

A Quick Guide to Using Cerebral in InnateDB



- Cerebral can be used to visualize interaction networks from a set of interactions from InnateDB.
- Cerebral uses subcellular localization annotations to provide more biologically intuitive pathway-like lay-outs of interaction networks.
- Note: the subcellular localizations in Cerebral should only be used as a guide. There are many proteins with no annotated subcellular localizations and many others that have multiple possible localizations (only 1 will be shown, nuclear, extracellular and membrane localizations will take precedence over cytoplasm if there are multiple).
- InnateDB batch searching allows users to upload a list of genes along with associated gene expression data from up to 10 different conditions.
- Gene expression data can be overlaid on network data and you can visualize this in Cerebral.

Visualize Interactions in a subcellular localization-based layout using the Cerebral plugin for Cytoscape.



Click here to visualize interactions in Cerebral
You must have a recent version of Java installed.

InnateDB
A Knowledge Resource For Innate Immunity Interactions & Pathways

Home About Search Browse Download Resources

Display Options (Show/Hide)

Sorted by: Interaction Level ascending then by Group ID ascending Sort

Click here to show redundant interactions

Download XML TAB MS Excel CSV SIF Visualize Cerebral (?)

Viewing interactions 1 to 20 of 66 hits matching query (Participant idphysical_molecule: 90782)

Page(s): 1 2 3 4 [Next]

Group ID	Interaction	Interactors	Species	Interaction level	Interaction type	Supporting Publications	
14062	Coimmunoprecipitation reveals interaction between the pellino protein homolog 1(Pellino) and Interleukin-1 receptor-associated kinase 1 (IRAK) and the Interleukin-1 receptor-associated kinase-4 (IRAK4) proteins	IRAK1 :: IRAK4 :: PELI1	<i>Homo sapiens</i>	direct interaction	physical interaction	1	Interaction Details
14064	IRAK4 phosphorylates IRAK1	IRAK1 :: IRAK4	<i>Homo sapiens</i>	direct interaction	phosphorylation	1	Interaction Details
14224	IRAK1 phosphorylates TOLLIP	IRAK1 :: TOLLIP	<i>Homo sapiens</i>	direct interaction	phosphorylation	1	Interaction Details
14237	IRAK1 phosphorylates IRAK3	IRAK1 :: IRAK3	<i>Homo sapiens</i>	direct interaction	phosphorylation	1	Interaction Details
16078	IRAK1 phosphorylates IRAK2	IRAK1 :: IRAK2	<i>Homo sapiens</i>	direct interaction	phosphorylation	1	Interaction Details



Opening Interaction Data in Cerebral from an Interaction Results page in InnateDB.

- You will be prompted to open a .jnlp file.
- You are recommended to save this file to your computer and then open it – this will allow you save a copy of this dataset.
- Opening the .jnlp file directly without saving sometimes causes Cerebral to hang when loading large datasets.
- Note: to use Cerebral you need to install Java version 6 or greater.
- You can get this from <http://java.com/en/download/index.jsp>

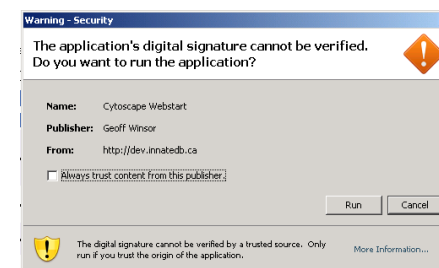
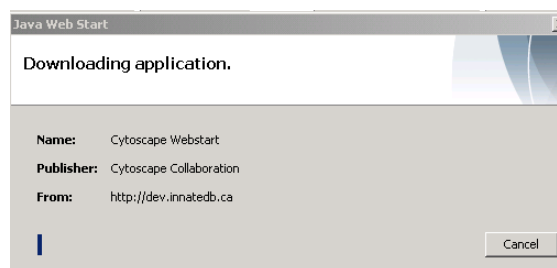
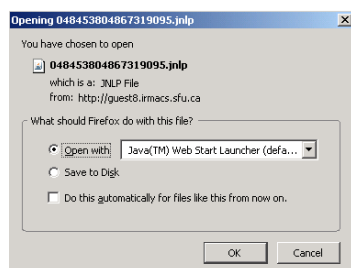
The screenshot shows the InnateDB website interface. At the top, there is a navigation bar with links: Home, About, Search, Browse, Download, Resources, Statistics, Contact, Help. Below the navigation bar, there are sorting options: "Sorted by: Interaction Level ascending then by Group ID ascending Sort". A "File Download" dialog box is open in the foreground, asking "Do you want to open or save this file?". The dialog box contains the following information: Name: temp_05658339911273171.jnlp, Type: JNLP File, From: dev.innatedb.ca. Below the dialog box, a table of interaction data is visible. The table has columns: Group ID, Interaction, Interaction Level, Interaction type, Supporting Publications, and Interaction Details. The table contains three rows of data:

Group ID	Interaction	Interaction Level	Interaction type	Supporting Publications	Interaction Details
14062	Coimmunoprecipitation reveals interaction between pellino protein homolog 1(Pellino) and Interleukin-1 associated kinase 1 (IRAK) and the Interleukin-1 receptor associated kinase-4 (IRAK4) proteins	direct interaction	physical interaction	1	Interaction Details
14064	IRAK4 phosphorylates IRAK1	direct interaction	phosphorylation	1	Interaction Details
14224	IRAK1 phosphorylates TOLLIP	direct interaction	phosphorylation	1	Interaction Details
14237	IRAK1 phosphorylates IRAK3	direct interaction	phosphorylation	1	Interaction Details



Opening Cerebral

- Cerebral is a Java plugin for the Cytoscape Visualization software.
- When you open the .jnlp file Cytoscape will begin downloading.
- You will then be prompted – “Do you want to run the application” – click Run.





Cerebral is now open and displays interactions based on protein subcellular localizations.

Cytoscape Desktop (New Session)

File Edit View Select Layout Plugins Help

Cerebral Search: []

CytoPanel 1

temp_05658339911273171_sif.sif

Network Editor Cerebral

Edge curviness: Straight Bundled

Label density: Dense Sparse

Group label size: Off Small Large

Show function clusters

Show layer separators

High quality rendering

Relayout

Supporting publications: 1 2 or 3 4 or more

Expression color scale: -16 0 16

Comparison color scale: -16 0 16

Significance cut-off: 1 0.1 0.01 0.001 0.05

Expression cutoff: ±0 ±1 ±2 ±3 ±4 1.5

Expression data are ratios

Add group Delete group

Node Attribute Browser Edge Attribute Browser Network Attribute Browser Parallel Coordinates

Welcome to Cytoscape 2.4.1 Right-click + drag to ZOOM Middle-click + drag to PAN

Extracellular

Cell surface

Plasma membrane

Cytoplasm

Nucleus

Unknown

IL10

TRIP6

IRAK2

IL1R1

NTRK3

Irak1

STIP1

IKBKB

TRAF6

TRAF3

SQSTM1

SUMO1P3/SUMO1

ITGAM

TRAF4

IRAK1

PRKCI

MAP3K7IP1

IRAK4 ::

PELI1

NGFR ::

PRKCI

IRF7

Re-size the Network



Click here to re-size the network display to full-screen.

