

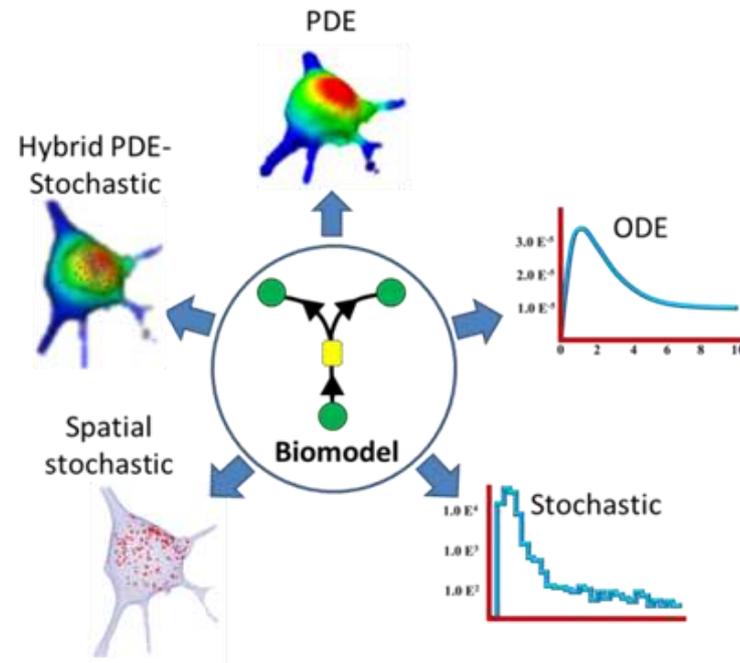
Virtual Cell Tutorials

VCell

modeling environment for
mathematical simulation of
cellular events.

To run VCell go to:

vcell.org



Virtual Cell is developed by the Center for Cell Analysis and Modeling at the University of Connecticut Health Center. It is funded as a Biomedical Technology Research Resource by the National Institute of General Medical Sciences (NIGMS)

VCell Tutorial

VCell Pathway Commons Tutorial

Using external pathway databases to construct a biomodel

In this tutorial...

- Use the database navigator to interact with pathway databases such as Biocompare.net, Pathway Commons or SabioRK
- Import pathways or components of pathways into the VCell workspace
- Edit pathway links in VCell models and annotate links
- Use tips for working with large network models in VCell

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The screenshot displays the VCell 5.3 (build 4) software interface. The main window is titled "BioModel2: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)". The interface is divided into several sections:

- Left Panel:** A tree view showing the project structure under "BioModel2". The "Physiology" folder is expanded, showing "Reaction Diagram" (highlighted in blue), "Reactions (0)", "Structures (1)", and "Species (0)". Below this are "Applications (0)", "Parameters and Functions", and "Pathway".
- Top Panel:** A toolbar with icons for "Reaction Diagram", "Reactions", "Structures", and "Species". Below these are various drawing and editing tools, including a mouse cursor, a green circle, a black arrow, a dashed line, a horizontal line, a magnifying glass, and a red cluster of dots. The text "ANN EAL" and "REL AX" is also visible.
- Main Canvas:** A large white area with the text "c0" centered on it.
- Bottom Panel:** A section for "Object Properties" and "Problems (0 Errors, 0 Warnings)". It contains a search bar and a message: "Select only one object (e.g. species, reaction, simulation) to view/edit properties."

A red box highlights the "Pathway Comm" button in the bottom-left corner of the interface. A red arrow points from this button to a yellow text box that reads: "To use the Pathways Commons database, click 'Pathway Comm'".

At the bottom left, a status bar shows "CONNECTED (tanyamiller1221)". At the bottom right, a status bar shows "70.3MB / 103.3MB".

The screenshot shows the BioModel2 application window. The title bar reads "BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)". The interface includes a menu bar (File, View, Server, Tools, Help), a left-hand tree view for "BioModel2" with sub-items like "Physiology", "Reaction Diagram", "Reactions (0)", "Structures (1)", "Species (0)", "Applications (0)", "Parameters and Functions", and "Pathway". The main workspace is titled "Reaction Diagram" and contains a single object labeled "c0". A toolbar with various icons is positioned above the workspace. At the bottom, there is a search panel with a text input field containing "egfr" and a "Search" button. Below the search panel is a list of search results, including "a6b 1 and a6b4 Integrin signaling", "Alpha6Beta4Integrin", "Alpha9 beta 1 integrin signaling events", "Arf6 downstream pathway", "Arf6 signaling events", "Arf6 trafficking events", "ATM pathway", "ATR signaling pathway", and "Axon guidance". A yellow callout box with a red border points to the search panel, containing the text: "To search Pathway Commons, type 'egfr' under Search and click 'Search'". The bottom status bar shows "CONNECTED (tanyamiller1221)" and "58MB / 145.9MB".

To search Pathway Commons, type "egfr" under Search and click "Search".

The screenshot shows the VCell 5.3 (build 4) interface. The main window displays a reaction diagram with a single species 'c0'. The left sidebar shows a tree view of the model structure, including 'Physiology', 'Reaction Diagram', 'Reactions (0)', 'Structures (1)', 'Species (0)', 'Applications (0)', 'Parameters and Functions', and 'Pathway'. Below the sidebar is a search bar with 'egfr' entered and a search button. A search result is displayed: 'Signaling by EGFR [Reactome, Homo sapiens]'. At the bottom left, a 'Filter' section is highlighted with a red box, containing a text input field with 'signaling by E' and a 'Sort' button. A yellow callout box with a red border and arrow points to the 'Sort' button, containing the text: 'To filter your search, type "signalling by egfr" under Filter and VCell will automatically search all names within Pathway Commons.' The bottom status bar shows 'CONNECTED (tanyamiller1221)' and '48.5MB / 107.5MB'.

To filter your search, type "signalling by egfr" under Filter and VCell will automatically search all names within Pathway Commons.

The screenshot shows the VCell 5.3 (build 4) interface. The main window displays a reaction diagram with a single species 'c0'. The left sidebar shows a tree view for 'BioModel2' with 'Physiology' expanded to 'Reaction Diagram'. Below the sidebar is a search bar with 'egfr' entered and a search button. The search results show 'Signaling by EGF' with a link to '[Reactome, Homo sapiens]'. A red box highlights this link, and a red arrow points to it from a yellow text box. The bottom status bar shows 'CONNECTED (tanyamiller1221)' and '58.1MB / 107.5MB'.

File View Server Tools Help

BioModel2

Physiology

- Reaction Diagram
- Reactions (0)
- Structures (1)
- Species (0)
- Applications (0)
- Parameters and Functions
- Pathway

VCCell DB BioModels.net Pathway Comm

Search

egfr Search

Signaling by EGF [Reactome, Homo sapiens]

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

Select only one object (e.g. species, reaction, simulation) to view/edit properties.

Filter

signaling by E Sort

Preview Open Web Link

CONNECTED (tanyamiller1221) 58.1MB / 107.5MB

The green text tells you where the pathway comes from and the red text tells you what species the pathway occurs in.

The screenshot displays the VCell 5.3 (build 4) interface. The main window shows a reaction diagram with a single species 'c0'. On the left, a tree view under 'BioModel2' shows 'Physiology' expanded to 'Reaction Diagram'. Below this, a search bar contains 'egfr' and a search button. A search result is highlighted: 'Signaling by EGFR [Reactome, Homo sapiens]'. A red box highlights this result, and a red arrow points from it to a yellow callout box. The callout box contains the text: 'To learn more information about a pathway, click the pathway and "Open Web Link".' Below the search results, there is a 'Filter' section with 'signaling by E' and a 'Sort' dropdown. At the bottom of the search results, there are 'Preview' and 'Open Web Link' buttons. The 'Open Web Link' button is highlighted with a red box. The status bar at the bottom shows 'CONNECTED (tanyamiller1221)' and '59.6MB / 107.5MB'.

Pathway Commons:Signa x

www.pathwaycommons.org/pc/record2.do?id=485564

Find Pathways Find Molecules

Search

Current filters: All Organisms. All Data Sources. Set filters.

