

Bioinformatics, proteomics of cells: An introduction to techniques and tools of an emerging field.

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http://donaldson.uio.no/wiki/Protein_Interaction_Resources
<http://irefindex.uio.no>

What is a network?

What are networks used for?

Where do networks come from?

Where would you get network data?

Some simple tools.

Where to begin and further reading.

What is a network?

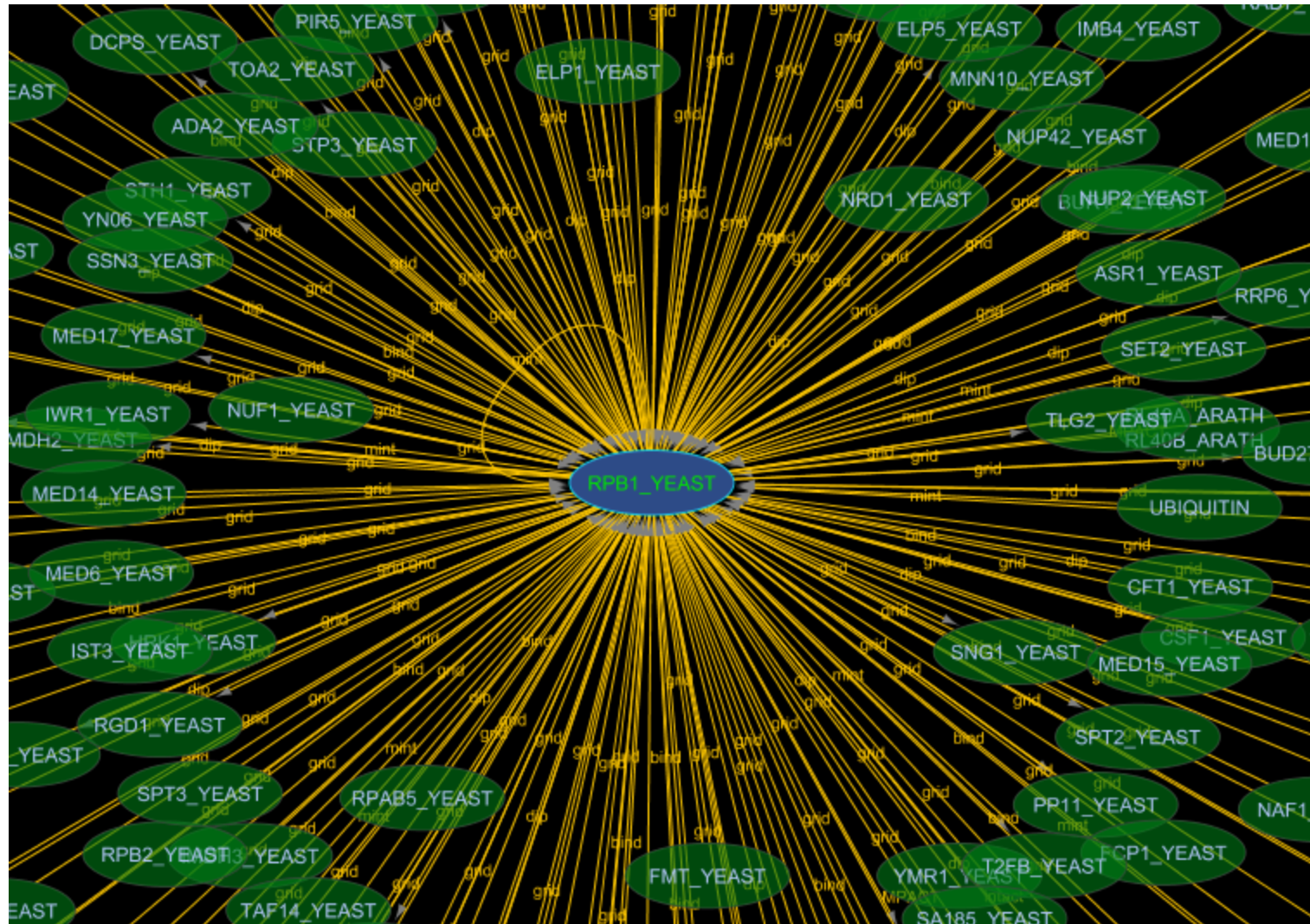
What are networks used for?

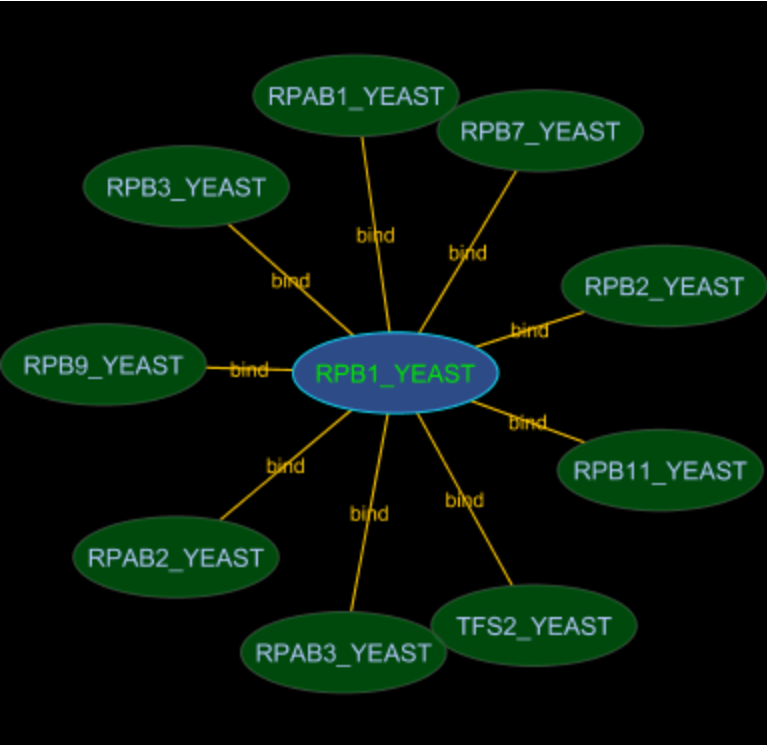
Where do networks come from?

Where would you get network data?

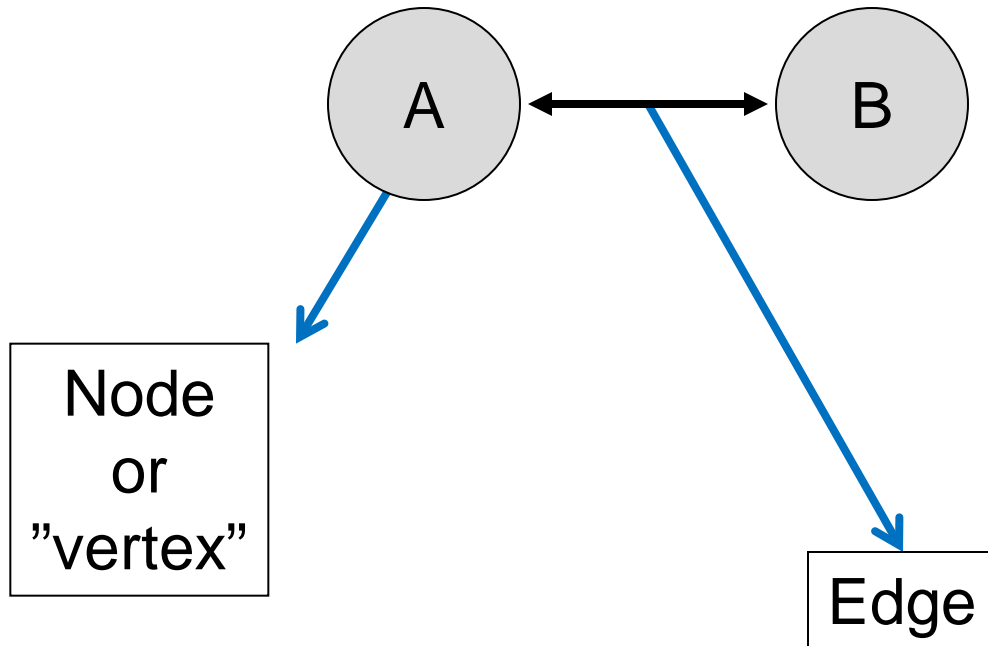
Some simple tools.

Where to begin and further reading.

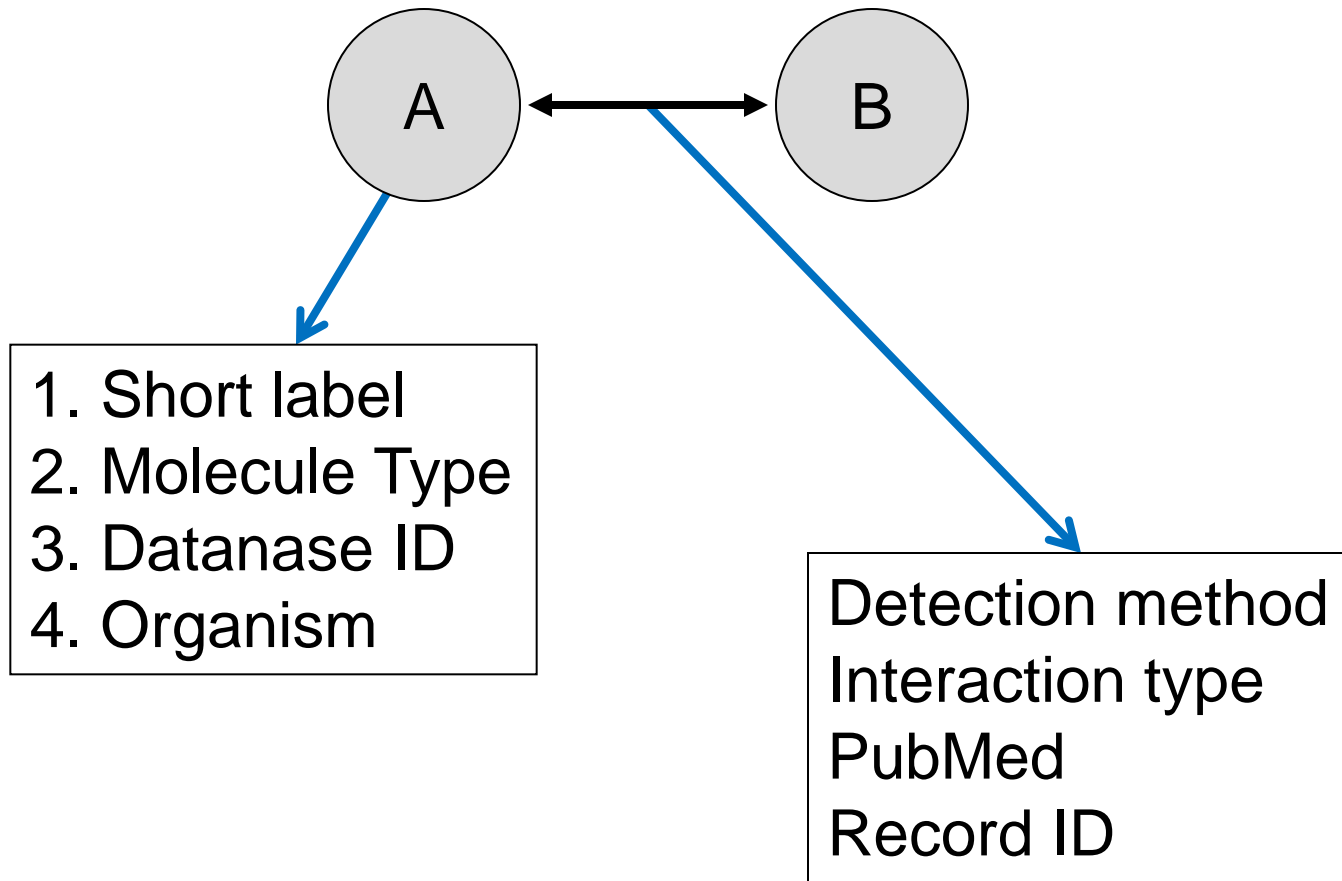




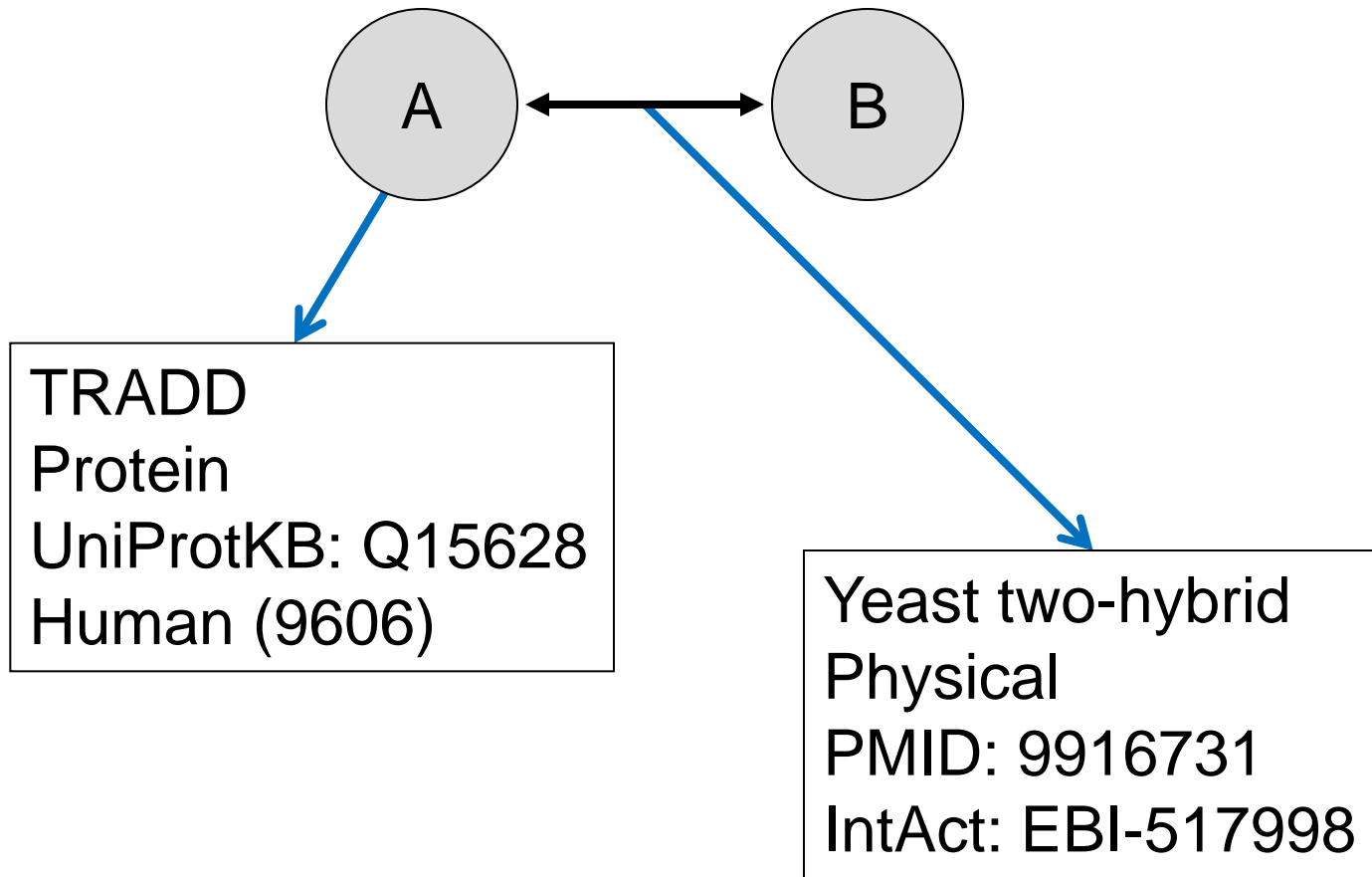
A simple interaction record



A simple interaction record



A simple interaction record



What is a network?

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How would you use it?

Where to begin and further reading.

What are networks used for?

What does my protein interact with?

What complexes is my protein a part of?

What are networks used for?

Given a list of genes with

**(SNP's,
altered somatic copy number,
altered gene expression, or
a shared phenotype),**

**how are they related and what pathways are
they likely to affect?**

What are networks used for?

Given a list of genes

**what other genes are likely to be involved
in the same process or pathway?**

Montejo J, et al. *Bioinformatics*. 2010. 26(22):2927-8. PMID: 20926419

Gillis, J. & Pavlidis, P. *Bioinformatics*. 2011. PMID: 21551147

What would you use it for?

Given a list of genes with

**(altered somatic copy number or
altered gene expression
in some patient's tumor sample),**

what is the prognosis for the patient?

What is a network?

What are networks used for?

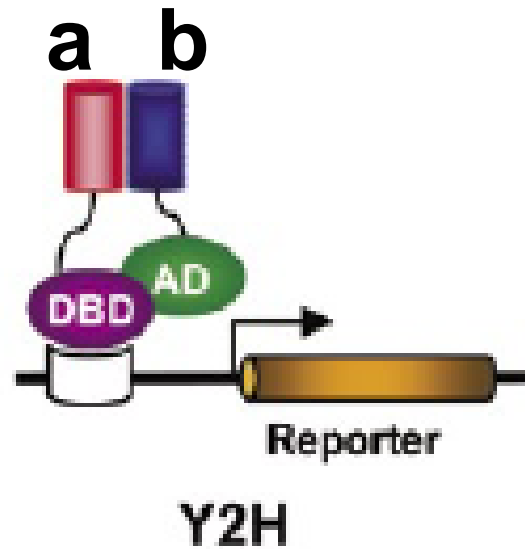
Where do networks come from?

Where would you get network data?

How would you use it?

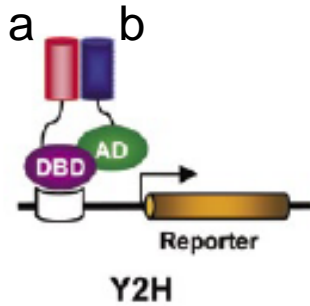
Where to begin and further reading.

Experimental methods – Yeast Two Hybrid

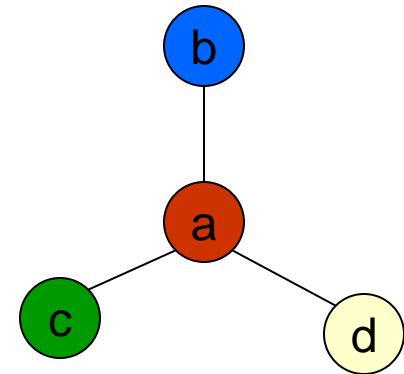


Representation of interaction data

binary data



Record	A	B
1	a	b
2	a	c
3	a	d



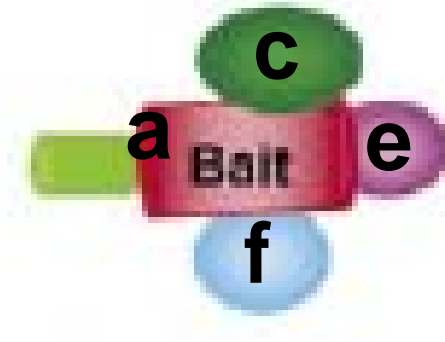
MITAB format of binary data

#uidA	uidB	...method...	pmids	interactionType	sourcedb	interactionIdentifier
uniprotkb: P04050	uniprotkb: P53617	MI:0018(two hybrid)	pubmed:12727883	MI:0407(direct interaction)	MI:0463(grid)	grid:142567
uniprotkb: P39081	uniprotkb: P04050	MI:0018(two-hybrid- test)	pubmed:12145212	-	MI:0462(bind)	bind:257718
uniprotkb: P04050	uniprotkb: P39081	MI:0018(two hybrid)	pubmed:12145212	-	MI:0465(dip)	dip:DIP-40350E

<http://code.google.com/p/psicquic/wiki/MITAB26Format>

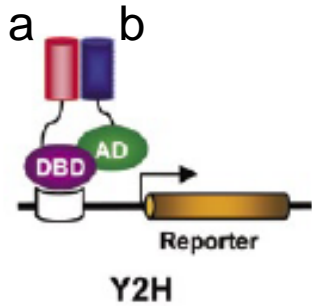
Experimental methods

Affinity purification

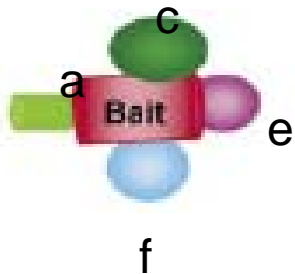
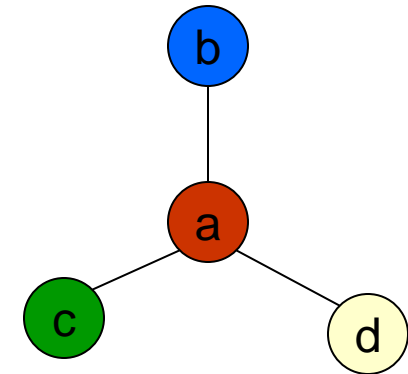


Representation of interaction data

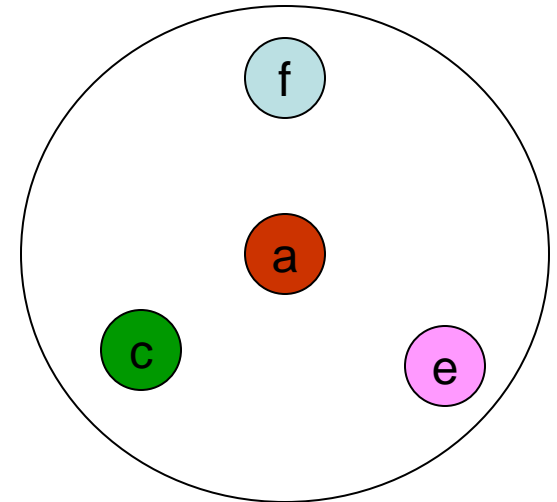
binary data versus n-ary data



Record	A	B
1	a	b
2	a	c
3	a	d

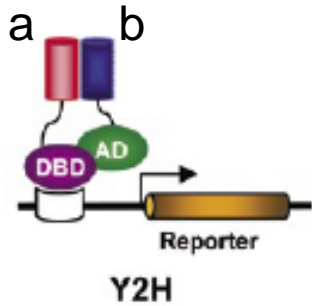


?

