

CURATION GUIDE

InnateDB Project Leader: David Lynn

Submission System Development: Calvin Chan

Main Curation Team: Misbah Naseer, Melissa Yau, Giselle Ring, Ana Sribnaia, Kathleen Wee, Raymond Lo.

Assistant Curators: Patrick Taylor, Tracee Wee, Tom Yang.

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

Table of Contents

TABLE OF CONTENTS	2
CHAPTER 1: A GUIDE TO THE INNATEDB SUBMISSION SYSTEM.....	4
1.1 Logging In	4
1.2 Searching Interactions	5
1.3 Adding a New Interaction	7
1.3.1 Interaction	7
1.3.1.1 Interaction type	7
1.3.1.2 Full name.....	9
1.3.1.3 Comments	9
1.3.2 Participant	10
1.3.2.1 Molecule Type	10
1.3.2.2 Species (Human & Mouse Only!)	10
1.3.2.3 Molecule.....	10
1.3.2.4 Biological Role.....	13
1.3.3 Evidence	14
1.3.3.1 PubMed ID	15
1.3.3.2 Interaction Detection Method	15
1.3.3.6 Host System and Host Organism	16
1.3.3.7 Cell Status	17
1.3.3.8 Cell Line	17
1.3.3.9 Cell Type	17
1.3.3.10 Tissue Type.....	18
1.3.3.11 Subcellular localization	18
1.3.3.12 Participant Identification Method and Experimental Role	20
1.3.3.13 Accession Number.....	23
1.3.3.14 Comments	23
1.4 Editing an Interaction	25
1.4.1 Editing a Curated Interaction	25
1.4.2 Editing a Public Interaction	26
1.5 Deleting an interaction	27
1.5.1 Deleting a Curated interaction	28
1.5.2 Deleting a Public interaction	28
1.6 Annotating Innate Immune Genes	29
1.6.1 Adding annotation for a gene	29
1.6.2 Editing/Deleting an annotation	31
CHAPTER 2: CURATION RELATED ISSUES	34
2.1 Confirming Species	34
2.2 Recording Subcellular Localization for a Gene	34
2.3 Using Pathogenomics Wiki Site	35
2.3.1 Guidelines for submitting interactions	35

2.3.2 Track Curation Progress	36
2.3.3 Record immune genes and their function	37

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.



InnateDB
A Knowledge Resource For Innate Immunity Interactions & Pathways

Home

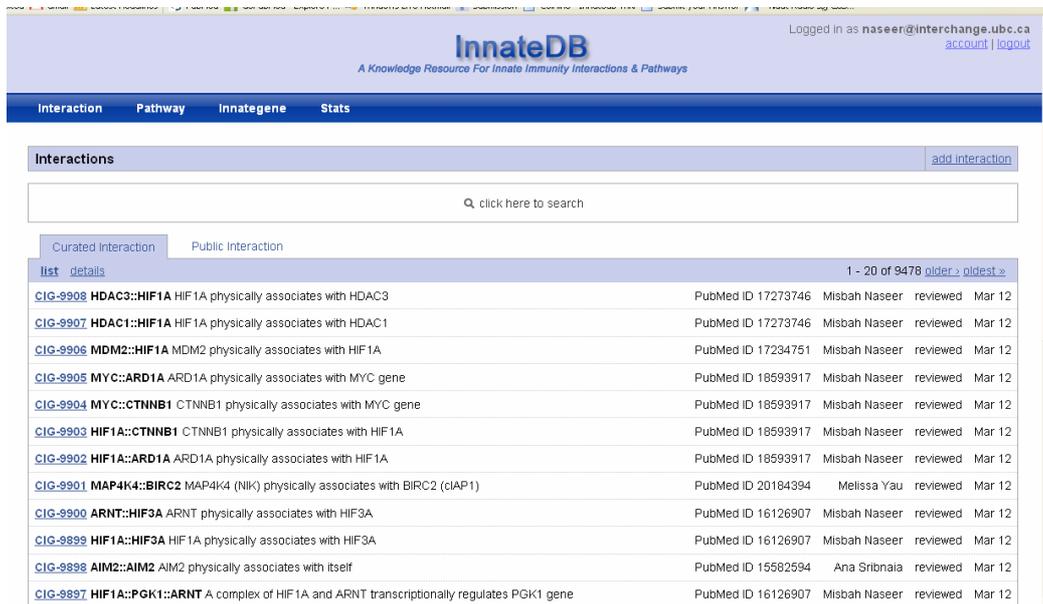
System Login

Email

Password

Login

First Page allows users to view & review submitted interactions:



InnateDB
A Knowledge Resource For Innate Immunity Interactions & Pathways

Logged in as naseer@interchange.ubc.ca
[account](#) | [logout](#)

Interaction Pathway Innatogene Stats

Interactions [add interaction](#)

Q click here to search

Curated Interaction Public Interaction

list	details	1 - 20 of 9478 older oldest »			
CIG-9908	HDAC3::HIF1A HIF1A physically associates with HDAC3	PubMed ID 17273746	Misbah Naseer	reviewed	Mar 12
CIG-9907	HDAC1::HIF1A HIF1A physically associates with HDAC1	PubMed ID 17273746	Misbah Naseer	reviewed	Mar 12
CIG-9906	MDM2::HIF1A MDM2 physically associates with HIF1A	PubMed ID 17234751	Misbah Naseer	reviewed	Mar 12
CIG-9905	MYC::ARD1A ARD1A physically associates with MYC gene	PubMed ID 18593917	Misbah Naseer	reviewed	Mar 12
CIG-9904	MYC::CTNNB1 CTNNB1 physically associates with MYC gene	PubMed ID 18593917	Misbah Naseer	reviewed	Mar 12
CIG-9903	HIF1A::CTNNB1 CTNNB1 physically associates with HIF1A	PubMed ID 18593917	Misbah Naseer	reviewed	Mar 12
CIG-9902	HIF1A::ARD1A ARD1A physically associates with HIF1A	PubMed ID 18593917	Misbah Naseer	reviewed	Mar 12
CIG-9901	MAP4K4::BIRC2 MAP4K4 (NIK) physically associates with BIRC2 (cIAP1)	PubMed ID 20184394	Melissa Yau	reviewed	Mar 12
CIG-9900	ARNT::HIF3A ARNT physically associates with HIF3A	PubMed ID 16126907	Misbah Naseer	reviewed	Mar 12
CIG-9899	HIF1A::HIF3A HIF1A physically associates with HIF3A	PubMed ID 16126907	Misbah Naseer	reviewed	Mar 12
CIG-9898	AIM2::AIM2 AIM2 physically associates with itself	PubMed ID 15582594	Ana Sriboiaia	reviewed	Mar 12
CIG-9897	HIF1A::PGK1::ARNT A complex of HIF1A and ARNT transcriptionally regulates PGK1 gene	PubMed ID 16126907	Misbah Naseer	reviewed	Mar 12

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.

Interactions add interaction

Match **all** of the following rules:

(1) PubMed ID	is		-	+
(2) Interaction Name	contains		-	+
(3) Interaction Type	is	OBO term select...	-	+
(4) Participant Molecule	is	select...	-	+
(5) Interaction Detection Method	is	select...	-	+
(6) Evidence Comments	contains		-	+
(7) Submission Status	is	pending	-	+
(8) Submitter	is	select...	-	+

Reset Search

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

Interaction Pathway innatgene Stats

Interactions add interaction

Match the following rule:

(1) Participant Molecule **is** **IRAK1**

Reset Search

Curated Interaction		Public Interaction		
list	details	1 - 20 of 86 older oldest		
CIG-9320	IRAK1::VASP	IRKA1 physically associates with VASP	PubMed ID 20044140	Ana Sribnaia reviewed Mar 07
CIG-9128	IRAK1::Ptpn6	IRAK1 physically associates with Ptpn6 (Shp-1)	PubMed ID 18391954	Misbah Naseer reviewed Mar 07
CIG-8738	PEL3::IRAK1	IRAK1 phosphorylates PEL3	PubMed ID 17997719	Misbah Naseer reviewed Nov 04
CIG-8737	PEL1::IRAK1	IRAK1 phosphorylates PEL1	PubMed ID 17997719	Misbah Naseer reviewed Nov 04
CIG-8736	IKBKG::IRAK1	IKBKG physically associates with polyubiquitinated IRAK1	PubMed ID 17997719	Misbah Naseer reviewed Mar 07
CIG-8692	TRAF6::IRAK1	TRAF6 physically associates with IRAK1	PubMed ID 19716405	Misbah Naseer reviewed Mar 07
CIG-8691	TOLLIP::IRAK1	TOLLIP physically associates with IRAK1	PubMed ID 19716405	Misbah Naseer reviewed Mar 07
CIG-8690	RCAN1::IRAK1	RCAN1 (DSCR1) physically associates with IRAK1	PubMed ID 19716405	Misbah Naseer reviewed Mar 07
CIG-5744	PEL3::IRAK1	PEL3 physically interacts with IRAK1	PubMed ID 19081057	Giselle Ring reviewed Mar 07
CIG-5743	PEL2::IRAK1	PEL2 physically interacts with IRAK1	PubMed ID 19081057	Giselle Ring reviewed Mar 07
CIG-5742	Pel1::IRAK1	Pel1 physically interacts with IRAK1	PubMed ID 19081057	Giselle Ring reviewed Mar 07
CIG-4834	hsa-mir-146b::IRAK1	MIRN146B MicroRNA inhibits IRAK1 mRNA translation through its 3' UTR	PubMed ID 16885212	Misbah Naseer reviewed Mar 07