Home Data Sources Download FAQ Web Service About

Send us your [feedback](#). Sign up for Pathway Commons [announcements](#). [RSS](#)

Data Source:

- Reactome, Release: 38 [20-Sep-11]



Organism:

- Homo sapiens

Synonyms:

- Epidermal Growth Factor Receptor (EGFR) signaling

Cytoscape:

 [View in Cytoscape](#)

Links:

- GO: 0007173
- Reactome: REACT_9417

Pathway: Signaling by EGFR

Reviewed: Muthuswamy, S, Heldin, CH, 2008-02-28 15:20:51 [more...](#)

[Biochemical Reactions \(5\)](#) [Catalysis Reactions \(3\)](#) [Sub-Pathways \(5\)](#) [Molecules \(216\)](#)

Showing 1-5 of 5

- EGF_HUMAN (in plasma membrane) (chain coordinates ^) → EGF_HUMAN (in extracellular region) (chain coordinates ^)
 - CATALYZED by ADAM:Zn2+
- EGF:EGFR dimer + ATP → EGF:p-6Y-EGFR + ADP
 - CATALYZED by SRC (chain coordinates ^)
- EGF:EGFR dimer + ATP → ADP + EGF:p-6Y-EGFR
 - CATALYZED by EGF:EGFR dimer
- EGF:EGFR → EGF:EGFR dimer
- EGFR_HUMAN (chain coordinates ^) + EGF_HUMAN (chain coordinates ^) → EGF:EGFR

Your internet browser will open to the online Pathway Commons database, where you can read resources about specific reactions, pathways and molecules within a particular pathway.

The screenshot shows the VCell 5.3 (build 4) interface. The main window is titled "BioModel2: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)". The left sidebar shows a tree view under "BioModel2" with "Physiology" expanded to show "Reaction Diagram" selected. Below this is a search bar with "egfr" entered and a "Search" button. A search result "Signaling by EGFR [Reactome, Homo sapiens]" is highlighted with a red box. A yellow callout box with a red border points to this result and contains the text: "To begin the process of importing a pathway, click on a pathway and click 'Preview'". Below the search results is a "Filter" section with "signaling by E" and a "Sort" dropdown. At the bottom of the search results, a "Preview" button is highlighted with a red box. The main workspace shows a "Reaction Diagram" tab with a toolbar and a central area containing the text "c0". The bottom status bar shows "CONNECTED (tanyamiller1221)" and "63.4MB / 107.5MB".

To begin the process of importing a pathway, click on a pathway and click "Preview".

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram**
 - Reactions (0)
 - Structures (1)
 - Species (0)
- Applications (0)
- Parameters and Functions
- Pathway

Reaction Diagram | Reactions | Structures | Species

ANN EAL REL AX

c0

Search: egfr

Signaling by EGFR [Reactome, Homo sapiens]

Filter: signaling by E|

Preview | Open Web Link

Object Properties | Problems (0 Errors, 0 Warnings) | Pathway Preview

Signaling by EGFR

Entity Name	Type	Imported?
Active PLC-gamma1 dissociates from EGFR	biochemical reaction	<input type="checkbox"/>
Sustained activation of SRC kinase by SHP2	biochemical reaction	<input type="checkbox"/>
PKA phosphorylates CREB	biochemical reaction	<input type="checkbox"/>
CBL escapes CDC42-mediated inhibition by down-regulating the adaptor molecule Beta-Pix	biochemical reaction	<input type="checkbox"/>
CaMK IV phosphorylates CREB	biochemical reaction	<input type="checkbox"/>
EGFR_non-clathrin mediated endocytosis	biochemical reaction	<input type="checkbox"/>

1 - 200 of 319

Search: Import

CONNECTED (tanyamiller1221)

94.1MB / 119.5MB

To filter entities by type, click "Type".

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram**
 - Reactions (0)
 - Structures (1)
 - Species (0)
- Applications (0)
- Parameters and Functions
- Pathway

VCCell DB BioModels.net Pathway Comm

Search
egfr Search

Signaling by EGFR [Reactome, Homo sapiens]

Filter
signaling by E Sort

Preview Open Web Link

Reaction Diagram Reactions Structures Species

ANN EAL REL AX

c0

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Signaling by EGFR

Entity Name	Type	Imported?
CBL binds to GRB2	biochemical reaction	<input type="checkbox"/>

To search for a specific entity, type the name of the entity in the Search box. In this example type "CBL binds to"

Search CBL binds to Import

CONNECTED (tanyamiller1221) 66.1MB 133.7MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram**
 - Reactions (0)
 - Structures (1)
 - Species (0)
- Applications (0)
- Parameters and Functions
- Pathway

VCCell DB BioModels.net Pathway Comm

Search: egfr

Signaling by EGFR [Reactome, Homo sapiens]

Filter: signaling by E

Preview Open Web Link

Reaction Diagram Reactions Structures Species

c0

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Signaling by EGFR

Entity Name	Type	Imported?
CBL binds to GRB2	biochemical reaction	<input type="checkbox"/>

Search: CBL binds to

Import

CONNECTED (tanyamiller1221) 72.4MB / 33.7MB

To import specific entities, click the entities and click "Import" > "Selected Only".

The screenshot displays the BioModel2 application window. The main area shows a pathway diagram with nodes labeled CBL:GRB2, GRB2, and CBL_HUMAN. A red box highlights the 'Pathway Diagram' option in the left-hand navigation tree. A yellow callout box with a red border points to this option and contains the text: "To view imported pathways, click 'Pathway Diagram'". Below the navigation tree is a search panel with the text 'egfr' and a search button. The search results show 'Signaling by EGFR [Reactome, Homo sapiens]'. At the bottom of the window, there is a status bar showing 'CONNECTED (tanyamiller1221)' and a memory usage indicator '77.6MB / 133.7MB'.

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (1)
 - Species (0)
- Applications (0)
- Parameters and Functions
- Pathway
 - Pathway Diagram**
 - Pathway Objects (4)
 - BioPAX Summary

Pathway Diagram Pathway Objects BioPAX Summary BioPAX Tree

CBL:GRB2 GRB2 CBL_HUMAN

To view imported pathways, click "Pathway Diagram".

Search

egfr Search

Signaling by EGFR [Reactome, Homo sapiens]

Filter

signaling by E Sort

Preview Open Web Link

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Select only one object (e.g. species, reaction, simulation) to view/edit properties.

CONNECTED (tanyamiller1221) 77.6MB / 133.7MB

To reorganize the pathway layout, click one of the layout icons.

The screenshot displays the BioModel2 software interface. On the left is a navigation tree with categories like Physiology, Applications, and Pathway. The main window shows a pathway diagram with nodes GRB2, CBL_HUMAN, and CBL:GRB2, and a reaction labeled 'CBL binds to GRB2'. A toolbar above the diagram contains layout icons: a magnifying glass, a square, a circle, a triangle, a diamond, and a hexagon. A red box highlights these icons, with a red arrow pointing to the text box above. Below the diagram are buttons for 'Group', 'Delete', and 'Physiology Links'. At the bottom, there is a search bar with 'egfr' and a 'Search' button, and a 'Filter' section with 'signaling by E' and a 'Sort' dropdown. The status bar at the bottom shows 'CONNECTED (tanyamiller1221)' and '91.5MB / 133.7MB'.

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (1)
 - Species (0)
- Applications (0)
- Parameters and Functions
- Pathway
 - Pathway Diagram
 - Pathway Objects (4)
 - BioPAX Summary

Pathway Diagram | Pathway Objects | BioPAX Summary | BioPAX Tree

To view information on a specific entity, click on the entity and view "Object Properties".

VCCell DB | BioModels.net | Pathway Comm

Search: egfr [Search]

Signaling by EGFR [Reactome, Homo sapiens]

Group | Delete | Physiology Links | Search

Object Properties | Problems (0 Errors, 0 Warnings) | Pathway Preview

Property	Value
Type	protein
Name	GRB2 (double-click lookup)
Role(s)	Participant
Comment	DOMAIN The SH3 domains mediate interaction with RALGPS1 and S...
Xref	UNIPROT:P62993-1
Xref	CPATH:504167

CONNECTED (tanyamiller1221) 70.5MB / 134.2MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (1)
 - Species (0)
- Applications (0)
- Parameters and Functions
- Pathway
 - Pathway Diagram**
 - Pathway Objects (4)
 - BioPAX Summary

VCell DB BioModels.net Pathway Comm

Search

egfr Search

Signaling by EGFR [Reactome, Homo sapiens]

Filter

signaling by E Sort

Preview Open Web Link

CONNECTED (tanyamiller1221)

76.8MB / 134.2MB

Pathway Diagram Pathway Objects BioPAX Summary BioPAX Tree

GRB2 CBL binds to GRB2 CBL_HUMAN CBL:GRB2

To select all entities within a pathway, click a corner of the diagram. Drag your cursor over all entities and release your cursor to finalize.

