

# CYTOSCAPE VIEW FOR PROTEIN ONTOLOGY HIERARCHY DOCUMENTATION

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## 1 INTRODUCTION

**Cytoscape View for Protein Ontology (PRO) Hierarchy** is a quick, neat and informative way of browsing entries' relations. It supports search, customization of the layout and display, and save the network. We updated the view page with "Cytoscape.js" JavaScript graph library, which made the view page compatible with most modern browsers (Chrome, Firefox, Safari, IE, etc.) and devices (PC and Mobile).

## 2 OVERVIEW

We recommend using the latest version of [Chrome](#) or [Safari](#) ([Safari for Windows](#)) to browse the view page. [Firefox](#) or [IE](#) users may experience non-fluency mouse movement or other minor functionality differences, but it doesn't influence the major functions.

### 2.1 ACCESS CYTOSCAPE VIEW

Cytoscape can be accessed via the  icon in the PRO entry report page (Figure 1) or in the search result page (Figure 2).

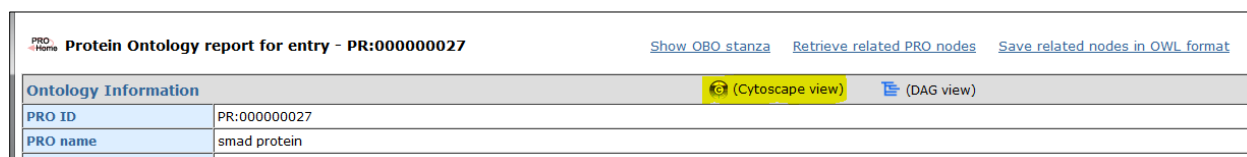


Figure 1 Access Cytoscape View from PRO entry report page

PRO ID	PRO Name	PRO Term Definition	Category	Parent	Matched Fields
<a href="#">GO:0071141</a>	SMAD protein complex	A protein complex that consists of SMAD proteins; may be homomeric or heteromeric. [GOC:mah, PMID:9670020]		<a href="#">GO:0043234</a>	PRO Name=>SMAD; PRO Name Synonyms=>SMAD; PRO Term Definition=>SMAD
<a href="#">GO:0071142</a>	SMAD2 protein complex	A protein complex that consists of a SMAD2 homotrimer. [GOC:mah, PMID:9670020]		<a href="#">GO:0071141</a>	PRO Name=>smad; PRO Name Synonyms=>smad; PRO Term Definition=>smad
<a href="#">GO:0071144</a>	SMAD2-SMAD3 protein complex	A heteromeric SMAD protein complex that contains SMAD2 and SMAD3. [GOC:mah, PMID:9670020]		<a href="#">GO:0071141</a>	PRO Name=>smad; PRO Name Synonyms=>smad; PRO Term Definition=>SMAD; PRO Term

Figure 2 Access Cytoscape View from PRO batch retrieval result page

## 2.2 CYTOSCAPE VIEW PAGE

The view page (Figure 3) main body displays the requested hierarchy network. A top panel bar provides various functions, such as: legend of network, display customization, search an entry in current network, save options, batch terms retrieval and a link to help documentation.