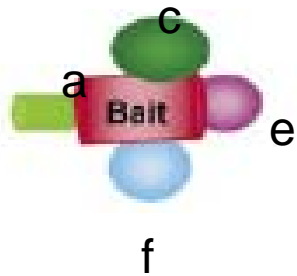
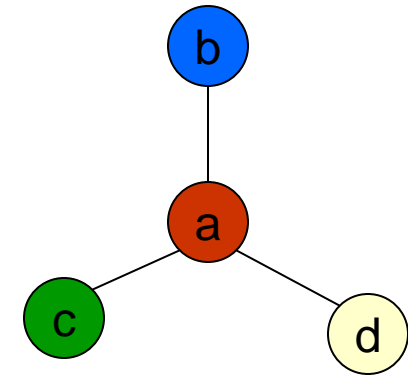


Representation of interaction data

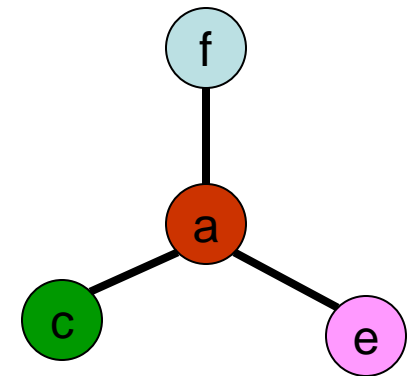
binary data versus n-ary data



Record	A	B
1	a	b
2	a	c
3	a	d



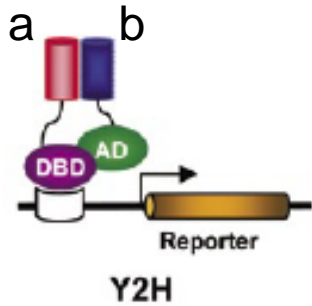
Record	A	B
1	a	c
2	a	e
3	a	f



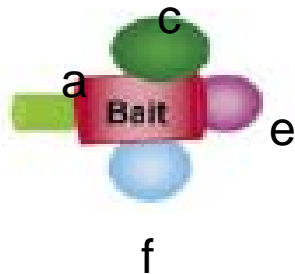
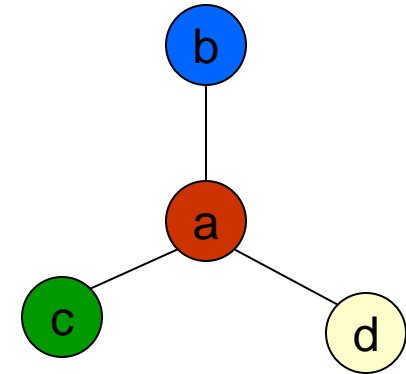
spoke model

Representation of interaction data

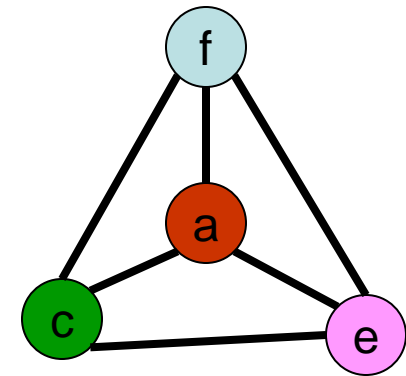
binary data versus n-ary data



Record	A	B
1	a	b
2	a	c
3	a	d



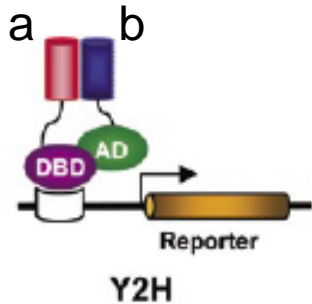
Record	A	B
1	a	c
2	a	e
3	a	f
4	f	e
5	e	c
6	c	f



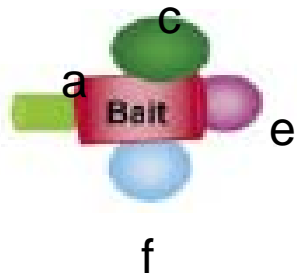
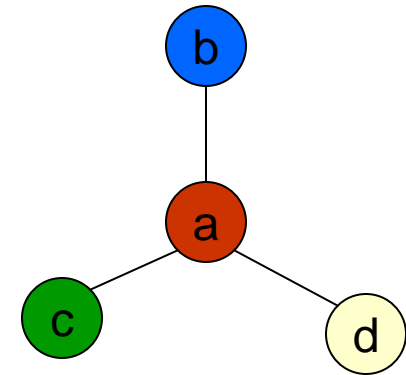
matrix model

Representation of interaction data

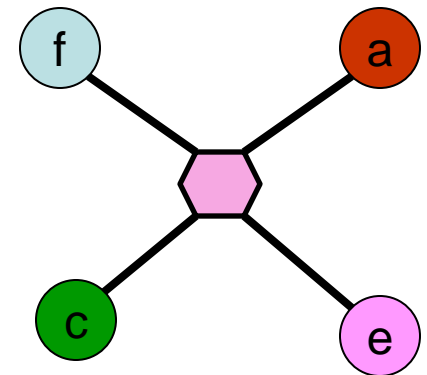
binary data versus n-ary data



Record	A	B
1	a	b
2	a	c
3	a	d



Record	A	B
1	Complex 1	f
1	Complex 1	a
1	Complex 1	c
1	Complex 1	e



Bipartite model

MITAB format of n-ary data

(using a bipartite model)

#uidA	uidB	method	pmids	Interaction Type	sourcedb	interactionIdentifier
complex:1	uniprotkb:P19659	MI:0000(11805826)	pubmed:11805826	-	MI:0462(bind)	bind:17408
complex:1	uniprotkb:P32259	MI:0000(11805826)	pubmed:11805826	-	MI:0462(bind)	bind:17408
complex:1	uniprotkb:P40356	MI:0000(11805826)	pubmed:11805826	-	MI:0462(bind)	bind:17408
complex:1	uniprotkb:P47821	MI:0000(11805826)	pubmed:11805826	-	MI:0462(bind)	bind:17408

<http://code.google.com/p/psicquic/wiki/MITAB26Format>

More about methods and interaction types that they support

<http://www.ebi.ac.uk/ontology-lookup/browse.do?ontName=MI>

The screenshot displays the Ontology Lookup Service (OLS) interface in a Mozilla Firefox browser window. The page title is "Ontology Lookup Service (OLS) - Mozilla Firefox". The main content area is titled "OLS - Ontology Lookup Service" and "MI Ontology Browser". The interface includes a navigation menu with options like "Databases", "Tools", "EBI Groups", "Training", "Industry", "About Us", and "Help". A search bar is present with the text "All Databases" and "Enter Text Here". The main content area shows a tree view of the "molecular interaction" ontology, with sub-classes like "interaction detection method", "participant identification method", "feature detection method", "interaction type", "genetic interaction", "colocalization", "association", "alias type", "interactor type", "feature range status", "experimental preparation", "cross-reference type", "database citation", "experimental role", and "biological role". A "Help (hide)" section provides instructions on how to use the browser, such as "Double-click a term to see its children" and "Click to highlight a term to see any information associated with it". There are also sections for "Relations", "Term Information" (with fields for ID and Name), "Associated information", and "Term Hierarchy" (with radio buttons for "Paths to Root" and "Child relationships").

Ontology Lookup Service (OLS) - Mozilla Firefox

EMBL-EBI EB-eye Search All Databases Enter Text Here Go Reset Advanced Search Give us feedback

Databases Tools EBI Groups Training Industry About Us Help Site Index

OLS - Ontology Lookup Service

MI Ontology Browser

Help (hide)

Double-click a term to see its children. The ontology browser is populated dynamically. If there are many children for a given term, there may be a small delay while the browser fetches Click to highlight a term to see any information associated with it. Hover over a term to see its relation with its immediate parent. Root terms will not display any relational information.

Relations

Term Information

ID: Zoom

Name:

Associated information

Highlight a term to view its associated information.

Term Hierarchy

Paths to Root: Child relationships:

You can zoom the ontology browser by clicking on a term in the graph.

Done Tor Disabled

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Interaction databases

BIND	inactive
BioGRID	IMEX (Observer)
CORUM	complexes
DIP	IMEX (Archival)
HPRD	human resource
IntAct	IMEX (Archival)
MATRIX	extracellular matrix
MINT	IMEX (Topical)
MPACT	IMEX (Topical) yeast
MPIDB	IMEX (Observer) prokaryotic
MPPI	mammalian
OPHID/I2D	predicted
Many others	

See <http://www.pathguide.org/> for URLs

Interaction databases

IMEx

International Molecular Exchange Consortium

IMEx partners exchange data and share curation tasks.

Set standards

They also accept interaction data submissions pre and post publication.

Data consolidation and exchange is an active area of research.

See <http://www.imexconsortium.org/>

Interaction databases: IntAct

The screenshot shows the IntAct website interface. At the top, there is a search bar with the text "Enter Text Here" and a "Find" button. Below the search bar, there are navigation menus for "Databases", "Tools", "Research", "Training", "Industry", "About Us", and "Help". The main content area features a search box and a "Search" button. Below the search box, there are tabs for "Home", "Search", "Interactions (268920)", "Browse", "Lists", "Interaction Details", "Molecule View", and "Graph". The "Interactions (268920)" tab is selected. Below the tabs, there is a section titled "Search IntAct" with a paragraph explaining how to perform a search. Below this, there are examples of search terms: "Gene name: e.g. BRCA2", "UniProtKB Ac: e.g. Q06609", "UniProtKB Id: e.g. dmc1", and "Pubmed Id: e.g. 10831611". A feedback box asks users to provide feedback to the helpdesk. Below the feedback box, there is an "Introduction" section and a "Dataset of the month: August" section. The "Dataset of the month" section lists four publications with their respective IntAct and PSI-MI scores. The "License" section at the bottom states that the software is available under the Apache License version 2.0 and the data is under the Creative Commons Attribution License.

Gene name: [BRCA2](#)
UniProtKB Ac: [Q06609](#)
UniProtKB Id: [dmc1](#)
Pubmed Id: [10831611](#)

Please supply your feedback to [helpdesk](#). We thank you for your help in further developing IntAct.

Introduction
IntAct provides a freely available, open source platform for the submission and curation of protein-protein interactions. Submissions and are freely available.

Dataset of the month: August

- Linking Chromatin remodelling, D
Yao et al *IntAct* [PSI-MI 2.5](#)
[PSI-MI 1.0](#)
- Wu et al *IntAct* [PSI-MI 2.5](#) [PSI-MI TAB](#)
[PSI-MI 1.0](#)
- Chen et al *IntAct* [PSI-MI 2.5](#) [PSI-MI TAB](#)
[PSI-MI 1.0](#)
- Jiang et al *IntAct* [PSI-MI 2.5](#) [PSI-MI TAB](#)
[PSI-MI 1.0](#)

Go to [Archive](#).

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<http://www.ebi.ac.uk/intact>

Interaction databases: IntAct

IntAct
www.ebi.ac.uk/intact/main.xhtml?conversationContext=1

EMBL-EBI
Enter Text Here Find Help | Feedback

Databases Tools Research Training Industry About Us Help Site Index

IntAct
EBI > Databases > Pathways & Networks > IntAct > View

Search: Rpb1 Search Clear Show Advanced Fields MIQL syntax reference

Home Search Interactions (607) Browse Lists Interaction Details Molecule View Graph

Browse by taxonomy, gene ontology, ChEBI ontology What is this view

> 607 binary interactions were found in IntAct. 442 of them are originated from spoke expanded co-complexes and you may want to filter them.
> Your query also matches 2,305 interaction evidences from 5 other databases.

Previous 1-30 of 607 Next 30 Export to: Select format... Export Change Columns Displayed Previous 1-30 of 607 Next 30

	Name molecule A	Links molecule A	Name molecule B	Links molecule B	Aliases molecule A	Aliases molecule B	Species molecule A	Species molecule B	Publication Identifier	Interaction Detection Method	Interaction AC	Expansion Method
1	RPC53	UniProt Dasty2	RPO31	UniProt Dasty2	RPC4; YDL150W; D1557; [+]	RPC160; RPC1; YOR116C; [+]	559292	559292	11805826	tandem affinity purification	EBI-42328	Spoke
2									16429126	tandem affinity purification	EBI-800569	Spoke
3	SET2	UniProt Dasty2	YDJ1	UniProt Dasty2	EZL1; YJL168C; J0520; [+]	MASS; YNL064C; N2418; [+]	559292	559292	19536198	tandem affinity purification	EBI-3664308	
4	CMD1	UniProt Dasty2	SET2	UniProt Dasty2	YBR109C; YBR0904; calm_ yeast	EZL1; YJL168C; J0520; [+]	559292	559292	16606443	protein array	EBI-939510	
5	INP52	UniProt Dasty2	SET2	UniProt Dasty2	YNL106C; N2160; SJL2; [+]	EZL1; YJL168C; J0520; [+]	559292	559292	18467557	dihydrofolate reductase reconstruction	EBI-2067822	
6	GABARAP	UniProt Dasty2	POLR1A	UniProt Dasty2	GABA(A) receptor-associated protein; MM46; FLC3B; [+]	DNA-directed RNA polymerase I subunit A; DNA-directed RNA polymerase I largest subunit; RNA polymerase I 194 kDa subunit; [+]	9606	9606	20562859 IM-15184	anti tag coimmunoprecipitation	EBI-3050465	Spoke
7	SET2	UniProt Dasty2	SIP2	UniProt Dasty2	EZL1; YJL168C; J0520; [+]	SPM2; YGL208W; G1155; [+]	559292	559292	16606443	protein array	EBI-939582	
8	RPC19	UniProt Dasty2	RPO31	UniProt Dasty2	YNL113W; N1937; DNA-directed RNA polymerases I and III 16 kDa polypeptide; [+]	RPC160; RPC1; YOR116C; [+]	559292	559292	11805826	tandem affinity purification	EBI-42328	Spoke
9									16429126	tandem affinity purification	EBI-800569	Spoke
10	RPC31	UniProt Dasty2	RPO31	UniProt Dasty2	ACP2; RPC8; YNL151C; [+]	RPC160; RPC1; YOR116C; [+]	559292	559292	11805826	tandem affinity purification	EBI-42328	Spoke

26/07/2011
UniProt collaboration on annotation of protein interactions to MIMx standard
UniProt curators will now curate protein interaction data to MIMx standards as part of their normal workflow, directly within the IntAct database. These interactions will form a part of the IntAct dataset, which also includes IMEx-level curation. A subset of binary interactions is extracted from this dataset and exported to the "Binary interactions" section of UniProtKB entries, determined using a simple scoring system, coupled to a score threshold that has been deliberately chosen to exclude interactions supported by only one experimental observation (for more details see the FAQ)

Remember...

Only a fraction of all interaction data is present in interaction databases

You always have recourse to text-mining and predicted interactions.

Not all interaction data is equal ...

Look at the methods and the original papers

Was the paper a high-throughput paper?

See Ipr score in irefweb/irefindex interfaces later.

Where would you get network data?

- **Interaction databases**
- **Text mining**
- **Predicted interactions**
- **Consolidated interaction databases**

Text mining resources

Most are based on co-occurrence of gene name mentions.

Two examples are

iHOP <http://www.ihop-net.org/UniPub/iHOP/>

PubGene <http://www.pubgene.org/>

Complete list maintained at

http://zope.bioinfo.cnio.es/bionlp_tools

Text mining resources: iHOP

iHOP - Information Hyperlinked over Proteins - Mozilla Firefox

http://www.ihop-net.org/UniPub/iHOP/index.html?field=all&search=RAD51&organism_id=0

Most Visited Entrez PubMed Post to CiteULike Library of Medicine and ... The Biotechnology Cen... BBC - bbc.co.uk home... Home page - The Rese... W Wikipedia

Stumble! I like it! Send to Channels: Favorites Friends Tools

iHOP - Inf... EBIMed FACTA PubGene - Find... Chilbot: finding... MedEvi - a per... FABLE - Overvi... BioCreative Met... BioText Search ...

iHOP
Information hyperlinked over proteins

Search Gene
RAD51

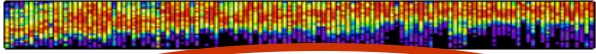




























































Gene Model Developer's Zone
How to cite iHOP

Contact Links Help

UNIVERSITY OF WASHINGTON CENTER FOR PROTEIN SCIENCE
ESTABLISHED 1987

cocoon

Concept & Implementation by Robert Hoffmann

Symbol	Name	Synonym/ DB-reference	Organism	Results
	 Life cycles of successful genes			↓
RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)		Homo sapiens	   
Rad51	RAD51 homolog (S. cerevisiae)		Mus musculus	   
RAD51	Strand exchange protein, forms a helical filament with DNA that searches for ...		Saccharomyces cerevisiae	   
rad51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)		Danio rerio	   
RAD51	LeRAD51		Lycopersicon esculentum	   
rad51	rad51 protein		Xenopus laevis	   
RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)		Gallus gallus	   
RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)		Canis familiaris	   
rad51	DNA repair protein Rad51 homolog		Guillardia theta	   
rad51	DNA repair protein		Giardia lamblia ATCC 50803	   
RAD51L1	RAD51-like 1 (S. cerevisiae)		Homo sapiens	   
RAD51C	RAD51 homolog C (S. cerevisiae)		Homo sapiens	   
RAD51L3	RAD51-like 3 (S. cerevisiae)		Homo sapiens	   
RAD51AP1	RAD51 associated protein 1		Homo sapiens	   
Rad51l3	RAD51-like 3 (S. cerevisiae)		Mus musculus	   

Interaction information for this gene.

Find: dmc1 Next Previous Highlight all Match case Reached end of page, continued from top

javascript:if(window.name=="") { window.location.href='./nil'; } else { doaction('IHOP', 91604, 1); }



Search Gene

Show overview

Find in this Page

Filter and options

Gene Model

Developer's Zone

Help

Concept & Implementation by Robert Hoffmann

WARNING: Please keep in mind that gene detection is done automatically and can exhibit a certain error. Read more about synonym ambiguity and the iHOP confidence value.

Found in this page: interacts (21)

Find in this Page

(Click here to show sentences in the default order)

Sentences in this view contain interactions of RAD51 - Interaction Information is available whenever you see this symbol - Read more.