Select only one object (e.g. species, reaction, simulation) to view/edit properties.

The screenshot displays the BioModel2 software interface. The main window shows a pathway diagram with three nodes: GRB2, CBL_HUMAN, and CBL:GRB2. The relationship is labeled "CBL binds to GRB2". The interface includes a left sidebar with a tree view of the model's structure, a search bar, and a filter section. A context menu is open over the "Physiology Links" button, with the "Import into Physiology..." option highlighted. A yellow callout box with a red border points to the "Physiology Links" button and the "Import into Physiology..." option.

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (1)
 - Species (0)
- Applications (0)
- Parameters and Functions
- Pathway
 - Pathway Diagram
 - Pathway Objects (4)
 - BioPAX Summary

Pathway Diagram Pathway Objects BioPAX Summary BioPAX Tree

GRB2 CBL_HUMAN CBL binds to GRB2 CBL:GRB2

VCCell DB BioModels.net Pathway Comm

Search egfr Search

Group Delete Physiology Links Search

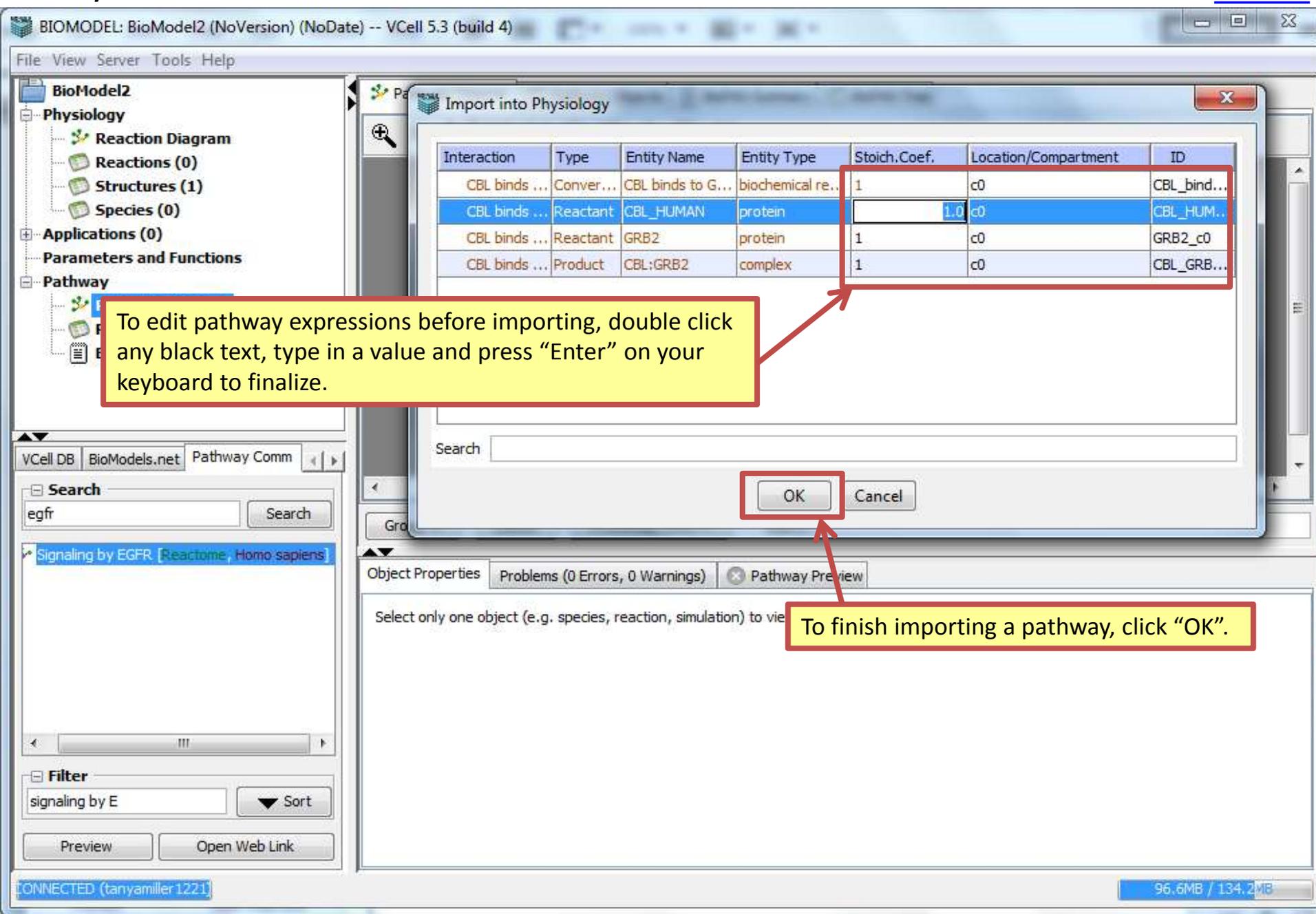
- Show Linked Physiology Objects
- Edit Physiology Links...
- Import into Physiology...

Click "Physiology Links" > "Import into Physiology".

Filter signaling by E Sort

Preview Open Web Link

CONNECTED (tanyamiller1221) 89.9MB / 134.2MB



To edit pathway expressions before importing, double click any black text, type in a value and press "Enter" on your keyboard to finalize.

To finish importing a pathway, click "OK".

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram
 - Reactions (1)
 - Structures (1)
 - Species (3)
- Applications (0)
- Parameters and Functions
- Pathway
 - Pathway Diagram
 - Pathway Objects (4)
 - BioPAX Summary

Pathway Diagram Pathway Objects BioPAX Summary BioPAX Tree

Info

The following pathway object(s) have been covered in the physiology model:

- Reaction: 'CBL_binds_to_GRB2_c0'
- Species: 'CBL_GRB2_c0'
- Species: 'GRB2_c0'
- Species: 'CBL_HUMAN_c0'

VCell will automatically inform you of which pathway objects you have imported into your physiology. Click "OK".

OK

Search egfr Search

Signaling by EGFR [Reactome, Homo sapiens]

Group Delete Physiology Links Search

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Select only one object (e.g. species, reaction, simulation) to view/edit properties.

CONNECTED (tanyamiller1221)

97.2MB / 134.2MB

The screenshot displays the BioModel2 software interface. On the left, a tree view shows the project structure under 'BioModel2', with 'Pathway Objects (4)' selected. The main window shows a reaction diagram with a species 'CBL_GRB2_c0' highlighted by a red box. Below the diagram, the 'Object Properties' panel is open, showing the 'Species Name' as 'CBL_GRB2_c0' and 'Linked Pathway Object(s)' as 'CBL:GRB2', which is also highlighted by a red box. A yellow callout box with a red border contains the text: 'To return to a pathway object, click on a specific species and double-click the link next to "Linked Pathway Objects"'. A red arrow points from this callout to the 'CBL:GRB2' link in the 'Object Properties' panel. The top of the window shows the title bar 'BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)' and a menu bar with 'File View Server Tools Help'. The bottom status bar shows 'CONNECTED (tanyamiller1221)' and '75MB / 41MB'.