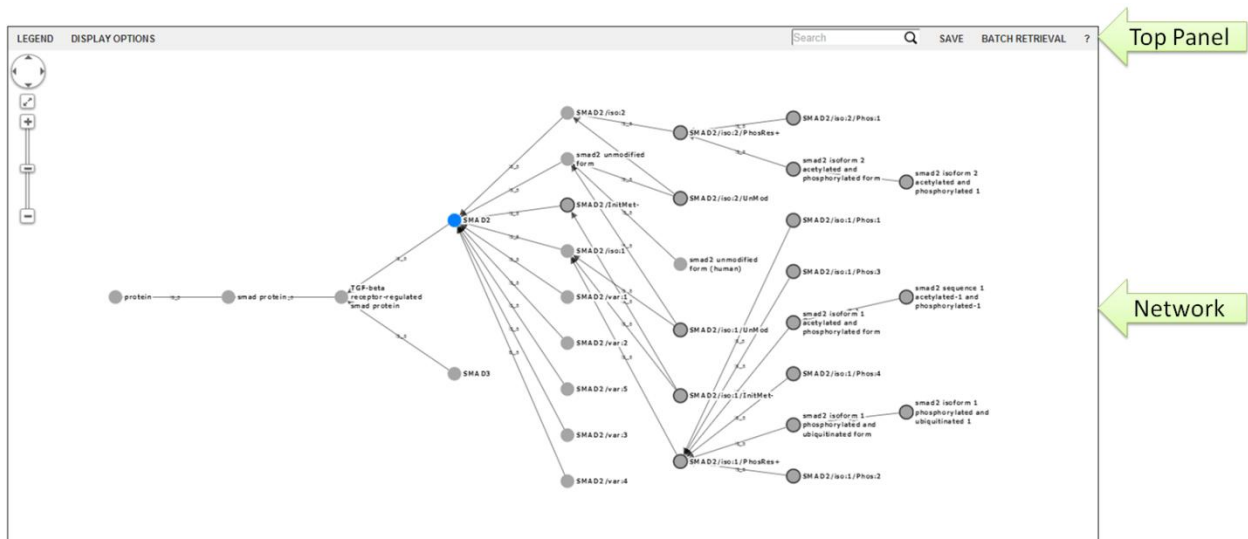


Figure 3 Cytoscape View for entry "PR:000000364"

## 2.3 NETWORK ELEMENTS

Network elements are nodes and edges. For every requested entry, the **basic hierarchy** ([how to show basic hierarchy only](#)) contains an entry's parents, siblings and children (Figure 4, elements in shaded area). It focuses on "is\_a" relation. The Cytoscape View page shows an entry's **expanded hierarchy by default** (Figure 4, all elements). Based on the basic hierarchy, the expanded hierarchy contains protein and complex information, which are connected with "has\_component" relation.

More specifically, when requesting a protein entry, besides basic protein hierarchy, we find all complexes containing at least one of the children and retrieve those complexes hierarchy up to complex root, then connect complexes' components to protein root; when requesting a complex entry, besides basic complex hierarchy, we find all complexes' components and connect those components with protein root.

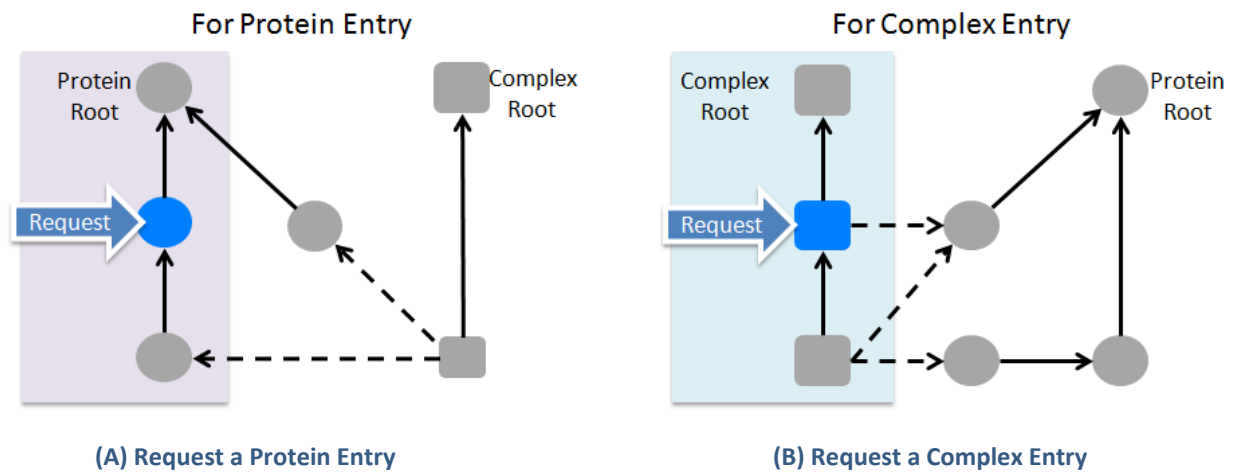


Figure 4 Network Elements

### 3 QUICKSTART (FUNCTION INDEX)

#### Available Function

- [Legend](#)
- [Display options](#)
  - [Control network element](#)
  - [Control label visibility](#)
  - [Control node color](#)
  - [Layout](#)
- [Find a node by ID or label](#)
- [Save network](#)
- [Property table](#)
- [Pan zoom bar](#)
- [Right click functions menu](#) for [one](#) or [more](#) nodes
  - Add node to batch retrieval
  - Hide node
  - Hide node label

#### Link to other Cytoscape View page

- [Property table](#): one entry only
- [Batch retrieval](#): one or multiple entries

#### Mouse gesture in network area

- [Hover](#) a node: highlight first neighbors
- [Left click](#) a node: show property table
- [Right click](#) a node or several: show functions menu
- [Left click and drag](#) the network: move the network
- [Scroll](#): Zoom in or out

## 4 FUNCTIONS

### 4.1 FUNCTIONS IN NETWORK AREA

The network consists of nodes and edges: each node is a PRO entry, and each edge connecting two nodes is the relation between them.