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)

Interaction Pathway Innategene Stats

Interactions [add interaction](#)

Match the following rule:

(1) Participant Molecule is IRAK1

[Reset](#) [Search](#)

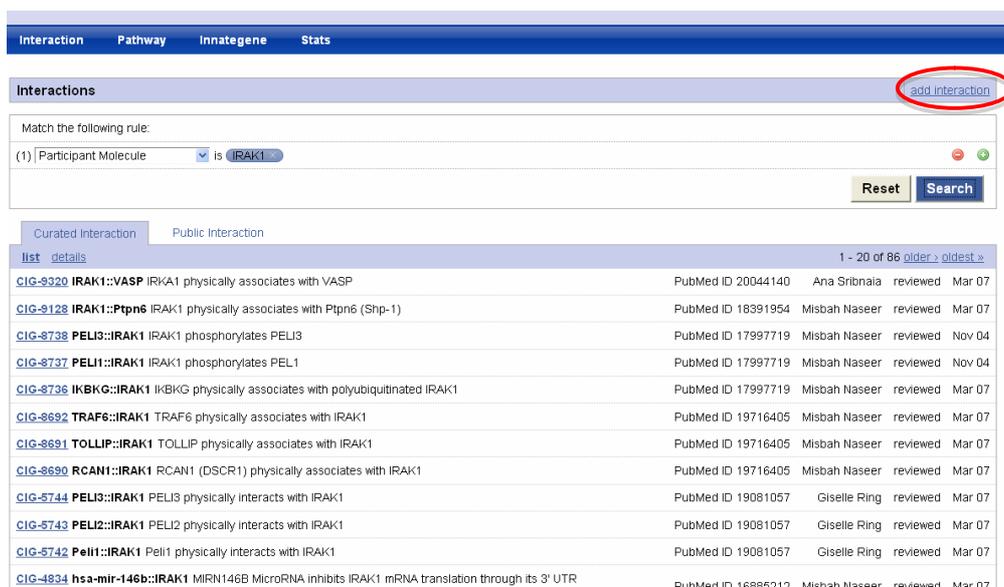
[Curated Interaction](#) [Public Interaction](#)

1 - 20 of 86 [older](#) [oldest](#)

CIG-9320	IRAK1::VASP	IRAK1 physically associates with VASP	PubMed ID 20044140	Ana Sribnaia	reviewed	Mar 07
CIG-9128	IRAK1::Ptpn6	IRAK1 physically associates with Ptpn6 (Shp-1)	PubMed ID 18391954	Misbah Naseer	reviewed	Mar 07
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1.3 Adding a New Interaction

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



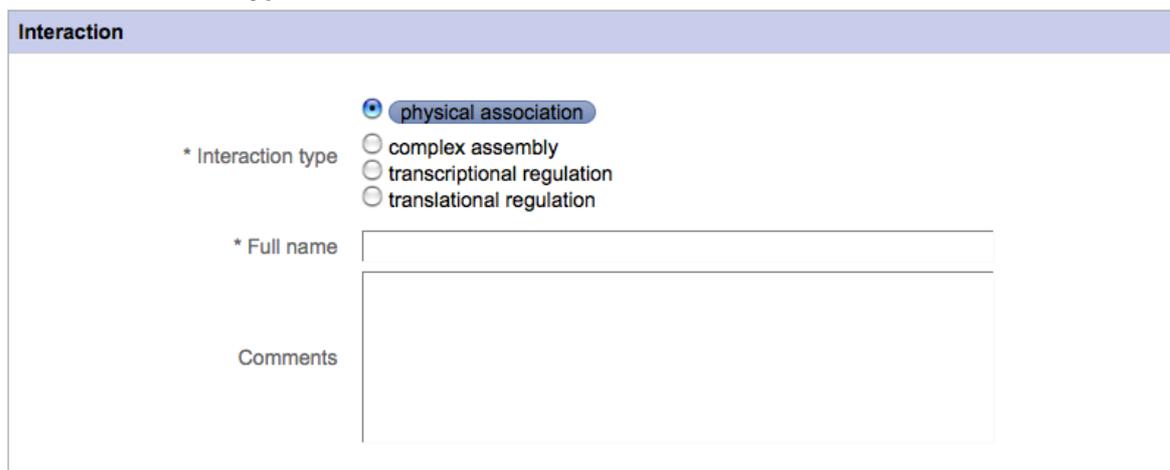
The screenshot shows the 'Interactions' page with a navigation bar at the top containing 'Interaction', 'Pathway', 'Innategene', and 'Stats'. Below the navigation bar, there is a search bar with the text 'Match the following rule:' and a dropdown menu showing '(1) Participant Molecule' with a selected value of 'IRAK1'. To the right of the search bar is a red circle around the 'add Interaction' button. Below the search bar are 'Reset' and 'Search' buttons. The main content area shows a list of interactions with columns for ID, description, PubMed ID, author, status, and date. The list includes entries like 'CIG-9320 IRAK1::VASP IRAK1 physically associates with VASP' and 'CIG-4834 hsa-mir-146b::IRAK1 MIRN146B MicroRNA inhibits IRAK1 mRNA translation through its 3' UTR'.

list	details	1 - 20 of 86	older >	oldest >
CIG-9320	IRAK1::VASP IRAK1 physically associates with VASP	PubMed ID 20044140	Ana Sribnaia	reviewed Mar 07
CIG-9128	IRAK1::Ptpn6 IRAK1 physically associates with Ptpn6 (Shp-1)	PubMed ID 18391954	Misbah Naseer	reviewed Mar 07
CIG-8738	PEL13::IRAK1 IRAK1 phosphorylates PEL13	PubMed ID 17997719	Misbah Naseer	reviewed Nov 04
CIG-8737	PEL11::IRAK1 IRAK1 phosphorylates PEL11	PubMed ID 17997719	Misbah Naseer	reviewed Nov 04
CIG-8736	IKBKG::IRAK1 IKBKG physically associates with polyubiquitinated IRAK1	PubMed ID 17997719	Misbah Naseer	reviewed Mar 07
CIG-8692	TRAF6::IRAK1 TRAF6 physically associates with IRAK1	PubMed ID 19716405	Misbah Naseer	reviewed Mar 07
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CIG-5744	PEL13::IRAK1 PEL13 physically interacts with IRAK1	PubMed ID 19081057	Giselle Ring	reviewed Mar 07
CIG-5743	PEL12::IRAK1 PEL12 physically interacts with IRAK1	PubMed ID 19081057	Giselle Ring	reviewed Mar 07
CIG-5742	Pel11::IRAK1 Pel11 physically interacts with IRAK1	PubMed ID 19081057	Giselle Ring	reviewed Mar 07
CIG-4834	hsa-mir-146b::IRAK1 MIRN146B MicroRNA inhibits IRAK1 mRNA translation through its 3' UTR	PubMed ID 16885212	Misbah Naseer	reviewed Mar 07

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

1.3.1 Interaction

1.3.1.1 Interaction type



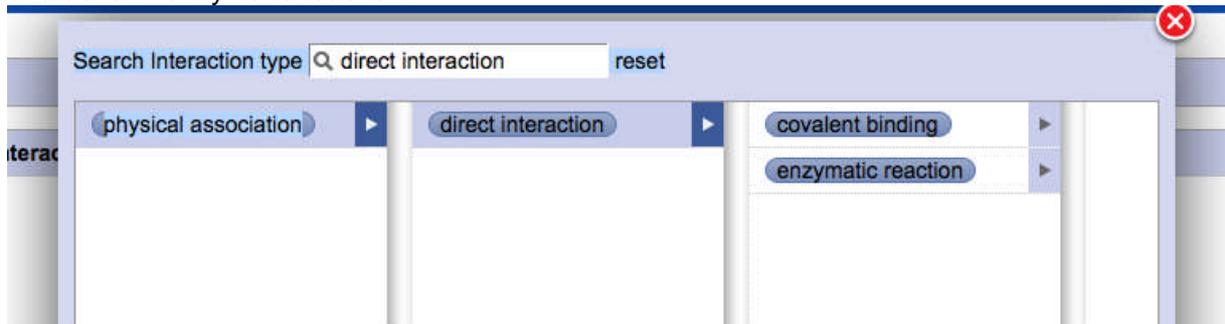
The screenshot shows the 'Interaction' form with a section for 'Interaction type'. There are four radio button options: 'physical association' (selected), 'complex assembly', 'transcriptional regulation', and 'translational regulation'. Below this is a field for '* Full name' and a larger text area for 'Comments'.