The screenshot shows the Cytoscape Desktop interface with a network diagram. A callout box points to the full-screen icon in the top toolbar. The network diagram is organized into layers: Extracellular, Cell surface, Plasma membrane, Cytoplasm, Nucleus, and Unknown. Nodes are represented by colored circles, and edges are lines connecting them. The interface includes a menu bar, a toolbar, a search bar, and a sidebar with various settings and filters. The bottom of the window shows the status bar with the text "Welcome to Cytoscape 2.4.1" and "Right-click + drag to ZOOM Middle-click + drag to PAN".

File Edit View Select Layout Plugins Help

Cerebral Search:

temp_05658339911273171_sif

Extracellular
Cell surface
Plasma membrane
Cytoplasm
Nucleus
Unknown

IL10
TRIP6
IL1RAP ::
IRAK1
IL1R1
TLR4
NTRK3
IRAK2
IRAK1
HRAS
STIP1
IKBKB
SQSTM1
TRAF6
TRAF3
SUMO1P3/SUMO1
IRF7
ITGAM
TRAF4
IRAK1
PRKCI
MAP3K7IP1
IRAK4 ::
NGFR ::

Off Small Large
 Show function clusters
 Show layer separators
 High quality rendering
Relayout

Supporting publications
1 2 or 3 4 or more

Expression color scale
-16 0 16

Comparison color scale
-16 0 16

Significance cut-off
1 0.1 0.01 0.001 0.05

Expression cutoff
±0 ±1 ±2 ±3 ±4 1.5

Expression data are ratios
Add group Delete group

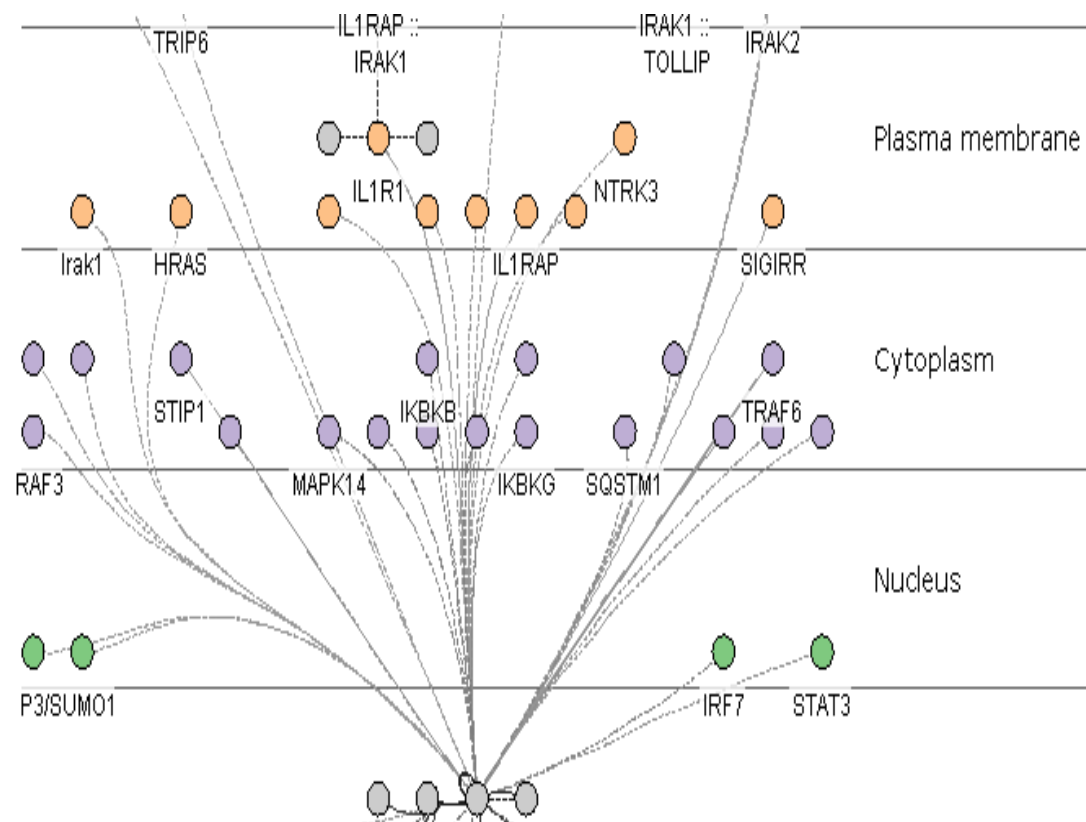
Node Attribute Browser Edge Attribute Browser Network Attribute Browser Parallel Coordinates

Welcome to Cytoscape 2.4.1 Right-click + drag to ZOOM Middle-click + drag to PAN



Navigating in Cerebral

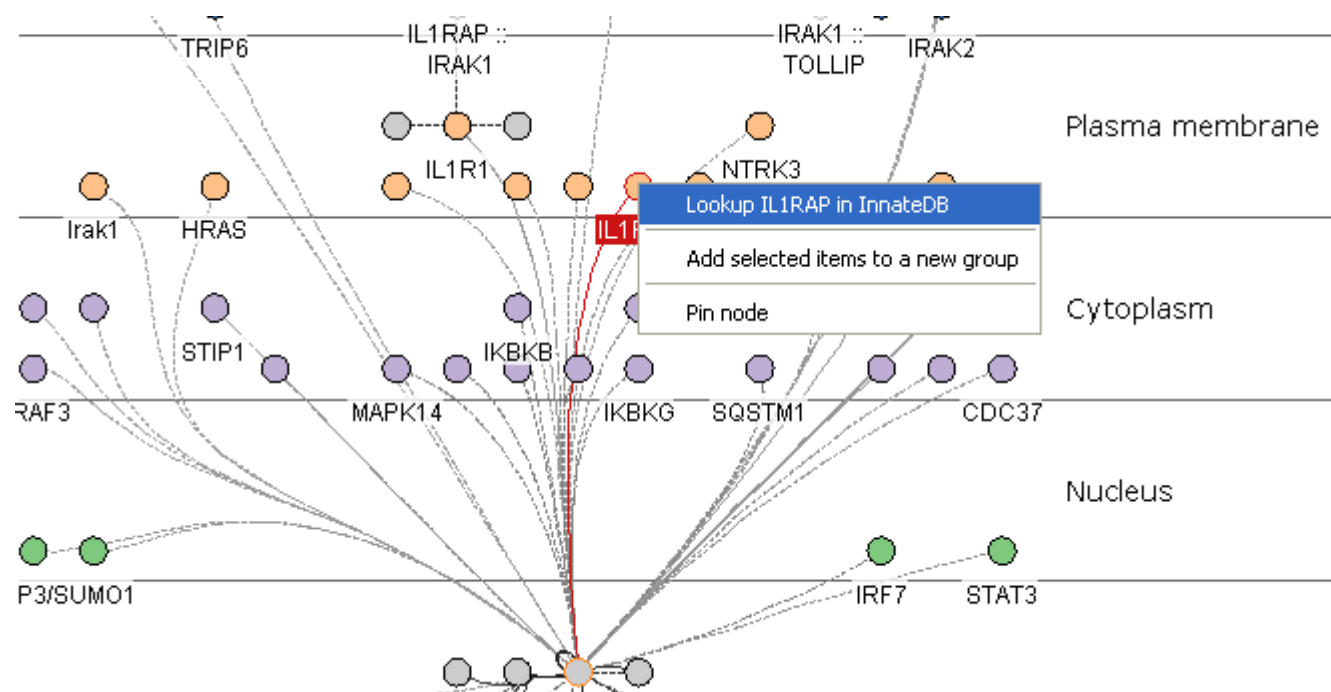
- Right click and push your mouse forward or back to zoom.
- Hold middle button of your mouse and drag to navigate around the network.
- Grey nodes do not have an annotated subcellular localization (from Gene Ontology data in InnateDB).
- Lines connecting nodes represent interactions. Dashed lines have only 1 supporting publication in InnateDB. The thicker the line the more publications support the interaction.