New Cytoscape View incorporate a lot of mouse gestures with view page functions, for example, adjusting network size and position, show node property table by left click a node.

To **move** a network, left click and hold mouse button, then drag the network around.

To adjust network graph **size**, scroll the mouse middle button.

A pan-zoom bar (Figure 5) on the top left of the network can also move the network and zoom in/out.



Figure 5 Pan Zoom Bar

To view an entry's direct partners (**first neighbors**), user can move the mouse pointer on (hover) an entry. All undirected linked nodes will fade out. They will show again when the mouse pointer leaves the entry.

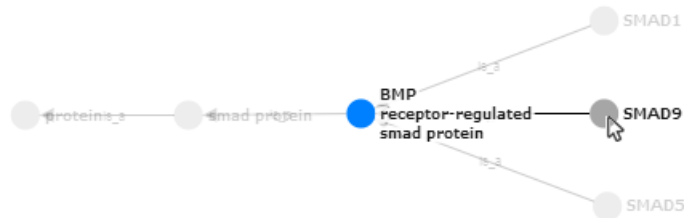


Figure 6 Mouse hover an entry to show its first neighbor

To check a node's **property**, left click it. The node is highlighted in yellow and its property table shows nearby. Node's attributes include ID, Label, Name, Definition, Category and Mapping (relations among PRO and UniProt entry). There are links at the table header: "Jump to its Cytoscape Web view" can open a new view page for the clicked node, "DAG view", "PRO entry report" and "OBO stanza" can link to corresponded PRO page.

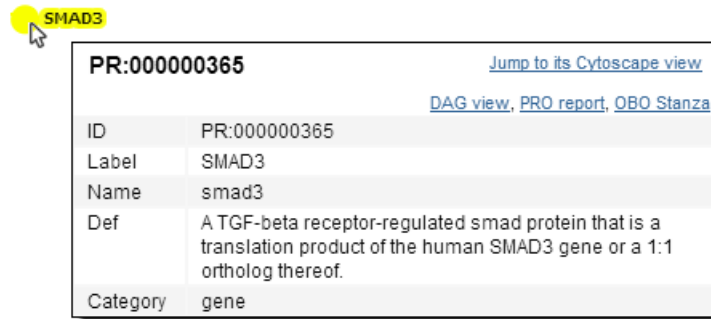


Figure 7 Left click a node to show node property table

If a relation (edge) is clicked, edge property table shows. Edge's attributes includes ID (in the format of "Entry A (interaction type) Entry B"), interaction type and source.

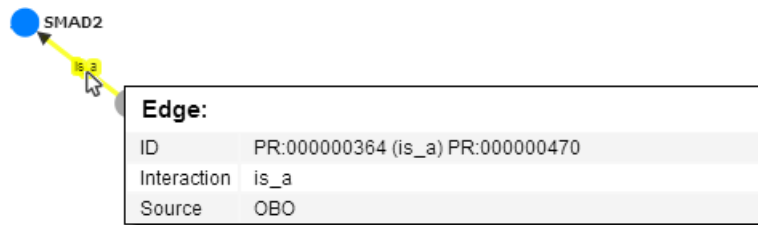


Figure 8 Left click an edge to show edge property table

More entry functions are in the **right click functions menu**: add node to "Batch Retrieval" list, hide a node ([how to show hidden node](#)), hide/show node label and select node first neighbor. For single entry, right click directly on the entry to show the functions menu.

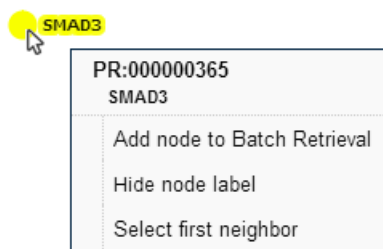
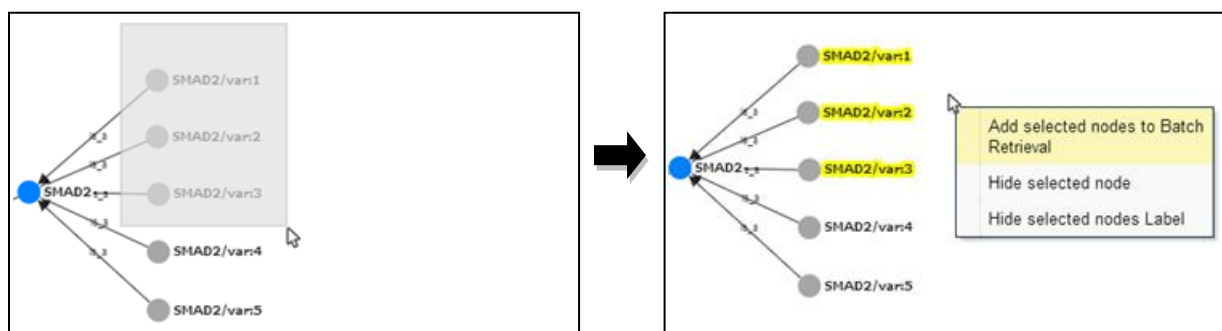


