immune genes and their function in specific scientific publications while curating. This information can also be extracted from review articles, however experimentally defined role of the gene/protein is preferred.