Interactively Link back to InnateDB to Look up Information on Particular Genes/Interactions of Interest.

- Right-click on a node (protein/gene) or edge (interaction line) to link to the relevant gene or interaction details page in InnateDB.





Nodes can be dragged to other layers as desired.

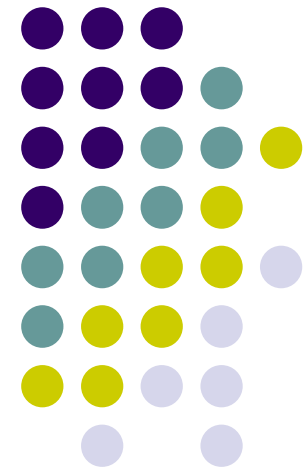
Click on & drag nodes to other layers.

Click "Node Attribute Browser" and select from list to see node attributes.

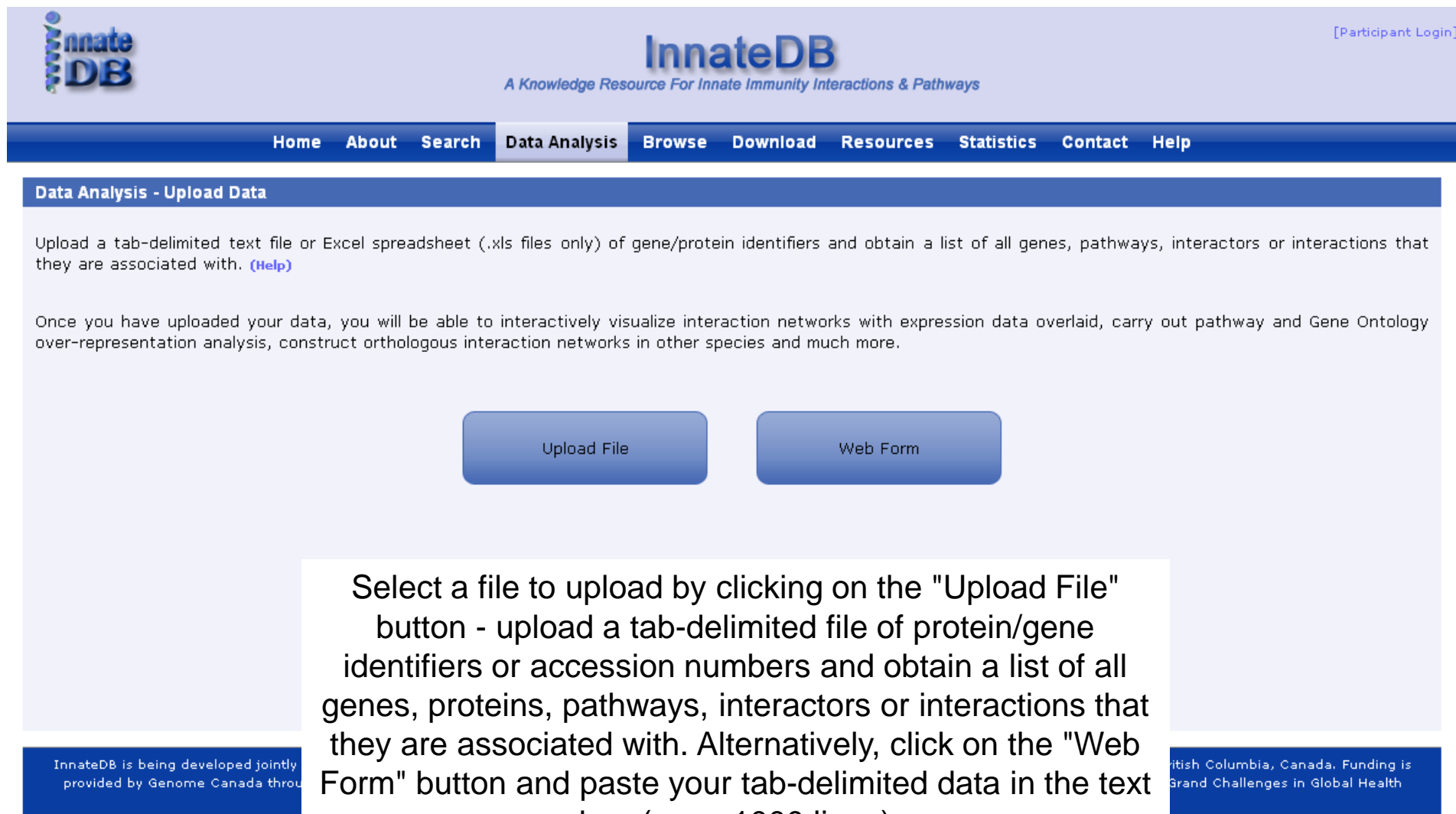
The screenshot shows the Cytoscape Desktop interface with a network diagram. The diagram is organized into layers: Extracellular, Cell surface, Plasma membrane, Cytoplasm, Nucleus, and Unknown. Nodes are represented by colored circles, and edges are lines connecting them. A node labeled 'IRAK1BP1' is highlighted in red. The Node Attribute Browser table at the bottom lists various nodes and their attributes.

ID	Function	InnateDB...	Localization	canonical...
MAP3K...	Signaling	http://dev.i...	Cytoplasm	MAP3K7IP2
IRAK4	Interleukin	http://dev.i...	Unknown	IRAK4
SQSTM...				SQSTM1 ...
NLRP12	Hydrolase	http://dev.i...	Cytoplasm	NLRP12
IRF7	Nucleic A...	http://dev.i...	Nucleus	IRF7
MAP3K7	Kinase	http://dev.i...	Unknown	MAP3K7
CAV1	Membran...	http://dev.i...	Cell surfa...	CAV1
AKT1	Kinase	http://dev.i...	Cytoplasm	AKT1

Overlay Gene Expression Data on Interaction Networks



Upload Gene/Protein List to InnateDB Along with Any Associated Quantitative Data



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[Participant Login]

Home About Search **Data Analysis** Browse Download Resources Statistics Contact Help

Data Analysis - Upload Data

Upload a tab-delimited text file or Excel spreadsheet (.xls files only) of gene/protein identifiers and obtain a list of all genes, pathways, interactors or interactions that they are associated with. ([Help](#))

Once you have uploaded your data, you will be able to interactively visualize interaction networks with expression data overlaid, carry out pathway and Gene Ontology over-representation analysis, construct orthologous interaction networks in other species and much more.