Select the appropriate interaction type from the list.

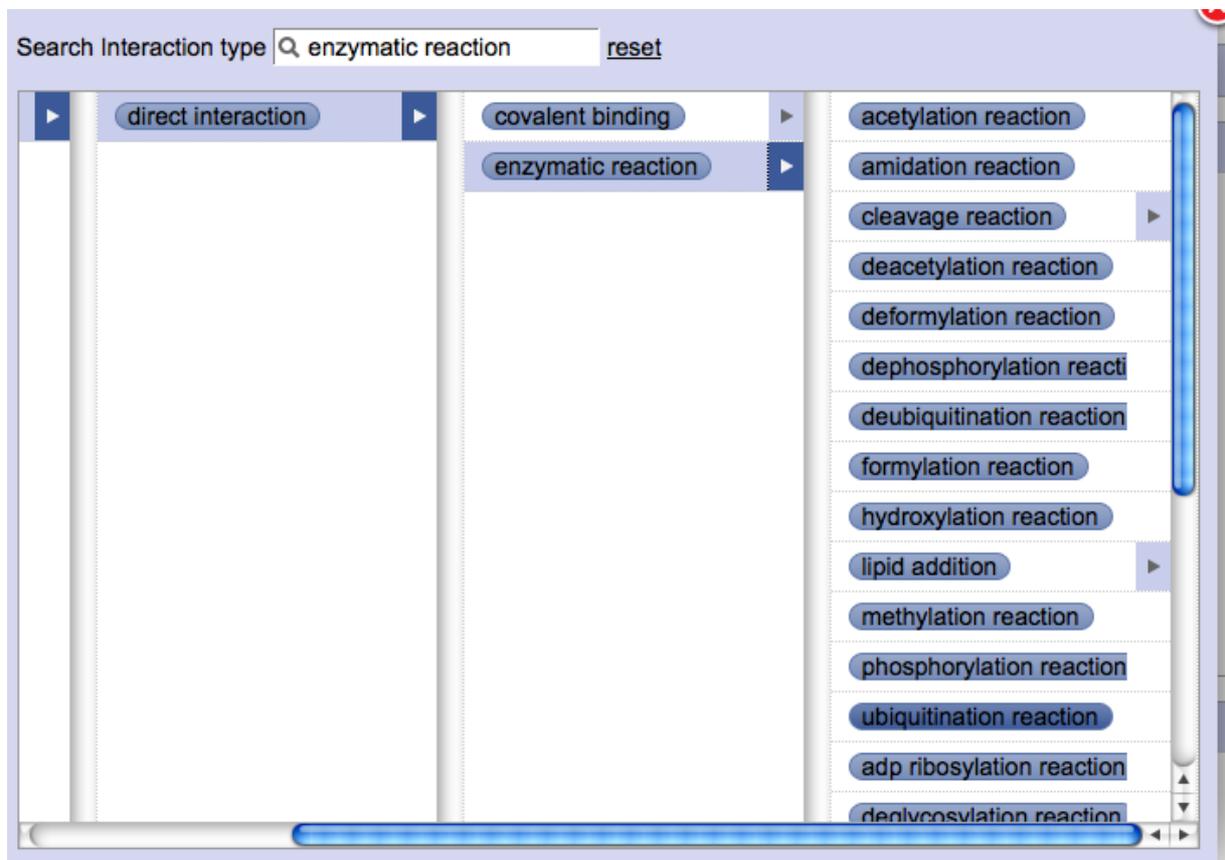
“**Physical Association**” is the most general term used to describe an interaction and should only be used when no other information is available (This is frequently the case).

“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

Participant 2

Participant 1

* Molecule type

* Species

* Molecule

* Biological role

Participant 2

* Molecule type

* Species

* Molecule

* Biological role

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.

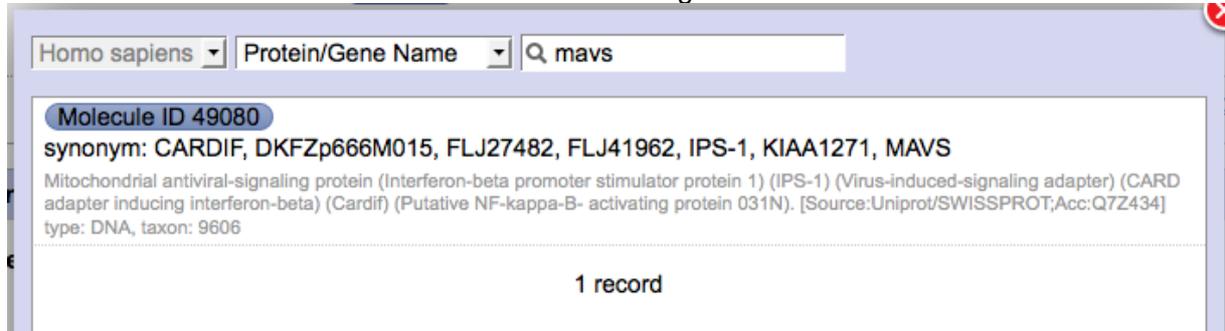
[Moran ST](#), [Haider K](#), [Ow Y](#), [Milton P](#), [Chen L](#), [Pillai S](#).

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 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 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.

The screenshot shows a search interface with a dropdown menu set to 'Homo sapiens', a search box containing 'mekk3', and a search button. Below the search bar, the results for 'MAP3K3' are displayed, including its molecule ID (63432), synonyms (MAPKKK3, MEKK3), and a description: 'mitogen-activated protein kinase kinase kinase 3'. The taxon is listed as DNA, 9606. At the bottom of the results section, it indicates '1 record'.

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.

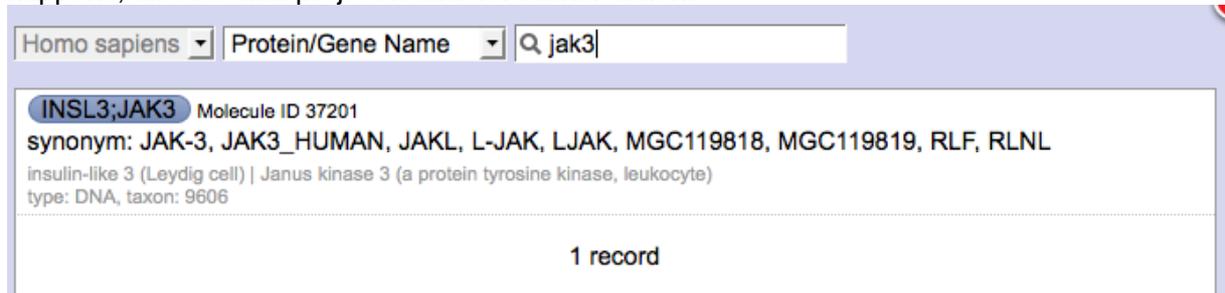


The screenshot shows a search interface for InnateDB. The search criteria are set to 'Homo sapiens' and 'Protein/Gene Name' with the search term 'mavs'. The results display a single record with the following details:

- Molecule ID 49080**
- synonym: CARDIF, DKFZp666M015, FLJ27482, FLJ41962, IPS-1, KIAA1271, MAVS**
- Mitochondrial antiviral-signaling protein (Interferon-beta promoter stimulator protein 1) (IPS-1) (Virus-induced-signaling adapter) (CARD adapter inducing interferon-beta) (Cardif) (Putative NF-kappa-B- activating protein 031N).** [Source:Uniprot/SWISSPROT;Acc:Q7Z434]
- type: DNA, taxon: 9606**

At the bottom of the record, it indicates '1 record'.

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



The screenshot shows a search interface for InnateDB. The search criteria are set to 'Homo sapiens' and 'Protein/Gene Name' with the search term 'jak3'. The results display a single record with the following details:

- INSL3;JAK3** Molecule ID 37201
- synonym: JAK-3, JAK3_HUMAN, JAKL, L-JAK, LJAK, MGC119818, MGC119819, RLF, RLNL**
- insulin-like 3 (Leydig cell) | Janus kinase 3 (a protein tyrosine kinase, leukocyte)**
- type: DNA, taxon: 9606**

At the bottom of the record, it indicates '1 record'.