To return to a pathway object, click on a specific species and double-click the link next to "Linked Pathway Objects"

Linked Pathway Object(s) [CBL:GRB2](#)

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram**
 - Reactions (1)
 - Structures (1)
 - Species (4)
- Applicat
- Parame
- Pathway
 - p
 - Pathway Objects (4)
 - BioPAX Summary

Reaction Diagram Reactions Structures Species

To add a species, click the species tool and double click on any point within the compartment.

c0

CBL_HUMAN_c0
CBL_GRB2_c0
GRB2_c0

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Species Name s3

Linked Pathway Object(s)

Annotation

Preview Open Web Link

CONNECTED (tanyamiller1221) 78.4MB / 141MB

The screenshot displays the BioModel2 software interface. On the left, a tree view shows the project structure under 'BioModel2', including 'Physiology', 'Reaction Diagram', 'Reactions (1)', 'Structures (1)', 'Species (4)', 'Applications (0)', 'Parameters and Functions', and 'Pathway'. The 'Pathway' section is expanded, showing 'Pathway Diagram', 'Pathway Objects (4)', and 'BioPAX Summary'. The main window shows a 'Reaction Diagram' with a toolbar and a central workspace. A red box highlights a species icon labeled 's3' in the workspace. A yellow callout box with a red border points to this icon, containing the text: "To add species to a pathway, click on a specific species. Click 'Pathway Links' > 'Edit Pathway Links...'" Below the workspace, a 'Pathway Links' dropdown menu is open, and a red box highlights the 'Edit Pathway Links...' option. The dialog box below shows fields for 'Species name' (containing 's3'), 'Linked Pathway Object(s)', and 'Annotation'. At the bottom left, a status bar shows 'CONNECTED (tanyamiller1221)' and at the bottom right, it shows '81.7MB / 41MB'.

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram
 - Reactions (1)
 - Structures (1)
 - Species (4)
- Applications (0)
- Parameters and Functions
- Pathway
 - Pathway Diagram
 - Pathway Objects (4)
 - BioPAX Summary

Reaction Diagram Reactions Structures Species

c0

s3

CBL_HUMA

To add species to a pathway, click on a specific species. Click "Pathway Links" > "Edit Pathway Links..."

VCCell DB BioModels.net Pathway Comm

Search egfr Search

Signaling by EGFR [Reactome, Homo sapiens]

Delete Pathway Links

Show Linked Pathway Objects

Edit Pathway Links...

Pathway Preview

Object Properties

Species name s3

Linked Pathway Object(s)

Annotation

Preview Open Web Link

CONNECTED (tanyamiller1221)

81.7MB / 41MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram
 - Reactions (1)
 - Structures (1)
- BioPAX Summary

VCCell DB BioModels.net Pathway Comm

Search: egfr Search

Signaling by EGFR [Reactome, Homo sapiens]

Filter: signaling by E Sort

Preview Open Web Link

CONNECTED (tanyamiller1221) 31.1MB / 143.7MB

Reaction Diagram

Edit Pathway Links

Edit pathway links by checking or unchecking the Link boxes.

Link	Entity Name	Type
<input type="checkbox"/>	CBL:GRB2	complex
<input checked="" type="checkbox"/>	GRB2	protein
<input type="checkbox"/>	CBL_HUMAN	protein

Search Show linked pathway entities only

Delete Pa

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Species Name s3

Linked Pathway Object(s)

Annotation

Close

To link a species to an entity in the imported pathway, click a box in the "Link" column, next to the entity's name.

To finish linking a species to a pathway, click "Close".

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram
 - Reactions (1)
 - Structures (1)
 - Species (4)
- Applications (0)
- Parameters and Functions
- Pathway
 - Pathway Diagram
 - Pathway Objects (4)
 - BioPAX Summary

VCCell DB BioModels.net Pathway Comm

Search: egfr

Signaling by EGFR [Reactome, Homo sapiens]

Reaction Diagram

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Signaling by EGFR

Entity Name	Type	Imported?
	biochemical reaction	<input type="checkbox"/>
	biochemical reaction	<input type="checkbox"/>
	biochemical reaction	<input type="checkbox"/>
SOS1-mediated nucleotide exchange of RAS (EGF:EGFR:SHC1:GRB2:SOS1)	biochemical reaction	<input type="checkbox"/>
Phosphorylation of CREB by CaMKIV	biochemical reaction	<input type="checkbox"/>
Binding of GRB2 to GAB1	biochemical reaction	<input type="checkbox"/>

Search:

Import

CONNECTED (tanyamiller1221) 59MB / 143.7MB

To begin importing an entire pathway, go to the Pathway Preview pane and clear "Search" of any text.

Search

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram
 - Reactions (1)
 - Structures (1)
 - Species (4)
- Applications (0)
- Parameters and Functions
- Pathway
 - Pathway Diagram
 - Pathway Objects (4)
 - BioPAX Summary

Reaction Diagram Reactions Structures Species

ANN EAL REL AX

c0

s3

CBL_HUMAN_c0

CBL_GRB2 GRB2_c0

VCeLl DB BioModels.net Pathway Comm

Search
egfr

Signaling by EGFR [Reactions, Homo sapiens]

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Signaling by EGFR

Entity Name	Type	Imported?
RAF1 phosphorylates MEK1	biochemical reaction	<input type="checkbox"/>
CBL ubiquitinates Sprouty	biochemical reaction	<input type="checkbox"/>
Dephosphorylation of PAG by SHP2	biochemical reaction	<input type="checkbox"/>
SOS1-mediated nucleotide exchange of RAS (EGF:EGFR:SHC1:GRB2:SOS1)	biochemical reaction	<input type="checkbox"/>
Phosphorylation of CREB by CaMKIV	biochemical reaction	<input type="checkbox"/>
Binding of GRB2 to GAB1	biochemical reaction	<input type="checkbox"/>

1 - 200 of 319

Search

Preview Open Web Link

Import ▾

CONNECTED (tanyamiller1221)

68.5MB / 143.7MB

To select all entities on a page, press "ctrl" and "a" at the same time on your keyboard.

To import entities, click "Import" > "Selected Only".

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram
 - Reactions (1)
 - Structures (1)
 - Species (4)
- Applications (0)
- Parameters and Functions
- Pathway
 - Pathway Diagram**
 - Pathway Objects (334)
 - BioPAX Summary

Pathway Diagram Pathway Objects BioPAX Summary BioPAX Tree

EGF:EGFR dimer, inositol-3,4,5-trisphosphate, the binding to phospho-Gab1, CDC42:GTP, Sprouty, Calmodulin activates Cam-PDE 1, p21 RAS:GTP, AKT cap, phospho-ERK-1:MEK1, EGF:p-6Y-EGFR:GRB2, PAG1_HUMAN, MEK2:ERK-2, Iophillin:Epsin:Eps15R:Eps15, Protein Kinase A, catalytic subunits [nucleoplasm], MEK2 phosphorylates ERK-2, Adenylate cyclase, IP3 receptor homotetramer, GAB1, G-beta-gamma, Phospho-CBL:GRB2, PHLP dephosphorylates S473, p-CDK inhibitor [cytosol], LST8_HUMAN, HGS_HUMAN, CBL_HUMAN, GAB1_HUMAN, CDK1_HUMAN

Search: egfr

Signaling by EGFR [Reactome, Homo sapiens]

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Signaling by EGFR

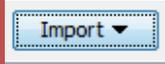
Entity Name	Type	Imported?
p-CDK inhibitor [cytosol]	protein	<input type="checkbox"/>
LST8_HUMAN	protein	<input type="checkbox"/>
HGS_HUMAN	protein	<input type="checkbox"/>
CBL_HUMAN	protein	<input type="checkbox"/>
GAB1_HUMAN	protein	<input type="checkbox"/>
CDK1_HUMAN	protein	<input type="checkbox"/>

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Import

CONNECTED (tanyamiller1221) 169.8MB / 267.4MB

If a pathway is extends to multiple pages, go back to the preview pane, click the right arrow icon to view the next page. Click within list and again press "ctrl" and "a" on your keyboard and click "Import" > "Selected Only".



BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

To view all pathway entities in list form, click "Pathway Objects".

Pathway Diagram | **Pathway Objects** | BioPAX Summary | BioPAX Tree

Pathway Entity	Type	Linked Physiology Objects
EGF:p-6Y-EGFR:GRB2:GAB1	complex	
CBL:SPRY1/2	complex	
EGF:p-6Y-EGFR:p-Y371-CBL:GRB2:CI...	complex	
Dimerisation of phospho-ERK-2	biochemical reaction	
STAM [cytosol]	protein	
Active PLC-gamma1 dissociates from E...	biochemical reaction	
phospho-CaMK IV:Calmodulin	complex	
Magnesium	small molecule	
EGF:p-6Y-EGFR:GRB2:p-Y627,659-GA...	complex	
3',5'-Cyclic AMP	small molecule	
AP2B1_HUMAN	protein	
Sprouty lures cytosolic CBL away from...	biochemical reaction	

1 - 200 of 319

Group Delete Physiology Links Search

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Select only one object (e.g. species, reaction, simulation) to view/edit properties.