[Upload File](#) [Web Form](#)

Select a file to upload by clicking on the "Upload File" button - upload a tab-delimited file of protein/gene identifiers or accession numbers and obtain a list of all genes, proteins, pathways, interactors or interactions that they are associated with. Alternatively, click on the "Web Form" button and paste your tab-delimited data in the text box (max. 1000 lines)

InnateDB is being developed jointly provided by Genome Canada through the Strategic Alliances Program and the British Columbia, Canada. Funding is provided by the Grand Challenges in Global Health.

Preview of Uploaded Data



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Data Analysis - Specify which data is in each column

Click on the column headers to specify which column in your data file contains the identifiers/accession numbers for each gene (and which database they come from). This is called the "Cross-reference ID". Please note that when using InnateDB identifiers, only gene IDs are valid, not interaction IDs!

If you have included gene expression data - identify which columns contain the gene expression values and their associated p-values.

You may also identify the column containing the probe IDs if you have included them in your file. [\(Help\)](#)

Dataset Preview

Column 1	Column 2	Column 3	Column 4	Column 5
Ensembl Gene	Day 3 fold change	Day 3 p-value	Day 4 fold change	Day 4 p-value
ENSG00000002586	-0.9	0.0080	-1.9	0.041
ENSG00000002834	1.2	0.046	1.6	0.01
ENSG00000004799	2.3	0.045	1.6	0.03
ENSG00000005249	-1.8	0.046	-2.3	0.017
ENSG00000005339	-0.2	0.03	-2.2	0.04
ENSG00000005381	2.3	0.042	2.4	0.043
ENSG00000005961	-0.8	0.02	-1.7	0.036
ENSG00000006075	1.4	0.021	1.8	0.014
ENSG00000006327	-1.6	0.0030	-1.1	0.048
ENSG00000006652	3.0	0.047	3.1	0.0020
ENSG00000008130	1.6	0.043	0.8	0.0060
ENSG00000011009	1.5	0.0020	2.0	0.02

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Click on the column headers to specify which column in your data file contains the identifiers/accession numbers for each gene.



If you have included gene expression data - identify which columns contain the gene expression values and their associated p-values.

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Home About Search **Data Analysis** Browse Download Resources Statistics Contact Help

Data Analysis - Specify which data is in each column

Click on the column headers to specify which column in your data file contains the identifier. Please note that when using InnateDB identifiers, only gene IDs are valid, not interaction IDs. This column is called the "Cross-reference ID".

If you have included gene expression data - identify which columns contain the gene expression values and their associated p-values.

You may also identify the column containing the probe IDs if you have included them in your data file.

This column is:

- (undefined)
- Cross-reference ID**
- Expression value
- P-Value
- Probe ID
- (undefined)

Dataset Preview

Column 1	Column 2	Column 3	Column 4	Column 5
Ensembl Gene	Day 3 fold change	Day 3 p-value	Day 4 fold change	Day 4 p-value
ENSG00000002586	-0.9	0.0080	-1.9	0.041
ENSG00000002834	1.2	0.046	1.6	0.01
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ENSG00000005249	-1.8	0.046	-2.3	0.017
ENSG00000005339	-0.2	0.03	-2.2	0.04
ENSG00000005381	2.3	0.042	2.4	0.043
ENSG00000005961	-0.8	0.02	-1.7	0.036
ENSG00000006075	1.4	0.021	1.8	0.014
ENSG00000006327	-1.6	0.0030	-1.1	0.048
ENSG00000006652	3.0	0.047	3.1	0.0020
ENSG00000008130	1.6	0.043	0.8	0.0060
ENSG00000011009	1.5	0.0020	2.0	0.02

20 Page 1 of 25 Displaying 1 to 20 of 491 items

If you have included gene expression data - identify which columns contain the gene expression values and their associated p-values.

Click Next.

Data Analysis - Specify which data is in each column

Click on the column headers to specify which column in your data file contains the identifiers/accession numbers for each gene (and which database they come from). This is called the "Cross-reference ID". Please note that when using InnateDB identifiers, only gene IDs are valid, not interaction IDs!

If you have included gene expression data - identify which columns contain the gene expression values and their associated p-values.

You may also identify the column containing the probe IDs if you have included them in your file. [\(Help\)](#)

Dataset Preview

Cross-reference ID	Exp.Value (Day3)	P-value (Day3)	Exp.Value (Day4)	P-value (Day4)
Ensembl Gene	Day 3 fold change	Day 3 p-value	Day 4 fold change	Day 4 p-value
ENSG00000002586	-0.9	0.0080	-1.9	0.041
ENSG00000002834	1.2	0.046	1.6	0.01
ENSG00000004799	2.3	0.045	1.6	0.03
ENSG00000005249	-1.8	0.046	-2.3	0.017
ENSG00000005339	-0.2	0.03	-2.2	0.04
ENSG00000005381	2.3	0.042	2.4	0.043
ENSG00000005961	-0.8	0.02	-1.7	0.036
ENSG00000006075	1.4	0.021	1.8	0.014
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ENSG00000006652	3.0	0.047	3.1	0.0020
ENSG00000008130	1.6	0.043	0.8	0.0060
ENSG00000011009	1.5	0.0020	2.0	0.02

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Data Analysis Options



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Data Analysis - Output

- Returning a list of **genes** provides detailed annotation for each gene in the uploaded list and is a prerequisite to performing a Gene Ontology over-representation analysis.
- Returning a list of **pathways** provides pathway annotation for each gene in the uploaded list and is a prerequisite to performing a pathway over-representation analysis.
- Returning a list of **interactors** allows one to identify all molecules in InnateDB which interact with the genes (or their encoded products) in the uploaded list.
- Returning a list of **interactions** allows one to identify all interactions in InnateDB in which the genes (or their encoded products) in the uploaded list are a participant and to construct a network of these interactions for visualization and further analysis.
- Returning a list of **Predicted TF Interactions** allows one to identify transcription factors which are predicted by the CisRED database to bind genes in the uploaded list and to construct a network of these interactions for visualization and further analysis.

Return a list of:

- Interactions ←
- Interactors
- Genes
- Pathways
- Predicted TF Interactions

Filter Interactions: [\(Help\)](#)

- Do not filter the results
- Only show interactions *between* uploaded molecules ←
- Filter for interactions in pathway

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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.

*This will only return molecular interactions **between** the genes and their encoded products in the uploaded list*

i.e. will not return interactions with other genes/proteins not in the uploaded list.

Results: Visualize Gene Expression Data in an Interaction Network Context

Click here to visualize interactions in Cerebral with overlaid gene expression data.
Open Cerebral as previously shown.