Show all Order by relevance

For a summary overview of the information in this page click here. new

The results provide insight into why mutation in just one of the eight BRC repeats would affect the way that BRCA2 protein interacts with the RAD51 filament. [2005]



The RAD51 recombinase interacts directly with the breast cancer-associated tumour suppressor BRCA2, an interaction that is required for normal recombination proficiency, radiation resistance and genome stability. [2003]



It is known that BRCA2 interacts directly with RAD51 through a series of degenerative motifs known as the BRC repeats. [2004]



The breast cancer susceptibility gene BRCA2 encodes a critical accessory protein that interacts with the RAD51 recombinase and this interaction fluctuates during the cell cycle. [2007]



BRCA2 protein interacts directly with the RAD51 recombinase and regulates recombination-mediated DSB repair, accounting for the high levels of spontaneous chromosomal aberrations seen in BRCA2-defective cells. [2007]



Whereas BRCA2 interacts directly with and regulates RAD51, the role of BRCA1 in this process is unclear. [2005]



RAD51 is an important component of double-stranded DNA-repair mechanisms that interacts with both BRCA1 and BRCA2. [2007]



Previous data report that wild-type p53 suppresses homologous recombination and physically interacts with Rad51. [2006]



p53 interacts with hRAD51 and hRAD54, and directly modulates homologous recombination. [2003]



Previously we reported that HsRad51 interacts with XRCC3, and Rad51C interacts with XRCC3, Rad51B, and HsRad51. [2003]



Find: dmc1

Next Previous Highlight all Match case Reached end of page, continued from top

Done



Text mining resources: PubGene

Network based on co-occurrence in article for the "RAD51" Gene and Proteins in Homo sapiens - Mozilla Firefox

File Edit View History Bookmarks Diigo Tools Help

http://www.pubgene.org/ biotext

Most Visited Entrez PubMed Post to CiteULike Library of Medicine and ... The Biotechnology Cen... BBC - bbc.co.uk home... Home page - The Rese... Wikipedia Google Translate

Stumble! I like it! Send to Channels: All Favorites Friends Tools

PubGene - Find ... Chilbot: finding ... MedEvi - a perm... FABLE - Overview BioCreative Met... BioText Search ... RAD51 - Google... RAD51 - Google... Network base...

Beta PubGene
FAQ
Users Guide
Demo Tutorials
Feedback

Bio Networks Bio Associations Sequence Homology My Workspace Login

Browse literature or sequence neighbours.

Organism Homo sapiens Select one or "all organisms"

Gene / Protein * RAD51 Terms separated by comma, eg. *BRCA1, LEP*

Biological term and/or One term, eg. *Alzheimer Disease*. Supported categories
Network displays genes/proteins important for the biological term

Submit Advanced Options Network Parameters

Network based on co-occurrence in article for the "RAD51" Gene and Proteins in Homo sapiens

Send selected terms to Choose PubGene Tool Legend ?

Information about 'RAD51'

Key information Related terms

Property	Value
Term	RAD51
Name	RAD51 homolog (Re...
Organi...	Homo sapiens
Article ...	4905
Term T...	PubGene Gene/Prot...
Externa...	EG
Chrom...	
Alt. Sym...	BRCC5
Alt. Sym...	HRAD51
Alt. Sym...	HsRad51
Alt. Sym...	HsT16930
Alt. Sym...	RAD51A
Alt. Sym...	RECA

Network view Table view

```
graph TD; RAD51 --- POLG2; RAD51 --- ATRX; RAD51 --- POLA1; RAD51 --- RAD52; RAD51 --- BRCAX; RAD51 --- BRCA2; RAD51 --- DIAPH8; RAD51 --- TP53; RAD51 --- STK32C; RAD51 --- ATP5E; BRCAX --- TP53; BRCA2 --- TP53; DIAPH8 --- STK32C; TP53 --- STK32C; STK32C --- ATP5E;
```

Find: dmc1 Next Previous Highlight all Match case Reached end of page, continued from top

Applet pubgenegraph.GraphController started

Predicted interaction resources

STRING

<http://string.embl.de/>

OPHID/I2D

<http://ophid.utoronto.ca/ophidv2.201/>

FunCoup

<http://FunCoup.sbc.su.se>

Consolidated databases

APID2NET

<http://bioinfow.dep.usal.es/apid/apid2net.html>

Pathway Commons

<http://www.pathwaycommons.org/pc/>

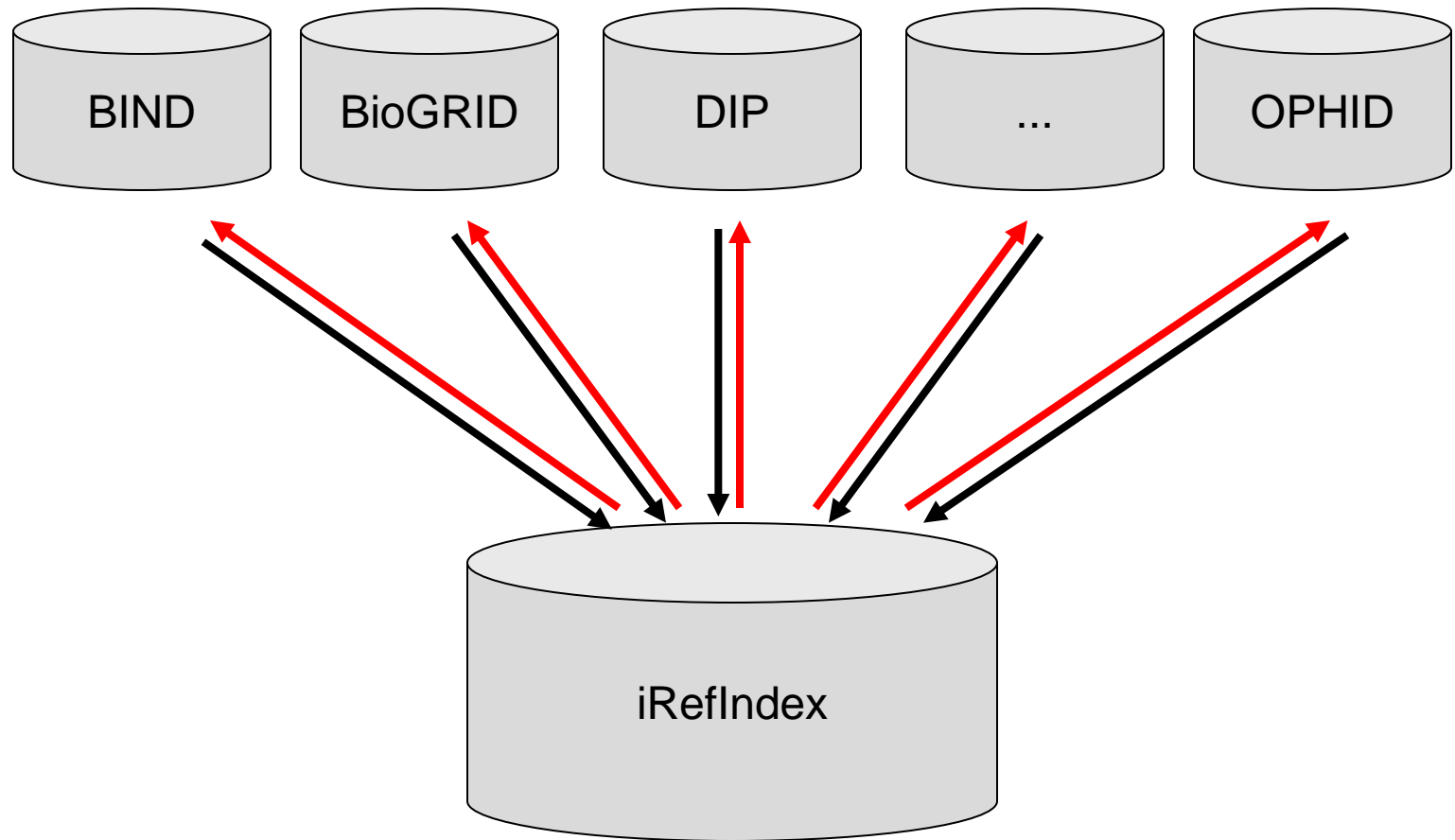
MiMI

<http://mimi.ncibi.org/MimiWeb/main-page.jsp>

iRefIndex

<http://irefindex.uio.no/wiki/iRefIndex>

iRefIndex: Integration and feedback



What is a network?

What are networks used for?

Where do networks come from?

Where would you get network data?

Some simple tools.

Where to begin and further reading.

http://irefindex.uio.no/

iRefIndex - Donaldson Group

irefindex.uio.no/wiki/iRefIndex

Bio

Page Discussion View source History



iRefIndex

Contents [hide]

- 1 A reference index for protein interaction data
- 2 Long term goals of the iRefIndex project
- 3 iRefIndex availability via download
- 4 Source data for the current build
- 5 iRefWeb: Data availability via web interface
 - 5.1 iRefWeb in the NCBI LinkOut programme
- 6 iRefScape: Data availability via Cytoscape
- 7 iRefR: Data availability via R
- 8 PSICQUIC: Data availability via Web services
- 9 Feedback files
- 10 License
- 11 Disclaimer
- 12 Statistics
- 13 Credits
- 14 Citation
- 15 References
- 16 Citations
- 17 Other Resources
- 18 Contact
- 19 iRefIndex Google Group
- 20 All iRefIndex Pages

iRefWeb

iRefScape



Take the video tour

Navigation

- Donaldson Group
- iRefIndex home
- Recent changes

Tools

- Help
- Bugzilla
- FTP usage statistics
- PSICQUIC usage statistics
- PSISCORE usage statistics


Search

Toolbox

- What links here
- Related changes
- Special pages
- Printable version
- Permanent link

A reference index for protein interaction data

iRefIndex provides an index of protein interactions available in a number of primary interaction databases including [BIND](#), [BioGRID](#), [CORUM](#), [DIP](#), [HPRD](#), [IntAct](#), [MINT](#), [MPact](#), [MPPI](#) and [OPHID](#). This index includes multiple interaction types including physical and genetic (mapped to their corresponding protein products) as determined by a multitude of methods.



Search - iRefWeb - Wodak L x

wodaklab.org/iRefWeb/search/index

Home Tools/Data Research Resources Info People Sponsors Publications

Wodak Lab
Research Institute - SickKids Toronto

iRefWeb 3.8 In collaboration with [Ian Donaldson](#) — using iRefIndex [Version 8.0](#)
Watch a webinar (or browse the slides) on how to use iRefWeb [here](#).

About **Search** Statistics PubMed Annotations FAQ Release Notes

1. Search Terms

Protein/Gene IDs and Aliases

LEFT:
Enter your protein/gene IDs and aliases below, or you can paste in a whole list, to find interactions that match any of them. Autocomplete begins after 3 characters.

RIGHT (optional):
If you wish, constrain your search to find interactions between any protein/gene in the left box with any entered or pasted in the right box.

PubMed IDs

Full Text

Lists of genes or proteins aliases and PubMed IDs should be delimited by whitespace or new lines.

2. Search Filters

Display filter counts and search results by: protein (0) interaction (454941)

[Expand All Filters](#) — [Collapse All Filters](#) — [Show Filter Help](#)

Source Database Organism Nature of Interaction

Number of Publications Lowest Experiment Size (LPR) Highest Experiment Size (HPR)

Interaction Detection Method Interaction Type

3. Search

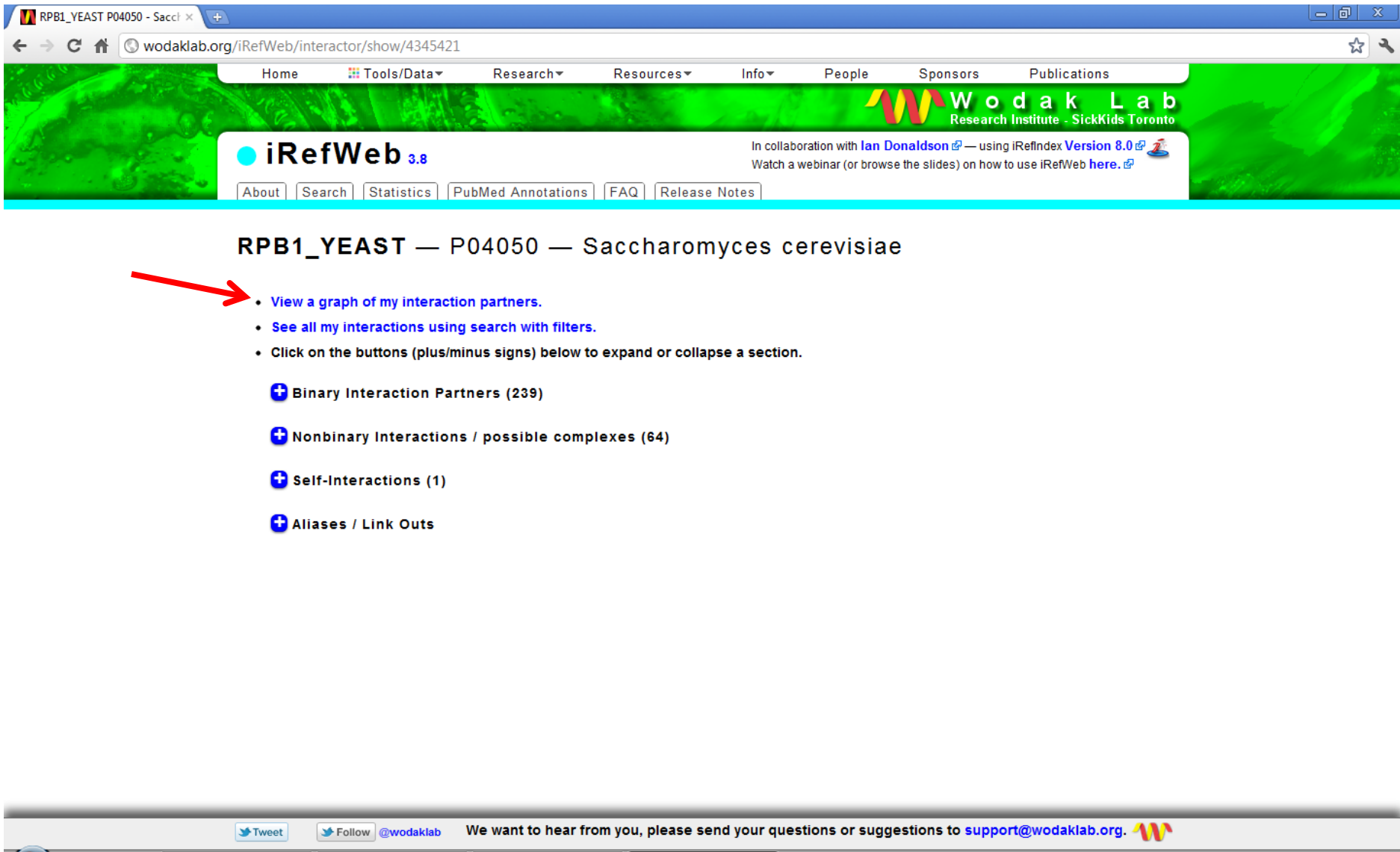
Search Download Interatome Clear/New Search Show Search Help

4. Search Results Summary

Showing 1 - 20 of 454941 results. | Page: 1 2 3 4 5 .. 22748 > | 20 Results per page.

Tweet Follow @wodaklab We want to hear from you, please send your questions or suggestions to support@wodaklab.org.

http://wodaklab.org/iRefWeb/



RPB1_YEAST P04050 - Saccl x

wodaklab.org/iRefWeb/interactor/show/4345421

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iRefWeb 3.8

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Watch a webinar (or browse the slides) on how to use iRefWeb [here](#).

About Search Statistics PubMed Annotations FAQ Release Notes

RPB1_YEAST — P04050 — *Saccharomyces cerevisiae*

- [View a graph of my interaction partners.](#)
- [See all my interactions using search with filters.](#)
- Click on the buttons (plus/minus signs) below to expand or collapse a section.

- + Binary Interaction Partners (239)
- + Nonbinary Interactions / possible complexes (64)
- + Self-Interactions (1)
- + Aliases / Link Outs

Tweet Follow @wodaklab We want to hear from you, please send your questions or suggestions to support@wodaklab.org.

http://wodaklab.org/iRefWeb/

RPB1_YEAST - Netility - Wo x

wodaklab.org/netility/network/show/id/189344

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Wodak Lab
Research Institute - SickKids Toronto

Netility 2.0 BETA Powered By: *Cytoscape Web*

About Search My Networks Release Notes

Netility — Network — RPB1_YEAST

Network Actions

PNG Export Network Save Network

Force Directed Apply or Reapply Layout

Save My Display Preferences

Node Label Attributes

Accession Type Organism

Name MINT Score Internal ID

Node Filters (Node Counts)

Gene (1) Enzyme (1)

Protein (87) Domain (8)

Mesh Term (0)

GO term: BiologicalProcess (2)

GO term: Molecular Function (3)

GO term: Cellular Component (2)

Non-binary Interaction* (14)

*Self interaction, n-ary interaction (possible complex)

Note: Human and Yeast interactions with MINT scores < 0.4 have been removed.

Edge Filters (Edge Counts)

Enzyme Function (2) Domain Annotation (8)

Paralog (0) Ortholog (0)

Interactor (136) Disease Annotation (0)

Physical Interaction (170) Genetic Interaction (96)