Figure 9 Right click a node to show functions menu

Those right click functions work for **multiple nodes** as well. Use the selection box to select multiple nodes at one time (left click on empty area and drag, release when selection finished (Figure 9, A)). Then right click on any empty area to show functions menu (Figure 9, B).



(A) Select several nodes with selection box

(B) Right click empty area to open functions menu

**Figure 10 Functions menu for several nodes**

## 4.2 TOP PANEL FUNCTIONS

### 4.2.1 LEGEND

#### NODE LEGEND

The default node is a grey circle.

Protein is a circle. Complex is a rectangle. Chemical entity (ChEBI) is a triangle.

Modified entry has a darker border.

Organism specific entry is smaller than taxon general entry.

Requested entry node is always colored blue and selected entry node is highlighted yellow.

More node coloring options are found in "[Display Options](#)".

#### EDGE LEGEND

There are three types of hierarchical relations: "is\_a", "derives\_from" and "has\_component".

"is\_a" describes parent-child relation. It is a black solid line with an arrow pointing to parent.

"derives\_from" is also a black solid line with an arrow pointing to parent form.

"has\_component" describes complex-component relation. It is in a navy blue dash line with an arrow pointing to component.



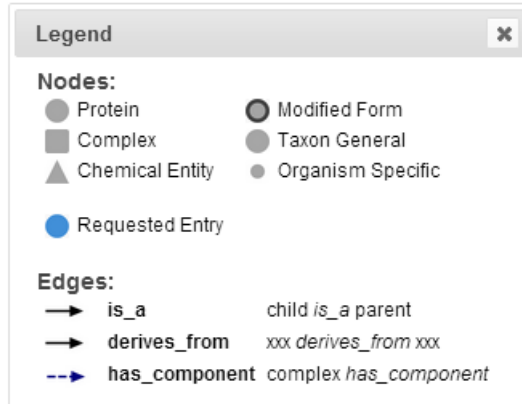


Figure 11 Edge legend

#### 4.2.2 DISPLAY OPTIONS

Display Options controls how elements are presenting in the network. These options include controlling network elements show/hide, elements label, node color and network layout.

##### PART A: NETWORK ELEMENT CONTROLS

Here user can customize which part of the network they want to show/hide.

The first section is options for network hierarchy. These options include: parent, sibling and children. For children option, a drop-down list allows selecting specific children level. A following organism checkbox can control show/hide species specific entries.

To show the requested entry's [basic hierarchy](#) (entry's parents, siblings and children only, Figure 4, elements in shaded area), a checkbox "Show requested hierarchy only" is presented.

The second section is options for node type. For example, after un-checking "all complex", network graph will only shows protein and ChEBI nodes.

The third section is an option "Show all right-click hidden nodes". If no element is hidden, the checkbox is un-clickable. When one or more nodes are hidden by [right click functions menu](#), the checkbox is editable. After checking it, all hidden nodes are shown again.

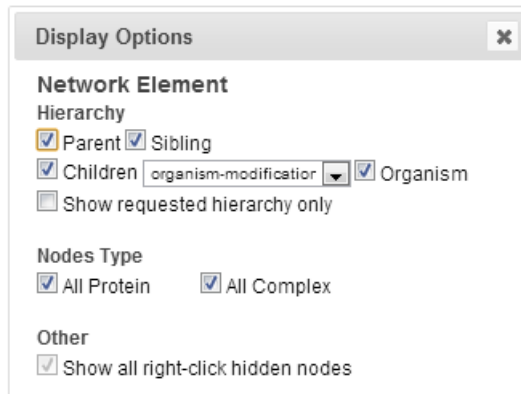


Figure 12 Display Options Part A: network element controls

#### PART B: LABEL CONTROL.

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Set whether node or edge label is visible.

When network contains more than 100 nodes, nodes label are hidden automatically when loading the view page.