Home About Search Data Analysis Browse Download Resources Statistics

Display Options (Show/Hide)

Sorted by: Name (query) ascending then by Interaction Type ascending Sort

Download XML TAB MS Excel CSV SIF Show Orthologous Interactions Visualize **Cerebral** (Help)

Viewing interactions 1 to 20 of 1053 hits matching query

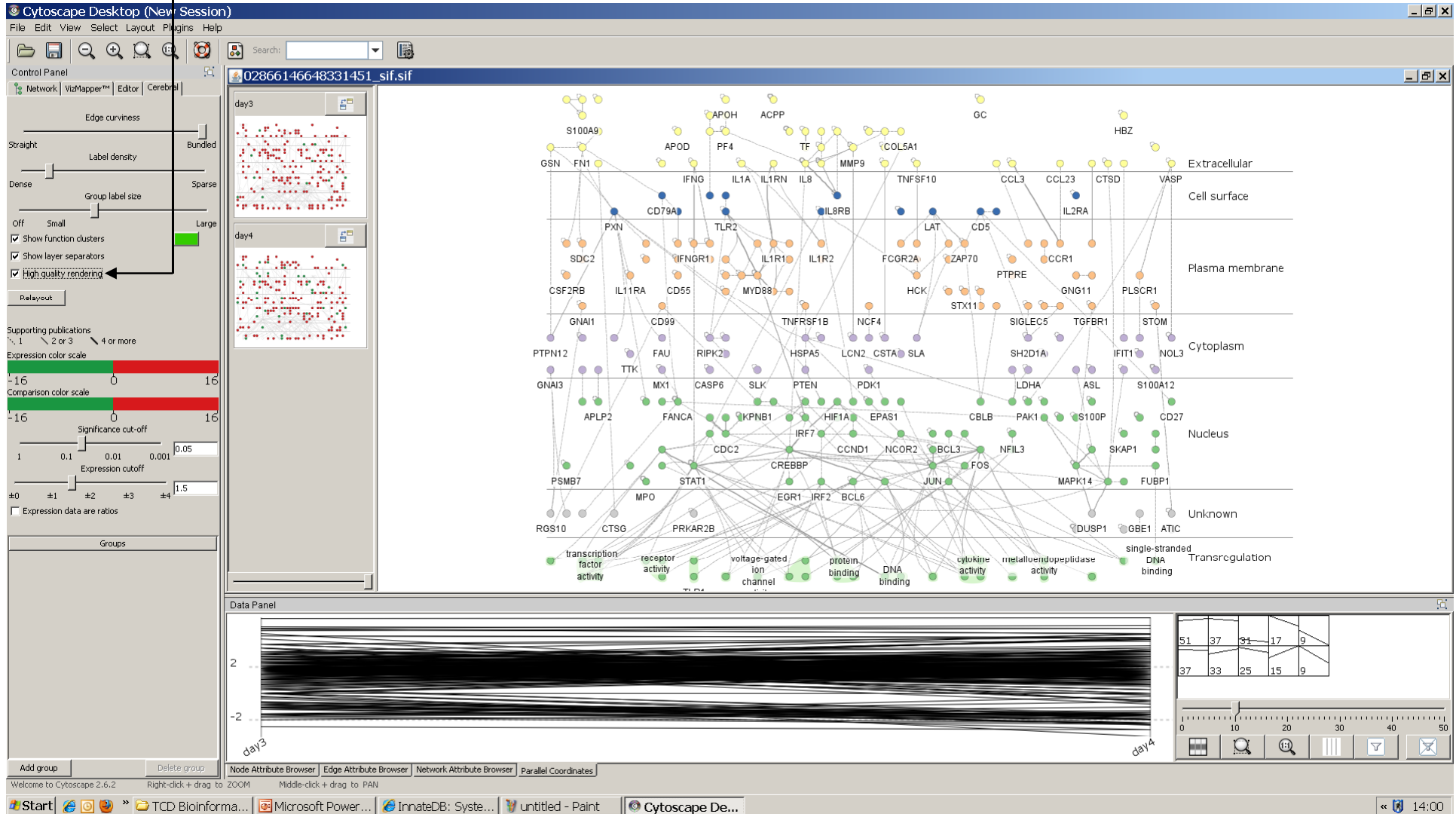
Page(s): 1 2 3 4 5 6 7 8 9 10 [Next]

Query Xref	Query Name	day3 (fold change)	P-Value	day4 (fold change)	P-Value	Group ID	Interaction Level	Interaction	Interactors	Interactor Species	Interaction Type	Supporting Publications	
ENSG00000128274	A4GALT	1.5	0.015	1.7	0.014			No interactions					
ENSG00000140526	ABHD2	1.6	0.006	2.1	0.013			No interactions					
ENSG00000014257	ACPP	2.0	0.049	1.7	0.011	6475	direct interaction	ACPP (complex)	ACPP	<i>Homo sapiens</i>	physical association	1	Interaction Details
ENSG00000014257	ACPP	2.0	0.049	1.7	0.011	6476	direct interaction	ACPP interacts with ACPP	ACPP :: ACPP	<i>Homo sapiens</i>	unspecified	5	Interaction Details
ENSG00000151726	ACSL1	3.7	0.014	4.7	0.013			No interactions					
ENSG00000135074	ADAM19	1.0	0.007	1.6	0.049			No interactions					
ENSG00000147872	ADFP	1.0	0.006	2.9	0.049			No interactions					
ENSG00000148926	ADM	3.1	0.036	3.0	0.012			No interactions					
ENSG00000100077	ADRBK2	2.2	0.032	3.0	0.026			No interactions					
ENSG00000177674	AGTRAP	1.8	0.043	1.2	0.048	25636	direct interaction	AGTRAP interacts with AGTRAP	AGTRAP :: AGTRAP	<i>Homo sapiens</i>	physical association	1	Interaction Details
ENSG00000177674	AGTRAP	1.8	0.043	1.2	0.048	25635	direct interaction	AGTRAP interacts with AGTRAP	AGTRAP :: AGTRAP	<i>Homo sapiens</i>	unspecified	1	Interaction Details
ENSG00000106992	AK1		0.026	1.6	0.014			No interactions					
ENSG00000131016	AKAP12	0.0	0.023	1.7	0.004			No interactions					
ENSG00000111275	ALDH2	2.0	0.047	1.0	0.039	27028	direct interaction	ALDH2 interacts with ALDH2	ALDH2 :: ALDH2	<i>Homo sapiens</i>	unspecified	3	Interaction Details
ENSG00000132746	ALDH3B2	-1.3	0.018	-2.0	0.032			No interactions					