Domain RNA_pol_Rpb1_1

Protein SPO1_YEAST

Protein BRZ2_YEAST

Protein UBP3_YEAST

Protein RND1_YEAST

Protein RND2_YEAST

Protein RND3_YEAST

Protein RND4_YEAST

Protein RND5_YEAST

Protein RND6_YEAST

Protein RND7_YEAST

Protein RND8_YEAST

Protein RND9_YEAST

Protein RND10_YEAST

Protein RND11_YEAST

Protein RND12_YEAST

Protein RND13_YEAST

Protein RND14_YEAST

Protein RND15_YEAST

Protein RND16_YEAST

Protein RND17_YEAST

Protein RND18_YEAST

Protein RND19_YEAST

Protein RND20_YEAST

Protein RND21_YEAST

Protein RND22_YEAST

Protein RND23_YEAST

Protein RND24_YEAST

Protein RND25_YEAST

Protein RND26_YEAST

Protein RND27_YEAST

Protein RND28_YEAST

Protein RND29_YEAST

Protein RND30_YEAST

Protein RND31_YEAST

Protein RND32_YEAST

Protein RND33_YEAST

Protein RND34_YEAST

Protein RND35_YEAST

Protein RND36_YEAST

Protein RND37_YEAST

Protein RND38_YEAST

Protein RND39_YEAST

Protein RND40_YEAST

Protein RND41_YEAST

Protein RND42_YEAST

Protein RND43_YEAST

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Protein RND89_YEAST

Protein RND90_YEAST

Protein RND91_YEAST

Protein RND92_YEAST

Protein RND93_YEAST

Protein RND94_YEAST

Protein RND95_YEAST

Protein RND96_YEAST

Protein RND97_YEAST

Protein RND98_YEAST

Protein RND99_YEAST

Protein RND100_YEAST

Domain RNA_pol_Rpb1_2

Domain RNA_pol_Rpb1_4

Domain RNA_pol_Rpb1_5

Protein RND101_YEAST

Protein RND102_YEAST

Protein RND103_YEAST

Protein RND104_YEAST

Protein RND105_YEAST

Protein RND106_YEAST

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Protein RND189_YEAST

Protein RND190_YEAST

Protein RND191_YEAST

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Protein RND195_YEAST

Protein RND196_YEAST

Protein RND197_YEAST

Protein RND198_YEAST

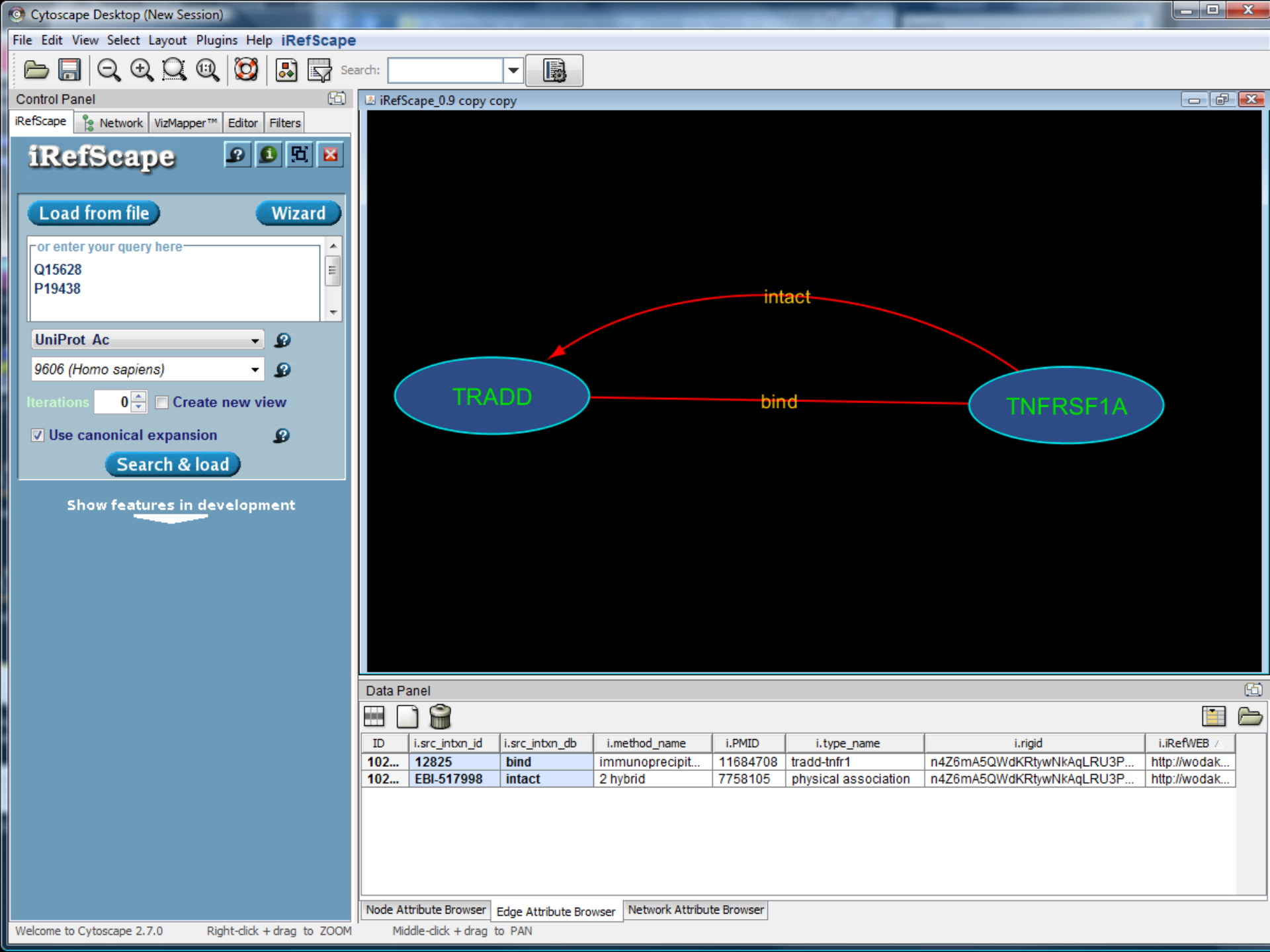
Protein RND199_YEAST

Protein RND200_YEAST

Cytoscape and iRefScape plugin

<http://cytoscape.org>

<http://irefindex.uio.no/wiki/iRefScape>



Control Panel

iRefScape Network VizMapper™ Editor Filters

Search: [] []

iRefScape

Load from file **Wizard**

or enter your query here

Q15628
P19438

UniProt Ac [?] [?]

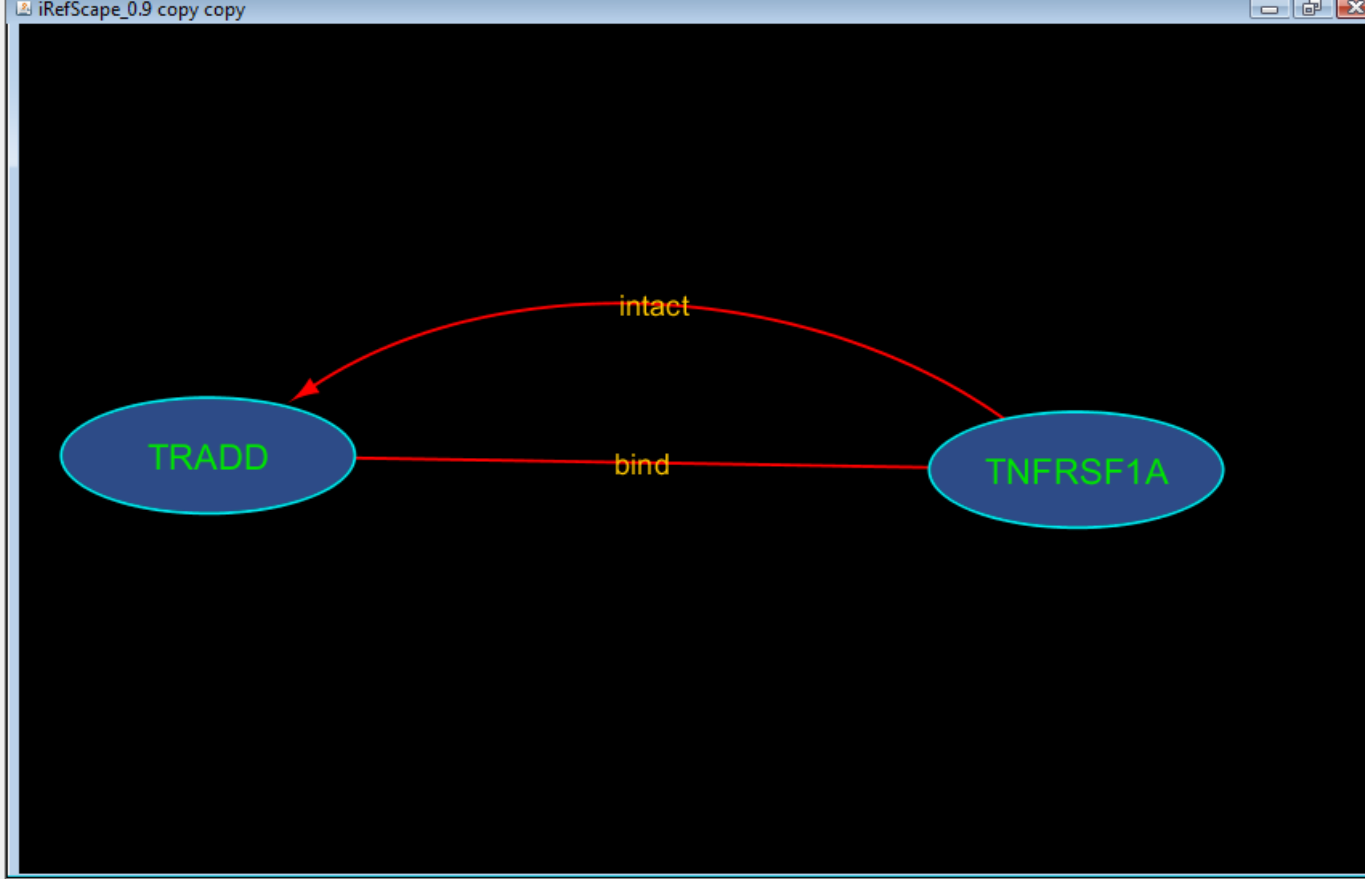
9606 (Homo sapiens) [?] [?]

Iterations 0 [?] [?] Create new view

Use canonical expansion [?]

Search & load

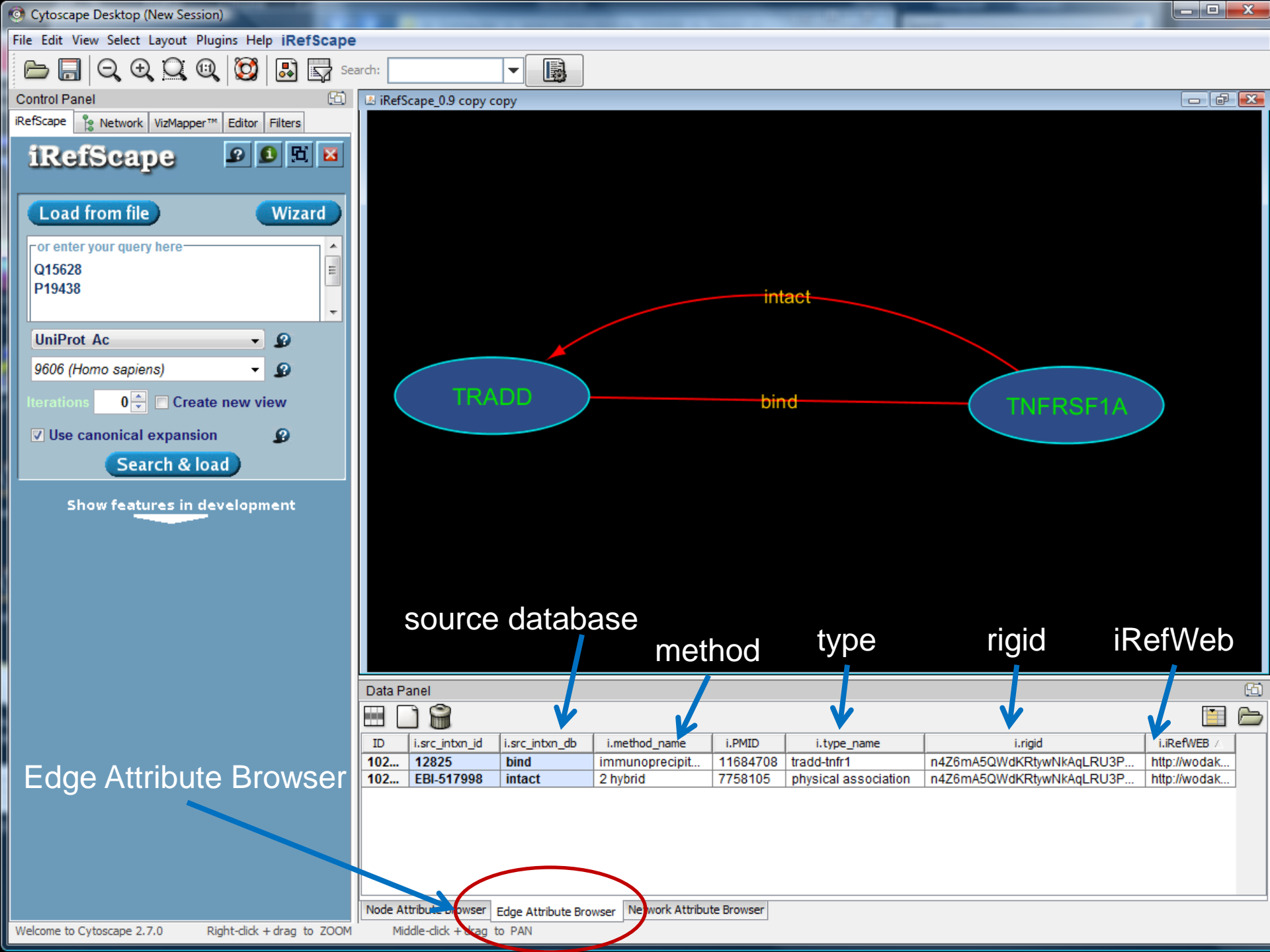
Show features in development



Data Panel

ID	i.src_intxn_id	i.src_intxn_db	i.method_name	i.PMID	i.type_name	i.rigid	i.iRefWEB
102...	12825	bind	immunoprecipit...	11684708	tradd-tnfr1	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...
102...	EBI-517998	intact	2 hybrid	7758105	physical association	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...

Node Attribute Browser Edge Attribute Browser Network Attribute Browser



iRefScape

Load from file Wizard

or enter your query here

Q15628
P19438

UniProt Ac

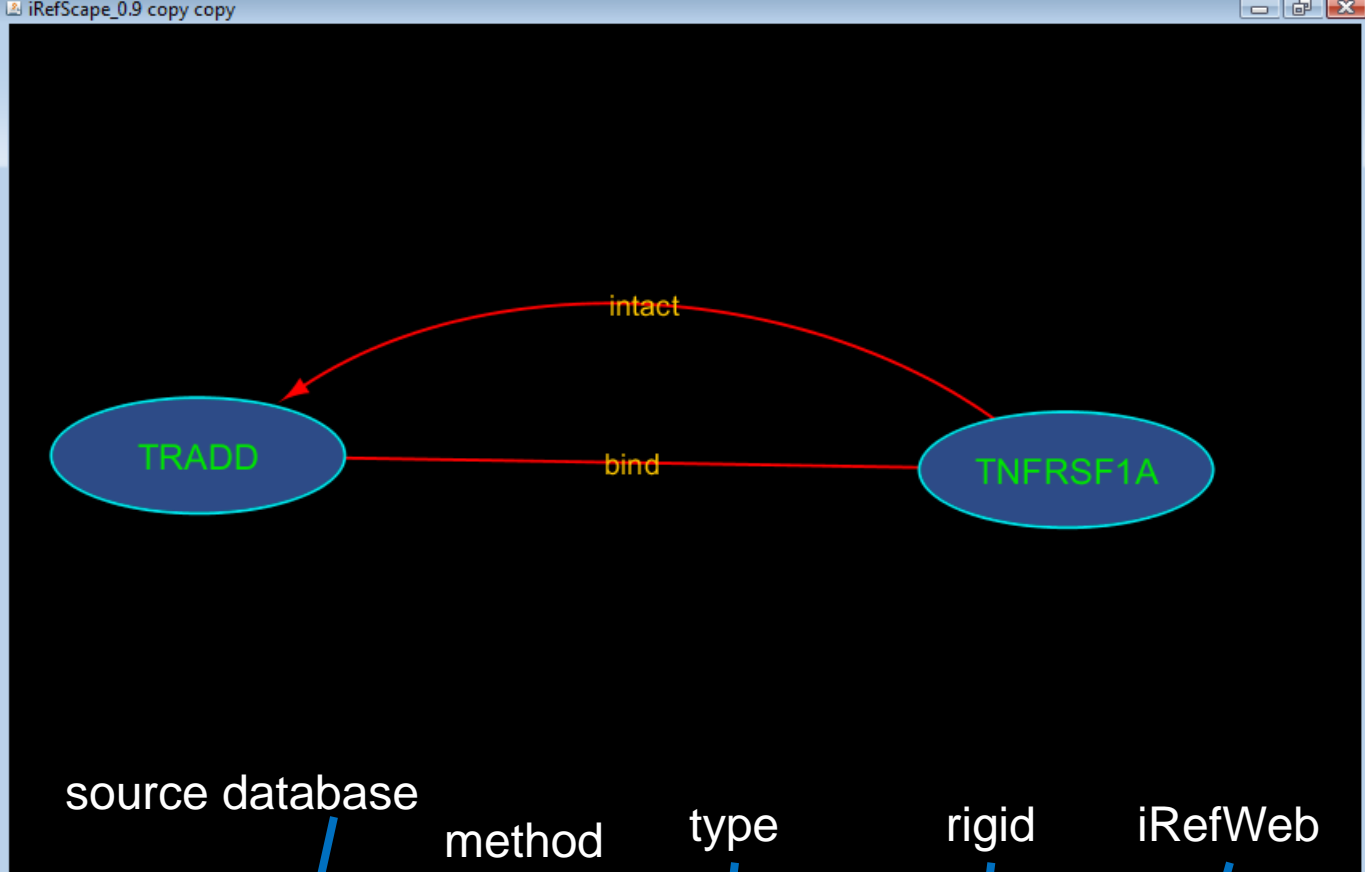
9606 (Homo sapiens)

Iterations 0 Create new view

Use canonical expansion

Search & load

Show features in development



source database

method

type

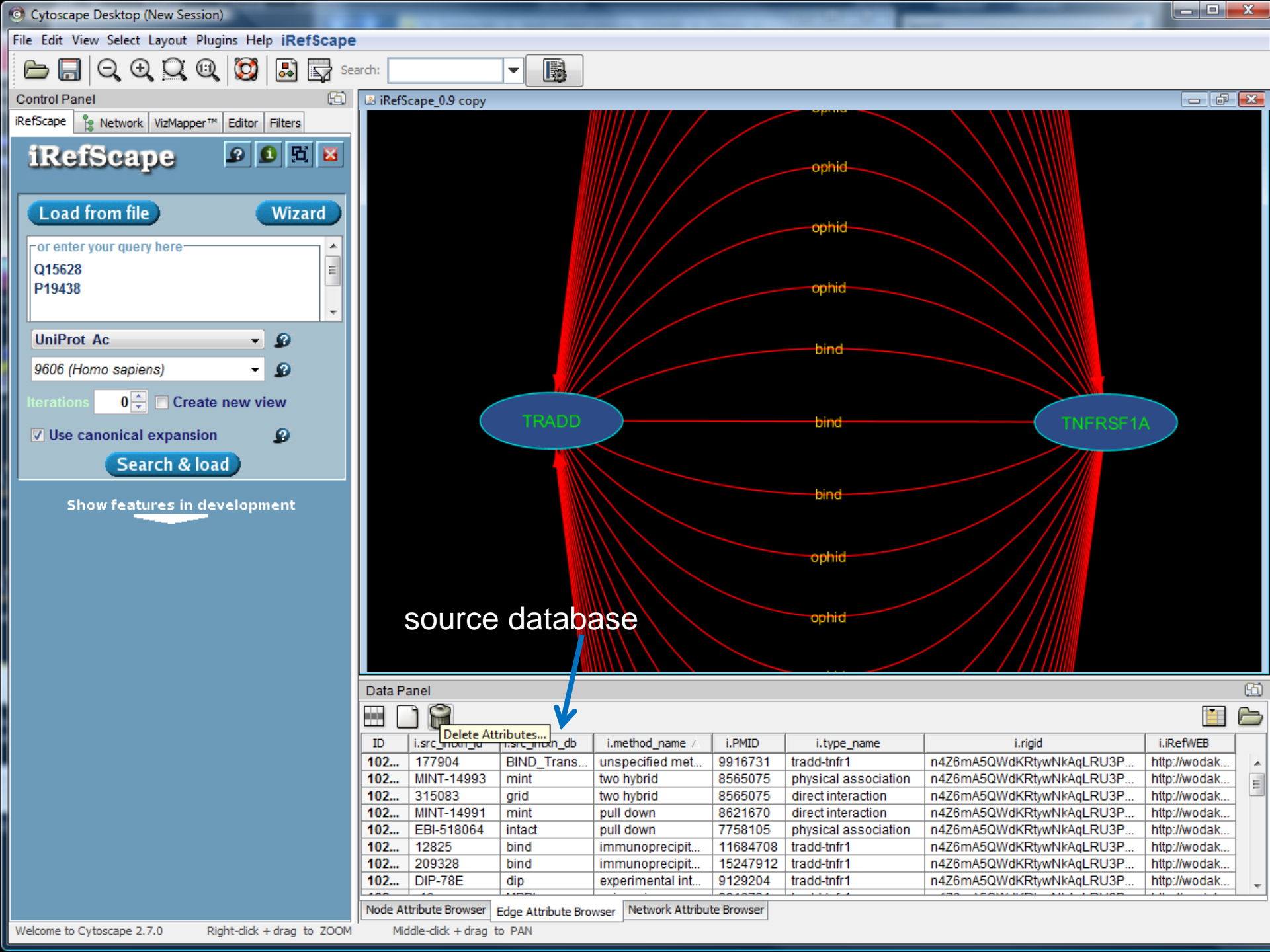
rigid

iRefWeb

Data Panel

ID	i.src_inbx_id	i.src_inbx_db	i.method_name	i.PMID	i.type_name	i.rigid	i.iRefWEB
102...	12825	bind	immunoprecipit...	11684708	tradd-tnfr1	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...
102...	EBI-517998	intact	2 hybrid	7758105	physical association	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...