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.

interaction type
 transcriptional regulation
 translational regulation

Homo sapiens Protein/Gene Name TUBB

RP11-631M21.2 Molecule ID 43552
 synonym: FLJ40100, TUBB8
 Tubulin beta-8 chain [Source:UniProtKB/Swiss-Prot;Acc:Q3ZCM7]
 type: DNA, taxon: 9606

TUBB Molecule ID 76778
 synonym: M40, MGC117247, MGC16435, OK/SW-cl.56, TUBB1, TUBB5
 tubulin, beta
 type: DNA, taxon: 9606

TUBB Molecule ID 126212
 Tubulin beta chain (Tubulin beta-5 chain) [Source:UniProtKB/Swiss-Prot;Acc:P07437]
 type: DNA, taxon: 9606

TUBB Molecule ID 299022
 Tubulin beta chain (Tubulin beta-5 chain) [Source:UniProtKB/Swiss-Prot;Acc:P07437]
 type: DNA, taxon: 9606

TUBB Molecule ID 299260
 Tubulin beta chain (Tubulin beta-5 chain) [Source:UniProtKB/Swiss-Prot;Acc:P07437]
 type: DNA, taxon: 9606

TUBB Molecule ID 299290
 Tubulin beta chain (Tubulin beta-5 chain) [Source:UniProtKB/Swiss-Prot;Acc:P07437]
 type: DNA, taxon: 9606

TUBB Molecule ID 299374
 Tubulin beta chain (Tubulin beta-5 chain) [Source:UniProtKB/Swiss-Prot;Acc:P07437]
 type: DNA, taxon: 9606

add new participant

InnateDB
 A Knowledge Resource For Innate Immunity Interactions & Pathways

Home About Search Data Analysis Browse Download Resources Statistics Contact Help

Display Options (Show/Hide)

Sorted by: Gene symbol ascending then by Organism ascending Sort

Download MS Excel TAB CSV Show Orthologs

Viewing genes 1 to 10 of 10 hits matching query (Name 'tubb')

Page(s): 1

InnateDB ID	Ensembl Gene ID	Organism	Chromosome	Gene symbol	Gene name	Interactions	
IDBG-299439	ENSG00000235067	Homo sapiens	HSCHR6_MHC_DBB	TUBB	Tubulin beta chain (Tubulin beta-5 chain)		Gene Details
IDBG-299374	ENSG00000227739	Homo sapiens	HSCHR6_MHC_COX	TUBB	Tubulin beta chain (Tubulin beta-5 chain)		Gene Details
IDBG-76778	ENSG00000196230	Homo sapiens	6	TUBB	tubulin, beta	21	Gene Details
IDBG-126212	ENSG00000183311	Homo sapiens	HSCHR6_MHC_QBL	TUBB	Tubulin beta chain (Tubulin beta-5 chain)	32	Gene Details
IDBG-299260	ENSG00000229684	Homo sapiens	HSCHR6_MHC_MCF	TUBB	Tubulin beta chain (Tubulin beta-5 chain)		Gene Details
IDBG-299290	ENSG00000232421	Homo sapiens	HSCHR6_MHC_SSTO	TUBB	Tubulin beta chain (Tubulin beta-5 chain)		Gene Details
IDBG-299480	ENSG00000232575	Homo sapiens	HSCHR6_MHC_MANN	TUBB	Tubulin beta chain (Tubulin beta-5 chain)		Gene Details
IDBG-57522	ENSG00000137267	Homo sapiens	6	TUBB2A	tubulin, beta 2A	36	Gene Details
IDBG-299022	ENSG00000224156	Homo sapiens	HSCHR6_MHC_APD	TUBB	Tubulin beta chain (Tubulin beta-5 chain)		Gene Details
IDBG-193657	ENSMUSG00000062591	Mus musculus	17	Tubb4	tubulin, beta 4		Gene Details

InnateDB is being developed jointly by the Brinkman Laboratory, Simon Fraser University and the Hancock Laboratory, University of British Columbia, Vancouver, British Columbia, Canada and the Lynn

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.

Search Biological role [reset](#)

- unspecified role
- enzyme
- enzyme target
- self
- inhibitor
- cofactor
- stimulator
- putative self
- donor
- acceptor

1.3.3 Evidence

Evidence

Reference type: PubMed ID Book Website

* PubMed ID:

Interaction detection method:

[add additional method](#)

Host system: In Vitro In Vivo Ex Vivo unspecified

Host organism:

Cell status: Primary Cell-line unspecified

Participants

Cell line:

Cell type:

Tissue type:

Subcellular localization:

Comments:

[add new 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.

Evidence 1

Reference type: PubMed ID

* PubMed ID:

Interaction detection method:

[add additional method](#)

Host system: In Vitro In Vivo Ex Vivo unspecified

Host organism:

Cell status: Primary Cell-line unspecified

Cell line:

Cell type:

Tissue type:

Subcellular localization:

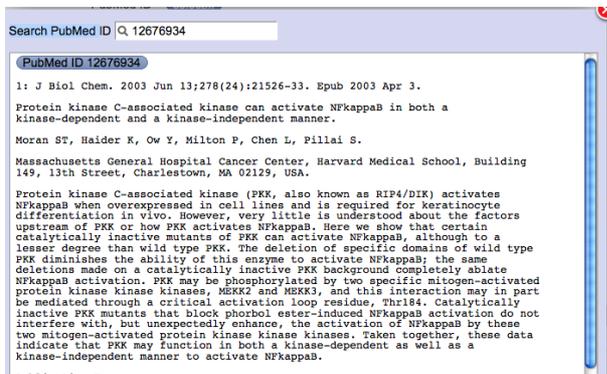
Comments:

Participant	Participant identification method	Experimental role	Accession number
(1)	<input type="text"/>	<input type="text"/>	<input type="text"/>
(2)	<input type="text"/>	<input type="text"/>	<input type="text"/>

[add new evidence](#)

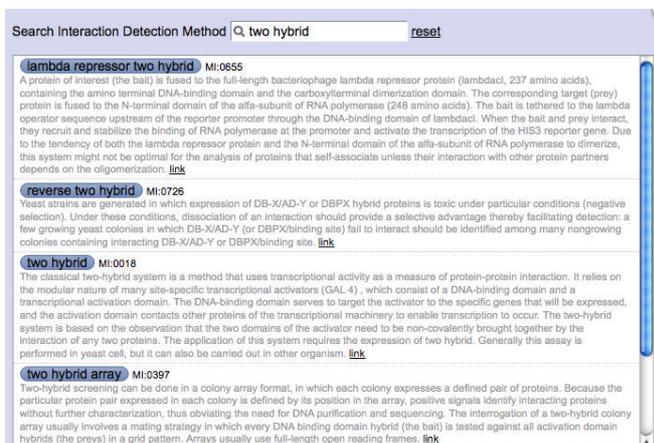
1.3.3.1 PubMed ID

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.

Search Interaction Detection Method [reset](#)

biophysical ▶	cosedimentation ▶	deacetylase assay ▶
protein complementation ▶	cross-linking study ▶	protein kinase assay ▶
genetic interference ▶	chromatography technol ▶	phosphatase assay ▶
post transcriptional interf ▶	affinity technology ▶	protease assay ▶
biochemical ▶	enzymatic study ▶	methyltransferase assay ▶
imaging techniques ▶	footprinting ▶	polymerase assay ▶
	comigration in gel electrc ▶	phosphotransfer assay ▶
		demethylase assay ▶
		nucleoside triphosphatas ▶
		acetylation assay ▶
		ribonuclease assay ▶

Following are some OBO terms used for common detection methods:

- *coimmunopercipiatiion/ 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 In Vivo Ex Vivo unspecified

Host organism

Host System:

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

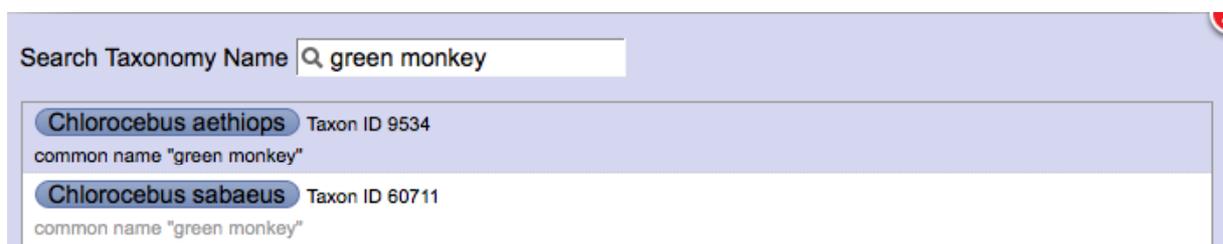
In Vivo – experiments performed in an organism or with cells extracted from an organism which have not been subject to any treatment.