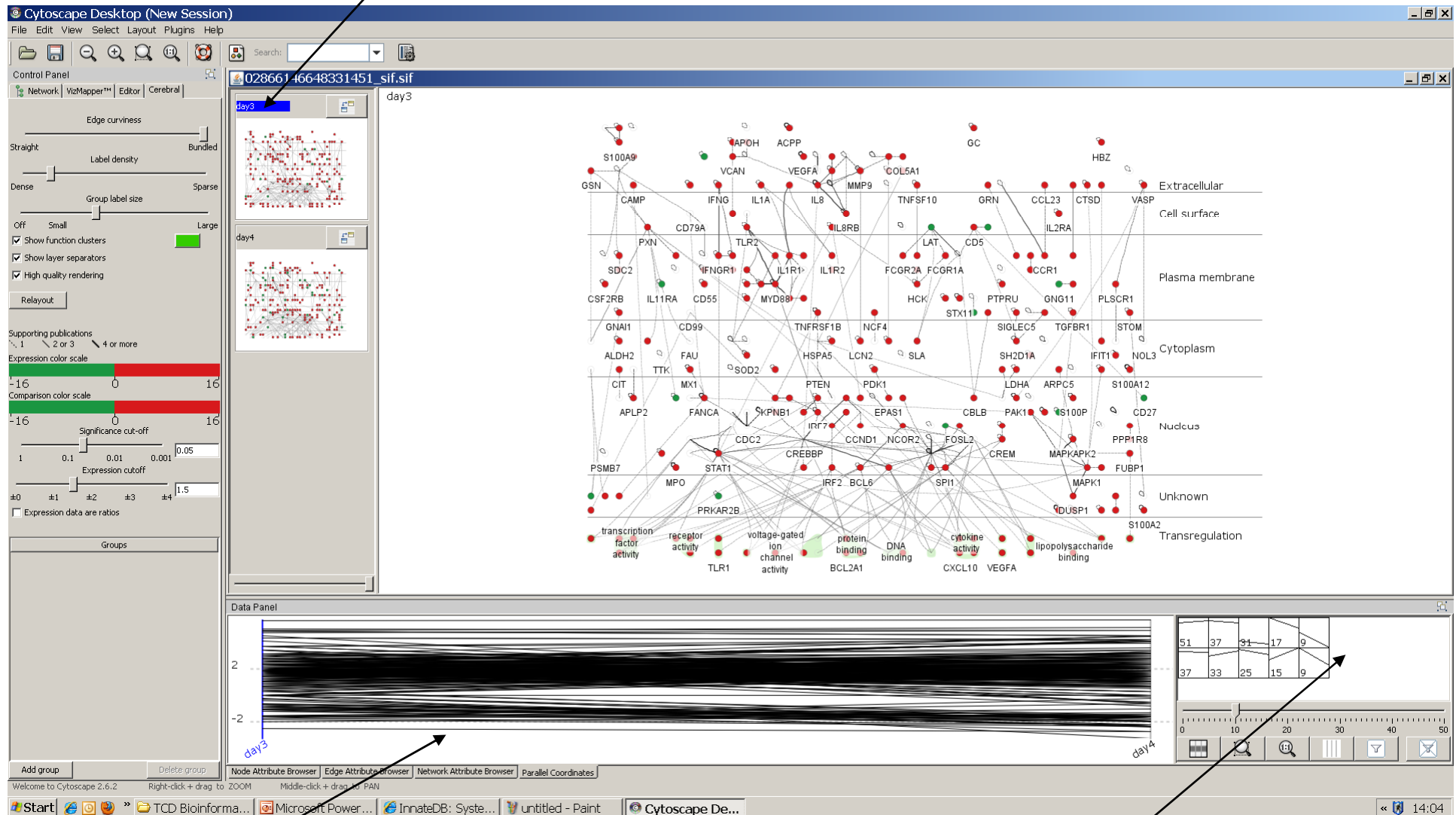
Multi-experiment View in Cerebral

Check this box
To sharpen image

Mini-windows show overlaid gene expression data for each condition.
Red = upreg. Green = downreg.



Click on one of the mini-windows to view data for condition in large window.



Graph of changes in gene expression across time-points

K-means clustering – clusters genes with similar patterns of gene expression

Click on these buttons in 2 different mini-windows to display changes in gene expression from 1 condition to another in the bigger window.

The screenshot shows the Cytoscape Desktop interface with a network diagram and a data panel. The network diagram displays various genes and their interactions, categorized by cellular compartments. The data panel shows a heatmap of gene expression levels across two conditions, 'day3' and 'day4'.

Network Diagram Details:

- Extracellular:** S100A9, APOH, ACPP, GC, HBZ, FN1, APOD, PF4, TF, THBS1, TNFSF10, GRN, TNFSF13, TNFSF12, TNF.
- Cell surface:** CD79A, IL1A, PPBP, IL8RB, IL2RA, CD5, CD79A, TLR2, CYBB, FCGR2A, FCGR1A, CCR1, IL2RA.
- Plasma membrane:** SDC2, IFNGR1, MYD88, HCK, PTPRU, GNG11, PLSCR1, CSF2RB, IL11RA, CD55, TNFRSF1B, NCF4, STX11, SIGLEC5, TGFB1, STOM.
- Cytoplasm:** GNAI1, CD99, HSPA5, LCN2, SLA, SH2D1A, IFIT1, NOL3, ALDH2, TTK, FAU, SOD2, PTEN, PDK1, LDHA, ARPC5, S100A12, CIT, MX1, FANCA, SKP1, EPAS1, CBLB, BNIP3, CD27, RHOB, FANCA, SKP1, EPAS1, CBLB, BNIP3, PPP1R8.
- Nucleus:** PSMB7, MX2, STAT1, CREBBP, CCND1, NCOR2, BCL3, FOS, MAPK1, MAPK2, FUBP1, PRKAR2B, IRF2, BCL6, JUN, IRF2, BCL6, JUN, FOS, MAPK1, MAPK2, FUBP1, DUSP1, S100A2.
- Unknown:** S100A2.
- Transregulation:** S100A2.
- Other categories:** transcription factor activity, receptor activity, voltage-gated ion channel activity, protein binding, DNA binding, cytokine activity, lipopolysaccharide binding, TLR1, BCL2A1, CXCL10, VEGFA.

Data Panel Details:

The data panel shows a heatmap of gene expression levels across two conditions, 'day3' and 'day4'. The y-axis represents gene expression levels, ranging from -2 to 2. The x-axis represents the two conditions. A table in the top right corner of the data panel shows the following values:

49	40	30	18	9
47	36	20	11	4

The data panel also includes a zoom slider and a search bar.

Cytoscape Desktop (New Session)

File Edit View Select Layout Plugins Help

Search:

Control Panel

Network VizMapper™ Editor Cerebral

Edge curviness

Straight Bundled

Label density

Dense Sparse

Group label size

Off Small Large

Show function clusters

Show layer separators

High quality rendering

Relayout

Supporting publications

1 2 or 3 4 or more

Expression color scale

-16 0 16

Comparison color scale

-16 0 16

Significance cut-off

1 n1 n n1 n11 0.05

Expression cutoff

±0 ±1 ±2 ±3 ±4 1.5

Expression data are ratios

Groups

02866146648331451_sif.sif

day3

day4

day3

day4

Extracellular

Cell surface

Plasma membrane

Cytoplasm

Nucleus

Unknown

Transregulation

transcription factor activity

receptor activity

voltage-gated ion channel activity

protein binding

DNA binding

cytokine activity

lipopolysaccharide binding

IL8RB

CD5

CD27

CD2

CD99

CD55

CD70A

CD11A

CD11B

CD11C

CD11D

CD11E

CD11F

CD11G

CD11H

CD11I

CD11J

CD11K

CD11L

CD11M

CD11N

CD11O

CD11P

CD11Q

CD11R

CD11S

CD11T

CD11U

CD11V

CD11W

CD11X

CD11Y

CD11Z

CD12A

CD12B

CD12C

CD12D

CD12E

CD12F

CD12G

CD12H

CD12I

CD12J

CD12K

CD12L

CD12M

CD12N

CD12O

CD12P

CD12Q

CD12R

CD12S

CD12T

CD12U

CD12V

CD12W

CD12X

CD12Y

CD12Z

CD13A

CD13B

CD13C

CD13D

CD13E

CD13F

CD13G

CD13H

CD13I

CD13J

CD13K

CD13L

CD13M

CD13N

CD13O

CD13P

CD13Q

CD13R

CD13S

CD13T

CD13U

CD13V

CD13W

CD13X

CD13Y

CD13Z

CD14A

CD14B

CD14C

CD14D

CD14E

CD14F

CD14G

CD14H

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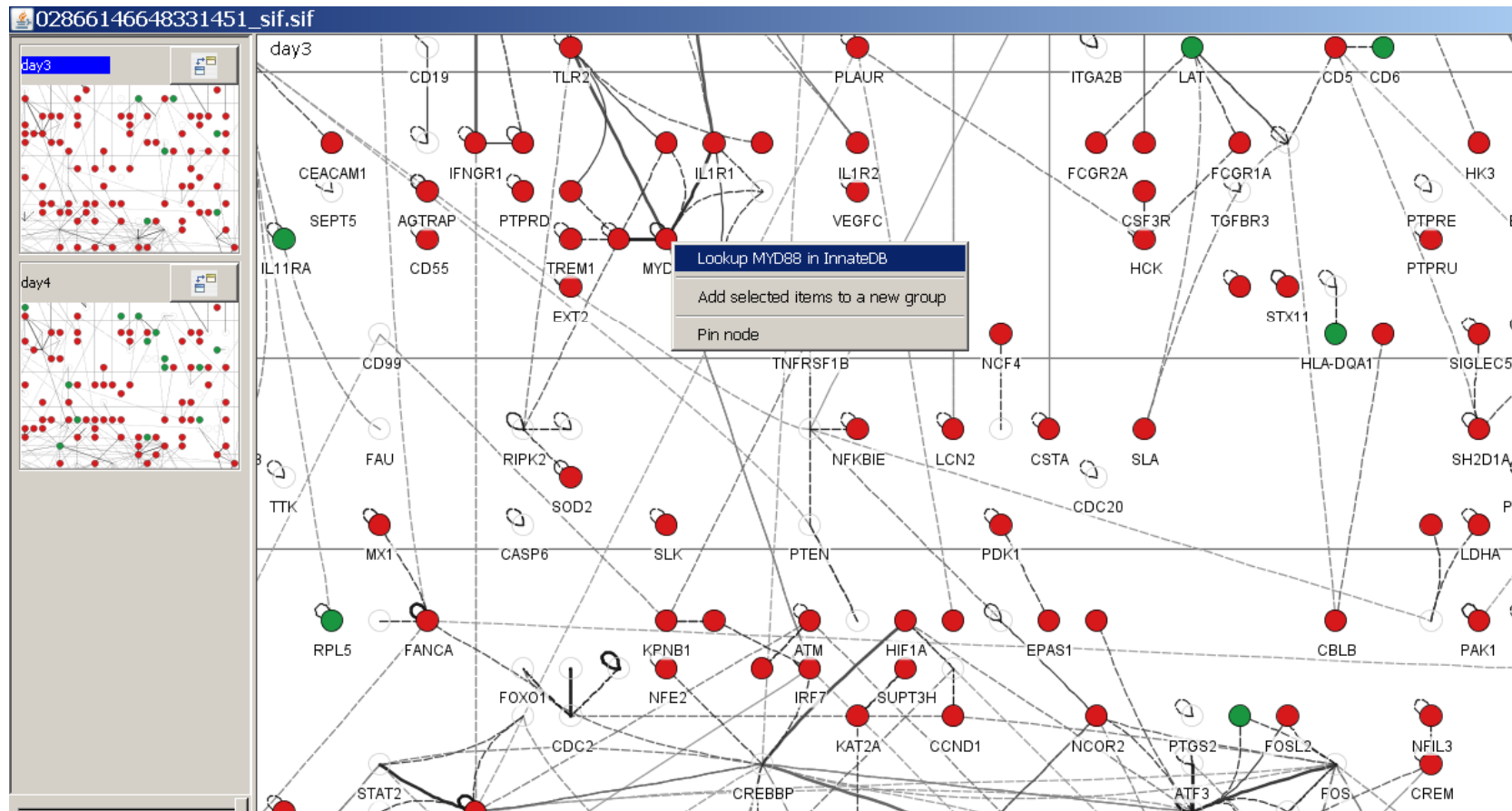
CD56E

CD56F

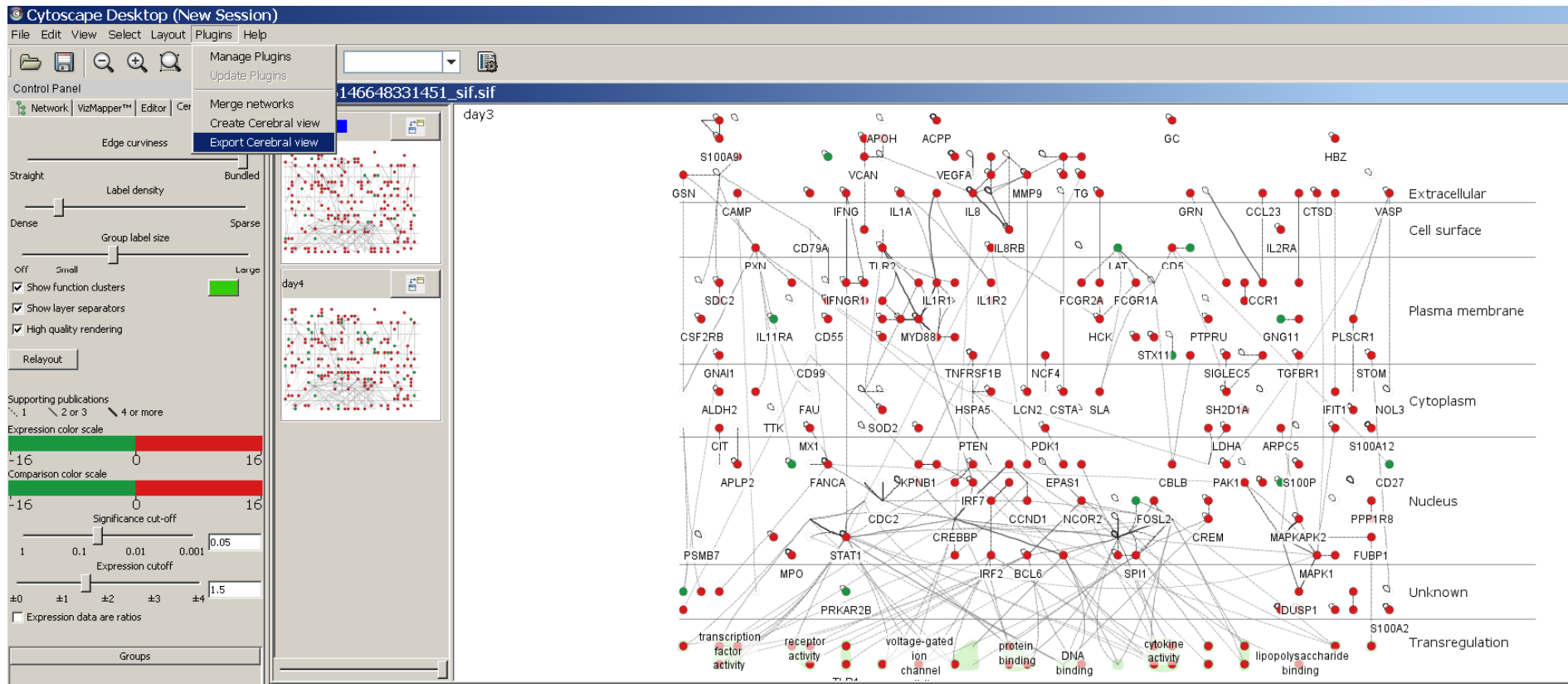
CD56G

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Interactively Link back to InnateDB to Look up Information on Particular Genes/Interactions of Interest – Right Click on a Node or an Edge.