Edge Attribute Browser



Control Panel

iRefScape Network VizMapper™ Editor Filters

iRefScape ? ⓘ

Load from file Wizard

or enter your query here

Q15628
P19438

UniProt Ac ⓘ

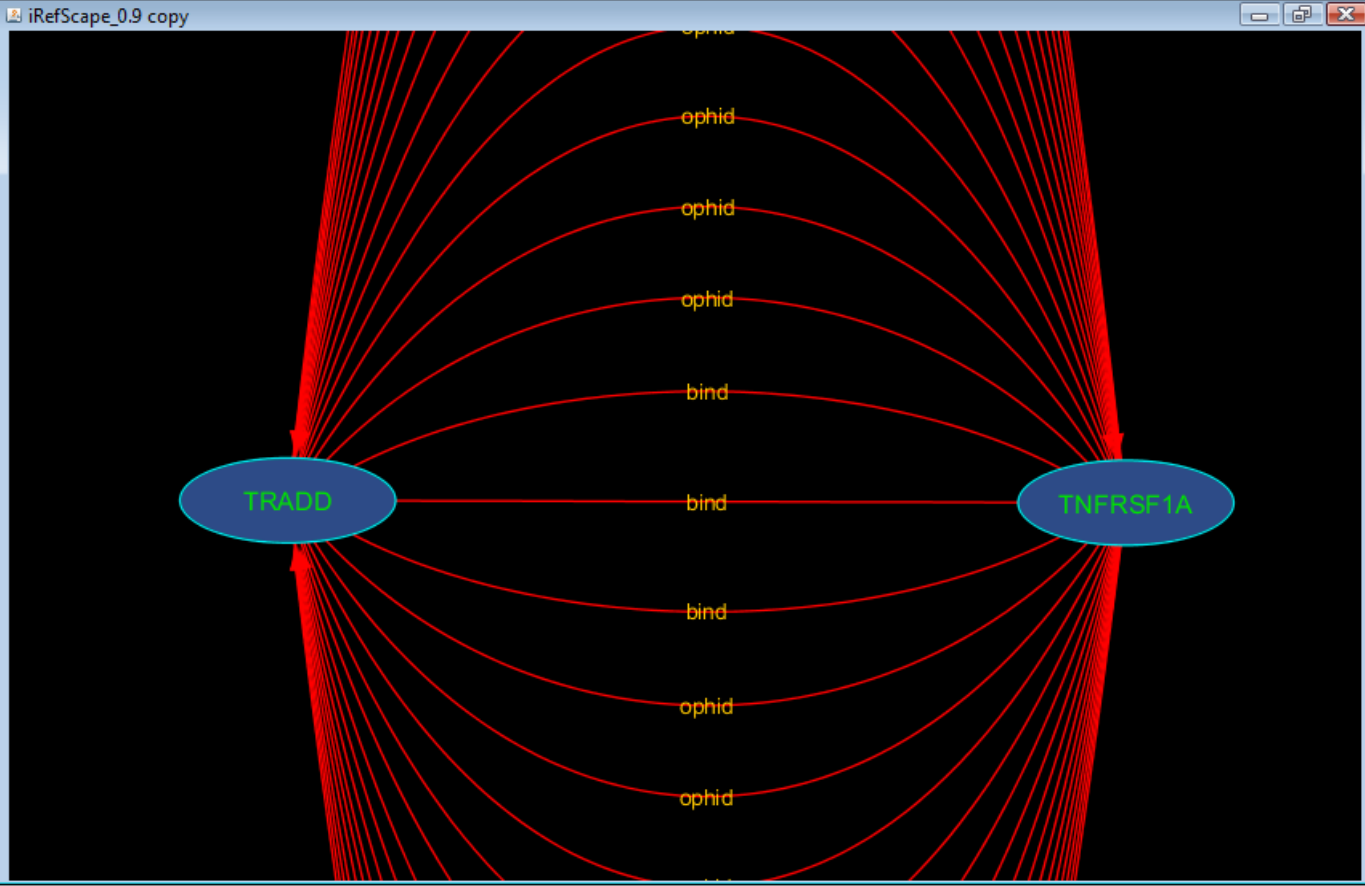
9606 (Homo sapiens) ⓘ

Iterations 0 Create new view

Use canonical expansion ⓘ

Search & load

Show features in development



Data Panel

ID	i.src_inbx_id	i.src_inbx_db /	i.method_name	i.PMID	i.type_name	i.rigid	i.iRefWEB
102...	NA	ophid	OPHID Predict...	15657099	aggregation	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...
102...	NA	ophid	OPHID Predict...	15657099	aggregation	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...
102...	NA	ophid	OPHID Predict...	15657099	aggregation	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...
102...	NA	ophid	OPHID Predict...	15657099	aggregation	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...
102...	NA	ophid	OPHID Predict...	15657099	aggregation	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...
102...	NA	ophid	OPHID Predict...	15657099	aggregation	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...
102...	NA	ophid	OPHID Predict...	15657099	aggregation	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...
102...	NA	ophid	OPHID Predict...	15657099	aggregation	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...

Node Attribute Browser Edge Attribute Browser Network Attribute Browser

iRefScape

Load from file Wizard

or enter your query here

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P19438

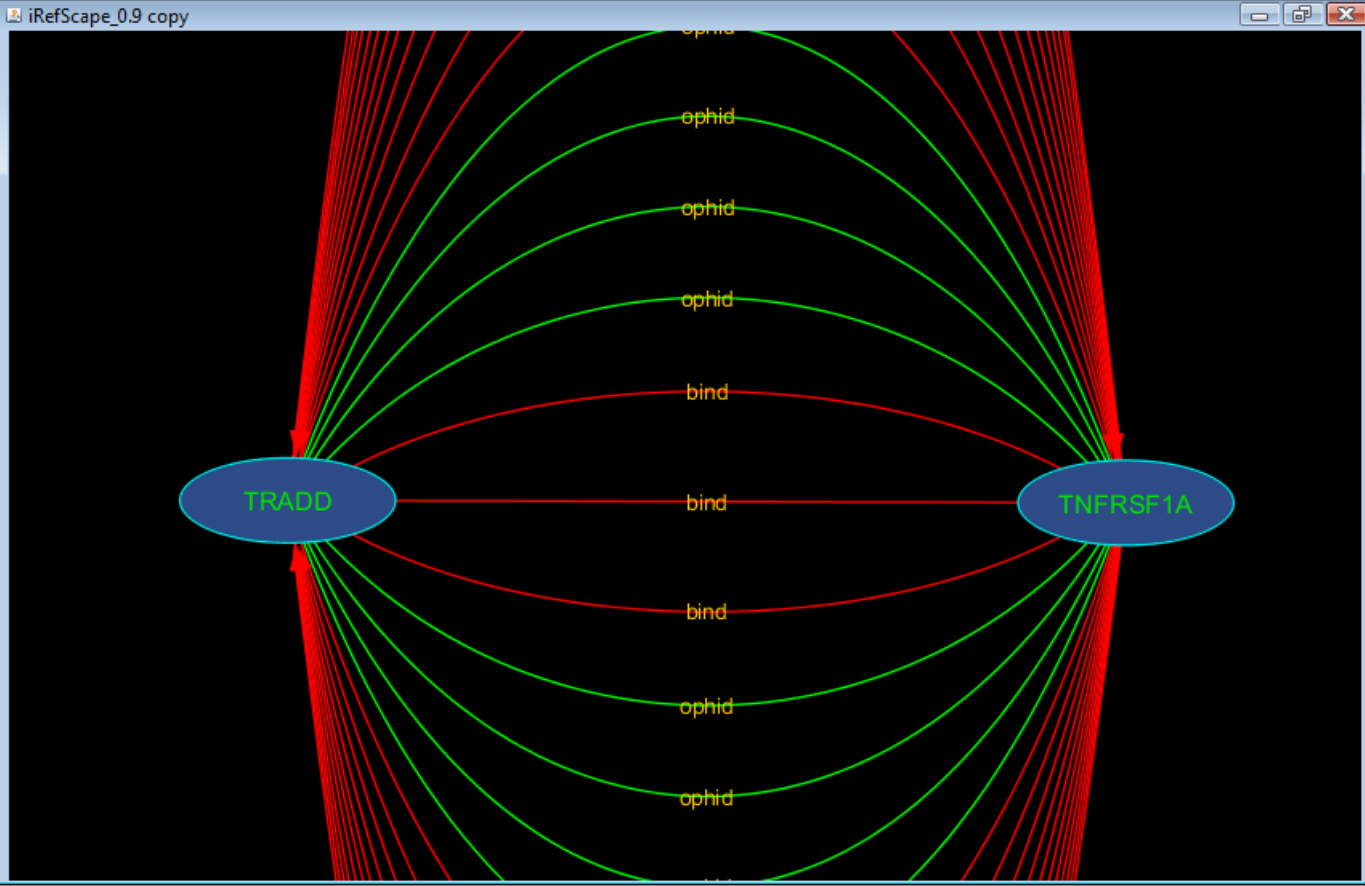
UniProt Ac

9606 (Homo sapiens)

Iterations 0 Create new view

Use canonical expansion

Search & load

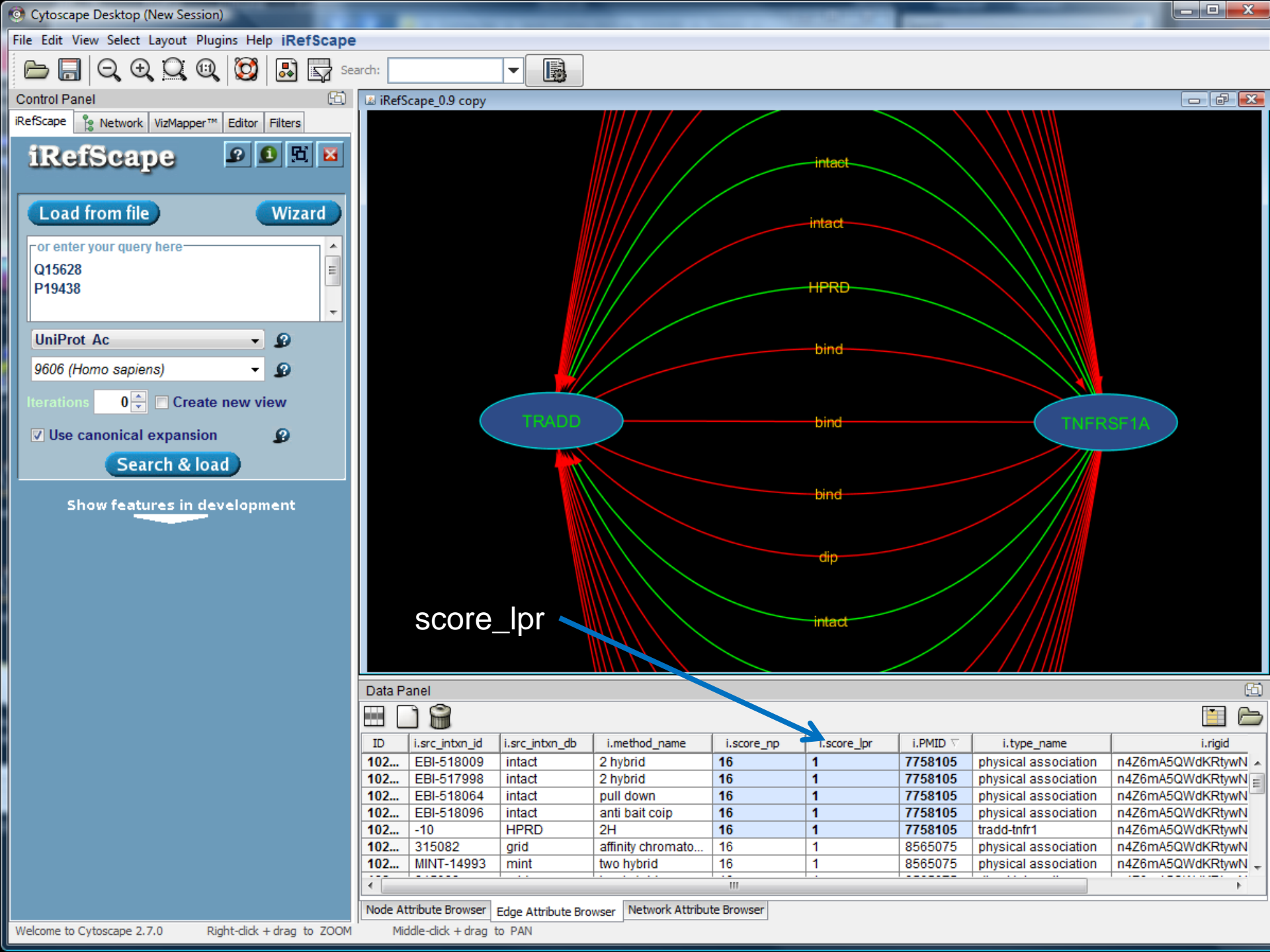


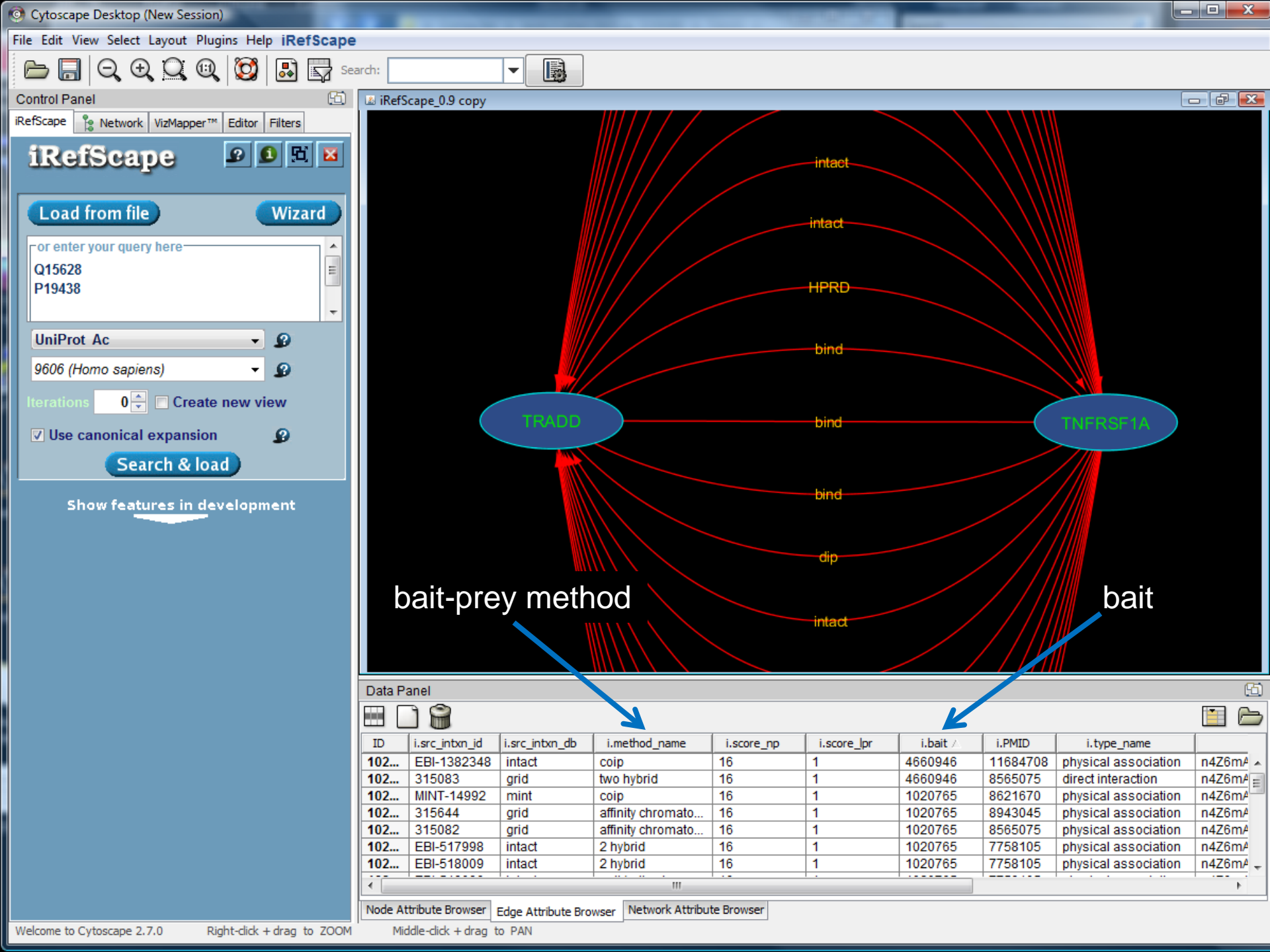
Data Panel

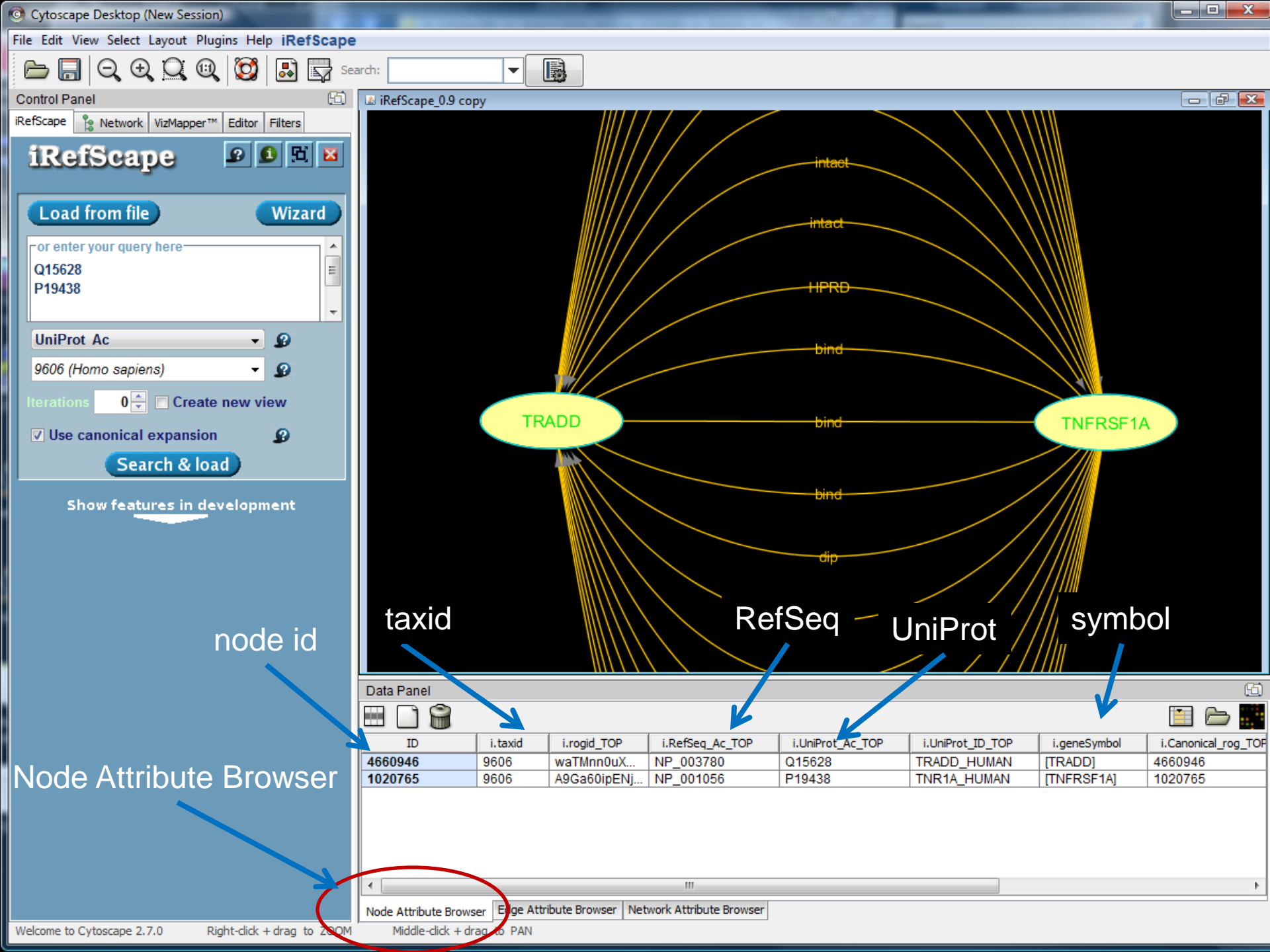
ID	i.src_inbxn_id	i.src_inbxn_db	i.method_name	i.PMID	i.type_name	i.rigid	i.iRefWEB
102...	NA	ophid	OPHID Predict...	15657099	aggregation	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...
102...	NA	ophid	OPHID Predict...	15657099	aggregation	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...
102...	NA	ophid	OPHID Predict...	15657099	aggregation	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...
102...	NA	ophid	OPHID Predict...	15657099	aggregation	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...
102...	NA	ophid	OPHID Predict...	15657099	aggregation	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...
102...	NA	ophid	OPHID Predict...	15657099	aggregation	n4Z6mA5QWdKRtywNkAqLRU3P...	http://wodak...
102...	MINT-14993	mint	two hybrid	8	i.PMID	RtywNkAqLRU3P...	http://wodak...