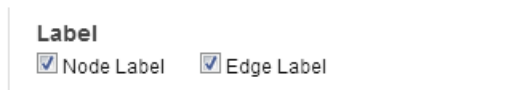


Figure 13 Display Options Part B: Label controls

#### PART C: COLOR CONTROL.

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Set node color according to node attribute.

Requested entry is always colored blue. PTM enzyme is colored in red tone color: kinase is in pink and other PTM enzyme (like acetylase) is in red. By checking corresponded checkbox, node is colored accordingly. If a node contains more than one color, it will be divided into several color sections (Figure 15).

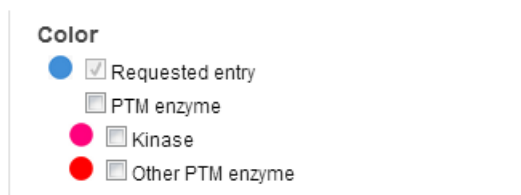


Figure 14 Display Options Part C: Color controls



Figure 15 Multi-color nodes

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#### PART D: LAYOUT.

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Layout options help arrange nodes into either an organized structure or a random structure.

Layout options includes: hierarchy (default), force directed, circle, grid and random. The reset layout button help recover network layout after moving or hiding nodes. It re-apply selected layout to current network making all elements well-spaced.

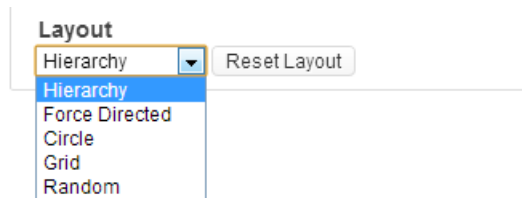


Figure 16 Display Options Part D: Network layout

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#### 4.2.3 SEARCH

Search box is used to find a node in CURRENT network by entry's ID or label.



Figure 17 Search

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#### 4.2.4 SAVE

The network can be saved in PNG format or XGMML format. Xgmml file can be imported into Cytoscape desktop version. [Step by step instruction](#).

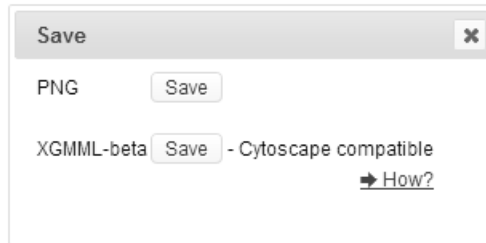


Figure 18 Save

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#### 4.2.5 BATCH RETRIEVAL

Batch Retrieval functions is used to create a new multi-entries view request.

##### ADD NODES

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There are three ways to add nodes to batch retrieval list. If a new network is based on the current one, click “add current requested entries” to the list. To add node in current network, user can right click the node and select “add node to batch retrieval” in the functions menu. To add other entry not in the current network, user can “enter valid PRO/GO IDs” in the textbox. The textbox can recognize multiple IDs separated by comma “,”, partially entered PRO ID or GO ID. For example, PRO ID can be written as “66” (“PR:000000066”) for short, “go71141” (“GO:0071141”) for short.

##### EDIT THE LIST

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All checked entries will be submitted to new view page. The top checkbox is used to select or deselect all listed entries. A number next to “ID” shows how many checked entries in the list.

“Clear all” button at the bottom left is used to empty the list.

##### SUBMIT

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When editing is finished, click the Submit button at the bottom right to the new Cytoscape View page.

**Batch Retrieval** [X]

**Add nodes**

Add current requested entries

Right-click node(s) in current network

Seperate multiple id by comma ","

**Edit the list**

<input checked="" type="checkbox"/> ID (3)	Label
<input checked="" type="checkbox"/>	PR:000002190 AKT1
<input checked="" type="checkbox"/>	PR:000003912 AKT2
<input checked="" type="checkbox"/>	PR:000003913 AKT3

Figure 19 Batch retrieval

## ABOUT

Cytoscape.js (v 2.0.2) is downloaded from github: <https://github.com/cytoscape/cytoscape.js>

Save functions are using FileSaver.js: <https://github.com/eligrey/FileSaver.js>

Network data is extracted from PRO OBO stanza ([ftp://ftp.pir.georgetown.edu/databases/ontology/pro\\_obo](ftp://ftp.pir.georgetown.edu/databases/ontology/pro_obo)) and integrated by an in-house python script. All tools are written in jQuery and jQuery UI (<http://jqueryui.com/>).

## CONTACT

If you have further questions or need assistance with the tool please send an email to <mailto:pirmail@georgetown.edu>.