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:

The screenshot shows the ATCC website interface. At the top right, the 'Search Catalog' dropdown menu is open, showing 'Cell Lines and Hybridomas' selected and 'SW480' entered in the search box. Below the search bar, there are links for 'Login' and 'Search Options'. The main navigation bar includes 'About', 'Cultures and Products', 'Science', 'Standards', 'Deposit Services', 'Custom Services', and 'Product Use Policy'. A 'Home' link is also present. A world map is displayed in the background. On the right, there are 'Highlights' including 'Available Now... -ATCC® Primary Cell Solutions™: a new product line designed to...' and 'ATCC Achieves ISO Guide 34 Accreditation -ATCC was...'. The main content area is titled 'Cell Biology' and displays details for 'CCL-228™' (SW480). The 'ATCC® Number' is CCL-228™, 'Designations' is SW480 [SW-480], 'Biosafety Level' is 1, 'Medium & Serum' is 'See Propagation', 'Organism' is 'Homo sapiens (human)', 'Source' includes 'Organ: colon', 'Tumor Stage: Dukes' type B', and 'Disease: colorectal adenocarcinoma'. 'Cellular Products' include 'carcinoembryonic antigen (CEA) 0.7 ng/10 exp6 cells/10 days; keratin; transforming growth factor beta'. 'Permits/Forms' information is provided, and 'Applications' are listed as 'transfection host(technology from amaxa)'. The price is \$244.00, deposited by A Leibovitz, shipped frozen, and grows adherent. The morphology is epithelial. A 'PHOTO' icon is visible below the morphology field. A 'Related Cell Culture Products' link is at the bottom right.

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

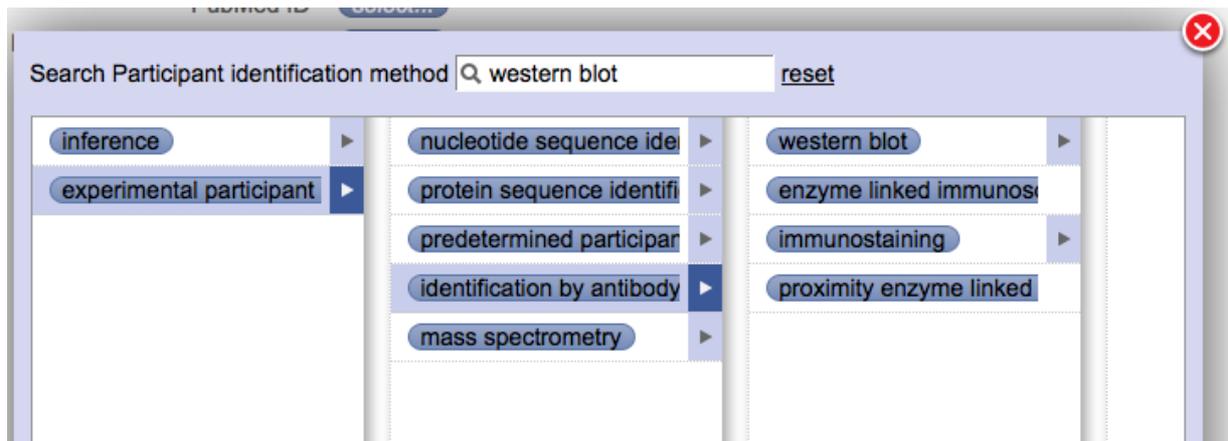
If specified, this is where the location within the cell in which the **interaction** is observed and NOT the subcellular localization of where a protein is normally located. When inputting subcellular localization, only controlled terms are allowed and thus this is a searchable field. Once search terms 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 [reset](#)

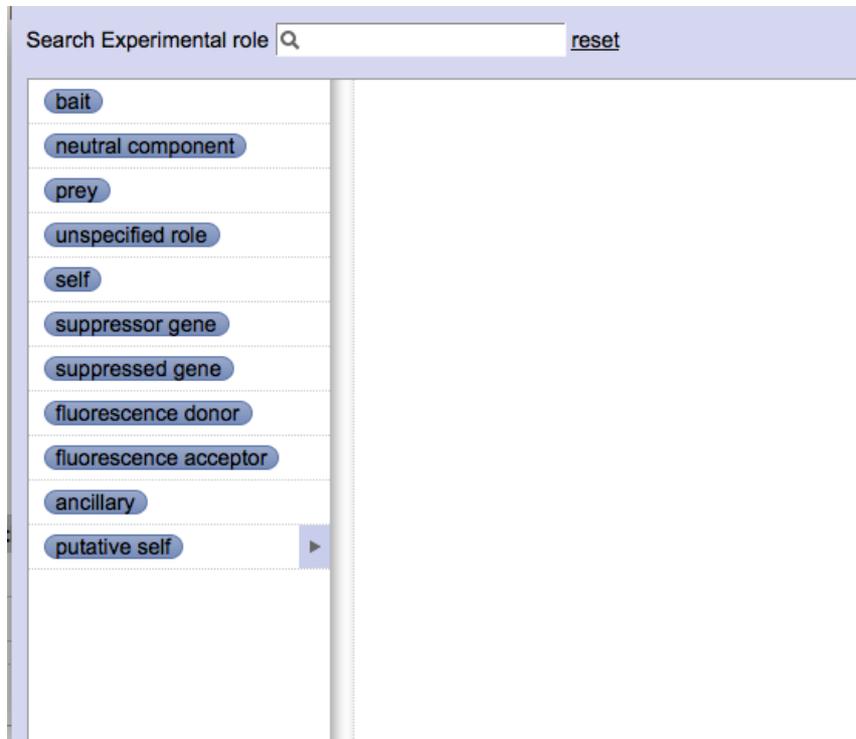
cilium	nuclear envelope	nuclear inner membrane
cytoplasm	nuclear lumen	nuclear outer membrane
cytoplasmic vesicle	nuclear lamina	
cytoskeleton	nuclear matrix	
endoplasmic reticulum	nuclear membrane	
extracellular region	nuclear pore	
golgi apparatus	nucleolus	
membrane	nucleoplasm	
mitochondrion		
nucleus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

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 many 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	<ul style="list-style-type: none"> • Bait • Prey 	Plasmid verified by nucleotide sequencing Positive clones verified by nucleotide sequencing
Coimmunoprecipitation	<ul style="list-style-type: none"> • Bait • Prey 	<ul style="list-style-type: none"> - Western blot (mono/polyclonal if specified) or - Plasmid was verified by nucleotide sequencing Western blot (mono/polyclonal if specified)
Anti Tag Coimmunoprecipitation	<ul style="list-style-type: none"> • Bait • Prey 	Western blot (mono/polyclonal if specified) or tag western blot <ul style="list-style-type: none"> - Anti tag western blot or - Western blot (mono/polyclonal if specified)
Pull down Chromatin Immunopercipitation Assays Electrophoretic Mobility Shift Assay	<ul style="list-style-type: none"> • Bait • Prey • Neutral Component • Neutral Component • Neutral Component • Neutral Component 	Predetermined participant <ul style="list-style-type: none"> - Western blot (mono/polyclonal if specified) or - Autoradiography if used in vitro translated 35S-labelled protein - Primer specific PCR (gene) - Identification by antibody (protein) - 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 V60 H-2 cells (Reith *et al.*, 1990).

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 *PvuII* 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 (λ ZAPIII 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 had a different poly(A) tail. The sequence of pSK-Socs1 has been deposited in the DDBJ/EMBL/GenBank database (accession No. AF120490).

Northern blot analysis

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.

Participant	Participant identification method	Experimental role	Accession number
(1)	experimental participant identification ▾	unspecified role	<input type="text"/>
(2)	select...	unspecified role	<input type="text"/>

[+ add new evidence](#)

Discard
Save Draft
Preview »

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

Evidence
1

Evidence 1

- InnateDB ID
- Cross-reference
- Submission status
- Reference type pmid
- PubMed ID 12676934
- Interaction detection method coimmunoprecipitation
- Host system invitro
- Host organism 9606
- Cell status cell line
- Cell line hela
- Cell type epithelial cell
- Tissue type cervical cancer cell line
- Subcellular localization
- Comments

Participant	Participant identification method	Experimental role	Accession number
(1) 90782	western blot	bait	
(2) 28022	western blot	prey	

« Previous
Commit »



Accepted

Curated Interaction Group has been created as [CIG-4737](#).

To create a new interaction, click [New Submission]

To create a new interaction with last submission data, click [Copy Submission]

[New Submission](#)[Copy Submission](#)

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 then make the appropriate changes. Click on “Preview” to review the interaction.

The screenshot shows the InnateDB web interface. At the top, it says "InnateDB" and "A Knowledge Resource For Innate Immunity Interactions & Pathways". The user is logged in as "meyau@interchange.ubc.ca". The main content area shows the details of a curated interaction group, CIG-4754. The interaction details are as follows:

Interaction	
Short name	ILK:CASP9
Full name	ILK physically associates with CASP9
Interaction type	physical association
Comments	

Below the interaction details, there is a section for participants:

Participant 1	
Molecule type	protein
Species	9606
Molecule	29381
Biological role	unspecified role

In the top right corner of the interaction details section, there are "edit" and "select" buttons. The "edit" button is circled in red in the screenshot.

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

Cell line	hi60
Cell type	
Tissue type	promyelocytic leukemia cell
Subcellular localization	
Comments	ILK recruits CASP9 4 hr. after irradiation in suspension cultures. Reciprocal coimmunoprecipitation was also performed. Treatment: irradiation with 0 Gy and 10 Gy

Participant	Participant identification method	Experimental role	Accession number
(1) 29381	western blot	bait	
(2) 90895	western blot	prey	

« Previous **Commit** »

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.