Node Attribute Browser Edge Attribute Browser Network Attribute Browser

15657099







node id

Node Attribute Browser

taxid

RefSeq

UniProt

symbol

ID

i.taxid

i.rogid_TOP

i.RefSeq_Ac_TOP

i.UniProt_Ac_TOP

i.UniProt_ID_TOP

i.geneSymbol

i.Canonical_rog_TOP

4660946

9606

waTMnn0uX...

NP_003780

Q15628

TRADD_HUMAN

[TRADD]

4660946

1020765

9606

A9Ga60ipENj...

NP_001056

P19438

TNR1A_HUMAN

[TNFRSF1A]

1020765

Node Attribute Browser

Edge Attribute Browser

Network Attribute Browser

Control Panel

iRefScape Network VizMapper™ Editor

iRefScape

Load from file **Wizard**

or enter your query here

Q15628
P19438

UniProt Ac ?

9606 (Homo sapiens) ?

Iterations 0 Create new view

Use canonical expansion ?

Search & load

Show features in development

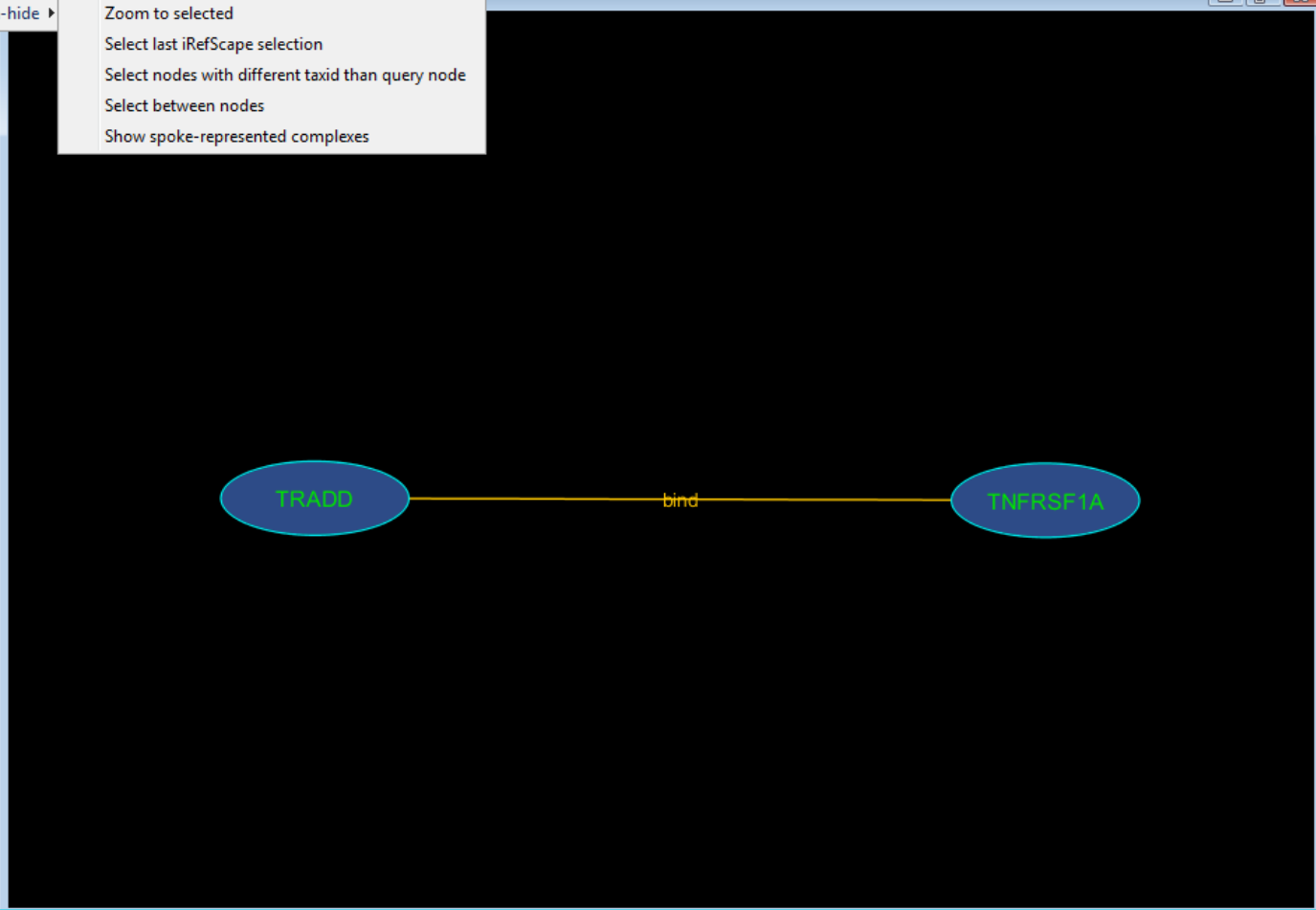
Node Attribute Browser | Edge Attribute Browser | Network Attribute Browser

Search tools

View tools

Hide/Un-hide

- Toggle selected multi-edges
- Zoom to selected
- Select last iRefScape selection
- Select nodes with different taxid than query node
- Select between nodes
- Show spoke-represented complexes



Data Panel

ID	i.taxid	i.rogid_TOP	i.RefSeq_Ac_TOP	i.UniProt_Ac_TOP	i.UniProt_ID_TOP	i.geneSymbol	i.Canonical_rog_TOP	i.geneID_



Control Panel

iRefScape Network VizMapper™ Editor Filters

iRefScape

Load from file Wizard

or enter your query here
Q15628
P19438

UniProt Ac

9606 (Homo sapiens)

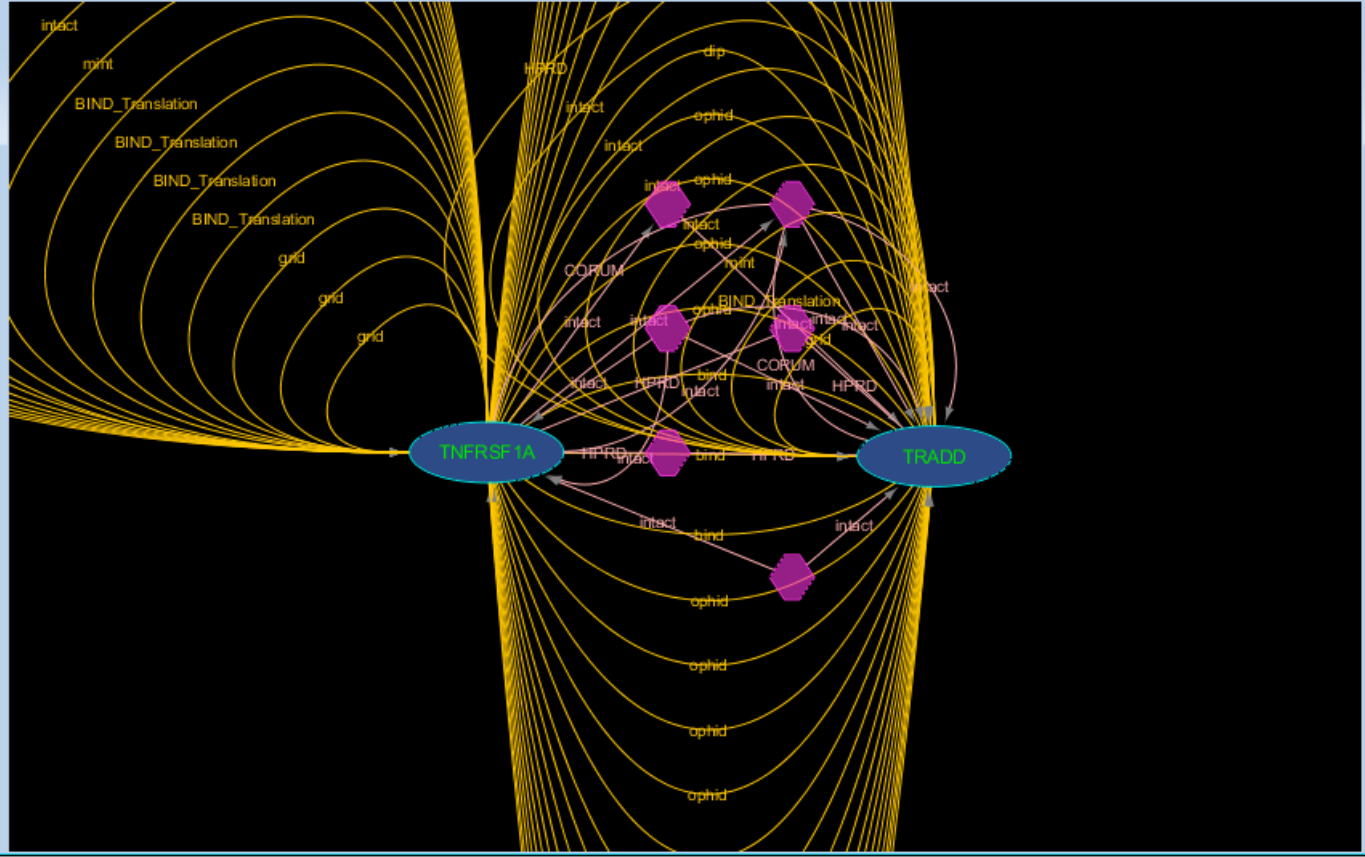
Iterations 0 Create new view

Use canonical expansion

Search & load

Show features in development

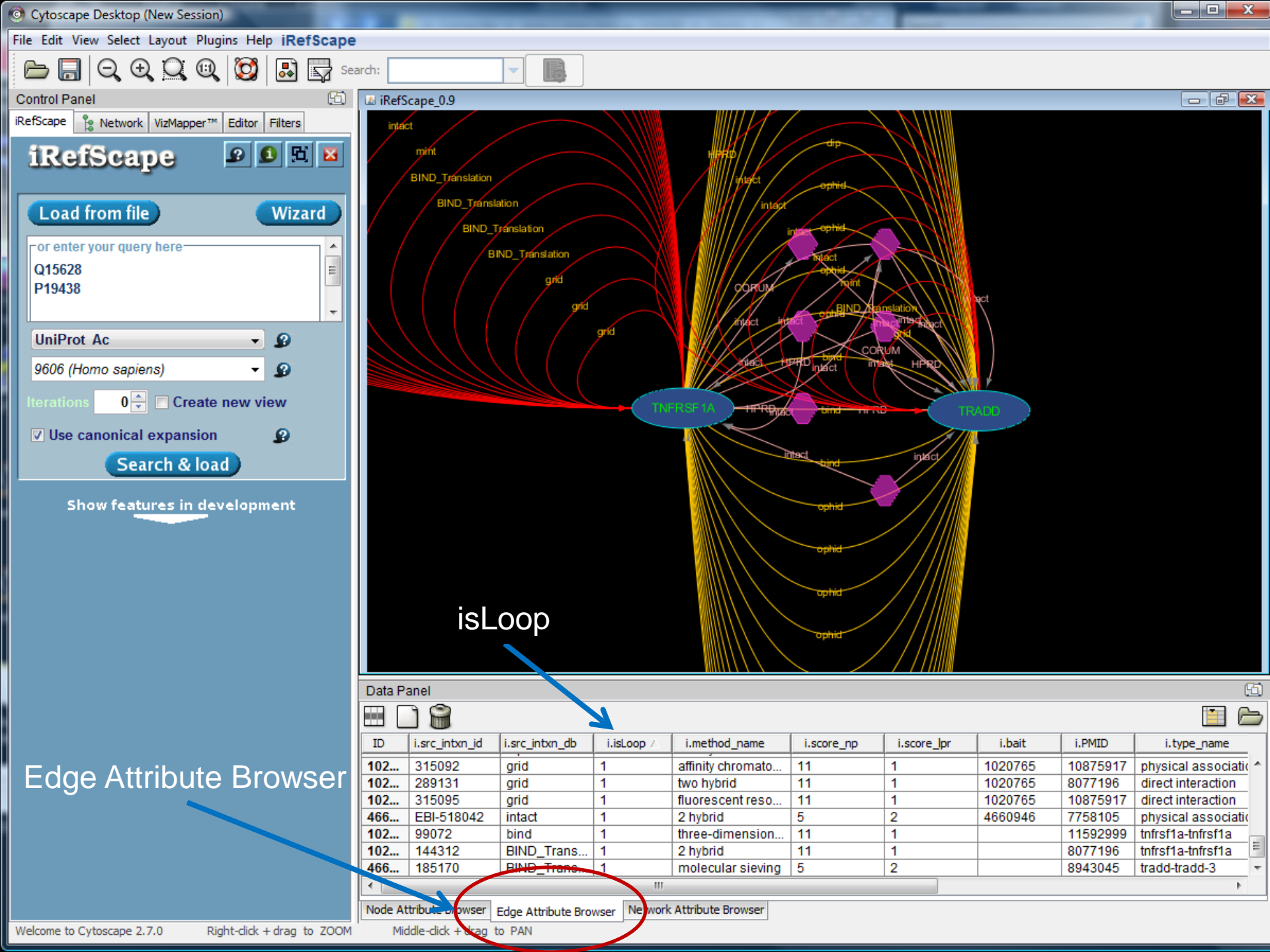
iRefScape_0.9

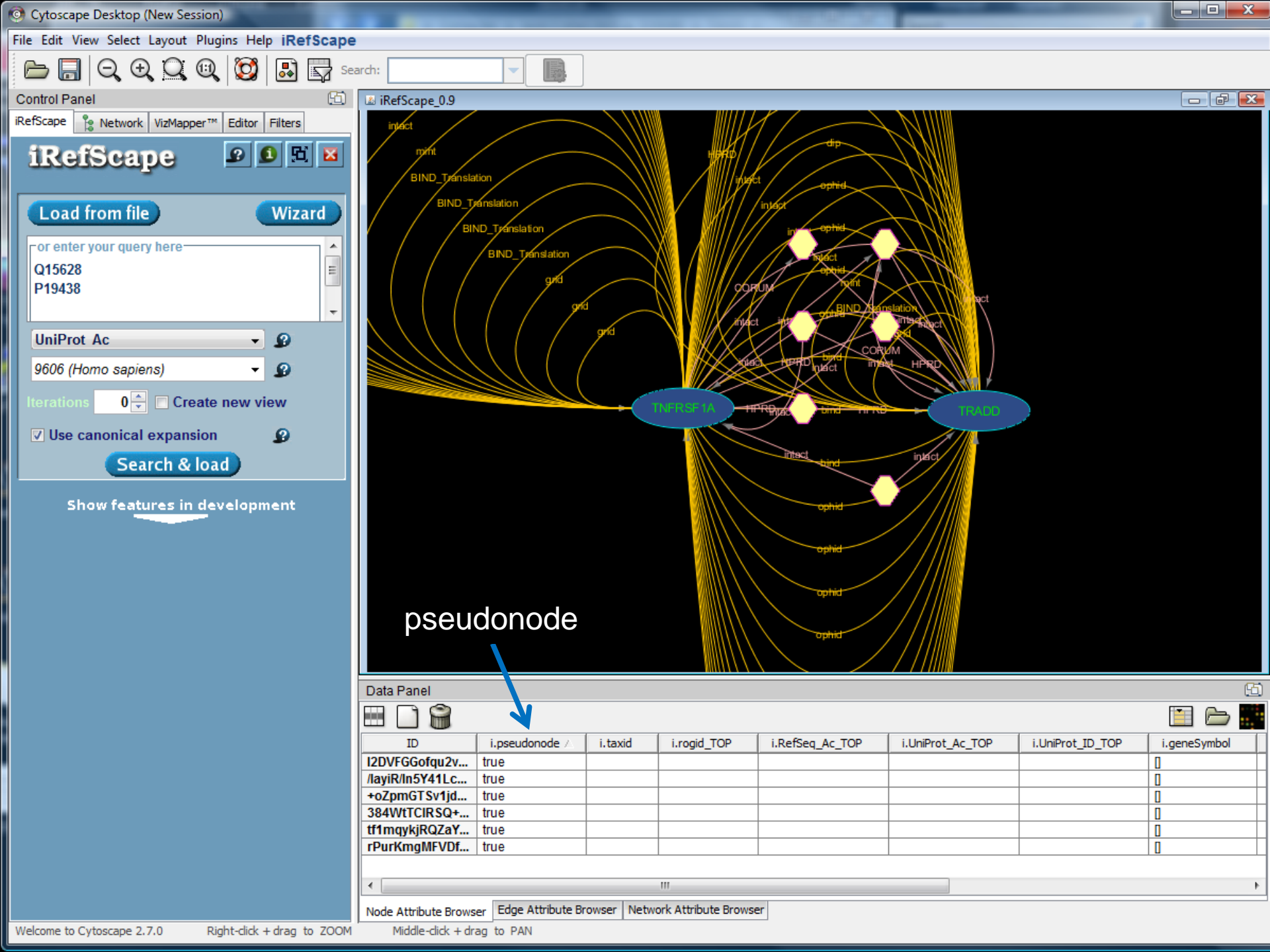


Data Panel

ID	i.src_intxn_id	i.src_intxn_db	i.isLoop	i.method_name	i.score_np	i.score_pr /	i.bait	i.PMID	i.type_name

Node Attribute Browser Edge Attribute Browser Network Attribute Browser





iRefScape

Load from file Wizard

or enter your query here

Q15628
P19438

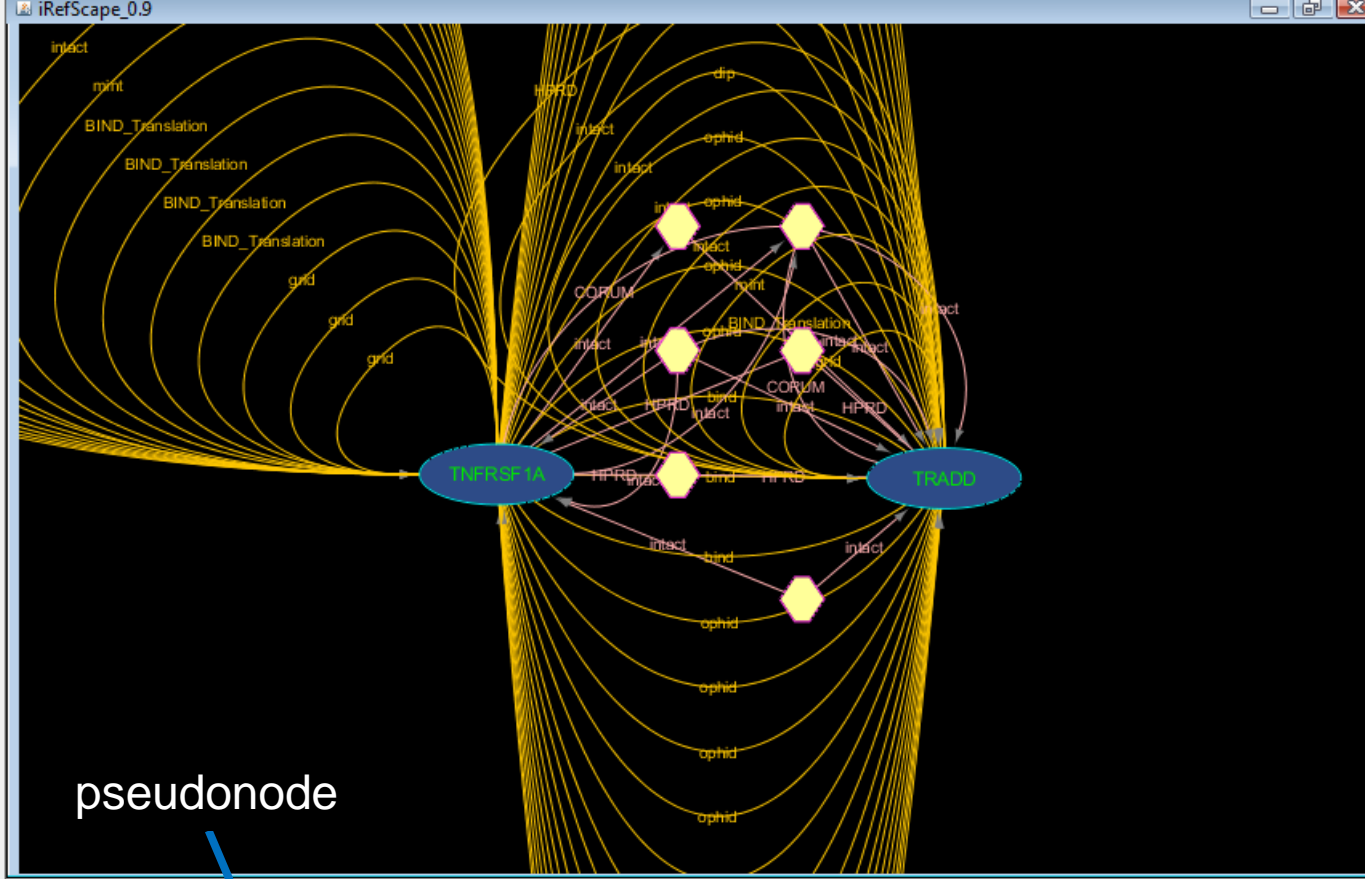
UniProt Ac

9606 (Homo sapiens)

