VCell Pathway Commons Tutorial

Using an external database
To use the Pathways Commons database, click “Pathway Comm”. 
To search Pathway Commons, type under Search and click “Search”.
To filter your search, type under “Filter” and it will automatically search all names within Pathway Commons.
The green text tells you where the pathway comes from and the red text tells you what species the pathway occurs in.
To learn more information about a pathway, click the pathway and “Open Web Link”.
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.
To begin the process of importing a pathway, click on a pathway and click “Preview”.
To filter entities by type, click “Type”.

- Gab1:Grb2 binds to EGF:Phospho-EGFR
- Stabilisation of RAF by further phosphorylation
- CBL binds to GRB2
- Sprouty lures cytosolic CBL away from EGFR
- Dephosphorylation of PAG by SHP2
- AKT phosphorylates BAD
- IP3 binds to the IP3 receptor, opening the endoplasmic reticulum Ca2+ channel
To search for a specific entity, type the name of the entity next to “Search”.
To import specific entities, click the entities and click “Import” > “Selected Only”.
To view imported pathways, double click “Pathway” and click “Pathway Diagram”.
To reorganize pathways, click the circle icons.
To view information on a specific entity, click on the entity and view “Object Properties”.
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.
Click “Physiology Links” > “Import into Physiology”.
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”.

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”.
VCell will automatically inform you of which pathway objects you have imported into your physiology. Click “OK”.
To return to a pathway object, click on a specific species and click the link next to “Linked Pathway Objects”
To add a species, click the species tool and click on any point within the compartment.
To add species to a pathway, click on a specific species. Click “Pathway Links” > “Edit Pathway Links...”
To link a species to an entity, check a box in the “Link” column, next to the entity’s name.

To finish linking a species to a pathway, click “Close”.
To begin importing an entire pathway, go to “Pathway Preview” and clear “Search” of any text.
To select all entities on a page, hit “ctrl+a”.

To import entities, click “Import” > “Selected Only”.
If a pathway is extends to multiple pages, click the right arrow icon to view the next page. Press “ctrl+a” on your keyboard and click “Import” > “Selected Only”.
Click “Pathway Objects” to organize the entities into list form.
Click a Pathway Object to find more Object Properties.
Use “Search” to find a specific pathway entity, type in the name of the object next to “Search".
To select all pathway entities on a page, press “ctrl+a”.

To import pathway entities into your physiology, click “Physiology Links” > “Import into Physiology...”
VCell will automatically notify you if anything you have selected to import into your physiology has already been imported. Click “OK’.
To edit entity 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 into your physiology, click “OK”.

To finish importing a pathway into your physiology, click “OK”.
VCell will automatically notify you of what species and reactions have been successfully imported into your physiology model. Click “OK”.

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

- Species: 'CBL_SPRY1_2_c0'
- Species: 'CDC42_GTP_c0'
- Reaction: 'Gab1_Grb2_binds_to_EGF_Phospho_EGFR_c0'
- Reaction: 'Stabilisation_of_RAF_by_further_phosphorylation_unidentified'
- Species: 'Protein_kinase_C__alpha__gamma_delta__cytosol_c0'
- Species: 'MEK2_ERK_2_c0'
- Reaction: 'Sprouty_lures_cytosolic_CBL_away_from_EGFR_c0'
- Species: 'GRB2_GAB1_PIK3R1_c0'
- Species: 'TRIB3_HUMAN_c0'
- Species: 'Active_AKT_cytosol_c0'
- Species: 'CBL_BetaPix_c0'
- Species: 'KCC4_HUMAN_c0'
- Species: 'NR4A1_HUMAN_c0'
- Reaction: 'Dephosphorylation_of_PAG_c0'
- Species: 'PHLP1_HUMAN_c0'
- Reaction: 'AKT_phosphorylates_BAD_c0'
- Species: 'Phospho_Forkhead_box_transcription_factor_nucleoplasm_c0'
To view reactions in list form, click “Reactions”.
To view a reaction’s kinetic type and forward and reverse rate constants, click a reaction and view “Object Properties”.
To create a new deterministic application, click “Applications” > “Add New” > “Deterministic”.
To specify conditions for species, double click the new application and click “Specifications” > “Species”.
To select all species on a page, press “ctrl+a” on your keyboard.

To simultaneously give multiple species the same initial condition, right click on selected species and hover your cursor over “Initial Condition”. Type a value and press “Enter” on your keyboard to finalize. For this tutorial, the value “1” was used.
To view parameters and functions, click “Parameters, Functions and Units”.

Check off the boxes next to “Defined In:” and “Type:” to narrow your search.
To search for a specific name, type in a name next to “Search”.

egfr

Search

Search kf
To select all constants on a page, press “ctrl+a”.

To simultaneously give multiple constants the same expression, right click on selected constants and hover your cursor over “Expression”. Type a value and press “Enter” on your keyboard to finalize. For this tutorial, the value “1” was used.
To change additional constants, clear "Search" and repeat the previous process. For this tutorial, the value "0.1" was used.
To add a simulation, click the add simulation icon.

Click “simulations”
To run and save a simulation, click the green play icon.

To run but not save a simulation, click the blue play button.
To select all items, press “ctrl+a” on your keyboard at the same time. To deselect an item, click on the specific item.

Check off different boxes to view more/less graphs.
To close the window, click “X”.

All of the fluxes start with “J”.

---

**BIOMODEL: PathwayCommons**

(Wed Jul 08 13:00:51 EDT 2015) -- **VCell 6.0 (build 3)**

---

**PathwayCommons**

**Physiology**

- Reaction Diagram
- Reactions (71)
- Structures (1)
- Species (175)
- Molecules (0)
- Observables (0)

**Applications**

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

**Search**

- Signaling by EGF, Reactome
  - Search
  - egrf

**Simulations**

- Simulation results for Simulation0
  - X Axis:
  - Y Axis:
    - Display Options:
      - Other
      - Reactions
      - Species

---

**Plot Legend:**

- J_AKT_phosphorylates_CREB_Active
- J_AKT_phosphorylates_GSK3_Active
- J_AKT_phosphorylates_MDM2_c0
- J_AKT_phosphorylates_TSC2_inhibit
- J_AK_cyclic_amplification_DN
- J_ASM_1d Regulatory alpha
- J_CALM binds calmodulin_c0
- J_CALM binds_CaMK_II
- J_CAMK IV autophosphorylation_c0
- J_CAMK IV phosphorylates_CREB_c0
- J_CAMK IV phosphorylates_KAP1_c0
- J_CAMK IV phosphorylates_KAP1_c0
- J_CALM binds_CaMK IV_c0