A Knowledge Resource For Innate Immunity Interactions & Pathways

Interaction	Pathway	Innategene	Stats
-------------	---------	------------	-------

Interactions **Public Interaction Group IDBG-76625** curate delete

Interaction

Short name: WDR62:WDR62
 Full name: WDR62 interacts with WDR62
 Interaction type: physical association
 Comments:

Participant 2

Participant 1

Molecule type: protein
 Species: 9606
 Molecule: 46287
 Biological role: unspecified role

Participant 2

Molecule type: protein
 Species: 9606
 Molecule: 46287
 Biological role: unspecified role

Evidence 2

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

Interactions » Public Interaction Group IDBG-76625 » Delete

Select a group member:

You cannot directly delete the whole group. Please select one of the following members to delete:

- [Public Interaction IDB-5181](#)
- [Public Interaction IDB-80406](#)

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.

Comments

Participant	Participant identification method	Experimental role	Accession number
(1) 46287		bait	C43379
(2) 46287		prey	C43379

Warning!

Once committed, this public interaction IDB-5181 **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.

I understand, please delete IDB-5181 & add as new curated interaction.

« Previous
Commit »

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.

InnateDB
A Knowledge Resource For Innate Immunity Interactions & Pathways

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[account](#) | [logout](#)

Interaction Stats

Interactions » Curated Interaction Group CIG-4754 [edit](#) [reject](#)

Interaction	
Short name	ILK: CASP9
Full name	ILK physically associates with CASP9
Interaction type	physical association
Comments	

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

Interactions » Curated Interaction Group CIG-4756 » Curated Interaction CI-6393 » Reject

Reject CI-6393?

Birc2::Birc3 Birc2 physically associates with Birc3

[Don't reject](#) [Reject](#)

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.

A Knowledge Resource For Innate Immunity Interactions & Pathways

Interaction Pathway Innategene Stats

Interactions » Public Interaction Group IDBG-76625 [curate](#) [delete](#)

Interaction	
Short name	WDR62: WDR62
Full name	WDR62 interacts with WDR62
Interaction type	physical association
Comments	

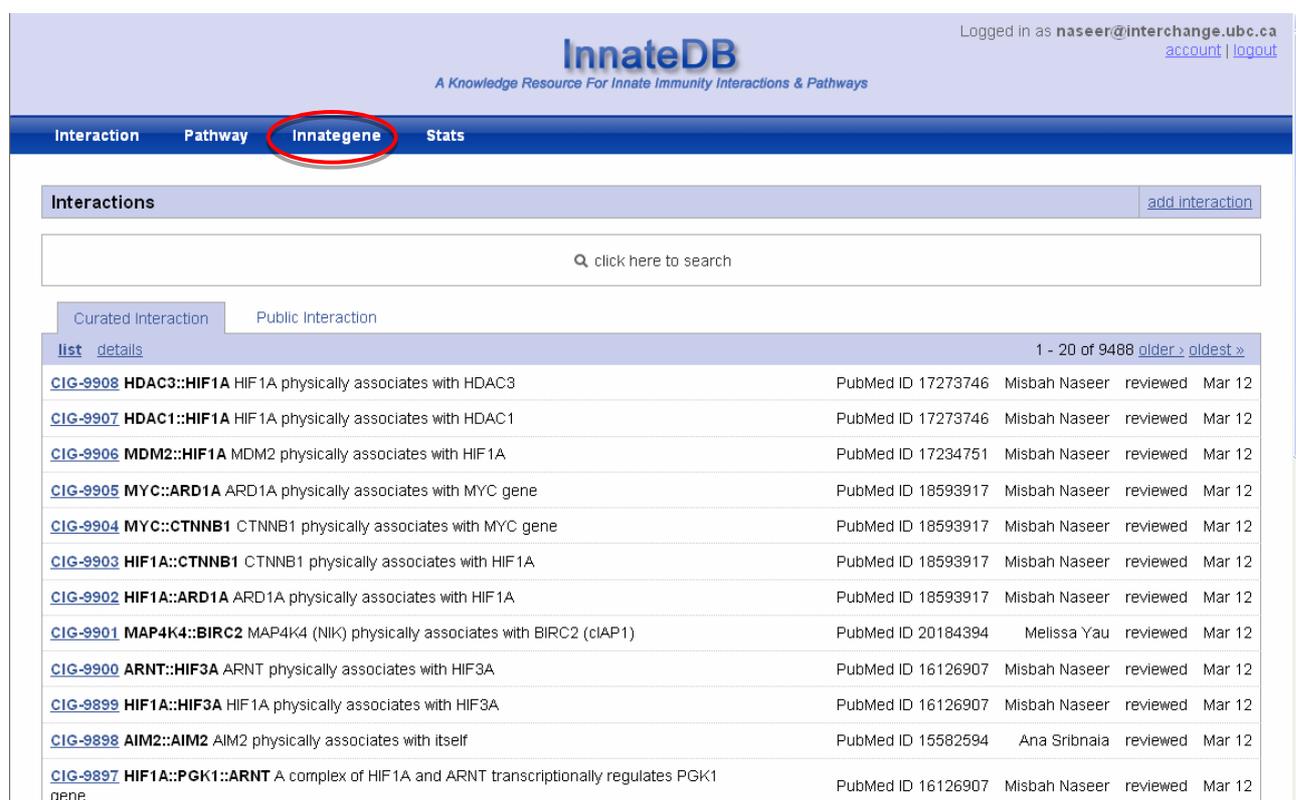
Participant	
Participant 1	
Molecule type	protein
Species	9606
Molecule	46287
Biological role	unspecified role
Participant 2	
Molecule type	protein
Species	9606
Molecule	46287
Biological role	unspecified role

Evidence	
----------	--

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.”



The screenshot shows the InnateDB website interface. The top navigation bar includes 'Interaction', 'Pathway', 'Innategene' (highlighted with a red circle), and 'Stats'. Below the navigation bar, there is a search bar and a list of interactions. The 'Curated Interaction' tab is selected, showing a list of interactions with columns for ID, description, PubMed ID, reviewer, and date.

list	details	1 - 20 of 9488	older >	oldest >>
CIG-9908	HDAC3::HIF1A HIF1A physically associates with HDAC3	PubMed ID 17273746	Misbah Naseer	reviewed Mar 12
CIG-9907	HDAC1::HIF1A HIF1A physically associates with HDAC1	PubMed ID 17273746	Misbah Naseer	reviewed Mar 12
CIG-9906	MDM2::HIF1A MDM2 physically associates with HIF1A	PubMed ID 17234751	Misbah Naseer	reviewed Mar 12
CIG-9905	MYC::ARD1A ARD1A physically associates with MYC gene	PubMed ID 18593917	Misbah Naseer	reviewed Mar 12
CIG-9904	MYC::CTNNB1 CTNNB1 physically associates with MYC gene	PubMed ID 18593917	Misbah Naseer	reviewed Mar 12
CIG-9903	HIF1A::CTNNB1 CTNNB1 physically associates with HIF1A	PubMed ID 18593917	Misbah Naseer	reviewed Mar 12
CIG-9902	HIF1A::ARD1A ARD1A physically associates with HIF1A	PubMed ID 18593917	Misbah Naseer	reviewed Mar 12
CIG-9901	MAP4K4::BIRC2 MAP4K4 (NIK) physically associates with BIRC2 (cIAP1)	PubMed ID 20184394	Melissa Yau	reviewed Mar 12
CIG-9900	ARNT::HIF3A ARNT physically associates with HIF3A	PubMed ID 16126907	Misbah Naseer	reviewed Mar 12
CIG-9899	HIF1A::HIF3A HIF1A physically associates with HIF3A	PubMed ID 16126907	Misbah Naseer	reviewed Mar 12
CIG-9898	AIM2::AIM2 AIM2 physically associates with itself	PubMed ID 15582594	Ana Sribnaia	reviewed Mar 12
CIG-9897	HIF1A::PGK1::ARNT A complex of HIF1A and ARNT transcriptionally regulates PGK1 gene	PubMed ID 16126907	Misbah Naseer	reviewed Mar 12

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.