CONNECTED (tanyamiller1221) 167.8MB / 397.4MB

To view all pathway entities in list form, click "Pathway Objects".

Pathway Objects

- Structures (1)
- Species (4)
- Applications (0)
- Parameters and Functions
- Pathway
 - Pathway Diagram
 - Pathway Objects (369)**
 - BioPAX Summary

VCell DB BioModels.net Pathway Comm

Search egfr Search

Signaling by EGFR [Reactome, Homo sapiens]

Filter signaling by E Sort

Preview Open Web Link

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram
 - Reactions (1)
 - Structures (1)
 - Species (4)
- Applications (0)
- Parameters and Functions
- Pathway
 - Pathway Diagram
 - Pathway Objects (369)
 - BioPAX Summary

Pathway Diagram Pathway Objects BioPAX Summary BioPAX Tree

Pathway Entity	Type	Linked Physiology Objects
CBL binds and ubiquitinates phosphoryl...	biochemical reaction	
CBL binds to GRB2	biochemical reaction	Reaction:CBL_binds_to_GRB2_c0;

VCell DB BioModels.net Pathway Comm

Search
 egfr

Signaling by EGFR [Reactome, Homo

To search for a specific pathway entity, type in the name of the object next to "Search".

Pathway Preview

Select only one object (e.g. species, reaction, simulation) to view/edit properties.

Filter: signaling by E

CONNECTED (tanyamiller1221) 175.7MB / 397.4MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram
 - Reactions (1)
 - Structures (1)
 - Species (4)

Pathway Diagram Pathway Objects BioPAX Summary BioPAX Tree

Pathway Entity	Type	Linked Physiology Objects
EGF:p-6Y-EGFR:GRB2:GAB1	complex	
CBL:SPRY1/2	complex	
EGF:p-6Y-EGFR:p-Y371-CBL:GRB2:CI...	complex	
Dimerisation of phospho-ERK-2	biochemical reaction	
STAM [cytosol]	protein	
Active PLC-gamma1 dissociates from E...	biochemical reaction	
phospho-CaMK IV:Calmodulin	complex	
Magnesium	small molecule	
EGF:p-6Y-EGFR:GRB2:p-Y627,659-GA...	complex	
3',5'-Cyclic AMP	small molecule	
AP2B1_HUMAN	protein	
Sprouty lures cytosolic CBL away from...	biochemical reaction	

1 - 200 of 319

Search egfr Search

Group Delete Physiology Links Search

- Show Linked Physiology Objects
- Edit Physiology Links
- Import into Physiology...

Filter signaling by E Sort

Preview Open Web Link

CONNECTED (tanyamiller1221) 185.5MB / 397.4MB

To select all pathway entities on a page, press "ctrl" and "a" on your keyboard at the same time.

To import pathway entities into your physiology, click "Physiology Links" > "Import into Physiology..."

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram
 - Reactions (1)
 - Structures (1)
 - Species (4)
- Applications (0)
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 - Pathway Diagram
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VCell DB BioModels.net Pathway Comm

Search: egfr Search

Signaling by EGFR [Reactome, Homo sapiens]

Filter: signaling by E Sort

Preview Open Web Link

CONNECTED (tanyamiller1221) 205.7MB 397.4MB

Pathway Diagram Pathway Objects BioPAX Summary BioPAX Tree

Pathway Entity	Type	Linked Physiology Objects
EGF:p-6Y-EGFR:GRB2:GAB1	complex	
CBL:SPRY1/2	complex	
EGF:p-6Y-EGFR:p-Y371-CBL:GRB2:CI...	complex	
Dimerisation of phospho-ERK-2	biochemical reaction	
STAM [cytosol]	protein	
Active PLC-gamma1 dissociates from E...	biochemical reaction	

Warning:

 The following pathway object(s) have been associated with object(s) in the physiology model:

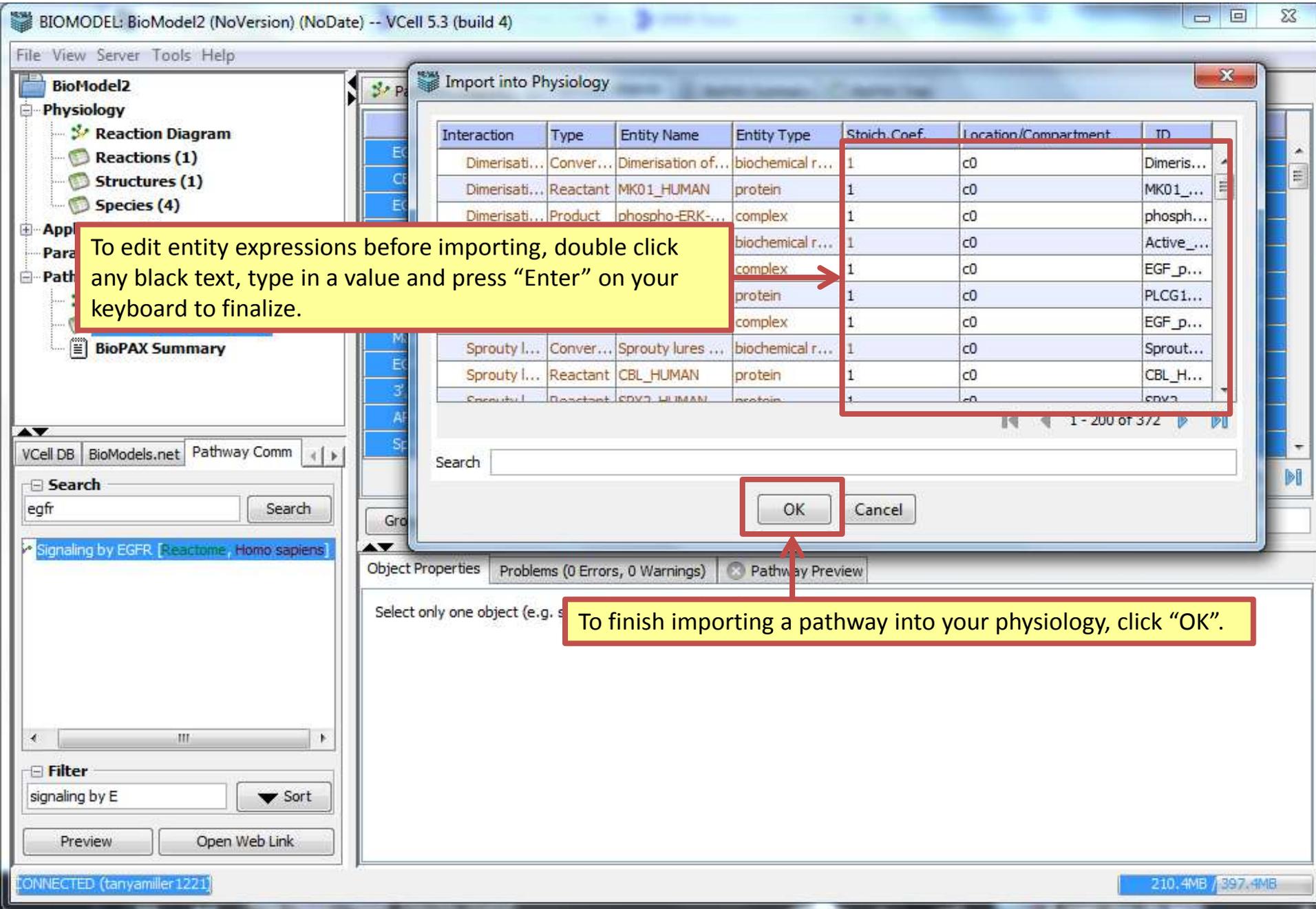
Species: 'CBL_HUMAN' =>
=> 'CBL_HUMAN_c0'

Reaction: 'CBL binds to GRB2' =>
=> 'CBL_binds_to_GRB2_c0'

They will NOT be converted to the physiology model.

OK

VCell will automatically notify you if anything you have selected to import into your physiology has already been imported. Click "OK".



BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram
 - Reactions (68)
 - Structures (1)
 - Species (172)
- Applications (0)
- Parameters and Functions
- Pathway
 - Pathway Diagram
 - Pathway Object
 - BioPAX Summary

Pathway Diagram Pathway Objects BioPAX Summary BioPAX Tree

Pathway Entity	Type	Linked Physiology Objects
EGF:p-6Y-EGFR:GRB2:GAB1	complex	
CBL:SPRY1/2	complex	

Info

The following pathway object(s) have been covered in the physiology model:

- Species: 'EGF_p_6Y_EGFR_GRB2_GAB1_c0'
- Species: 'CBL_SPRY1_2_c0'
- Species: 'EGF_p_6Y_EGFR_p_Y371_CBL_GRB2_CIN85_Endophilin_Epsin_Eps15R_c0'
- Reaction: 'Dimerisation_of_phospho_ERK_2_c0'
- Species: 'STAM_cytosol_c0'
- Reaction: 'Active_PLC_gamma1_dissociates_from_EGFR_c0'
- Species: 'phospho_CaMK_IV_Calmodulin_c0'
- Species: 'Magnesium_c0'
- Species: 'EGF_p_6Y_EGFR_GRB2_p_Y627_659_GAB1_SHP2_c0'
- Species: '_3_5_Cyclic_AMP_c0'
- Species: 'AP2B1_HUMAN_c0'
- Reaction: 'Sprouty_lures_cytosolic_CBL_away_from_EGFR_c0'
- Species: 'PXN_CSK_SRC_c0'

OK

VCell will automatically notify you of what species and reactions have been successfully imported into your physiology model. Click "OK".

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CONNECTED (tanyamiller1221)

210.4MB / 397.4MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram
 - Reactions (68)
 - Structures (1)
 - Species (172)
- Applications (0)
- Parameters and Functions
- Pathway
 - Pathway Diagram
 - Pathway Objects (369)**
 - BioPAX Summary

Pathway Diagram | **Pathway Objects** | BioPAX Summary | BioPAX Tree

Pathway Entity	Type	Linked Physiology Objects
AKT phosphorylates caspase-9	biochemical reaction	
AKT can phosphorylate NUR77	biochemical reaction	
phospho-ERK-1 dimer	complex	Species:phospho_ERK_1_dimer_c0;
AKT can phosphorylate forkhead box t...	biochemical reaction	
AKT phosphorylates MDM2	biochemical reaction	
EGF:p-6Y-EGFR:p-Y371-CBL:GRB2	complex	Species:EGF_p_6Y_EGFR_p_Y371_CBL_GRB2_c0;
KCC4_HUMAN	protein	Species:KCC4_HUMAN_c0;
Activated RAF1 complex	complex	Species:Activated_RAF1_complex_c0;
MTOR_HUMAN	protein	
Nuclear translocation of phospho-ERK...	biochemical reaction	
RAF1 phosphorylates MEK2	biochemical reaction	
EGFR_HUMAN	protein	Species:EGFR_HUMAN_c0;

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Group Delete **Physiology Links** Search

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

CONNECTED (tanyamiller1221) 203MB / 410MB

If a pathway extends to multiple pages, go back to the Pathway Objects view, and click the right arrow icon to view the next page. Press "ctrl" and "a" on your keyboard and click "Physiology Links" > "Import into Physiology..."

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
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 - Reactions (109)**
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VCell DB BioModels.net Pathway Comm

Search: egfr Search

Signaling by EGFR [Reactome, Homo sapiens]

Filter: signaling by E Sort

Preview Open Web Link

CONNECTED (tanyamiller1221) 207.2MB / 416.3MB

Reaction Diagram Reactions Structures

To view your physiology's reactions in list form, click "Reactions".

EGF_p_6Y_EGFR_p_Y371_CBL_CIN85_Endophilin_epsin..._p_6Y_EGFR_p_Y371_CBL_CIN85_Endophilin_epsin...

2ATP_c0 + KS6B2_HUMAN_c0 -> KS6B2_HUMAN_c0 + 2ADP_c0

CBL_HUMAN_c0 + EGF_p_6Y_EGFR_c0 -> EGF_p_6Y_EGFR_CBL_c0

p21_RAS_GTP_c0 + p_Raf1_S259_S621_14_3_3_protein_beta_alpha_c0 -> RAS_RAF_c0 + _1433B_HUMAN_c0

2ATP_c0 + AKTS1_HUMAN_c0 -> 2ADP_c0 + AKTS1_HUMAN_c0

Calmodulin_CaMK_IV_c0 -> Calmodulin_CaMK_IV_c0

EGF_p_6Y_EGFR_p_Y371_CBL_GRB2_c0 + CIN85_Endophilin_c0 -> EGF_p_6Y_EGFR_p_Y371_CBL_GRB2_CIN85_Endophilin_c0

EGF_EGFR_dimer_c0 + 12ATP_c0 -> 12ADP_c0 + EGF_p_6Y_EGFR_c0

THEM4_HUMAN_c0 + TRIB3_HUMAN_c0 + AKT_plasma_membrane_c0 -> AKT_CTMP_TRIB3_c0

_1_phosphatidyl_1D_myoinositol_3_4_5_trisphosphate_c0 + GRB2_GAB1_c0 -> GRB2_GAB1_PIP3_c0

EGF_EGFR_dimer_c0 + 12ATP_c0 -> EGF_p_6Y_EGFR_c0 + 12ADP_c0

SPY2_HUMAN_c0 + CBL_HUMAN_c0 -> CBL_SPRY1_2_c0

CREB1_HUMAN_c0 -> phospho_CREB_dimer_c0

Add New Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Select only one object (e.g. species, reaction, simulation) to view/edit properties.

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

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 - BioPAX Summary

Reaction Diagram Reactions Structures Species

EGF_p_6Y_EGFR_p_1371_CBL_CIN85_Endophilin_epsin_eps15R_eps15 + SPRK1_1_2_plasma_membrane_c0 -> EGF_p_6Y_EGFR_p_1371

2ATP_c0 + KS6B2_HUMAN_c0 -> KS6B2_HUMAN_c0 + 2ADP_c0

CBL_HUMAN_c0 + EGF_p_6Y_EGFR_c0 -> EGF_p_6Y_EGFR_CBL_c0

p21_RAS_GTP_c0 + p_Raf1_S259_S621_14_3_3_protein_beta_alpha_c0 -> RAS_RAF_c0 + _1433B_HUMAN_c0

2ATP_c0 + AKTS1_HUMAN_c0 -> 2ADP_c0 + AKTS1_HUMAN_c0

Calmodulin_CaMK_IV_c0 -> Calmodulin_CaMK_IV_c0

EGF_p_6Y_EGFR_p_Y371_CBL_GRB2_c0 + CTN85_Endophilin_c0 -> EGF_p_6Y_EGFR_p_Y371_CBL_GRB2_CTN85_Endophilin_c0

EGF_EGFR_dimer_c0 + 12ATP_c0 -> 12ADP_c0 + EGF_p_6Y_EGFR_c0

TRIM4_HUMAN_c0 + TRIB3_HUMAN_c0 + AKT_plasma_membrane_c0 -> AKT_CITMP_TRIB3_c0

_1_phosphatidyl_1D_myo_inositol_3_4_5_trisphosphate_c0 + GRB2_GAB1_c0 -> GRB2_GAB1_PIP3_c0

EGF_EGFR_dimer_c0 + 12ATP_c0 -> EGF_p_6Y_EGFR_c0 + 12ADP_c0

To view a reaction's kinetic type and forward and reverse rate constants, click a reaction and view "Object Properties".

Add New Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Reaction Name: EGFR_autophosphorylation_EGF_EGFR_dimer_c0

Kinetic Type: Mass Action [μM/s] (recommended for stochastic application) Convert to [molecules.s⁻¹]

Name	Description	Global	Expression
J	reaction rate	<input type="checkbox"/>	12.0 $(Kf \cdot EGF_EGFR_dimer_c0 \cdot (ATP_c0) - Kr \cdot (ADP_c0))$
Kf	forward rate constant	<input type="checkbox"/>	0.0
Kr	reverse rate constant	<input type="checkbox"/>	0.0
EGF_EGFR_dimer_c0	Species Concentration	<input checked="" type="checkbox"/>	Variable

Annotation and Pathway Links

CONNECTED (tanyamiller1221) 197.8MB / 417.3MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

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Name	Math Type	Annotation
<p>To create a new deterministic application, click "Applications" , select > "Add New" > "Deterministic".</p>		

VCell DB BioModels.net Pathway Comm

Search
 egfr Search

Signaling by EGFR [Reactome, Homo sapiens]

Filter
 signaling by E Sort

Preview Open Web Link

Problems (0 Errors, 0 Warnings) Pathway Preview

Select only one object (e.g. species, reaction, simulation) to view/edit properties.