Export an Image of the Network



The screenshot displays the Cytoscape Desktop interface for a network visualization. The window title is "Cytoscape Desktop (New Session)". The menu bar includes File, Edit, View, Select, Layout, Plugins, and Help. The Control Panel on the left contains several sections:

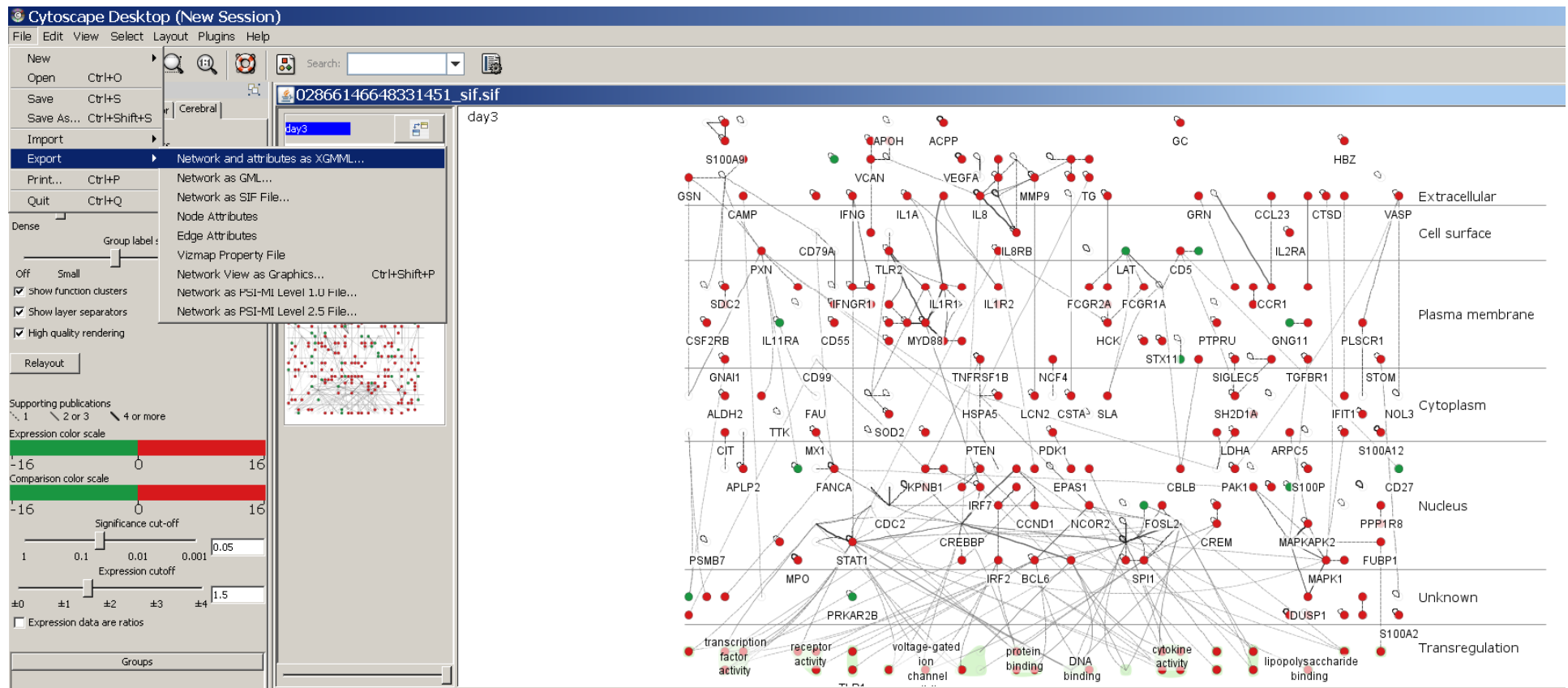
- Manage Plugins:** Includes "Update Plugins" and a search field.
- Control Panel:** Includes "Merge networks", "Create Cerebral view", and "Export Cerebral view" (highlighted).
- Edge curviness:** Sliders for "Straight" and "Bundled" styles.
- Label density:** Sliders for "Dense" and "Sparse" styles.
- Group label size:** Sliders for "Small" and "Large" styles.
- Rendering options:** Checkboxes for "Show function clusters", "Show layer separators", and "High quality rendering".
- Supporting publications:** A dropdown menu with options for 1, 2 or 3, and 4 or more.
- Expression color scale:** A horizontal scale from -16 to 16.
- Comparison color scale:** A horizontal scale from -16 to 16.
- Significance cut-off:** A slider with values 1, 0.1, 0.01, 0.001, and 0.05.
- Expression cutoff:** A slider with values ±0, ±1, ±2, ±3, and ±4.
- Expression data are ratios:** A checkbox.
- Groups:** A list of groups.

The main network graph shows a complex network of nodes and edges. The nodes are color-coded based on expression levels and are grouped into layers. The layers are labeled on the right side of the graph:

- Extracellular
- Cell surface
- Plasma membrane
- Cytoplasm
- Nucleus
- Unknown
- Transregulation

Key nodes and edges are visible, including S100A9, GSN, CAMP, IFNG, IL1A, IL8, MMP9, TG, GRN, CCL23, CTSD, VASP, CD79A, IL1R1, IL1R2, FCGR2A, FCGR1A, CCR1, IL2RA, CD55, MYD88, HCK, PTPRU, GNG11, PLSCR1, GNAI1, CD99, TNFRSF1B, NCF4, SIGLEC5, TGFBR1, STOM, ALDH2, FAU, HSPA5, LCN2, CSTA3, SLA, SH2D1A, IFIT1, NOL3, CIT, TTK, MX1, SOD2, PTEN, PDK1, LDHA, ARPC5, S100A12, APLP2, FANCA, SKPNB1, IRF7, EPAS1, CBLB, PAK1, S100P, CD27, CDC2, CREBBP, CCND1, NCOR2, FOSL2, CREM, MAPKAPK2, PPM1R8, PSMB7, STAT1, MPO, IRF2, BCL6, SPI1, MAPK1, FUBP1, PRKAR2B, and DUSP1. Functional annotations at the bottom include transcription factor activity, receptor activity, voltage-gated ion channel, protein binding, DNA binding, cytokine activity, and lipopolysaccharide binding.

Export the Graph as XGMML File to Use Later in Local Version of Cytoscape



The screenshot displays the Cytoscape Desktop interface with a network graph loaded. The 'Export' menu is open, showing options for exporting the network and its attributes as XGMML, GML, SIF, or PSI-MI Level 1.0 and 2.5 files. The graph is organized into layers representing cellular compartments: Extracellular, Cell surface, Plasma membrane, Cytoplasm, Nucleus, and Transregulation. Nodes are color-coded by expression levels, and edges represent interactions between them. The interface includes a menu bar, a toolbar, and various control panels for node and edge attributes, as well as a 'Relayout' button.