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InnateDB

A Knowledge Resource For Innate Immunity Interactions & Pathways

Interaction Pathway Innategene Stats

Innate Genes

Add Edit Delete Reset

Gene ID	Gene Symbol	Species	Descriptions	Created on
130586	Cd209a	10090	Has a role in the regulation of inflammation in a model of experimental colitis and	2010-03-11 10:43:10
103863	AIM2	9606	Recognizes cytosolic dsDNA and forms a caspase-1-activating inflammasome wit	2010-03-11 09:55:02
21100	HMGB1	9606	Functions as universal sentinel for nucleic-acid-mediated innate immune respons	2010-03-11 09:37:15
6462	SPON2	9606	SPON2 expression is upregulated during intestinal inflammation and may induce	2010-03-11 09:33:15
62191	IL31	9606	Antimicrobial Peptides Human (beta)-Defensins and Cathelicidin LL-37 Induce th	2010-03-11 09:31:25
32341	CAMP	9606	Activates human mast cells and is degraded by mast cell tryptase ; Vitamin D3 in	2010-03-11 09:28:58
18750	IDO1	9606	Induction of IDO-1 by Immunostimulatory DNA limits severity of experimental colit	2010-03-11 09:19:18
97039	TNFAIP3	9606	Restricts TLR signals by restricting ubiquitination of TRAF6; Accomplishes debu	2010-03-11 09:08:12
83441	INPP5D	9606	Absence of SHIP-1 results in constitutive phosphorylation of tank-binding kinase	2010-03-11 08:51:53
8115	RAC1	9606	LTA-induced MAPKs activation is mediated through the TLR-2/MyD88/PI3K/Rac1	2010-03-11 08:44:49

10 Page 1 of 47 Displaying 1 to 10 of 468 items

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.

Logged in as naseer@interch

InnateDB

A Knowledge Resource For Innate Immunity Interactions & Pathways

Interaction Pathway Innategene Stats

Innate Genes » [New Innate Genes](#)

Innate Genes Basic Information

InnateDB Gene ID select...

Gene Symbol

Species Homo sapiens

Associated Publication and Description

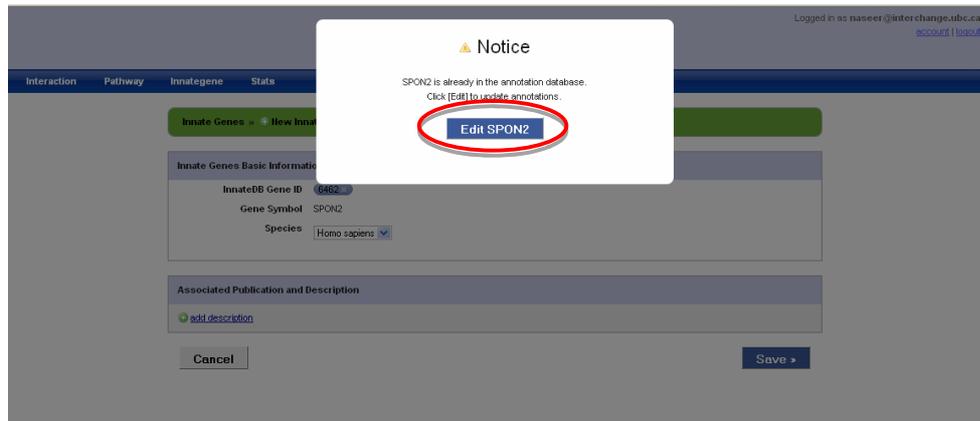
add description

Cancel
Save >

InnateDB is being developed jointly by the Brinkman Laboratory, Simon Fraser University and the Hancock Laboratory, University of British Columbia, Vancouver, British Columbia, Canada and the Lynn Laboratory, Teagasc Animal Bioscience Department, Ireland.

Funding is provided by Genome Canada through the Pathogenomics of Innate Immunity (PI2) project, and the Foundation for the National Institutes of Health through the Grand Challenges in Global Health initiative.

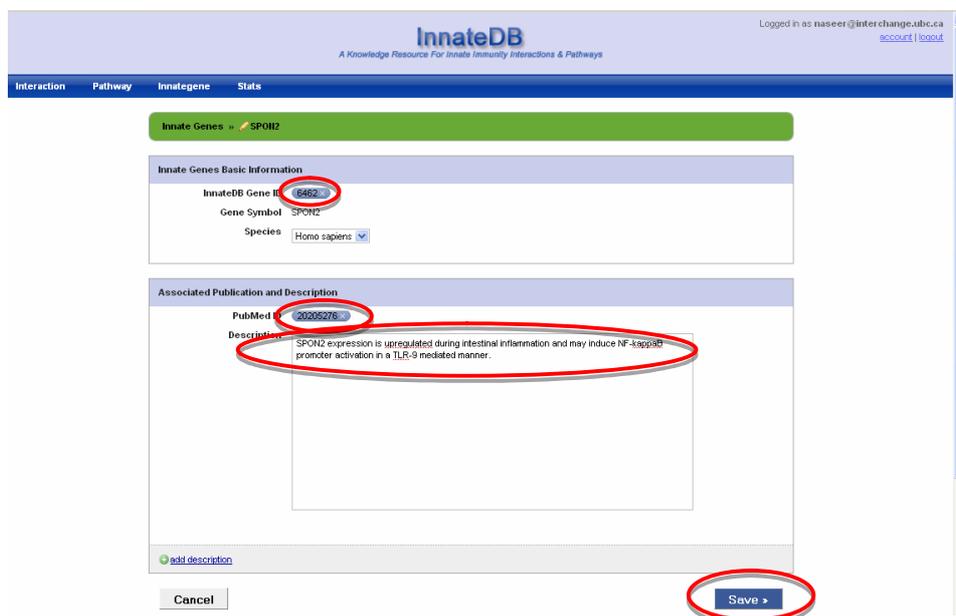
Note: When looking up a gene ID, a pop-up screen may appear notifying the user of an existing annotation for the gene. Click **EDIT [GENE SYMBOL]** button to continue.



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.

InnateDB
A Knowledge Resource For Innate Immunity Interactions & Pathways

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account | logout

Interaction Pathway Innategene Stats

Innate Genes

+ Add Edit Delete Reset

Gene ID	Gene Symbol	Species	Descriptions	Created on
130586	Cd209a	10090	Has a role in the regulation of inflammation in a model of experimental colitis and	2010-03-11 10:43:10
103863	AIM2	9606	Recognizes cytosolic dsDNA and forms a caspase-1-activating inflammasome wit	2010-03-11 09:55:02
21100	HMGB1	9606	Functions as universal sentinel for nucleic-acid-mediated innate immune respon	2010-03-11 09:37:15
6462	SPON2	9606	SPON2 expression is upregulated during intestinal inflammation and may induce	2010-03-11 09:33:15
62191	IL31	9606	Antimicrobial Peptides Human (beta)-Defensins and Cathelicidin LL-37 Induce th	2010-03-11 09:31:25
32341	CAMP	9606	Activates human mast cells and is degraded by mast cell tryptase ; Vitamin D3 in	2010-03-11 09:28:58
18750	IDO1	9606	Induction of IDO-1 by Immunostimulatory DNA limits severity of experimental coliti	2010-03-11 09:19:18
97033	TNFAIP3	9606	Restricts TLR signals by restricting ubiquitination of TRAF6, Accomplishes deubi	2010-03-11 09:08:12
83441	INPP5D	9606	Absence of SHIP-1 results in constitutive phosphorylation of tank-binding kinase	2010-03-11 08:51:53
8115	RAC1	9606	LTA-induced MAPKs activation is mediated through the TLR-2/MyD88/PI3K/Rac	2010-03-11 08:44:49

10 Page 1 of 47 Displaying 1 to 10 of 468 items

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

InnateDB
A Knowledge Resource For Innate Immunity Interactions & Pathways

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account | logout

Interaction Pathway Innategene Stats

Innate Genes

+ Add Edit Delete Reset

Gene ID	Gene Symbol	Species	Descriptions	Created on
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Quick Search: Gene ID/Gene Symbol Clear

10 Page 1 of 47 Displaying 1 to 10 of 468 items

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.

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Interaction Pathway Innategene Stats

Innate Genes

Gene ID	Gene Symbol	Species	Descriptions	Created on
90792	IRAK1	9606	Upregulates IL1 and binds to TRAF6 in TLR4 pathway. IRAK1 binds to the NFkB	2010-01-04 09:27:04

Quick Search | IRAK1 Gene ID/Gene Symbol

10 Page 1 of 1 Displaying 1 to 1 of 1 items

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.