CONNECTED (tanyamiller1221) 177MB / 418.9MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

Geometry Specifications Protocols Simulations Parameter Estimation

Species Reactions

To specify conditions for species, click "Specifications" > "Species".

Applications (1)

- Application0
 - Geometry
 - Specifications**
 - Protocols
 - Simulations
 - Parameter Estimation

Parameters and Functions

Pathway

Species	Structure	Clamped	Initial Condition
CBL_HUMAN_c0	c0	<input type="checkbox"/>	0.0
GRB2_c0	c0	<input type="checkbox"/>	0.0
CBL_GRB2_c0	c0	<input type="checkbox"/>	0.0
s3	c0	<input type="checkbox"/>	0.0
MK01_HUMAN_c0	c0	<input type="checkbox"/>	0.0
phospho_ERK_2_dimer_c0	c0	<input type="checkbox"/>	0.0
EGF_p_6Y_EGFR_p_Y472_771_783_1254_PLCG1_c0	c0	<input type="checkbox"/>	0.0
PLCG1_HUMAN_c0	c0	<input type="checkbox"/>	0.0
EGF_p_6Y_EGFR_c0	c0	<input type="checkbox"/>	0.0
SPY2_HUMAN_c0	c0	<input type="checkbox"/>	0.0
CBL_SBRV1_2_c0	c0	<input type="checkbox"/>	0.0

Search 1 - 200 of 212

Search

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Select only one object (e.g. species, reaction, simulation) to view/edit properties.

CONNECTED (tanyamiller1221)

226.5MB / 423.6MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

BioModel2

- Physiology
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 - Structures (1)
 - Species (212)
- Applications (1)
- Parameters and Functions
- Pathway

VCell DB BioModels.net Pathway Comm

Search egfr

Filter signaling

Preview Open Web Link

CONNECTED (tanyamiller1221) 214.1MB 425.7MB

Geometry Specifications Protocols Simulations Parameter Estimation

Species Reactions

Species	Structure	Clamped	Initial Condition
CBL_HUMAN_c0	c0	<input type="checkbox"/>	0.0
GRB2_c0	c0	<input type="checkbox"/>	0.0
CBL_GRB2_c0	c0	<input type="checkbox"/>	0.0
s3	c0	<input type="checkbox"/>	0.0
MK01_HUMAN_c0	c0	<input type="checkbox"/>	0.0
phospho_ERK_2_dimer_c0	c0	<input type="checkbox"/>	0.0
EGF_p_6Y_EGFR_p_Y472_771_783_1254_PLCG1_c0	c0	<input type="checkbox"/>	0.0
PLCG1_HUMAN_c0	c0	<input type="checkbox"/>	0.0
EGF_p_6Y_EGFR_c0		<input type="checkbox"/>	0.0
SPY2_HUMAN_c0		<input type="checkbox"/>	0.0
CBL_SPRY1_2_c0		<input type="checkbox"/>	0.0

Copy
Copy All
Paste
Paste All
Specify Column Value for Selected Row(s)
Clamped
Initial Condition

1
(Press Enter to commit)

1 - 200 of 212

To select all species on a page, press "ctrl" and "a" on your keyboard at the same time.

To simultaneously give multiple species the same initial condition, right click on selected species and hover your cursor over "Initial Condition". Type a value (use "1" for this tutorial) and press "Enter" on your keyboard to finalize.

Click the right arrow icon to view the next page of species. If desired, repeat the process of pressing "ctrl" and "a" on your keyboard, right clicking on species, and typing a value next to "Initial Condition".

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

Reactions (109)
Structures (1)
Species (212)
Applications (1)
Application0
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Specifications
Protocols
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Parameter Estimation
Parameters and Functions
Pathway
Pathway Diagram
Pathway Objects (369)
BioPAX Summary

Parameters and Functions Predefined Constants and Math Functions Model Unit System

Defined In: Global Reactions Applications Type: Parameters Functions

Defined In:	Name	Description	Expression
Model / Reaction (CBL_binds_to_GRB2_c0)	Kf	forward rate constant	0.0
Model / Reaction (CBL_binds_to_GRB2_c0)	Kr	reverse rate constant	0.0
Model / Reaction (Dimerisation_of_phospho_ERK_2_c0)	Kf	forward rate constant	0.0
Model / Reaction (Dimerisation_of_phospho_ERK_2_c0)	Kr	reverse rate constant	0.0
Model / Reaction (Active_PLC_gamma1_dissociates_from_EGFR_c0)	Kf	forward rate constant	0.0
Model / Reaction (Active_PLC_gamma1_dissociates_from_EGFR_c0)	Kr	reverse rate constant	0.0
Model / Reaction (Sprouty_lures_cytosolic_CBL_away_from_EGFR_c0)	Kf	forward rate constant	0.0
Model / Reaction (Sprouty_lures_cytosolic_CBL_away_from_EGFR_c0)	Kr	reverse rate constant	0.0
Model / Reaction (GRB2_SOS1_complex_binds_to_EGF_EGFR_complex_c0)	Kf	forward rate constant	0.0

Add New Global Parameter Delete Global Parameter(s) Search

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Select only one object (e.g. species, reaction, simulation) to view/edit properties.

Filter: signaling by E Sort

Preview Open Web Link

CONNECTED (tanyamiller1221) 295.5MB / 434.6MB

To view parameters and functions, click "Parameters and Functions".

Check off the boxes next to "Defined In:" and "Type:" to narrow your search.

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

Reactions (109)
Structures (1)
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Parameters and Functions
Pathway
Pathway Diagram
Pathway Objects (369)
BioPAX Summary

Parameters and Functions | Predefined Constants and Math Functions | Model Unit System

Defined In: Global Reactions Applications Type: Parameters Functions

Defined In:	Name	Description	Expr
Model / Reaction(CBL_binds_to_GRB2_c0)	Kf	forward rate constant	0.0
Model / Reaction(Dimerisation_of_phospho_ERK_2_c0)	Kf	forward rate constant	0.0
Model / Reaction(Active_PLC_gamma1_dissociates_from_EGFR_c0)	Kf	forward rate constant	0.0
Model / Reaction(Sprouty_lures_cytosolic_CBL_away_from_EGFR_c0)	Kf	forward rate constant	0.0
Model / Reaction(GRB2_SOS1_complex_binds_to_EGF_EGFR_complex_c0)	Kf	forward rate constant	0.0
Model / Reaction(Sustained_activation_of_SRC_kinase_by_SHP2_EGF_p_6Y_EGFR_GRB)	Kf	forward rate constant	0.0
Model / Reaction(PKA_phosphorylates_CREB_Protein_Kinase_A_catalytic_subunits)	Kf	forward rate constant	0.0
Model / Reaction(CBL_escapes_CDC42_mediated_inhibition_by_down_regulating_the)	Kf	forward rate constant	0.0
Model / Reaction(Dimerisation_of_phospho_ERK_1_c0)	Kf	forward rate constant	0.0

Object Properties | Problems (0 Errors, 0 Warnings) | Pathway Preview

Select only one object (e.g. To search for a specific name, type in a name next to "Search".