Iterations 0 Create new view

Use canonical expansion

Search & load



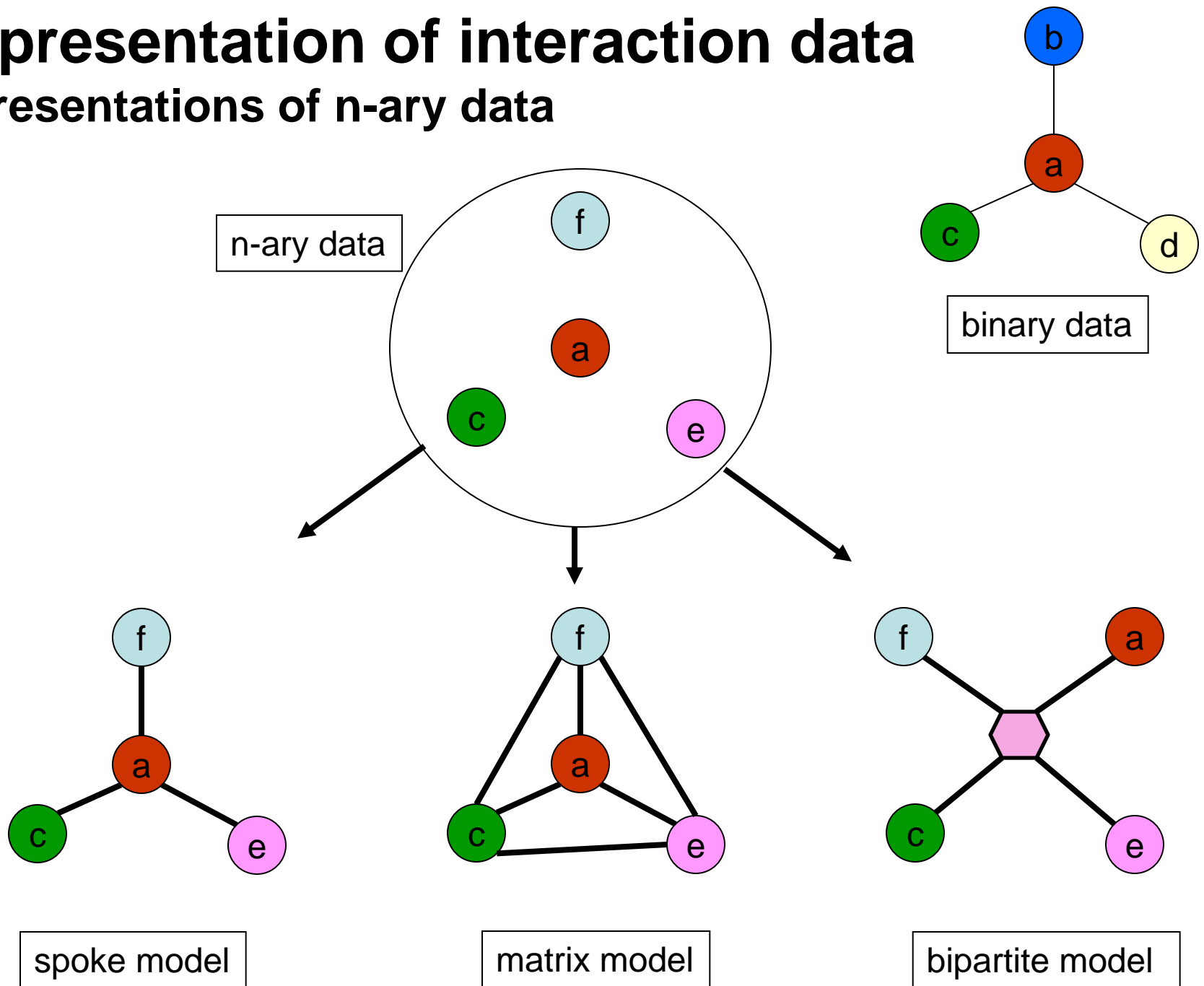
pseudonode

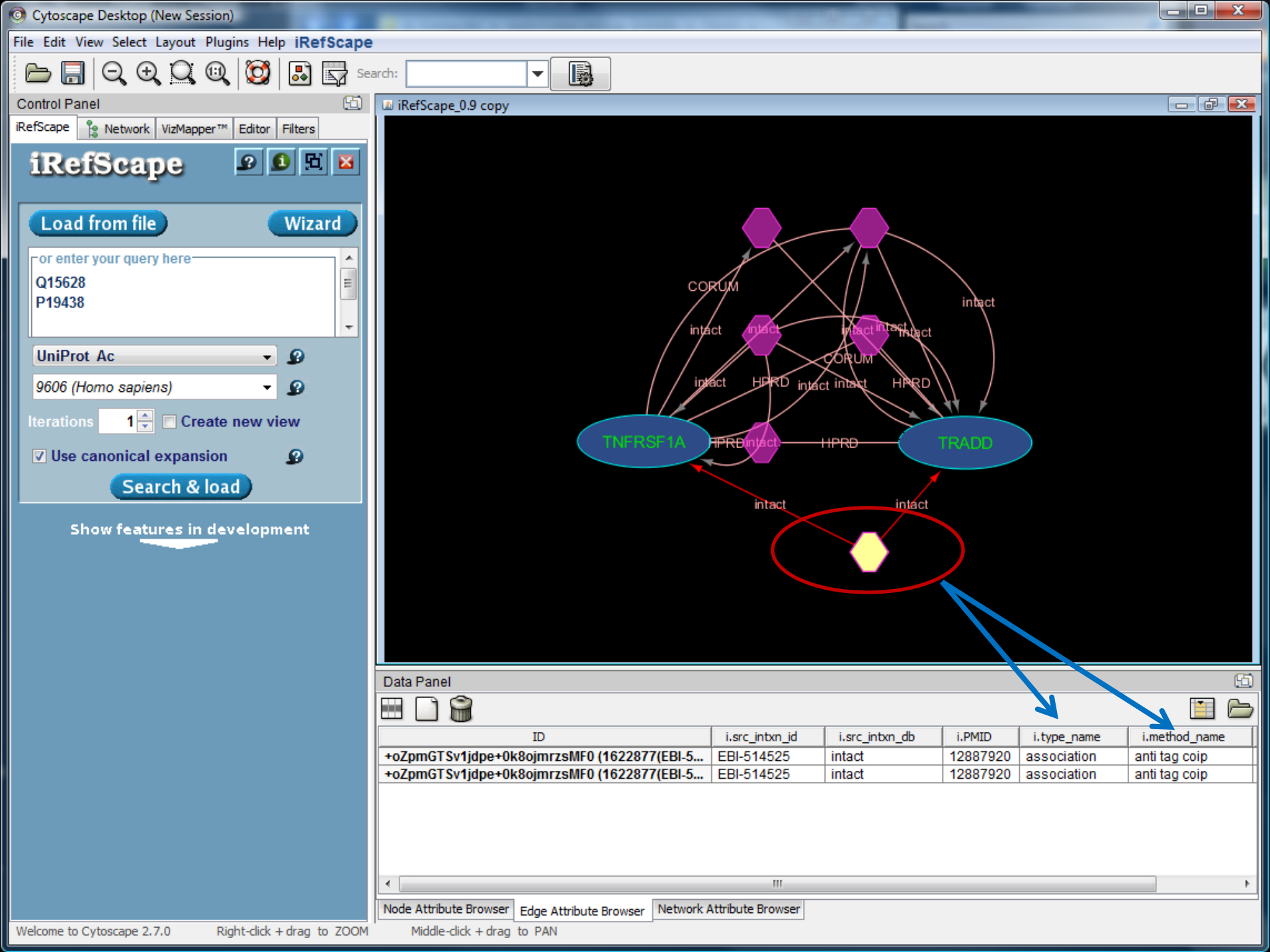
Data Panel

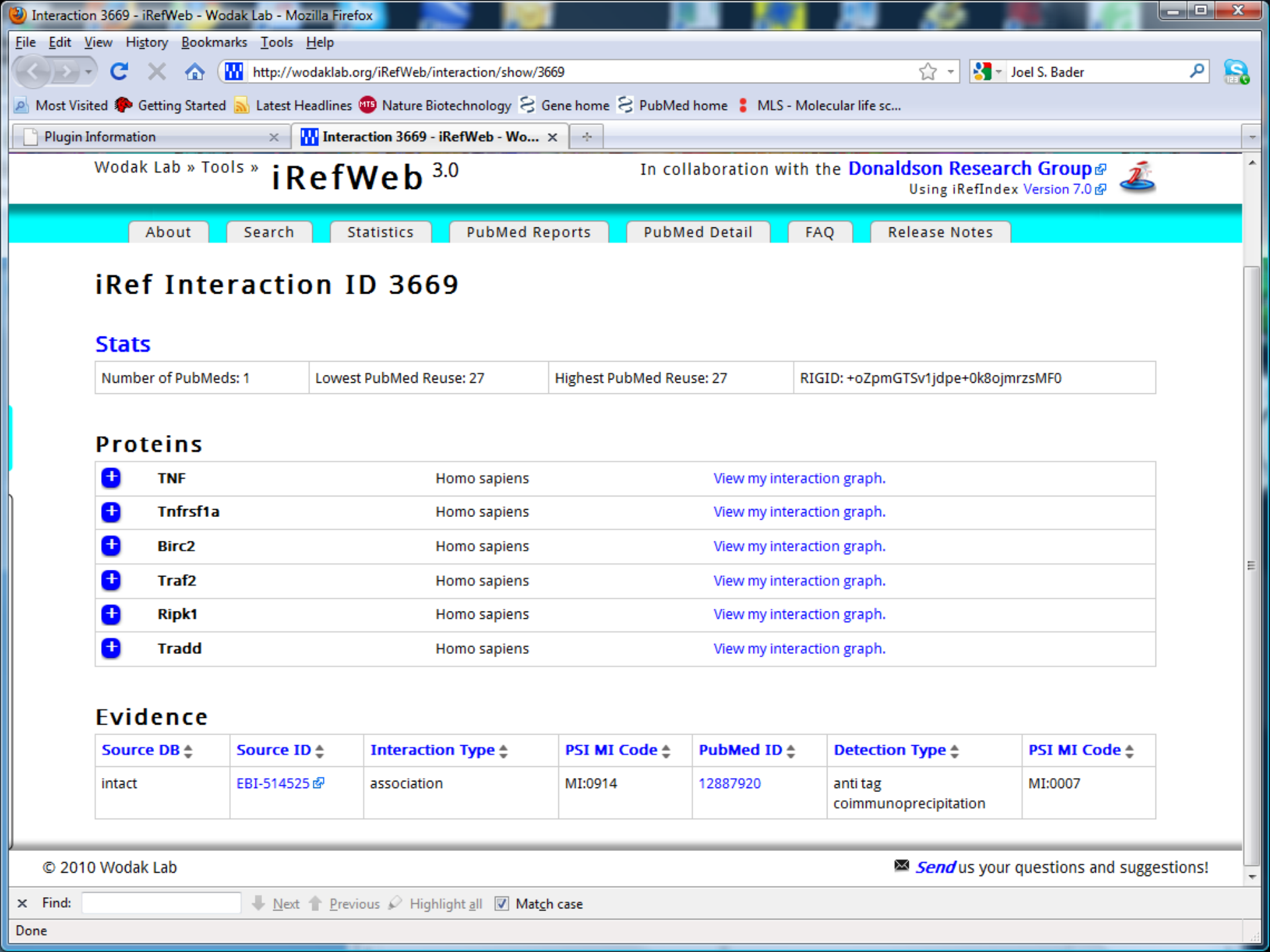
ID	i.pseudonode	i.taxid	i.rogid_TOP	i.RefSeq_Ac_TOP	i.UniProt_Ac_TOP	i.UniProt_ID_TOP	i.geneSymbol
I2DVFGGofqu2v...	true						∅
/layiR/In5Y41Lc...	true						∅
+oZpmGTSv1jd...	true						∅
384WtCIRSQ+...	true						∅
tf1mqykjRQZaY...	true						∅
rPurKmgMFVdf...	true						∅

Representation of interaction data

representations of n-ary data







iRef Interaction ID 3669

Stats

Number of PubMeds: 1	Lowest PubMed Reuse: 27	Highest PubMed Reuse: 27	RIGID: +oZpmGTSv1jdpe+0k8ojmrzsMF0
----------------------	-------------------------	--------------------------	------------------------------------

Proteins

+ TNF	Homo sapiens	View my interaction graph.
+ Tnfrsf1a	Homo sapiens	View my interaction graph.
+ Birc2	Homo sapiens	View my interaction graph.
+ Traf2	Homo sapiens	View my interaction graph.
+ Ripk1	Homo sapiens	View my interaction graph.
+ Tradd	Homo sapiens	View my interaction graph.

Evidence

Source DB	Source ID	Interaction Type	PSI MI Code	PubMed ID	Detection Type	PSI MI Code
intact	EBI-514525	association	MI:0914	12887920	anti tag coimmunoprecipitation	MI:0007

Disease browsing



Control Panel

iRefScape Network VizMapper™ Editor Filters

iRefScape

Load from file Wizard

or enter your query here
ichthyosis

dig title

Any

Iteration 1 Create new view

Use canonical expansion

Search & load

Hide advanced features

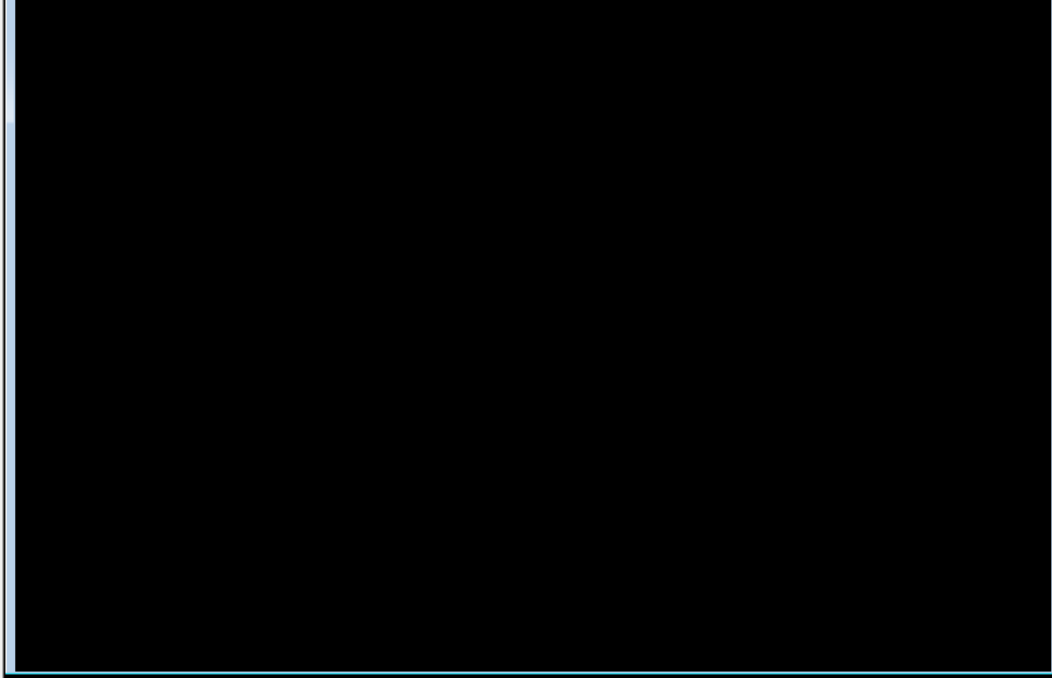
Loading options Import Export Filter
Statistics Compare Summary
Path parameters Preferences

Select additional search types ?

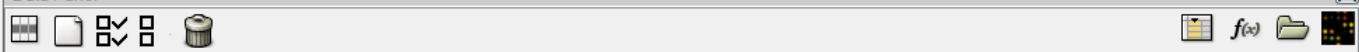
- rog
- PMID
- src_inbx_id
- omim
- digid
- RIGID
- dig_title

Refresh Set selected

iRefScape_1.16



Data Panel



ID	i.taxid	i.rogid_TOP	i.RefSeq_Ac_TOP	i.UniProt_Ac_TOP	i.UniProt_ID_TOP	i.interactor_shorttbl	i.geneSymbol	i.Canonical_rog_TOP
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Node Attribute Browser Edge Attribute Browser Network Attribute Browser

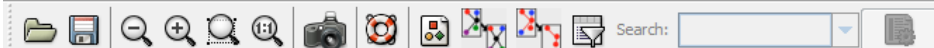
iRefScape info

Always on top Do not show this again Exit

Messages Search history Matrix_view query_helper

Save Clear Refresh ?