PubMed ID

Description

Functionally associates with PKC ζ and VASP in the regulation of macrophage migration

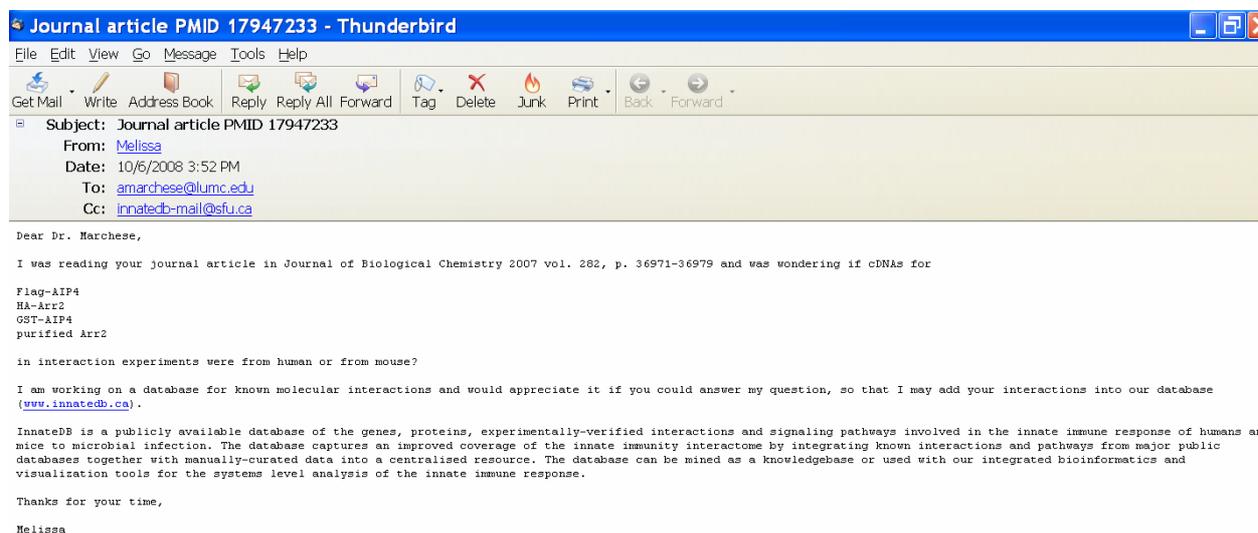
Chapter 2: Curation Related Issues

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:

- Guidelines for submitting interactions
- Track curation progress (requested and curated genes)
- 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.

Curators Group

Submission System [edit]

PARTICIPANTS

- Proteins with no HUGO symbol: search the innatEDB id for the **gene** encoding your protein of interest and enter it the "name" field.
- Biological Role:
 - Specifies the role of the protein in the particular interaction e.g. kinase-phospho donor; phosphorylated protein --phospho acceptor
 - Ubiquitination: Ubiquitinating molecule: Enzyme; Ubiquitinated molecule: Enzyme Target
 - Dephosphorylation: Dephosphorylating molecule: Enzyme; Dephosphorylated molecule: Enzyme Target
 - FRET (Fluorescent resonance energy transfer: CFP tag-protein: Fluorescence donor; YFP tag-protein: Fluorescence acceptor
 - Transcriptional regulation: title: transcriptionally downregulates/upregulates; biological role of the protein: transcription factor; interaction detection method: enzymatic study and mention the type of assay used to detect the upregulation or downregulation of the promoter of interest in comments

EVIDENCE

Experimental type:

- In order to add more than one experimental method from the same paper, add two separate evidences with same PMIDs.
- ELISA, in-gel kinase assay, Yeast two hybrid: No cell line, cell type, tissue defined. Usually "neutral component", except when doing a Y2H screen in which there is an obvious bait.
- GST pulldowns: (A) in-vitro translated proteins (at least one GST fusion protein), pulled down on glutathione-agarose beads; this type of pulldown does not have a cell type. (B) GST fusion protein transfected into the cell, and cell lysate is run on glutathione-agarose beads; this type of pulldown has a cell type (C) GST fusion protein also has a tag: if protein is pulled out using glutathione-agarose (or similar), this is called a GST pulldown; if GST fusion protein was pulled out using an anti-tag antibody, this is a co-immunoprecipitation.
- ALWAYS select anti-tag Co-IP for experiments with one or more tagged protein(s), specifying the tags in comments is optional.

Experimental Role

Select one of the following for each participant:

- bait
- prey
- neutral component e.g. kinase assays, ubiquitination assays, x-ray crystallography, Y2H in which no bait is used (i.e. binding domain of Protein 1 with Activating domain of other)
- unspecified role

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.

List of Genes - Curated and Requests - PI2 Wiki - Mozilla Firefox

File Edit View History Bookmarks Tools Help

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

Customize Links I.M.A.G.E. Single Clon...

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List of Genes - Curated and Requests

CURATED GENES

- AKT2 by Jaimmie & Aaron (18 human, 1 mouse, total 19)
- AZ2 (NAP1) by Melissa (8 human)
- BIRC4 Aug 2007 by Melissa and Raymond (70 human, 4 mouse; total: 74)
- CAMP by Ray
- CCL20 by Ray
- BTK by Misbah (25 human, 9 mouse; total: 34)
- CARD6 by Misbah (5 human, 1 mouse; total: 6)
- CARD9 by Misbah (6 human)
- CD14 by Jaimmie (2 human, 0 mouse; total: 2)
- CDH1 by Melissa (46 human, 20 mouse; total: 66)
- CENTB1 (ACAP1) by Misbah: (11 human, 1 mouse; total: 12)
- CHUK (IKK alpha) by Misbah (60 human, 7 mouse; total: 67)
- COP36 (CSN6) by Misbah (8 h)
- CTNNB1 by Melissa (118 human, 40 mouse; total: 158)
- DDX58 by Jaimmie (9 human, 0 mouse; total: 9)
- DHX58 (LGP2) by Melissa (5 human)
- DEDD by Melissa (6 human, 2 mouse; total: 8)
- DUSP16 (MLK7) by Misbah and Alex (8 human, 1 mouse; total: 9)
- ECSIT by Misbah (1 human)
- EPC1 by Misbah (9 human, 2 mouse, total: 11)
- ERBB2IP (ERBIN) by Misbah (46 human, 5 mouse, total: 53)
- FADD by Melissa (23 human, 1 mouse; total: 24)
- GAPDH by Misbah (9 human, 3 mouse; total: 12)
- GSR by Ray
- HRAS September 2007 by Melissa and Raymond (50 human, 6 mouse; total: 56)
- IFIH1 by Jaimmie (2 human, 0 mouse; total: 2)
- IFIT1 by Ray
- IKBKB by Misbah (69 human, 6 mouse; total: 75)
- IKBKE by Jaimmie (18 human, 0 mouse; total: 18)

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.

InnateDB curators list - PI2 Wiki - Mozilla Firefox

File Edit View History Bookmarks Tools Help

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

Customize Links I.M.A.G.E. Single Clon...

Meyau my talk preferences my watchlist my contributions log out

InnateDB curators list

Innate Immune Genes [edit]

HUGO Symbol: function

- ADIPOQ**: Adipose-specific protein adiponectin, member of pattern-recognition family of defense collagens, binds to C1Q and activates the classical pathway of complement; PMID 18179772
- ATG5**: ATG5-ATG12 conjugate associates with innate antiviral immune responses by its direct association with DDX58 and MAVS, which negatively regulates IFN production pathway by mediating autophagy PMID 17709747
- AXL**: Tyrosine protein kinase, acts with TYRO3 and MERTK as Pleiotropic Inhibitor of the Innate Immune Response in DCs; PMID 18063102
- AZ2(NAP1)**: NAP1 participates in both the TLR3 and cytoplasmic RIG pathways in type I IFN induction, binding to MAVS and DDX58 and MDA5 PMID 17142768
- BCL10**: selectively regulates JNK2 kinase in T cell receptor signalling pathway, serves as JNK-interacting protein like scaffold to assemble MAPK9, MAP3K7 and MAP2K7. The latter two kinases are recruited by BCL10 to activate MAPK9; PMID 17189706
- BDKRB2**: The bradykinin B2 receptor in the early immune response against Listeria infection—potentiates the production of IL-12p70 in human monocyte-derived dendritic cells PMID 18810490
- BECN1**: key factor in autophagosome formation, binds Th4, Myd88 and Ticam1 in mouse, Selective TLR signaling via its adaptor proteins reduces the binding of Becn1 to Bcl-2 by recruiting Becn1 into the TLR-signaling complex leading to autophagy. PMID 18772134
- BIRC2**: regulates TNF alpha-mediated NFkappa B activation by binding to TNFR1; PMID 18697935, Tumour necrosis factor receptor 2 signaling induces selective BIRC2-dependent ASK1 ubiquitination and terminates mitogen-activated protein kinase signaling PMID 17220297
- BIRC3**: regulates TNF alpha-mediated NFkappa B activation by binding to TNFR1; PMID 18697935
- BMX**: Tyrosine protein kinase, regulates TLR4 induced IL-6 in macrophages independent of MAPK14 (P38 alpha) and NFKB; PMID 18025155
- BTK**: Tyrosine protein kinase, downstream of B cell receptor regulating NFKB activation; PMID 12724322, negative regulator of Fas-mediated apoptosis PMID 9880544
- C1Q**: Recognition subunit of the classical complement C1 complex. PMID 15207504
- C1R**: Protease that mediates activation of the C1 complex of classical complement. PMID 11445589
- C1S**: Associates with C1R and C1Q to form the first component (C1) of the classical complement pathway. C1S is the modular serine protease responsible for cleavage of C4 and C2, the protein substrates for C1. PMID 16177097
- C2**: Complement component two is part of the classical and lectin complement pathways. C2 molecule binds to C4B and is cleaved by C1S protease into C2A and C2B fragments. The resulting C4B2A complex