Signaling by EGFR [Reactome, Homo sapiens]

CONNECTED (tanyamiller1221) 243.4MB / 435.7MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

File View Server Tools Help

Reactions (109)
Structures (1)
Species (212)
Applications (1)
Application0
Geometry
Specifications

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BioPAX Summary

VCell DB BioModels.net Pathway Comm

Search
egfr Search

Signaling by EGFR [Reactome, Homo sapiens]

Filter
signaling by E Sort

Preview Open Web Link

Parameters and Functions Predefined Constants and Math Functions Model Unit System

Defined In: Global Reactions Applications **Type:** Parameters Functions

Defined In:	Name	Description	Expr
Model / Reaction(CBL_binds_to_GRB2_c0)	Kf	forward rate constant	0.0
Model / Reaction(Dimerisation_of_phospho_ERK_2_c0)	Kf	forward rate constant	0.0
Model / Reaction(Active_PLC_gamma_1_dissociates_from_EGFR_c0)	Kf	forward rate constant	0.0
Model / Reaction(Sprouty_lures_cytosolic_CBL_away_from_EGFR_c0)	Kf	forward rate constant	0.0
Model / Reaction(GRB2_SOS1_complex_binds_to_EGF_EGFR_complex_c0)	Kf	forward rate constant	0.0
Model / Reaction(Sustained_activation_of_ERK1/2_c0)	Kf	forward rate constant	0.0
Model / Reaction(PKA_phosphorylates_CDC42_c0)	Kf	forward rate constant	0.0
Model / Reaction(CBL_escapes_CDC42_mediated_inhibition_by_down_regulating_its_activity_c0)	Kf	forward rate constant	0.0
Model / Reaction(Dimerisation_of_phospho_ERK_1_c0)	Kf	forward rate constant	0.0
Model / Reaction(PIP3_recruits_PDK1_and_AKT_to_the_membrane_unknown_c0)	Kf	forward rate constant	0.0
Model / Reaction(CaMK_IV_phosphorylates_CREB_phospho_CaMK_IV_Calmodulin_c0)	Kf	forward rate constant	0.0

Specify Column Value for Selected Row(s)

Expression 1

Add New Global

Object Properties

Select only on

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To select all constants on a page, press "ctrl" and "a" on your keyboard at the same time.

To simultaneously give multiple constants the same expression, right click on selected constants and hover your cursor over "Expression". Type a value ("1" for this tutorial) and press "Enter" on your keyboard to finalize.

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

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Parameters and Functions Predefined Constants and Math Functions Model Unit System

Defined In: Global Reactions Applications **Type:** Parameters Functions

Defined In:	Name	Description	Exp
Model / Reaction(CBL_binds_to_GRB2_c0)	Kr	reverse rate constant	0.0
Model / Reaction(Dimerisation_of_phospho_ERK_2_c0)	Kr	reverse rate constant	0.0
Model / Reaction(Active_PLC_gamma1_dissociates_from_EGFR_c0)	Kr	reverse rate constant	0.0
Model / Reaction(Sprouty_lures_cytosolic_CBL_away_from_EGFR_c0)	Kr	reverse rate constant	0.0
Model / Reaction(GRB2_SOS1_complex_binds_to_EGF_EGFR_complex_c0)	Kr	reverse rate constant	0.0
Model / Reaction(Specify Column Value for Selected Row(s))	Kr	reverse rate constant	0.0
Model / Reaction(Expression)	Kr	reverse rate constant	0.0
Model / Reaction(Cbl_escapes_LC42_mediated_inhibition_by_oo)	Kr	reverse rate constant	0.0
Model / Reaction(Dimerisation_of_phospho_ERK_1_c0)	Kr	reverse rate constant	0.0
Model / Reaction(PIP3_recruits_PDK1_and_AKT_to_the_membrane_unknown_c0)	Kr	reverse rate constant	0.0
Model / Reaction(CaMK_IV_phosphorylates_CREB_phospho_CaMK_IV_Calmodulin_c0)	Kr	reverse rate constant	0.0

0.1
(Press Enter to commit)

Add New Global Parameter Delete Global Parameter(s) Search kr

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Select only one object (e.g. s

To change additional constants, clear "Search" and repeat the previous process.

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Geometry Specifications Protocols Simulations Parameter Estimation

Simulations Output Functions Generated Math

+

Name	End Time	Output Option	Solver	Running Status	Results
Simulation0	1.0	keep every 1	Combined IDA/CVODE	not saved	no

To add a simulation, click the add simulation icon.

To view simulations, click "Simulations".

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Annotation:

Settings: max timestep output rel tol abs tol Sensitivity Analysis
1.0s keep every 1, at most 1000 1.0E-9 1.0E-9 no

Mesh Refinement: Finest Level Mesh:
Refinement ROI(s): View Level Mesh:

Parameters with values changed from defaults

Parameter Name	Default	New Value/Expression	Scan

166.6MB / 462.4MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

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Geometry Specifications Protocols Simulations Parameter Estimation

Simulations Output Functions Generated Math

To run and save a simulation, click the green play icon.

To run but not save a simulation, click the blue play button.

Name	End Time			Running Status	Results
Simulation0	1.0	keep every 1	Combined IDA/CVODE	not saved	no

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Annotation:

Settings: max timestep output rel tol abs tol Sensitivity Analysis
1.0s keep every 1, at most 1000 1.0E-9 1.0E-9 no

Mesh Refinement: Finest Level Mesh:
Refinement ROI(s): View Level Mesh:

Parameters with values changed from defaults

Parameter Name	Default	New Value/Expression	Scan
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BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

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Geometry Specifications Protocols Simulations Parameter Estimation

Simulations Output Functions Generated Math

Name	End Time	Output Option	Solver	Running Status	Results
Simulation0	1.0	keep every 1	Combined IDA/CVODE	not saved	o

To view the results, click the results icon once the simulation is completed.

Object Properties Problems (0 Errors, 0 Warnings) Pathway Preview

Annotation:

Settings: max timestep output rel tol abs tol Sensitivity Analysis
 1.0s keep every 1, at most 1000 1.0E-9 1.0E-9 no

Mesh Refinement: Finest Level Mesh:
 Refinement ROI(s): View Level Mesh:

Parameters with values changed from defaults

Parameter Name	Default	New Value/Expression	Scan

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

simulation results for Simulation0

X Axis: t

Y Axis: [Display Options: Reactions, Species]

Plot Legend:

- _1433B_HUMAN
- _1_phosphatidyl
- _1_phosphatidyl
- _3_5_Cyclic_A
- Activated_RAF1
- Activated_RAF1
- Activated_RAF1
- Activated_RAF1
- Active_AKT_cy
- Active_AKT_nu
- Active_AKT_pla
- Active_Calmodul
- active_Calmodul
- Active_Calmodul
- active_Cam_PDE
- active_PKC_alp

egfr

Signaling by EGFR [Reaction]

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312.9MB / 532.2MB

To select all items, press "ctrl" and "a" on your keyboard at the same time. To deselect an item, click on the specific item.

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 4)

simulation results for Simulation0

X Axis: t

Y Axis: 1.0

Plot Legend: J_p_RAF_binds_14

Display Options:

- Reactions
- Species

J_Localization_of_CBL_GRB2_to_the_r
J_MEK1_binds_ERK_1_c0
J_MEK1_phosphorylates_ERK_1_MEK1
J_MEK1_phosphorylates_ERK_1_p_ME
J_MEK2_binds_ERK_2_c0
J_MEK2_phosphorylates_ERK_2_MEK2
J_Nuclear_translocation_of_phospho
J_Nuclear_translocation_of_phospho
J_p_RAF_binds_14_3_3_beta_alpha_c
J_PDK1_phosphorylates_AKT_at_T308
J_PDK1_phosphorylates_AKT_at_T308
J_PHLPP_dephosphorylates_S473_in_
J_Phospholipase_C_gamma1_binds_to
J_Phosphorylation_of_CBL_EGFR_CB
J_Phosphorylation_of_CBL_EGFR_GR
J_Phosphorylation_of_CREB_by_CaMK
J_Phosphorylation_of_EGFR_by_SRC_
J_PIK3_catalytic_subunit_binds_to_EG
J_PIK3_converts_phosphatidylinositol
J_PIP3_recruits_PDK1_and_AKT_to_th
J_PKA_catalytic_subunit_translocates_
J_PKA_phosphorylates_CREB_Protein_
J_PKC_phosphorylates_GRK2_active_f
J_Pro_EGF_is_cleaved_to_form_matur
J_PTEN_dephosphorylates_PIP3_PTEN
J_RAF1_phosphorylates_MEK1_c0
J_RAF1_phosphorylates_MEK2_Activa

All fluxes' names start with "J_".

To close the window, click "X".

Finest Level Mesh:
View Level Mesh:
Scan

329.8MB / 549.5MB