ICHTHYOSIS -> ICHTHYOSIS PREMATUREITY SYNDROME, 608649 (3)
ICHTHYOSIS -> ICHTHYOSIS, LEUKOCYTE VACUOLES, ALOPECIA, AND SCLEROSING CHOLANGITIS, 607626 (3)
ICHTHYOSIS -> CEREBRAL DYSGENESIS, NEUROPATHY, ICHTHYOSIS, AND PALMOPLANTAR KERATODERMA SYNDROME, 609528 (3)
ICHTHYOSIS -> ICHTHYOSIS, LAMELLAR, AUTOSOMAL RECESSIVE, 242300 (3)
ICHTHYOSIS -> ICHTHYOSIS FOLLICULARIS, ATRICHIA, AND PHOTOPHOBIA SYNDROME, 308205 (3)
ICHTHYOSIS -> HYSTRIX-LIKE ICHTHYOSIS WITH DEAFNESS, 602540 (3)
ICHTHYOSIS -> KERAT **Double click or press enter after selecting to transfer the terms
to the query box (CTL+click and SHIFT+click supported)**
ICHTHYOSIS -> VOHWI
ICHTHYOSIS -> ICHTHYOSIS WITH HYPOTRICHOSIS, 610765 (3)
ICHTHYOSIS -> KERATOSIS LINEARIS WITH ICHTHYOSIS CONGENITA AND SCLEROSING KERATODERMA, 601952 (3)
ICHTHYOSIS -> ICHTHYOSIS, X-LINKED, 308100 (3)
ICHTHYOSIS -> ICHTHYOSIS VULGARIS, 146700 (3)
ICHTHYOSIS -> ICHTHYOSIS BULLOSA OF SIEMENS, 146800 (3)
ICHTHYOSIS -> ICHTHYOSIS HISTRIX, CURTH-MACKLIN PALMOPLANTAR KERATODERMA, NONEPIDERMOLYTIC, 600962 (3)
ICHTHYOSIS -> ICHTHYOSIS, CYCLIC, WITH EPIDERMOLYTIC HYPERKERATOSIS, 607602 (3)
ICHTHYOSIS -> ICHTHYOSIS, HARLEQUIN, 242500 (3)
ICHTHYOSIS -> ICHTHYOSIS, LAMELLAR 2, 601277 (3)



iRefScope Network VizMapper™ Editor Filters

iRefScope

Load from file

Wizard

```

)
"ICHTHYOSIS, HARLEQUIN, 242500 (3)"
"ICHTHYOSIS, LAMELLAR 2, 601277 (3)"
)
    
```

dig title

Any

Iteration 0 Create new view

Use canonical expansion

Search & load

Hide advanced features

Loading options Import Export Filter

Statistics Compare Summary

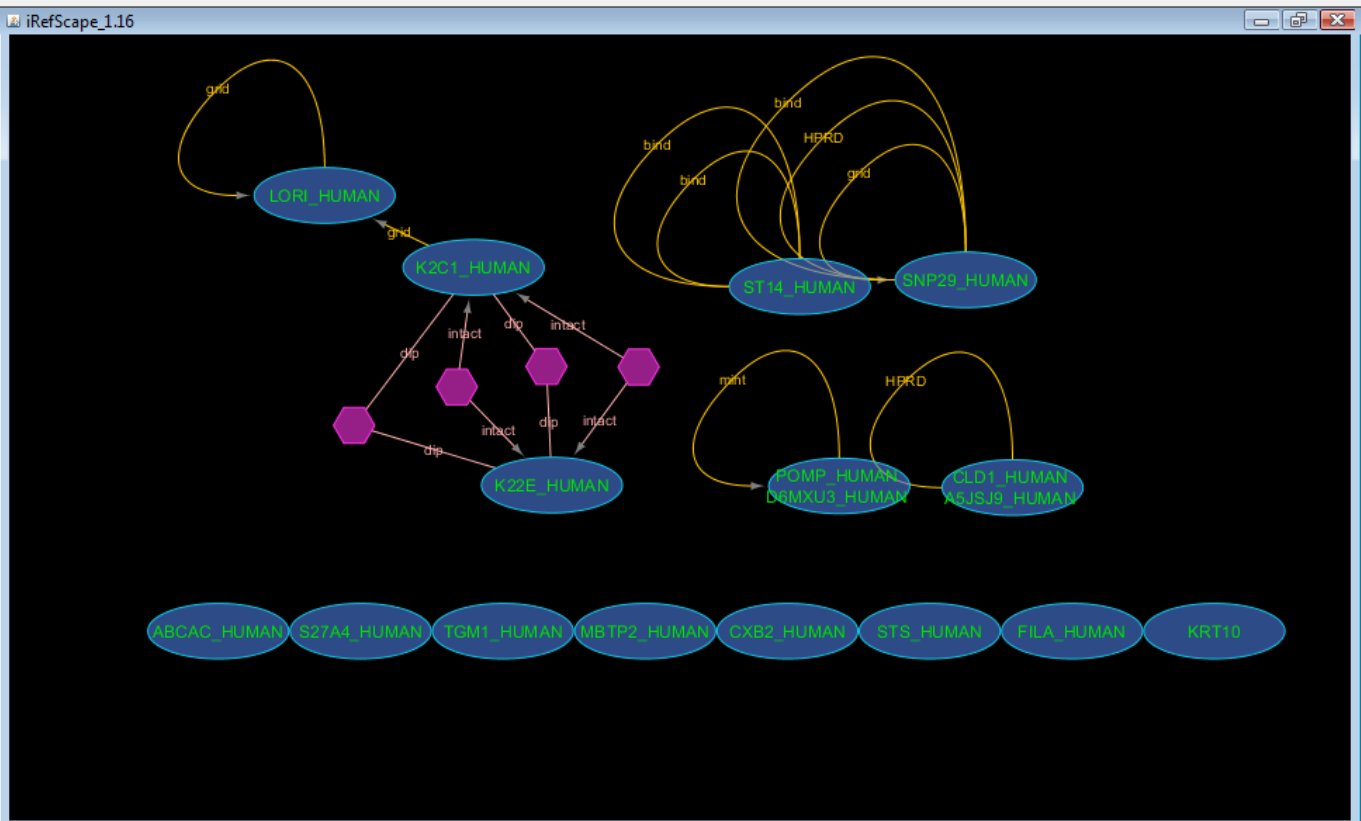
Path parameters Preferences

Select additional search types ?

- rog
- PMID
- src_inbn_id
- omim
- digid
- RIGID
- dig_title

Refresh

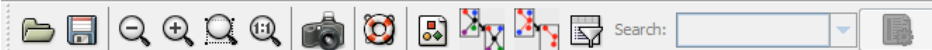
Set selected



Data Panel

ID	i.taxid	i.rogid_TOP	i.RefSeq_Ac_TOP	i.UniProt_Ac_TOP	i.UniProt_ID_TOP	i.interactor_shorttbl	i.geneSymbol

Node Attribute Browser Edge Attribute Browser Network Attribute Browser



iRefScope

Load from file

Wizard

```

)
"ICHTHYOSIS, HARLEQUIN, 242500 (3)"
"ICHTHYOSIS, LAMELLAR 2, 601277 (3
)"
    
```

dig title

Any

Iteration 1 Create new view

Use canonical expansion

Search & load

Hide advanced features

Type **Node**

Attribute **i.alive_degree**

Value **GREATER_THAN_OR_EQUAL**

Condition **2**

Refresh Set selected

Optional settings

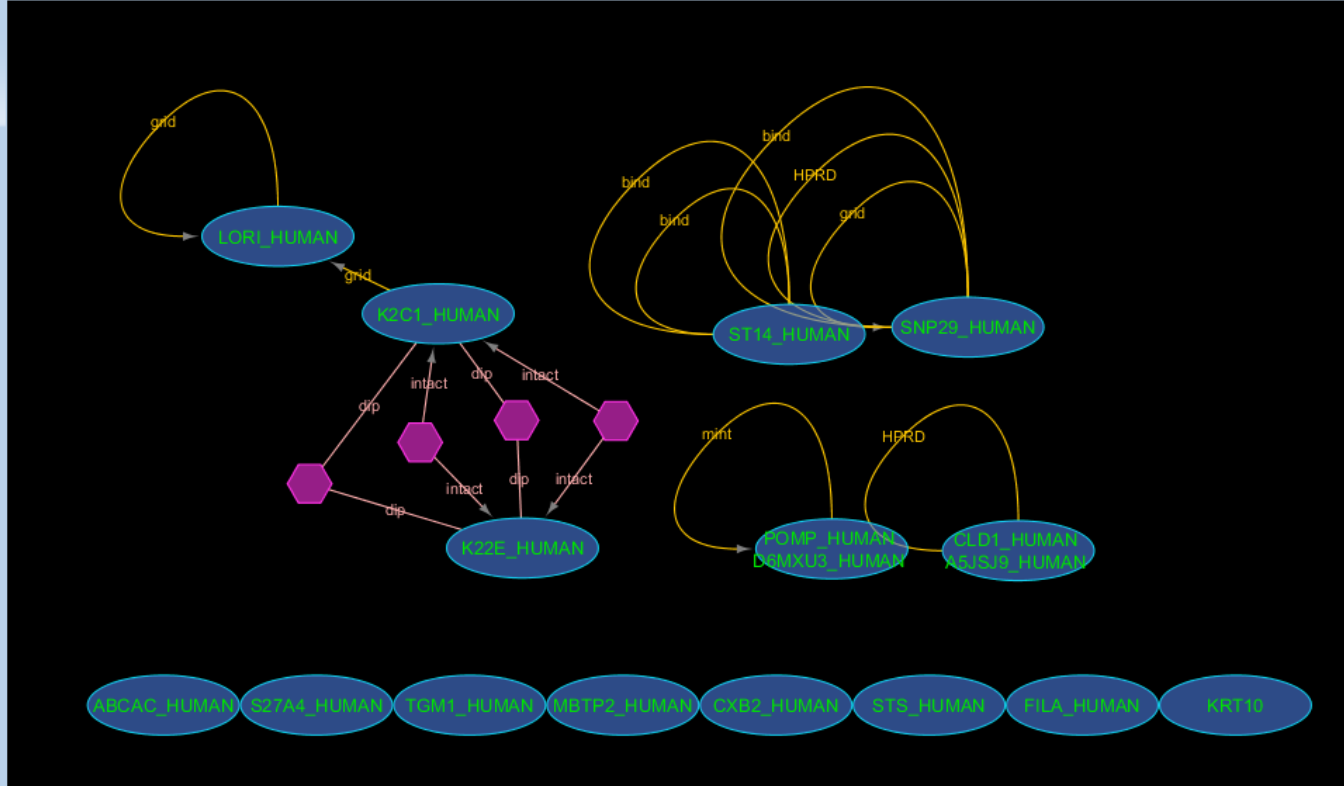
Selection **Select_not_in_current_selec...**

Set i.alive **Do_not_change**

Group_mode **Do not group**

Reset order for selection 19

Case sensitive Tabulate



Data Panel

ID	i.taxid	i.rogid_TOP	i.RefSeq_Ac_TOP	i.UniProt_Ac_TOP	i.UniProt_ID_TOP	i.interactor_shorttbl	i.geneSymbol

Node Attribute Browser Edge Attribute Browser Network Attribute Browser

Between nodes



Control Panel
iRefScope Network VizMapper™ Editor F

iRefScope

Load from file Wizard

```
"ICHTHYOSIS, HARLEQUIN, 242500 (3)"
"ICHTHYOSIS, LAMELLAR 2, 601277 (3)"
}"
```

dig title
Any

Iteration 1 Create new view

Use canonical expansion

Search & load

Hide advanced features

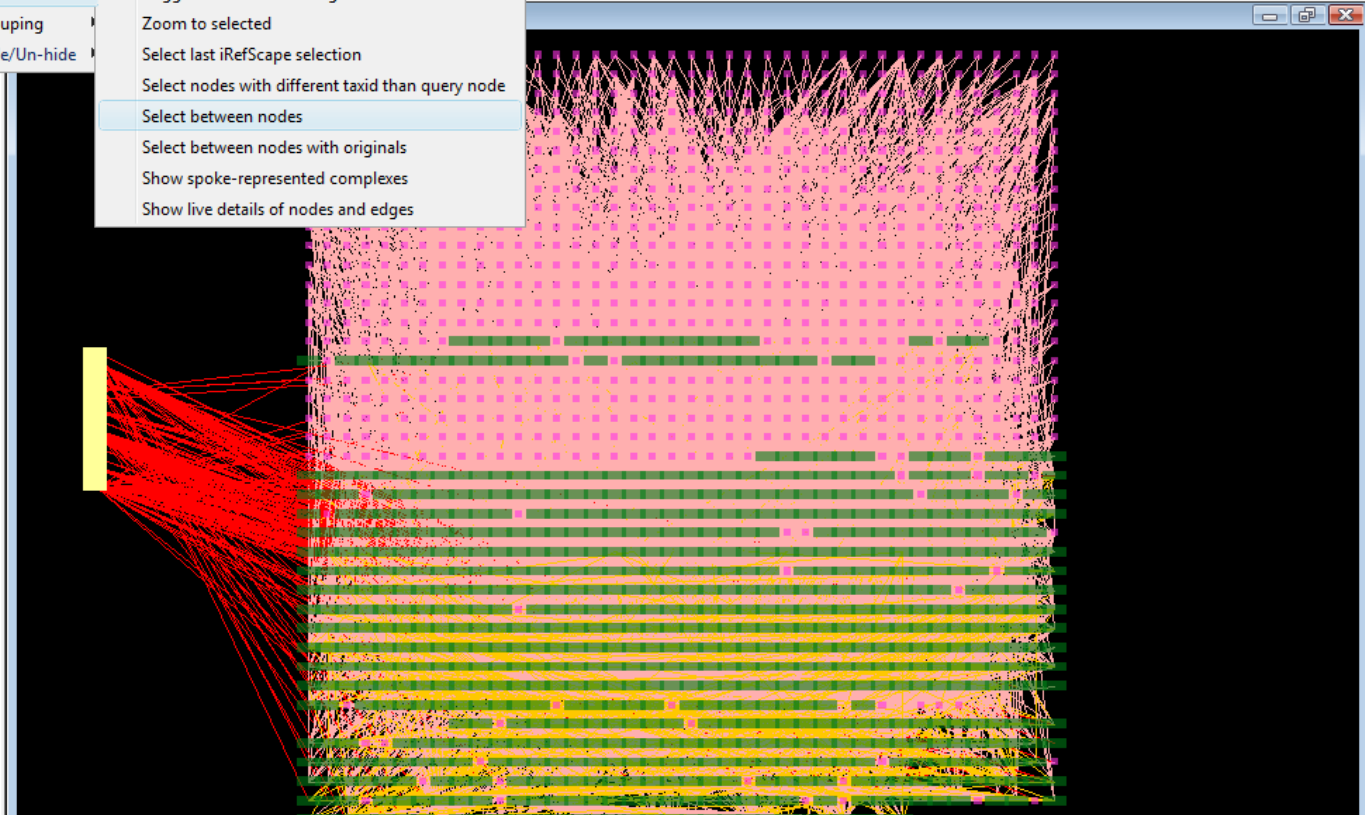
Statistics Compare Summary
Path parameters Preferences
Loading options Import Export Filter

Type Node
Attribute canonicalName
Value GREATER_THAN_OR_EQUAL
Condition 2

Refresh Set selected

Optional settings
Selection Select_not_in_current_selec...
Set i.alive Do_not_change
Group_mode Do not group
 Reset order for selection 19
 Case sensitive Tabulate

- Search tools
- View tools
 - Toggle selected multi-edges
 - Zoom to selected
 - Select last iRefScope selection
 - Select nodes with different taxid than query node
 - Select between nodes
 - Select between nodes with originals
 - Show spoke-represented complexes
 - Show live details of nodes and edges
- Grouping
- Hide/Un-hide



Data Panel

ID	i.alive_degree ▾	i.alive	i.order	i.taxid	i.rogid_TOP	i.RefSeq_Ac_TOP	i.UniProt_Ac_TOP	i.UniProt_ID
2974551	1	true	0	9606	m+0wD07fg...	NP_057016	Q9Y244	POMP_HUM
2462635	1	true	0	9606	lw04f5ViRM...	NP_068813	Q9Y5Y6	ST14_HUMA
9645225	0	true	0	9606	nrM8vPoc1A...	NP_000412		
530760	1	true	0	9606	4HyjERPnED...	NP_004773	O95721	SNP29_HUI
3157434	0	true	0	9606	n4lyRvHbJpb...	NP_000342	P08842	STS_HUMA
2307760	0	true	0	9606	HYJINDmk6a...	NP_056968	O43462	MBTP2_HUI
4182659	1	true	0	9606	TeAC3i2hWT...	NP_006112	P04264	K2C1_HUMA
2441415	2	true	0	9606	ISIQk0W6vO...	NP_000418	P23490	LORI_HUMA
620248	0	true	0	9606	5kr1FHRSYLL...	NP_000350	P22735	TGM1_HUM
4154807	0	true	0	9606	T7LeB8nkZz...	NP_000414	P35908	K22E_HUM
2314882	0	true	0	9606	Hzwv5T/e5F...	NP_003995	P29033	CXB2_HUM
426556	1	true	0	9606	38MxEaRUY...	NP_066924	O95832	CLD1_HUM
3951813	0	true	0	9606	RXgRbd4W6...	NP_002007	P20930	FILA_HUMA
9768971	0	true	0	9606	HZsVBkhHni...	NP_775099	Q86UK0	ABCAC_HUI

Node Attribute Browser Edge Attribute Browser Network Attribute Browser



Control Panel

iRefScope Network VizMapper™ Editor Filters

iRefScope

Load from file **Wizard**

"ICHTHYOSIS, HARLEQUIN, 242500 (3)"
"ICHTHYOSIS, LAMELLAR 2, 601277 (3)"

dig title
Any

Iteration 1 Create new view

Use canonical expansion

Search & load

Hide advanced features

Statistics Compare Summary
Path parameters Preferences
Loading options Import Export Filter

Type: Node

Attribute: canonicalName

Value: GREATER_THAN_OR_EQUAL

Condition: 2

Refresh **Set selected**

Optional settings

Selection: Select_not_in_current_selc...

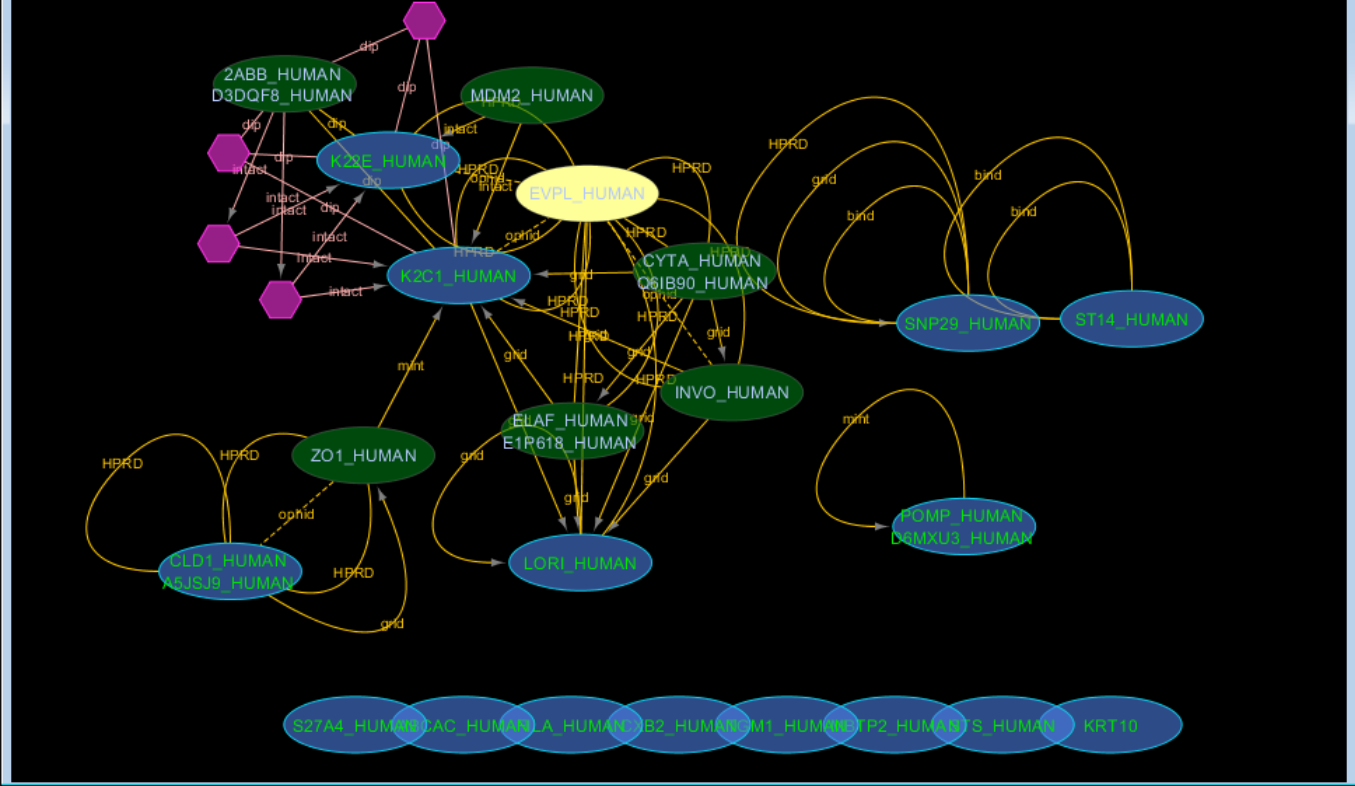
Set i.alive: Do_not_change

Group_mode: Do not group

Reset order for selection 19

Case sensitive Tabulate

iRefScope_116--child.2



Data Panel

ID	i.alive_degree ▾	i.alive	i.order	i.interactor_shorttbl	i.UniProt_ID_TOP	i.taxid	i.rogid_TOP	i.RefSeq_Ac_1
9644735	3	false	1	[EVPL, ENVOPLAKIN]	EVPL_HUMAN	9606	KPm640C6t...	NP_001979

Node Attribute Browser | Edge Attribute Browser | Network Attribute Browser

Where to begin and further reading.

Links and references in this talk.

Vidal M, Cusick ME, Barabási AL. Interactome networks and human disease. Cell. 2011 Mar 18;144(6):986-98.
Review. PubMed PMID: 21414488.

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http://donaldson.uio.no/wiki/Bioinformatics_course

FINITO

breast cancer

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3858

675

4014

5888

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51360

5290

51371

5245

6768

472

7051

3845

9076

367

9342

3161

207

1728

11200